



Sorghum in the 21st Century

Global Sorghum Conference

Resiliency and Sustainability in the Face of Climate Change

June 5-9 2023 The Corum Event Center, Montpellier, France

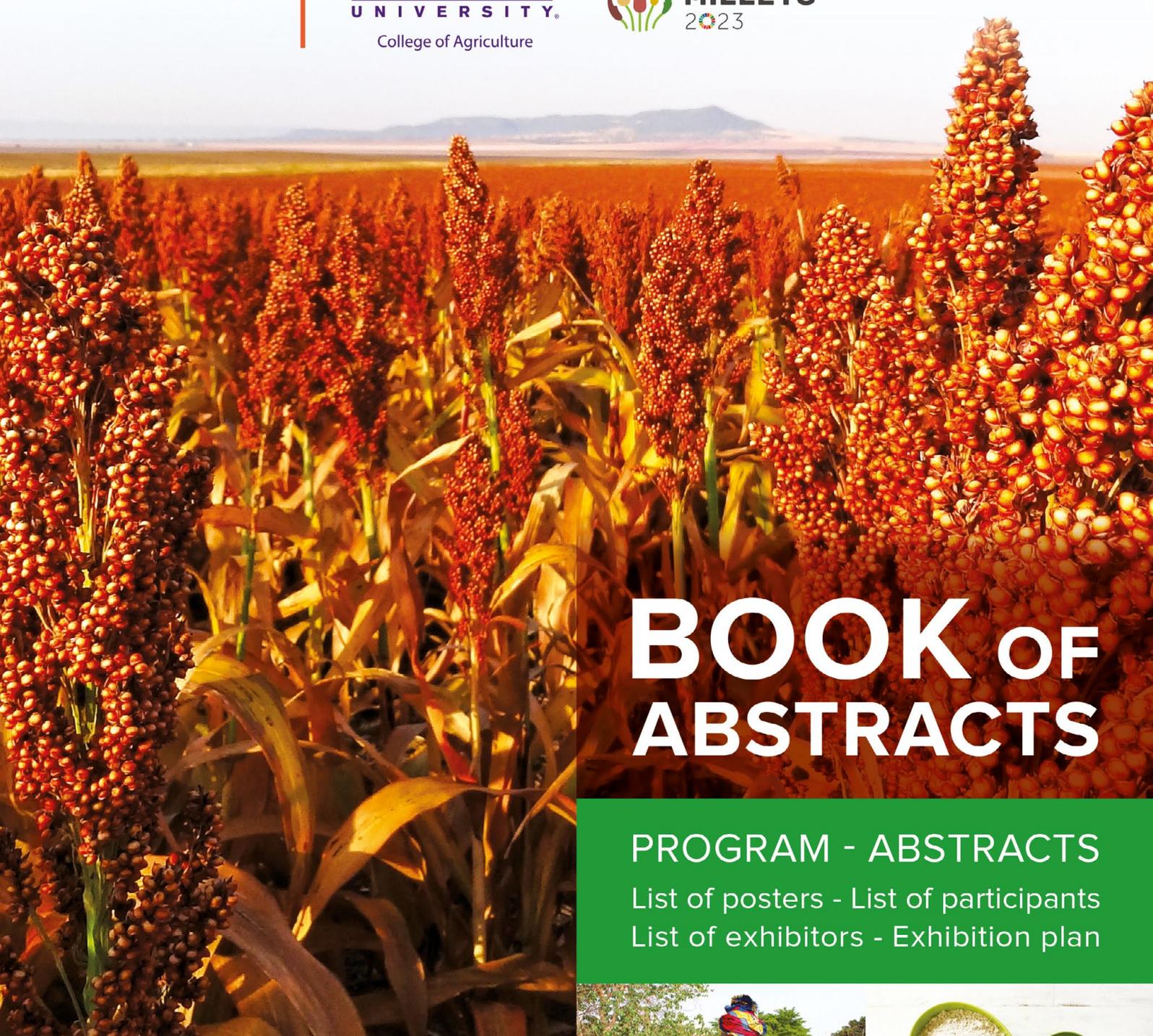
Lead Sponsor

KANSAS STATE UNIVERSITY

College of Agriculture

Supporting the

INTERNATIONAL YEAR OF
MILLETS
2023



BOOK OF ABSTRACTS

PROGRAM - ABSTRACTS

List of posters - List of participants

List of exhibitors - Exhibition plan



LEADING THE WAY IN SORGHUM INNOVATION

We engage globally, prioritizing climate-smart strategies while enhancing the global food system and preparing future leaders in agriculture.

Kansas is the No. 1 state in the U.S. in grain sorghum production. And, Kansas State University is a global leader in sorghum research and innovation.



**STOP BY OUR BOOTH IN THE EXHIBITION HALL
TO LEARN HOW K-STATE IS AT THE
HEART OF A GLOBAL SORGHUM NETWORK**



CENTER FOR
SORGHUM
IMPROVEMENT



GLOBAL COLLABORATION ON
SORGHUM & MILLET

ag.k-state.edu



Welcome to Montpellier!

On behalf of everyone who has contributed to the organization of the conference and the development of the scientific program, we want to welcome you to ***Sorghum in the 21st Century: Resiliency and Sustainability in the Face of Climate Change***. This conference and the scientific program build upon the groundwork established in Cape Town at the 2018 conference hosted by the University of Pretoria and the Feed the Future Innovation Lab for Collaborative Research on Sorghum and Millet. The primary objective of the 2023 conference continues to align with past goals: To build relationships between producers, consumers and the research and development community around the fascinating opportunities sorghum presents to address some of the world's greatest challenges facing agriculture. It is the primary purpose of this conference to advance this dialogue and update the community about the state of sorghum science, industry, development and novel opportunities to confront climate change. We must focus on creating additive knowledge and identifying the 'known unknowns' in order to build collaborative actions that break down geographical and scientific barriers and that increase resiliency and sustainability across the sorghum value chain.

We will address this need through exciting keynote, plenary and contributed presentations, a wide range of posters and exhibits, topical symposia, and student events such as the '3-Minute Thesis' competition that will identify the best and brightest minds that will move our work forward. Special scientific visits and tours, the addition of the 'Sorghum Idea Challenge' and social events in the most wonderful southern France style will further enhance out this experience. Our geographical focus on the European Union will be an eye-opening experience for all.

This event would not have been possible without generous funding from numerous sponsors from both the public and private sectors around the world. A special thank you is extended to Kansas State University as our lead event sponsor. This conference would not have been possible without the dedication and hard work of the local and international organizing committees over the past 24 months. Truly this has been a collaborative effort from like-minded individuals and organizations from around the world.

We hope you will leave the conference renewed and energized about the monumental and societal role of Sorghum in the 21st Century!

Timothy J. Dalton
Kansas State University
Chair of the international steering and program planning committee

Jean-Francois Rami
Cirad
Chair of the Local organizing committee

The most diverse range of sorghum hybrids

Benefiting from the 1st European breeding program, Lidea designs a range of sorghum varieties adapted to almost all outlets, grain and fodder, thus meeting the needs of farmers and processors.



Grain and fodder varieties as a **perfect ingredient in animal diets** thanks to its high nutritional values, digestibility and taste.



Grain varieties with high nutritional value are **suitable for human food**: for the production of bread, breakfast cereals, snacks, pasta, semolina, beer and spirits.



Grain and biomass hybrids for **bioenergy production** such as biomass, bioethanol, biofuel.





UNITED SORGHUM CHECKOFF PROGRAM

Fifteen Years of Innovation

Our Mission:

The Sorghum Checkoff commits to reveal the potential and versatility of sorghum through increased shared value.



Scan above to learn more about this producer-funded organization dedicated to improving the sustainability of the sorghum industry through research, promotion and education.



Global Leader in Sorghum Technology



Alta Seeds is a premium brand of Advanta Seeds in Europe and North America. Advanta Seeds is a global seed company adapting to rapidly increasing food insecurity and climate change by providing farmers with innovation and modern technologies.

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Advanta Seeds was ranked	#5 GLOBAL SEED COMPANY in the Access to Seeds Index 2019
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Alta Seeds was recognized by European Seeds as one of the '20 MOST CLIMATE FRIENDLY COMPANIES OVER 2021	

Advanta sorghum brands: Advanta / Alta Seeds / Pacific Seeds

1 In the world
imi sorghum

#1 Grain sorghum
company in
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#1 In sorghum
technology

+60 Years of
experience in
sorghum r&d



Sorghum in the 21st Century Global Sorghum Conference

Resiliency and Sustainability in the Face of Climate Change

June 5-9 2023 The Corum Event Center, Montpellier, France

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French Agricultural Research Centre for International Development

<https://www.cirad.fr/en/>



Collaborative Research
on Sorghum and Millet

FEED THE FUTURE INNOVATION LAB

Collaborative Research on Sorghum and Millet

<https://smil.k-state.edu>



SORGHUM ID

Sorghum - International Development

<https://www.sorghum-id.com/en/>



IRD

French National Research Institute for Sustainable Development

<https://en.ird.fr/>



CERAAS

Centre d'Étude Régionale pour l'Amélioration de l'Adaptation
à la Sécheresse

<https://ceraas.org>

WE ARE HONORED TO BE A PART OF THE
SORGHUM IN THE 21ST CENTURY CONFERENCE.

GLOBAL COLLABORATION *for* RESILIENT FOOD SYSTEMS

MCKNIGHT FOUNDATION

Together, we are working to cultivate
resilient food systems globally by
bridging farmer-centered agroecological
research, action, and influence.

ccrp.org



SEMENCES
DE PROVENCE

INVOLVED
IN SORGHUM
MARKET
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First breeding program in Europe with Eurosorgho.



EUROSORGHO SINCE 2009

A joint venture between Arterris and Euralis,
two French cooperative groups.

Breeding for grain and silage sorghum
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Seed production in different countries:
France, Spain, Hungary, USA...



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in the south of France.



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on the website: semencesdeprovence.com

Grain sorghum:
red and white



Silage sorghum:
feed and bioenergy



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Global Sorghum Conference

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COMMITTEES

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- **Timothy Dalton (chair)** - *Kansas State University/SMIL - USA*
 - **Valérie Brochet** - *SorghumID - France*
 - **Kira Everhart-Valentin** - *USA*
 - **David Jordan** - *University of Queensland - Australia*
 - **Ndjido Kane** - *CERAAS - Senegal*
 - **Jurandir Magalhães** - *EMBRAPA - Brazil*
 - **David Pot** - *Cirad - France*
 - **Jean-François Rami** - *Cirad - France*
 - **Gilles Trouche** - *Cirad - France*
 - **Vincent Vadez** - *IRD - France/Senegal*

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 - **Patricia Costeraste** - *Cirad - France*
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 - **Béatrice Dhellemmes** - *Cirad - France*
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 - **Olivier Ginestet** - *Alpha Visa - France*
 - **Martin Gomez** - *SorghumID - France*
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 - **Olivier Ginestet** - *Alpha Visa Congrès - France*
 - **Martin Gomez** - *SorghumID - France*
 - **Norma Ritz Johnson** - *Sorghum Checkoff - USA*
- **Nathanael Bascom** - *Kansas State University/SMIL - USA*

Administrative secretariat

Registration, accommodation & abstract submission - Sponsorship & exhibition

Alpha Visa Congrès / Sorghum 2023

624 rue des Grèzes - 34070 Montpellier - France

Tel: +33 4 67 03 03 00

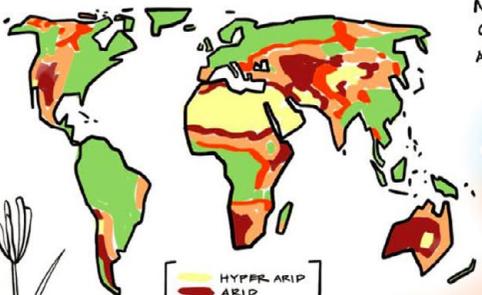
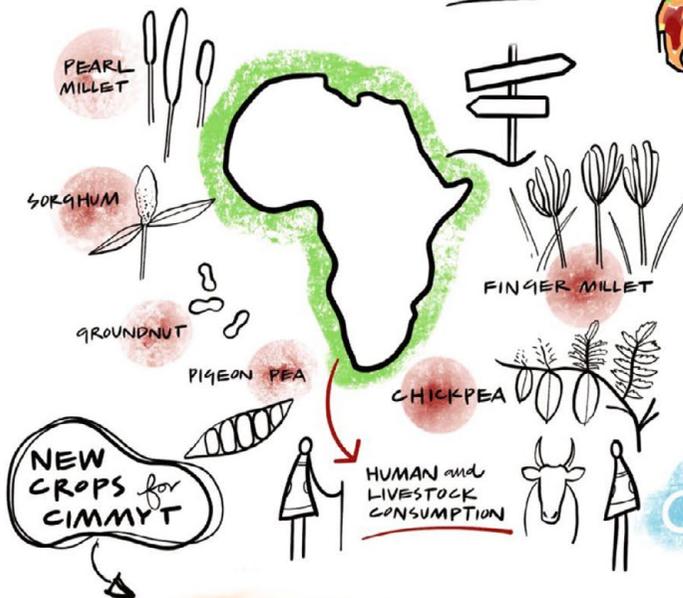
E-mail: sorghum@alphavisa.com - <https://www.21centurysorghum.org>

DRYLAND CEREALS & GRAIN LEGUMES —

FOCUS on AFRICA

WHERE are the DRYLANDS?

HOW?
NARES WILL CO-CREATE,
CO-DEVELOP, CO-IMPLEMENT
AND CO-OWN THE NETWORK!



NARES-LED CROP DEVELOPMENT NETWORKS

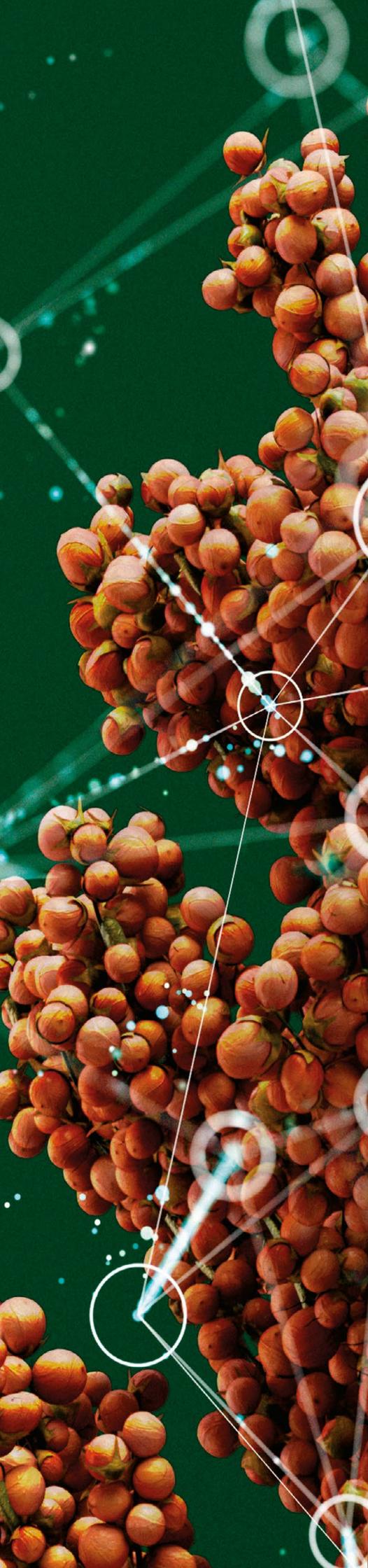


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(MODIFIED BY MARK NAS)

TO ACHIEVE THE VISION
for MAIZE and WHEAT
CROPPING SYSTEMS

- CIMMYT has worked on the **improvement of maize and wheat for 57 years**, through science and innovation.
- CIMMYT, a CGIAR Research Center, has initiated crop improvement for **sorghum, millet, and groundnut**, and has supported NARES with crop improvement efforts for **pigeon pea and chickpea**.
- CIMMYT has partnered with National Agricultural Research and Extension Systems (NARES) across Africa to advance a **crop improvement network approach** that develops improved seed varieties.
- These countries include **Kenya, Uganda, Tanzania, Ethiopia, Sudan, Malawi, South Sudan, Mozambique, Zambia, Zimbabwe, Nigeria, Ghana, Senegal, Togo, Burkina Faso, Mali, Niger, & Chad**.
- CIMMYT's work on dryland crops is a key part of the **strategy to achieve climate-resilient maize and wheat cropping systems**.





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ACKNOWLEDGMENT

The Organizers would like to thank our sponsors and public & private partners for their support of the 2023 Sorghum in the 21st Century Global Sorghum Conference.

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Gold sponsors



Silver sponsors



Supporting partners



OZ Sorghum is an alliance of Australian sorghum researchers

We are focused on improving the productivity and profitability of the Australian sorghum industry and end users via the best combination of genetics and agronomy.

We are globally recognized as leaders in sorghum research for our capacity to carry out integrated multi-disciplinary research with industry impact.

Partners in multi-disciplinary research

- Breeding
- Genomics
- HTP phenomics
- Crop physiology and modelling
- Cereal chemistry
- Entomology
- Pathology

Our discipline strengths include breeding, genetics, genomics, crop physiology, entomology, cereal chemistry and remote sensing. Our research links upstream science to industry problems and opportunities.

The majority of OZ Sorghum researchers work for the University of Queensland through the Queensland Alliance for Agriculture and Food Innovation (QAAFI) or for the Queensland Department of Agriculture and Fisheries (DAF).

CONTACT US: Professor David Jordan
📍 Hermitage Research Facility, Australia
☎ +61 (0) 7 4542 6700
✉ admin@aussorgm.org.au

🐦 @AusSORGM



**OZ
Sorghum**

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Creating future success!

Thinking in generations means:
acting sustainably.
#ThinkingInGenerations

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SEEDING
THE FUTURE
SINCE 1856



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TEXAS TECH
UNIVERSITY.

Texas Tech, established in 1923, is a comprehensive public research university. Working with faculty at the forefront of discovery and innovation and capitalizing on our geography, we will address issues of global consequence in areas including energy, sustainability, and water.

Research Strengths

99

Faculty Members Ranked
Among Top 2% of Most
Cited Researchers

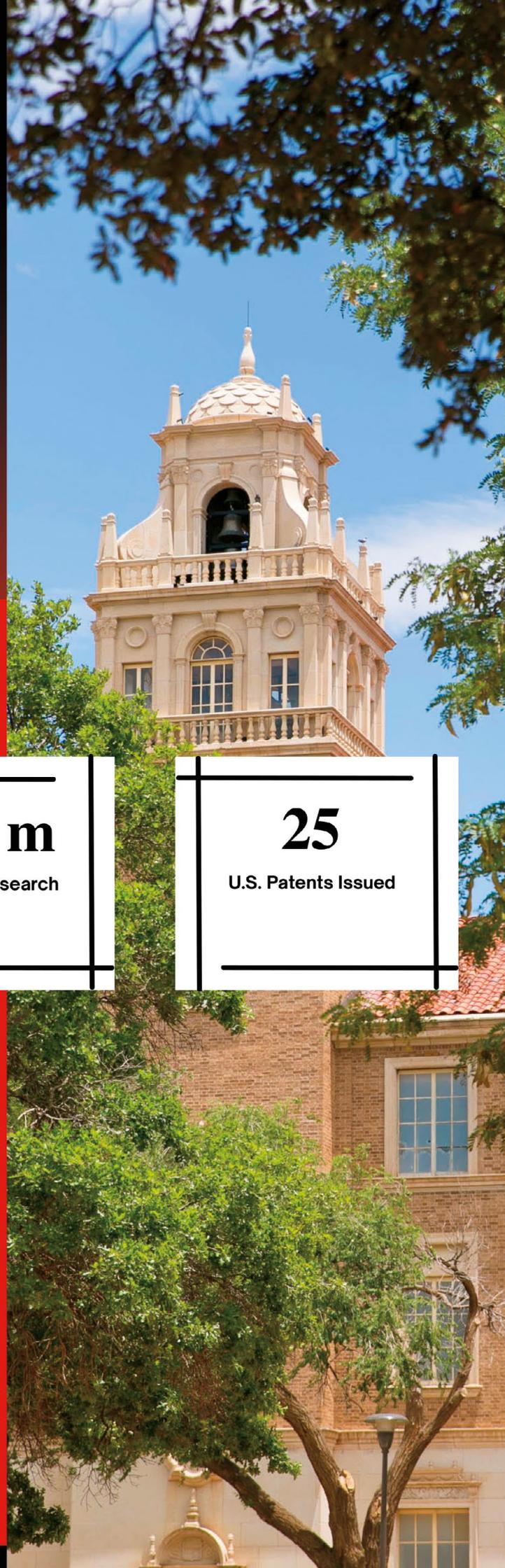
\$212 m

2022 Total Research
Expenditures

25

U.S. Patents Issued

- Genetically resilient crops
- Sustainable nitrogen-based fertilizer production from waste
- Energy efficiency and sustainability, energy storage, microgrids and grid integration and resiliency
- Zoonotic and vector-borne disease, chronic diseases, environmental impacts on health, food safety and security





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Industrial-grade
Sensing
Equipment



Real-time
Analytics &
Decisions



Customize The
System To Your
Specific Needs

PLOT #20X7Y



Disease Level:

Infested

PLOT #21X5Y



Plant Count

125

PLOT #22X8Y



Max Height

63.2_{cm}

PLOT #31X9Y



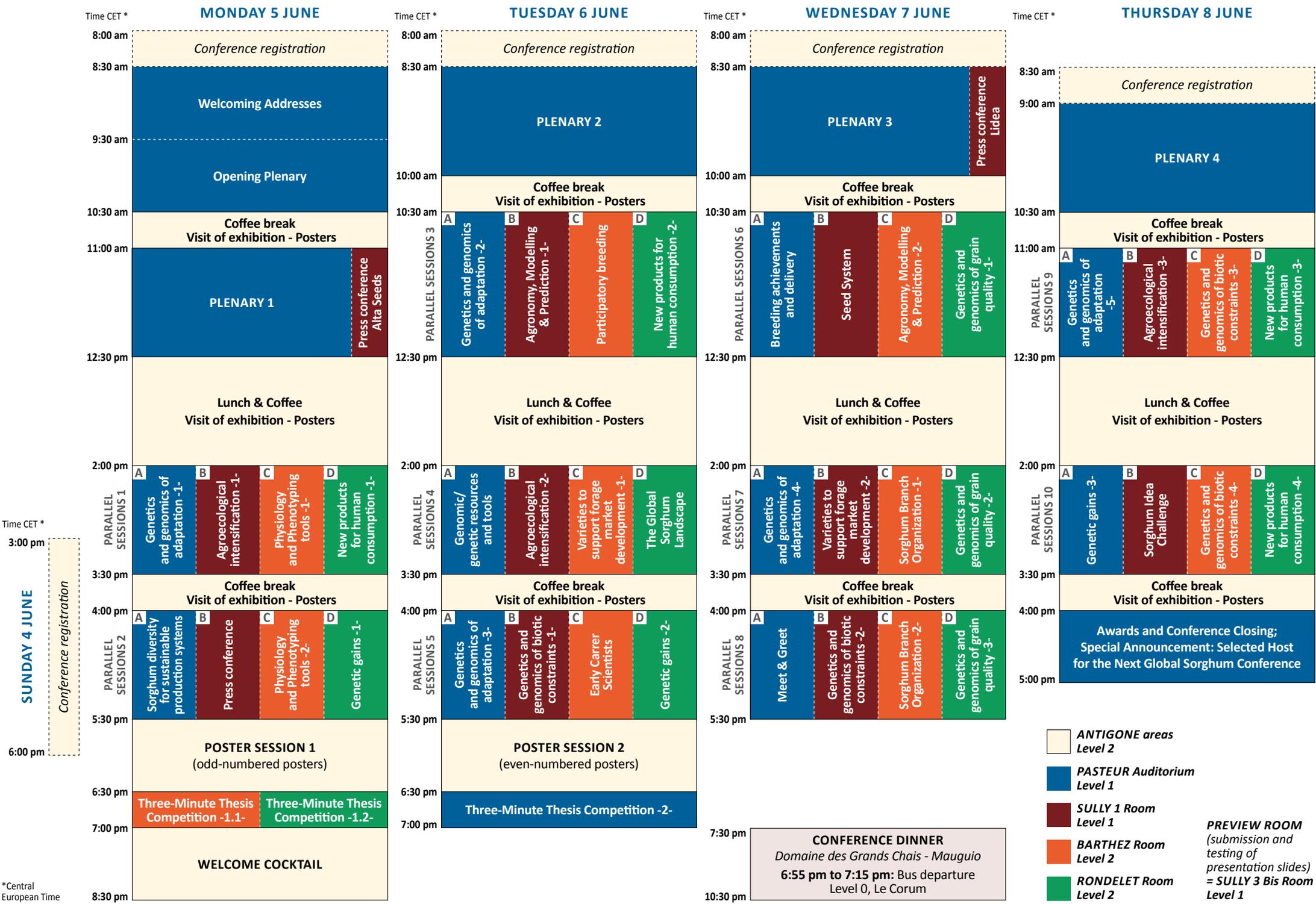
Plot Quality

Good

MEET US AT BOOTH 19

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SUNDAY 4 JUNE

Conference registration

*Central European Time

- ANTIGONE areas**
Level 2
 - PASTEUR Auditorium**
Level 1
 - SULLY 1 Room**
Level 1
 - BARTHEZ Room**
Level 2
 - RONDELET Room**
Level 2
- PREVIEW ROOM**
(submission and testing of presentation slides)
= **SULLY 3 Bis Room**
Level 1



**LE SORGHO,
UN ATOUT POUR
NOTRE AVENIR.**

Les semences européennes, Sorghum in the 21st Century

**Résilience et durabilité face au
changement climatique**

**Conférence Mondiale
du secteur sorgho
Du 5 au 9 juin 2023
Au Corum Event Center,
Montpellier, France**

Retrouvez-nous au stand n°16

Pour plus d'informations : <https://seedsforfuture.eu/>
Contact : martin.gomez@fnpsms.fr

Après le succès de la Conférence mondiale 2018 «Sorghum in the 21st Century» au Cap, en Afrique du Sud, la communauté mondiale du secteur sorgho se prépare à se réunir à nouveau en 2023 pour partager et en apprendre davantage sur les derniers développements en matière de recherche, d'innovation et d'utilisation industrielle.

Organisée par le Cirad en consortium avec ses partenaires internationaux, la conférence couvrira l'ensemble de la chaîne de valeur du sorgho, de la génétique à l'agronomie et aux utilisations finales, et mettra en lumière de nombreux défis clés auxquels l'utilisation du sorgho est actuellement confrontée dans le monde. Les conférences et les séances cibleront à la fois les chercheurs et le secteur privé, avec de nombreuses possibilités de construction de réseau intersectoriel. Cette conférence réunira des compétences au niveau mondial sur de nombreux sujets, notamment :

- Génétique et génomique
- Amélioration des plantes
- Gestion des systèmes de production
- Systèmes agricoles durables
- Solutions post-récolte
- Développement des produits agroalimentaires et du marché



MONDAY 5 JUNE

8:00 am - 8:30 am **Registration** *Antigone 1, 2 & 3 areas - Level 2*

PLENARY SESSIONS

8:30 am - 9:30 am **Welcoming Addresses** *Pasteur Auditorium - Level 1*9:30 am - 10:30 am **Opening Plenary** *Pasteur Auditorium - Level 1*9:30 am - 10:27 am • **In what climatic context does the evolution of agriculture take place?**
Nathalie de Noblet-Ducoudré (*CEA - Université Paris-Saclay, Gif-sur-Yvette, France*)10:30 am - 11:00 am **Coffee break - Visit of exhibition - Posters** *Antigone 1, 2 & 3 areas - Level 2*

PLENARY SESSION

11:00 am - 12:30 pm **Plenary 1** *Pasteur Auditorium - Level 1***Chair: David Jordan**11:00 am - 11:42 am • **The nexus between modelling and experimentation in understanding and predicting the ecophysiological basis of crop adaptation**
Graeme Hammer (*The University of Queensland, Brisbane, Australia*)11:42 am - 12:24 pm • **Developing sorghum hybrids to meet market needs**
Laura Mayor (*Corteva Agriscience, Manhattan, USA*)12:30 pm - 2:00 pm **Lunch break - Visit of exhibition - Posters** *Antigone 1, 2 & 3 areas - Level 2*

PARALLEL SESSIONS 1

2:00 pm - 3:30 pm **A - Genetics and genomics of adaptation -1-** *Pasteur Auditorium - Level 1***Chair: Gael Pressoir***Selected oral presentations*2:00 pm - 2:22 pm • **O01 - The genomics of local adaptation in sorghum landraces**
Aayudh Das (*Department of Biology, Pennsylvania State University, University Park, PA, USA*)2:22 pm - 2:44 pm • **O02 - Integration of sorghum genetics, human genetics, and environmental condition demystified tannin domestication**
Xianran Li (*USDA-ARS, Pullman, WA, USA*)2:44 pm - 3:06 pm • **O03 - Understanding sorghum race level diversity and development of sorghum genomic resources by using deep learning-based variant calling approach**
Abhishek Rathore (*CIMMYT, Medak, Telangana, India*)3:06 pm - 3:28 pm • **O04 - A brief history of stay-green in sorghum: Has it made a difference?**
Andrew Borrell (*Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Warwick, QLD, Australia*)2:00 pm - 3:30 pm **B - Agroecological intensification -1-** *Sully 1 Room - Level 1***Chair: Ana Carcedo***Selected oral presentations*2:00 pm - 2:22 pm • **O05 - Systems agronomy pathways for crop adaptation to heat stress and terminal droughts**
Daniel Rodriguez (*The University of Queensland, Centre for Crop Sciences (QAAFI), Gatton, QLD, Australia*)2:22 pm - 2:44 pm • **O06 - Adapting to heat stresses by sowing summer grain crops in late-winter: Sorghum root growth, water use, and yield**
Dongxue Zhao (*The University of Queensland, Gatton, QLD, Australia*)

... / ...

- 2:44 pm - 3:06 pm • **O07 - Wide row configurations in sorghum reduce crop water use efficiency and yield in marginal rainfall environments in Australia**
Loretta Serafin (*Summer Grains, NSW Department of Primary Industries, Calala, NSW, Australia*)
- 3:06 pm - 3:28 pm • **O08 - Effect of soil treatment with Methionine on *Striga* infection and sorghum growth under field conditions in Ethiopia**
Taye Tessema (*NABRC, Ethiopian Institute of Agricultural Research, Addis Ababa, Ethiopia*)
-
- 2:00 pm - 3:30 pm **C - Physiology and Phenotyping tools to support breeding -1-** Barthez Room - Level 2
Chair: Krishna Jagadish SV 
Selected oral presentations
- 2:00 pm - 2:22 pm • **O09 - Flowering response to photoperiod combines the effect of the daylength with the effects of the daily changes in sunrise and sunset times and of temperature acclimation**
Benoit Clerget (*UMR AGAP Institute, Cirad, Montpellier, France*)
- 2:22 pm - 2:44 pm • **O10 - Dissecting the genetic value and genetic variability for the limited transpiration trait in sorghum: from simulations to field phenomics**
Rubi Raymundo (*Soil and Crops sciences, Colorado State University, Fort Collins, CO, USA*)
- 2:44 pm - 3:06 pm • **O11 - Contrasts in leaf photosynthetic low-light response across temperatures generate differences in crop-scale radiation use efficiency**
Alex Wu (*QAAFI, The University of Queensland, Brisbane, Queensland, Australia*)
- 3:06 pm - 3:28 pm • **O12 - Plant response to a late heat stress can be modified by an earlier one: a case study on sorghum grain production**
Angelique Berger (*Agap Institut, Cirad, Montpellier, France*)
-
- 2:00 pm - 3:30 pm **D - Developing new products for human consumption -1-** Rondelet Room - Level 2
Chair: Rewati Raman Bhattarai 
Selected oral presentations
- 2:00 pm - 2:22 pm • **O13 - Nutritional characterization and technological aptitude of twenty-nine ICRISAT Sorghum varieties in Burkina Faso**
Fatoumata Ba-Hama (*Département technologie Alimentaire, IRSAT, Ouagadougou, Burkina Faso*)
- 2:22 pm - 2:44 pm • **O14 - Innovative food-to-food fortified sorghum flours to improve nutrition in rural West Africa**
Moustapha Moussa (*Institut National de la Recherche Agronomique du Niger (INRAN), Niamey, Republic of the Niger*)
- 2:44 pm - 3:06 pm • **O15 - Developing and marketing sorghum baked products: Acceptance of novel biscuits as influenced by sensory characteristics and information**
Pulane Nkhabutlane (*Consumer Science, National University of Lesotho, Lesotho, Roma, Lesotho*)
- 3:06 pm - 3:28 pm • **O16 - Supplementary Feeding on Soy-fortified cereal porridge improves the Nutritional Status of Pre-school Children aged 4-5 Yea**
Beatrice Were (*Biological, The University of Eldoret, Eldoret, Kenya*)
-
- 3:30 pm - 4:00 pm **Coffee break - Visit of exhibition - Posters** Antigone 1, 2 & 3 areas - Level 2
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- PARALLEL SESSIONS 2**
- 4:00 pm - 5:30 pm **A - Highlighting sorghum diversity as a key to develop sustainable production systems** Pasteur Auditorium - Level 1
Chair: Somashekhar Punnuri
Selected oral presentations
- 4:00 pm - 4:22 pm • **O17 - Sorghum wild relatives: The forgotten treasure-trove for unlocking the hidden hunger crises in Sudan**
Tilal Abdelhalim (*Biotechnology and Biosafety Research Center, Agricultural Research Corporation (ARC), Khartoum North, Sudan*)
- ... /...

4:22 pm - 4:44 pm	<ul style="list-style-type: none"> • O18 - Crop diversity and West African farmers: agroecological perspectives Christian Leclerc (<i>UMR AGAP Institut, Cirad, Montpellier, France</i>) 	
4:44 pm - 5:06 pm	<ul style="list-style-type: none"> • O19 - Investigations on pollen-mediated gene flow between grain sorghum (<i>Sorghum bicolor</i>) and johnsongrass (<i>Sorghum halepense</i>) Muthukumar Bagavathiannan (<i>Texas A&M University, College Station, TX, USA</i>) 	
5:06 pm - 5:28 pm	<ul style="list-style-type: none"> • O20 - Sorghum diversity for sustainable cropping systems in marginal environments in the deep south of Madagascar Kirsten Von Brocke (<i>AGAP, Cirad, Montpellier, France</i>) 	
4:00 pm - 5:30 pm	B - Press conference	<i>Sully 1 Room - Level 1</i>
4:00 pm - 5:30 pm	C - Physiology and Phenotyping tools to support breeding -2- <i>Chair: Alemu Tirefessa</i> <i>Selected oral presentations</i>	<i>Barthez Room - Level 2</i>
4:00 pm - 4:22 pm	<ul style="list-style-type: none"> • O21 - 3D Computer Vision for High-throughput Phenotyping Jan Masner (<i>Department of Information Technologies, Czech University of Life Sciences, Prague, Praha-Suchdol, Czechia</i>) 	
4:22 pm - 4:44 pm	<ul style="list-style-type: none"> • O22 - Evaluating variation in stem strength in response to artificial drought stress amongst sorghum genotypes Geetika Geetika (<i>The University of Queensland, Warwick, Queensland, Australia</i>) 	
4:44 pm - 5:06 pm	<ul style="list-style-type: none"> • O23 - Quantifying effects of high temperature stress on seed set of sorghum Erik Van Oosterom (<i>QAAFI (Queensland Alliance for Agriculture and Food Innovation), The University of Queensland, St Lucia, QLD, Australia</i>) 	
5:06 pm - 5:28 pm	<ul style="list-style-type: none"> • O24 - Deep learning pipeline for phenotyping sorghum panicles Chrisbin James (<i>School of Agriculture and Food Sciences, The University of Queensland, Brisbane, Queensland, Australia</i>) 	
4:00 pm - 5:30 pm	D - Optimizing breeding programs to maximize genetic gains -1- <i>Chair: Mitch Tuinstra</i> <i>Selected oral presentations</i>	<i>Rondelet Room - Level 2</i>
4:00 pm - 4:22 pm	<ul style="list-style-type: none"> • O25 - Effect of retraining on genomic prediction accuracy in sorghum Jean-Rigaud Charles (<i>CHIBAS, Faculté des Sciences de l'Agriculture et de l'Environnement, Université Quisqueya, Port au Prince, Haiti</i>) 	
4:22 pm - 4:44 pm	<ul style="list-style-type: none"> • O26 - Genetic gain from a rapid cycling genomic selection program for non photoperiodic dual use sorghum Gael Pressoir (<i>CHIBAS, Université Quisqueya, Port-au-Prince, Haiti</i>) 	
4:44 pm - 5:06 pm	<ul style="list-style-type: none"> • O27 - Improving rate of genetic gain through optimised breeding cycles Abhishek Rathore (<i>CIMMYT, Hyderabad, Telangana, India</i>) 	
5:30 pm - 6:30 pm	Poster Session 1 Odd-numbered posters	<i>Antigone 1, 2 & 3 areas - Level 2</i>
6:30 pm - 7:00 pm	Three-Minute Thesis Competition (3MT) -1.1-	 <i>OZ Sorghum</i> <i>Barthez Room - Level 2</i>
	Three-Minute Thesis Competition (3MT) -1.2-	 <i>OZ Sorghum</i> <i>Rondelet Room - Level 2</i>
7:00 pm - 8:30 pm	Welcome cocktail	<i>Antigone 1, 2 & 3 areas - Level 2</i>

Sponsored by



TUESDAY 6 JUNE

8:00 am - 8:30 am **Registration**

Antigone 1, 2 & 3 areas - Level 2

PLENARY SESSION

8:30 am - 10:00 am

Plenary 2

Pasteur Auditorium - Level 1

Chair: Jean-François Rami

8:30 am - 8:57 am

- **Sorghum in Europe: State of play and prospects**
Valérie Brochet (*Sorghum-ID, Montardon, France*)

8:57 am - 9:24 am

- **Can the analysis of the genetic diversity of stress responses challenge the consensus on the relative performance of maize and sorghum under drought scenarios?**
Boris Parent (*INRAE, Montpellier, France*)

9:24 am - 09:51 am

- **Breaking boundaries in sorghum value chains: the impact of Europe-Africa collaborations and future prospects**
David Pot (*Cirad, Montpellier, France*)

10:00 am - 10:30 am **Coffee break - Visit of exhibition - Posters**

Antigone 1, 2 & 3 areas - Level 2

PARALLEL SESSIONS 3

10:30 am - 12:30 pm

A - Genetics and genomics of adaptation -2-

Pasteur Auditorium - Level 1

Chair: Ian Goodwin*Selected oral presentations*

10:30 am - 10:52 am

- **O28 - Novel strategies to mine the relevant biodiversity from genebanks to enhance crop adaptations for changing climate: case study-harnessing sorghum drought adaptations**
Jana Kholova (*Department of Information Technologies, Czech University of Life Sciences Prague, Praha - Suchdol, Czechia*)

10:52 am - 11:14 am

- **O29 - The genetics basis of sorghum adaptation to a changing climate**
Karine Da Costa Bernardino (*Embrapa Maize and Sorghum, Sete Lagoas, Brazil*)

11:14 am - 11:36 am

- **O30 - Breeding for reproductive cold tolerance in sorghum**
Steffen Windpassinger (*Plant Breeding, Justus-Liebig-University Giessen, Giessen, Germany*)

11:36 am - 11:58 am

- **O31 - Early-Stage Phenotyping of Root Angle Provides Insights into the Drought Tolerance Level of Sorghum (*Sorghum bicolor* L. Moench) Landraces**
Temesgen Menamo (*Horticulture and Plant Sciences, Jimma University, Jimma, Oromia, Ethiopia*)

11:58 am - 12:20 pm

- **O32 - Identifying genotypic variation in transpiration efficiency (TE) among major sorghum races and examine their genetic association**
Abel Debebe (*Agricultural Biotechnology, Ethiopian Institute of Agricultural Research (EIAR), Adama, Oromia, Ethiopia*)

10:30 am - 12:30 pm

B - Agronomy / Modelling / Prediction -1-

Sully 1 Room - Level 1

Chair: Andrew Borrell*Selected oral presentations*

10:30 am - 10:52 am

- **O33 - Modeling adaptation of sorghum in Ethiopia with APSIM—opportunities with G×E×M**
Alemu Tirfessa (*Crop Research, Ethiopian Institute of Agricultural Research (EIAR), Adama, Oromia, Ethiopia*)

10:52 am - 11:14 am

- **O34 - The need for local data for moving forward food assessments in Africa: a review using sorghum crop modeling as case study**
Ana Julia Carcedo (*Kansas State University, Manhattan, Kansas, USA*)

11:14 am - 11:36 am

- **O35 - Foresighting sorghum production through integrating general circulation and biophysical crop models with remote sensing at regional scales across north-eastern Australia**
Andries Potgieter (*QAAFI, The University of Queensland, Gatton, QLD, Australia*)

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11:36 am - 11:58 am	<ul style="list-style-type: none"> • O36 - CropGen: A new tool for optimising sorghum crop design for drought adaptation Genevieve Durrington (<i>Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, Australia</i>) 	
11:58 am - 12:20 pm	<ul style="list-style-type: none"> • O37 - Automated processing of GxExM parametrized simulations Jan Pavlik (<i>Department of Information Technologies, Czech University of Life Sciences Prague, Prague, Praha - Suchdol, Czechia</i>) 	
10:30 am - 12:30 pm	<p>C - Optimizing variety development through farmers and value chain stakeholder involvements</p> <p>Chair: Bettina Haussmann</p> <p><i>Selected oral presentations</i></p>	<p><i>Barthez Room - Level 2</i></p>  
10:30 am - 10:52 am	<ul style="list-style-type: none"> • O38 - How farmer-breeder collaboration can increase functional sorghum diversity and reach larger-scale impact Bettina Haussmann (<i>DITSL, The Deutsches Institut für Tropische und Subtropische Landwirtschaft GmbH, Witzenhausen, Germany</i>) 	
10:52 am - 11:14 am	<ul style="list-style-type: none"> • O39 - The power of Farmer Research Network in technology promotion among smallholder farmers: The case of improved sorghum varieties in Eastern Uganda Moses Biruma (<i>National Semi-Arid Resources Research Institute (NaSARRI), National Agricultural Research Organisation (NARO), Soroti, Uganda</i>) 	
11:14 am - 11:36 am	<ul style="list-style-type: none"> • O40 - Participatory Selection of Introgression Lines Derived from Wild and Exotic Sorghum with Farmers in Western Kenya Evans Ouma (<i>Agronomy, Rongo University, Rongo, Migori, Kenya</i>) 	
11:36 am - 11:58 am	<ul style="list-style-type: none"> • O41 - Sorghum Breeding for Agroecology: Biodiversity considerations in West Africa Eva Weltzien (<i>Tracy Lab/Agronomy Dept., The University of Wisconsin-Madison, Remagen, Rhineland Palatinate, Germany</i>) 	
11:58 am - 12:20 pm	<ul style="list-style-type: none"> • O42 - Participatory sorghum development increased number of functional varieties and genetic diversity for climate resilience among smallholder farmers in Chirundu Lloyd Mbulwe (<i>Sorghum & Millets Improvement Programme/Crop Improvement and Agronomy, Zambia Agriculture Research Institute (ZARI), Chilanga, Zambia</i>) 	
10:30 am - 12:30 pm	<p>D - Developing new products for human consumption -2-</p> <p>Chair: Tadesse Teferra</p> <p><i>Selected oral presentations</i></p>	<p><i>Rondelet Room - Level 2</i></p>  
10:30 am - 10:52 am	<ul style="list-style-type: none"> • O43 - Nutritional and functional properties of infrared and microwave heat moisture-treated sorghum meals Rose Otema Baah (<i>Department of consumer and Food Science, The University of Pretoria, Pretoria, South Africa</i>) 	
10:52 am - 11:14 am	<ul style="list-style-type: none"> • O44 - Sorghum grains milling: filling the technological gaps for new functional flours and semolina production Reine Barbar (<i>UMR 1208 IATE, Univ Montpellier, INRAE, Institut-Agro Montpellier, Montpellier, France</i>) 	
11:14 am - 11:36 am	<ul style="list-style-type: none"> • O45 - End-use quality driven sorghum improvement: new opportunities for high value food products Tadesse Teferra (<i>Hawassa University, Hawassa, Ethiopia</i>) 	
11:36 am - 11:58 am	<ul style="list-style-type: none"> • O46 - Extrusion processing of sorghum grain (whole and decorticated) used as ingredients for breads, biscuits and arraw Cheikh N'Diaye (<i>Cereals, Institut de Technologie Alimentaire, Dakar, Senegal</i>) 	
11:58 am - 12:20 pm	<ul style="list-style-type: none"> • O47 - Prioritizing sorghum value chain preferred straits : lessons learned from the field in Burkina Faso and way forward Alex-Fabrice Zongo (<i>Institut de l'Environnement et de Recherches Agricoles, Ouagadougou, Burkina Faso</i>) 	
12:30 pm - 2:00 pm	<p>Lunch break - Visit of exhibition - Posters</p>	<p><i>Antigone 1, 2 & 3 areas - Level 2</i></p>

PARALLEL SESSIONS 4

2:00 pm - 3:30 pm	A - Developing genomic / Genetic resources and tools	Pasteur Auditorium - Level 1
	Chair: Geoffrey Morris	 
	<i>Selected oral presentations</i>	
2:00 pm - 2:22 pm	<ul style="list-style-type: none"> • O48 - Panning for genetic gold: pan-genomics and other omics resource for crop improvement Emma Mace (QAAF, The University of Queensland, Warwick, Queensland, Australia) 	
2:22 pm - 2:44 pm	<ul style="list-style-type: none"> • O49 - Editing the way to resilient high value cereals Ian Godwin (QAAFI, The University of Queensland, St Lucia, QLD, Australia) 	
2:44 pm - 3:06 pm	<ul style="list-style-type: none"> • O50 - Sorghum Mutation Breeding in the Age of Next-Generation Sequencing Doreen Ware (Cold Spring Harbor Laboratory, USDA ARS, Cold Spring Harbor, NY, USA) 	
3:06 pm - 3:28 pm	<ul style="list-style-type: none"> • O51 - Genotype–environment associations to reveal the molecular basis of environmental adaptation in sorghum Jesse Lasky (Pennsylvania State University, University Park, PA, USA) 	
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2:00 pm - 3:30 pm	B - Agroecological intensification -2-	Sully 1 Room - Level 1
	Chair: Ignacio Ciampetti	
	<i>Selected oral presentations</i>	
2:00 pm - 2:22 pm	<ul style="list-style-type: none"> • O52 - OGA (Fermented human urine) fertilizer an auto-innovation among women farmers in Niger Moussa Oumarou Hannatou (Institut National de Recherche Agronomique du Niger (INRAN), Maradi, Republic of the Niger) 	
2:22 pm - 2:44 pm	<ul style="list-style-type: none"> • O53 - Can low-input agriculture in semi-arid Burkina Faso feed its soil, livestock and people? Gildas Assogba (Plant Production Systems, Wageningen University, Wageningen, The Netherlands) 	
2:44 pm - 3:06 pm	<ul style="list-style-type: none"> • O54 - Co-designing sorghum-based cropping systems with rotations to improve soil fertility and yield in Burkina Faso Abdoul Rasmane Bagagnan (Plant production system (PPS), Wageningen University and Research/ Cirad, Ouagadougou, Burkina Faso) 	
3:06 pm - 3:28 pm	<ul style="list-style-type: none"> • O55 - Exploration of sorghum genetic variability for adaptation to intercropping with cowpea - case study in Burkina Faso Louis-Marie Raboin (AIDA, Cirad, Ouagadougou, Burkina Faso) 	
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2:00 pm - 3:30 pm	C - Developing varieties to support forage market development -1-	Barthez Room - Level 2
	Chair: Nathanael Bascom	
	<i>Selected oral presentations</i>	
2:00 pm - 2:22 pm	<ul style="list-style-type: none"> • O56 - Dual-purpose sorghum in Mali : adoption factors and producer perceptions Aminata Berthe (Système de production et gestion des ressources naturelles, IER, Bamako, Mali) 	
2:22 pm - 2:44 pm	<ul style="list-style-type: none"> • O57 - Brown midrib sorghum forages create new opportunities for animal producers in West Africa Ousmane Seyni Diakite (Cultures pluviales, INRAN, Niamey, Republic of the Niger) 	
2:44 pm - 3:06 pm	<ul style="list-style-type: none"> • O58 - Variability and Character Association among Forage Biomass and Nutritional Quality Traits of Sorghum Collections in Ethiopia Getachew Ayana (Plant protection, Ethiopian Institute of Agricultural Research (EIAR), Adama, Oromia, Ethiopia) 	
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2:00 pm - 3:30 pm	D - Joint session - Sorghum ID - OZ Sorghum - the United Sorghum Checkoff Program - Sorghum Movement	Rondelet Room - Level 2
	<ul style="list-style-type: none"> • The Global Sorghum Landscape: Opportunities and Challenges for Research and Industry Valérie Brochet, David Jordan, Tim Lust, Vinicius Guimarães 	
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3:30 pm - 4:00 pm	Coffee break - Visit of exhibition - Posters	Antigone 1, 2 & 3 areas - Level 2

PARALLEL SESSIONS 5

4:00 pm - 5:30 pm **A - Genetics and genomics of adaptation -3-** *Pasteur Auditorium - Level 1*

Chair: Erik Van Oosterom

Selected oral presentations

- 4:00 pm - 4:22 pm • **O59 - Enhancing the sustainable production of sorghum by exploiting biological nitrogen fixation by microbial symbionts associated with aerial roots**
Wilfred Vermerris (*Microbiology & Cell Science, The University of Florida, Gainesville, FL, USA*)
- 4:22 pm - 4:44 pm • **O60 - Understanding the spatiotemporal regulation of biosynthesis of sorgoleone, an inhibitor of nitrification secreted from sorghum root hair cells**
Sakiko Okumoto (*Texas A&M Agrilife research, Collegen Station, TX, USA*)
- 4:44 pm - 5:06 pm • **O61 - Harnessing root biology for sorghum adaptation to tropical environments with abiotic stresses**
Jurandir Viera de Magalhães (*Embrapa Maize and Sorghum, Sete Lagoas, MG, Brazil*)
- 5:06 pm - 5:28 pm • **O62 - Transcription factor nuclear trafficking elicited by aluminum sensing in the plasma membrane plays a role in the regulation of the sorghum SbMATE transporter**
Vanessa Barros (*Embrapa Maize and Sorghum, Sete Lagoas, Brazil*)

4:00 pm - 5:30 pm **B - Genetics and genomics of biotic constraints -1-** *Sully 1 Room - Level 1*

Chair: Graeme Hammer

Selected oral presentations

- 4:00 pm - 4:22 pm • **O63 - Sorghum aphid host plant resistance: Implications for global durability**
Carl Vangessel (*Crop Adaptation Lab, Colorado State University, Fort Collins, Colorado, USA*)
- 4:22 pm - 4:44 pm • **O64 - Impact of herbicide imidazolinone-resistance trait introgression in grain sorghum (Sorghum bicolor L. Moench)**
Pedro Pardo (*R&D, Advanta Seeds, Venado Tuerto, Santa Fe, Argentina*)
- 4:44 pm - 5:06 pm • **O65 - Population genomics of Low Germination Stimulant 1 enabled molecular breeding of Striga resistant sorghum varieties**
Fanna Maina (*INRAN - NIGER, Niamey, Republic of the Niger*)
- 5:06 pm - 5:28 pm • **O66 - PP37 multi-parent advanced generation inter-cross (MAGIC) population – a resource for Striga research**
Habte Nida (*Agronomy, Purdue University, West Lafayette, IN, USA*)

4:00 pm - 5:30 pm **C - Early Career Scientists Session** *Barthez Room - Level 2*

• **Special session**

Valérie Brochet, Krishna Jagadish, Timothy Dalton, Bettina Haussmann

4:00 pm - 5:30 pm **D - Optimizing breeding programs to maximize genetic gains -2-** *Rondelet Room - Level 2*

Chair: Eva Weltzien

Selected oral presentations

- 4:00 pm - 4:22 pm • **O67 - The IAVAO crop network: a NARS led regional platform for germplasm exchange and multi-environment trials**
Jean-François Rami (*UMR AGAP Institut, Cirad, Montpellier, France*)
- 4:22 pm - 4:44 pm • **O68 - Characterization of adaptation mechanisms in sorghum using a multi-reference back-cross nested association mapping design and envirotyping**
Vincent Garin (*ICRISAT, Patancheru, India ; Cirad, UMR AGAP, Montpellier, France*)
- 4:44 pm - 5:06 pm • **O69 - Performance of phenomic selection in sorghum : Exploring population structure and GXE effects on prediction accuracy**
Nicolas Salas (*AGAP/GIV/BIOS, Cirad, Montpellier, France*)

5:30 pm - 6:30 pm **Poster Session 2 Even-numbered posters** *Antigone 1, 2 & 3 areas - Level 2*

6:30 pm - 7:00 pm **Three-Minute Thesis Competition (3MT) -2-**  *Pasteur Auditorium - Level 1*

WEDNESDAY 7 JUNE

8:00 am - 8:30 am

Registration

Antigone 1, 2 & 3 areas - Level 2

PLENARY SESSION

8:30 am - 10:00 am

Plenary 3

Pasteur Auditorium - Level 1

Chair: Timothy Dalton• **Round table**Kwaku Gyebi Duodu (*University of Pretoria, Hatfield, South Africa*)Monia Caramma (*Sustainable Food Researcher, Switzerland*)Earl Roemer (*Nu Life Market, Scott City, USA*)

10:00 am - 10:30 am

Coffee break - Visit of exhibition - Posters

Antigone 1, 2 & 3 areas - Level 2

PARALLEL SESSIONS 6

10:30 am - 12:30 pm

A - Breeding Programs achievements and technology delivery

Pasteur Auditorium - Level 1

Chair: David Jordan*Selected oral presentations*

10:30 am - 10:52 am

- **O70 - ADVANTA Championing Future R&D Strategies in Genetic Improvement and Seed Treatment Technologies of Sorghum for Global Food, Feed, Fodder, Biofuel and Nutrition Security**
Vilas Tonapi (*Advanta Seeds, Advanta Enterprises Limited, Hyderabad, Telangana, India*)

10:52 am - 11:14 am

- **O71 - Dutch bred Dusormil sorghums HD100 and HD7, were found suitable for harvest with a dual purpose harvester unlocking a multipurpose crop and its applications**
Walter De Milliano (*Maatschap de Milliano-Meijer, Oostburg, Zeeland, Netherlands*)

11:14 am - 11:36 am

- **O72 - Genotype by Environment Interaction and Stability analysis of Sorghum [Sorghum bicolor (L.) Moench] Genotypes in Western Ethiopia**
Meseret Tola (*Plant breeding, Oromia Agricultural Research Institute, Bako Agrecultural Research Center, Addis Ababa, Oromia, Ethiopia*)

11:36 am - 11:58 am

- **O73 - Development of energy sorghum cultivars for bioenergy in Brazil**
Rafael Parrella (*Embrapa Maize and Sorghum, EMBRAPA, Sete Lagoas, MG, Brazil*)

11:58 am - 12:20 pm

- **O74 - Development of sorghum hybrids with good response to synthetic fertilizers to improve yield in Mali**
MacDonald Jumbo (*Accelerated Crop Improvement, International Crops Research Institute for the Semi-Arid Tropics, Bamako, Mali*)

10:30 am - 12:30 pm

B - Seed System

Sully 1 Room - Level 1

Chair: Timothy Dalton*Selected oral presentations*

10:30 am - 10:52 am

- **O75 - Sorghum Seed System Security situation among Smallholders in Semi-Arid Eastern Kenya**
Carolynne Khalayi Wafula (*Kenya Agricultural and Livestock Organization, Rongo, Kenya*)

10:52 am - 11:14 am

- **O76 - Dissemination process of new seed variety in Senegal: analysis of the interactions of the actors of the millet and sorghum sectors**
Cheikh Tidiane Diouf (*UMR innovation/BAME, Cirad /ISRA, Dakar, Senegal*)

11:14 am - 11:36 am

- **O77 - Scaling the pearl millet and sorghum seedball technology in the Sahel**
Moussa Oumarou Hannatou (*Institut National de Recherche Agronomique du Niger (INRAN), Maradi, Republic of the Niger*)

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11:36 am - 11:58 am	<ul style="list-style-type: none"> • O78 - Analysis of Macro-Institutional Determinants of the adoption of new sorghum/millet varieties in Burkina Faso Alex-Fabrice Zongo (<i>Université Thomas Sankara, Ouagadougou, Burkina Faso</i>) 	
11:58 am - 12:20 pm	<ul style="list-style-type: none"> • O79 - From demo plot to sorghum seed system construction: a journey with the tribal farmers of Adilabad District, India Marijn Voorhaar (<i>International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Telangana, India</i>) 	
10:30 am - 12:30 pm	<p>C - Agronomy / Modelling / Prediction -2-</p> <p>Chair: Emma Mace</p> <p><i>Selected oral presentations</i></p>	Barthez Room - Level 2 
10:30 am - 10:52 am	<ul style="list-style-type: none"> • O80 - Environment characterisation of sorghum (<i>Sorghum bicolor</i> L.) crops using climate, satellite imagery, and crop simulation modelling in Australia Javier Fernandez (<i>School of Agriculture and Food Sciences, The University of Queensland, Brisbane, QLD, Australia</i>) 	
10:52 am - 11:14 am	<ul style="list-style-type: none"> • O81 - Environment characterization in sorghum by modeling water-deficit and heat patterns in the US Great Plains region Ana Julia Carcedo (<i>Kansas State University, Manhattan, Kansas, USA</i>) 	
11:14 am - 11:36 am	<ul style="list-style-type: none"> • O82 - Field-scale greenhouse gas fluxes from sorghum in the U.S. Great Plains using eddy covariance Nithya Rajan (<i>Soil and Crop Sciences, Texas A&M University, College Station, TX, USA</i>) 	
11:36 am - 11:58 am	<ul style="list-style-type: none"> • O83 - Sorghum in France: climate-related yield and its perspectives Maeva Baumont (<i>SAGEP, Arvalis, Montardon, France</i>) 	
11:58 am - 12:20 pm	<ul style="list-style-type: none"> • O84 - Composts from two invasive species (<i>Hyptis suaveolens</i> and <i>Chromolaena odorata</i>) enhance stem sugar and grain production in photoperiodic sweet sorghum Thierry Tovignan (<i>CHIBAS, Université Quisqueya, Port au Prince, Haiti</i>) 	
10:30 am - 12:30 pm	<p>D - Genetics and genomics of grain quality -1-</p> <p>Chair: Nofou Ouerdarogo</p> <p><i>Selected oral presentations</i></p>	Rondelet Room - Level 2
10:30 am - 10:52 am	<ul style="list-style-type: none"> • O85 - Characterization of genetic variants in carotenoid biosynthesis pathway, a hub for sorghum crop improvement Clara Cruet-Burgos (<i>Department of Soil and Crop Science, Colorado State University, Fort Collins, Colorado, USA</i>) 	
10:52 am - 11:14 am	<ul style="list-style-type: none"> • O86 - Genomics of Sorghum Grain Carotenoid Bioavailability Rachel McDowell (<i>Horticulture and Landscape Architecture, Colorado State University, Fort Collins, Colorado, USA</i>) 	
11:14 am - 11:36 am	<ul style="list-style-type: none"> • O87 - Analysis of polysaccharide composition during sorghum grain development Camille Costes (<i>BIA, INRAE, Nantes, France</i>) 	
11:36 am - 11:58 am	<ul style="list-style-type: none"> • O88 - Sorghum grain germination reveals new opportunities to improve kafirin digestibility: biochemical insights and Mass-spectrometry label-free based quantitative proteomics Hamza Mameri (<i>UMR 1208 IATE, Univ. Montpellier, INRAE, L'Institut-Agro Montpellier, Montpellier, France</i>) 	
11:58 am - 12:20 pm	<ul style="list-style-type: none"> • O89 - Grain filling duration in sorghum: Opportunities for yield improvement Daniel Otwani (<i>QAAFI, The University of Queensland, Warwick, QLD, Australia</i>) 	
12:30 pm - 2:00 pm	Lunch break - Visit of exhibition - Posters	Antigone 1, 2 & 3 areas - level 2

PARALLEL SESSIONS 7

- 2:00 pm - 3:30 pm** **A - Genetics and genomics of adaptation -4-** *Pasteur Auditorium - Level 1*
Chair: MacDonald Jumbo
Selected oral presentations
- 2:00 pm - 2:22 pm • **O90 - What doesn't kill you makes you stronger: the benefits of being cyanogenic in a changing world**
 Ros Gleadow (*School of Biological Sciences, Monash University, Melbourne, Clayton, Vic, Australia*)
- 2:22 pm - 2:44 pm • **O91 - Modulating brassinosteroid signaling to confer drought tolerance in Sorghum**
 Juan Bautista Fontanet-Manzaneque (*Centre for Research in Agricultural Genomics, Barcelona, Spain*)
- 2:44 pm - 3:06 pm • **O92 - Differential responses of antioxidant enzymes in two sorghum lines contrasting in water deficit and salt tolerance**
 Ndiko Ludidi (*Department of Biotechnology, University of the Western Cape, Bellville, South Africa*)
- 3:06 pm - 3:28 pm • **O93 - Virus-induced gene silencing facilitated the discovery of a new gene affecting the photosynthetic capacity of sorghum under cold stress**
 Maria Salas Fernandez (*Iowa State University, Ames, Iowa, USA*)
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- 2:00 pm - 3:30 pm** **B - Developing varieties to support forage market development -2-** *Sully 1 Room - Level 1*
Chair: Habte Nida
Selected oral presentations
- 2:00 pm - 2:22 pm • **O94 - Brown Midrib brachytic dwarf sorghum silage as a high-quality forage alternative**
 Tomas Sundblad (*TD Lead America's Region, Advanta Seeds, Benavidez, Buenos Aires, Argentina*)
- 2:22 pm - 2:44 pm • **O95 - The brown midrib (bmr) mutants prevent stalk rots under drought conditions and improve sorghum biomass quality**
 Deanna Funnell-Harris (*Wheat, Sorghum and Forage Research Unit, US Department of Agriculture, Agricultural Research Service, Lincoln, Nebraska, USA*)
- 2:44 pm - 3:06 pm • **O96 - The brown midrib (bmr) mutants: a tool to tailor lignin synthesis in sorghum for forage end uses**
 Scott Sattler (*Wheat, Sorghum and Forage Research Unit, United States Dept. of Agriculture - Agriculture Research Service, Lincoln, NE, USA*)
- 3:06 pm - 3:28 pm • **O97 - Prussic-acid Free Sorghum Creates New Opportunities for Hay and Silage Production**
 Mitchell Tuinstra (*Department of Agronomy, Purdue University, West Lafayette, IN, USA*)
-
- 2:00 pm - 3:30 pm** **C - Sorghum Branch - Organization / Multi-actor organization -1-** *Barthez Room - Level 2*
Chair: Fanna Maina
Selected oral presentations
- 2:00 pm - 2:22 pm • **O98 - The Impact of Collaboration on Sorghum Research and Development System in Africa: The Case of Ethiopia**
 Firew Mekbib Hailemariam (*School of Plant Sciences, Haramaya University, Dire Dawa, Ethiopia*)
- 2:22 pm - 2:44 pm • **O99 - Communicating Research Effectively and Timely to Non-Research Audiences in Agriculture**
 Stacy Mayo-Martinez (*Martinez Media & Marketing Group, Manhattan, KS, USA*)
- 2:44 pm - 3:06 pm • **O100 - Overcoming Aspiration Failures in Sorghum Consumption in Africa**
 Paswel Marenya (*Sustainable Agrifood Systems, CIMMYT, Nairobi, Kenya*)
- 3:06 pm - 3:28 pm • **O101 - Potential contribution of sorghum to sustainable food systems in southern Africa: A case for Zimbabwe**
 Edmore Gasura (*The University of Zimbabwe, Harare, Zimbabwe*)

... / ...

2:00 pm - 3:30 pm	D - Genetics and genomics of grain quality -2-	<i>Rondelet Room - Level 2</i>
	Chair: Ndjido Kane	
	<i>Selected oral presentations</i>	
2:00 pm - 2:22 pm	<ul style="list-style-type: none"> • O102 - High-resolution spatiotemporal transcriptome landscape of sorghum seed development Yinping Jiao (<i>Institute of Genomics for Crop Abiotic Stress Tolerance, Texas Tech University, Lubbock, TX, USA</i>) 	
2:22 pm - 2:44 pm	<ul style="list-style-type: none"> • O103 - Digging into the transcriptome of a developing sorghum grain to find the culprits of protein content and low digestibility Nancy Terrier (<i>UMR AGAP Institut, INRAE, Montpellier, France</i>) 	
2:44 pm - 3:06 pm	<ul style="list-style-type: none"> • O104 - Exploring Natural and Induced Genetic Variation for Protein Digestibility in Sorghum Grain Elisabeth Diatta-Holgate (<i>Agronomy, Purdue University, West Lafayette, IN, United States</i>) 	
3:06 pm - 3:28 pm	<ul style="list-style-type: none"> • O105 - Transforming grain sorghum's yield potential and grain quality through trait-based ideotype breeding Krishna Jagadish SV (<i>Texas Tech University, Lubbock, Texas, USA</i>) 	

3:30 pm - 4:00 pm	Coffee break - Visit of exhibition - Posters	<i>Antigone 1, 2 & 3 areas - Level 2</i>
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PARALLEL SESSIONS 8

4:00 pm - 5:30 pm	A - Meet & Greet	<i>Pasteur Auditorium - Level 1</i>
	<ul style="list-style-type: none"> • Special session Tim Lust, Earl Romer, Dilys MacCarthy, Eva Wetzién 	
4:00 pm - 5:30 pm	B - Genetics and Genomics of biotic constraints -2-	<i>Sully 1 Room - Level 1</i>
	Chair: Elisabeth Diatta-Holgate	
	<i>Selected oral presentations</i>	
4:00 pm - 4:22 pm	<ul style="list-style-type: none"> • O106 - Does ecotypic variation in <i>Striga hermonthica</i> alter efficacy of LOW GERMINATION STIMULANT 1-based resistance in sorghum? Joel Masanga (<i>Lasky Lab, Department of Biology, The Pennsylvania State University, University Park, PA, USA</i>) 	
4:22 pm - 4:44 pm	<ul style="list-style-type: none"> • O107 - Count the cost: Trade-offs associated with LOW GERMINATION STIMULANT 1 resistance in <i>Sorghum bicolor</i> Chloee McLaughlin (<i>Intercollege Graduate Degree Program in Plant Biology, Pennsylvania State University, University Park, PA, USA</i>) 	
4:44 pm - 5:06 pm	<ul style="list-style-type: none"> • O108 - The sorghum mutant LOW GERMINATION STIMULANT 1 (<i>lgs1</i>) at the nexus of food security in Africa Sylvia Mutinda (<i>Institute for Basic Sciences, Technology and Innovation, Pan African University, Nairobi, Jkuat, Kenya</i>) 	
4:00 pm - 5:30 pm	C - Sorghum Branch - Organization / Multi-actor organization -2-	<i>Barthez Room - Level 2</i>
	Chair: Khady Nani Drame	
	<i>Selected oral presentations</i>	
4:00 pm - 4:22 pm	<ul style="list-style-type: none"> • O109 - Sorghum in Senegal: overview of work on pathology in the past five years Mame Penda Sarr Diawara (<i>Laboratory of plant pathology, ISRA, Bambey, Senegal</i>) 	
4:22 pm - 4:44 pm	<ul style="list-style-type: none"> • O110 - Designing an e-platform for promoting sorghum value chain networking arrangements and countering climate change induced food insecurity Tafadzwa Hungwe (<i>Department of Agricultural Business Development and Economics, The University of Zimbabwe, Harare, Zimbabwe</i>) 	

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- 4:44 pm - 5:06 pm • **O111 - Diagnostics on sorghum value chain challenges, market opportunities, and potential solutions for Ethiopia**
Tsebaot Kassa Gebremariam (*Analytics, Ethiopian Agricultural Transformation Institute, Addis Ababa, Ethiopia*)
- 5:06 pm - 5:28 pm • **O112 - Lessons from the impacts of a sorghum participatory breeding program addressing the needs of resource poor farmers in marginal areas of Nicaragua**
Gilles Trouche (*AGAP Institute, Cirad, Montpellier, France*)
-
- 4:00 pm - 5:30 pm** **D - Genetics and genomics of grain quality -3-** *Rondelet Room - Level 2*
Chair: David Pot
Selected oral presentations
- 4:00 pm - 4:22 pm • **O113 - High protein sorghums for improved health and productivity for smallholder communities**
Tesfaye Tesso (*Agronomy, Kansas state University, Manhattan, KS, USA*)
- 4:22 pm - 4:44 pm • **O114 - Digestibility, biochemical changes and Kafirin polymerization analysis during sorghum grain development**
Hamza Mameri (*UMR 1208 IATE, Univ. Montpellier, INRAE, Institut-Agro Montpellier, Montpellier, France*)
- 4:44 pm - 5:06 pm • **O115 - Evaluation of genotype and growing season impacts on the synthesis of phenolic compounds during sorghum (*Sorghum bicolor* (L.) Moench) grain development**
Carolina D'Almeida (*Laboratory of Bioactives, Food and Nutrition Graduate Program - UNIRIO, Rio de Janeiro, Brazil*)
- 5:06 pm - 5:28 pm • **O116 - Genetic enhancement to improve productivity, resilience and nutrition of sorghum in Sub-Saharan Africa**
MacDonald Jumbo (*Accelerated Crop Improvement, International Crops Research Institute for the Semi-Arid Tropics, Bamako, Mali*)
-
- 7:30 pm - 10:30 pm** **Conference dinner** *Domaine des Grands Chais, Mauguio*
- 6:55 pm - 7:15 pm • Bus departure (Level 0, Le Corum)
- 7:30 pm - 10:30 pm • Conference dinner

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THURSDAY 8 JUNE

8:30 am - 9:00 am

Registration

Antigone 1, 2 & 3 areas - Level 2

PLENARY SESSION

9:00 am - 10:30 am

Plenary 4

Pasteur Auditorium - Level 1

Chair: Ndjido Kane

9:00 am - 9:42 am

- **The Potential Hidden Within Sorghum Diversity Populations**
James Schnable (*University of Nebraska, Lincoln, NE, United States*)

9:42 am - 10:24 am

- **Resilience and Sustainability of Sorghum productivity in the face of Climate Change: Case of West Africa**
Dilys S. MacCarthy (*University of Ghana, Accra, Ghana*)



10:30 am - 11:00 am

Coffee break - Visit of exhibition - Posters

Antigone 1, 2 & 3 areas - Level 2

PARALLEL SESSIONS 9

11:00 am - 12:30 pm

A - Genetics and genomics of adaptation -5-

Pasteur Auditorium - Level 1

Chair: Jurandir Viera de Magalhães

Selected oral presentations

11:00 am - 11:22 am

- **O117 - The genetic control and consequences of heat induced partial fertility in CMS in sorghum**
David Jordan (*Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Warwick, QLD, Australia*)

11:22 am - 11:44 am

- **O118 - Integrating molecular genetics and precision phenotyping to elucidate gene function contributing to sorghum drought resilience**
Andrea Eveland (*Donald Danforth Plant Science Center, St. Louis, MO, USA*)

11:44 am - 12:06 pm

- **O119 - Identification of molecular basis of drought adaptation strategies in Sorghum bicolor**
S M Abdul-Awal (*Crop Adaptation Laboratory, Colorado State University, Fort Collins, Colorado, USA*)

12:06 pm - 12:28 pm

- **O120 - A new insight into proteomic responses of sorghum to combined drought and heat stress**
Ali Elnaeim Elbasheir Ali (*Department of Biotechnology, University of the Western Cape, Bellville, South Africa*)

11:00 am - 12:30 pm

B - Agroecological intensification -3-

Sully 1 Room - Level 1

Chair: Mame Penda Sarr Diawara

Selected oral presentations

11:00 am - 11:22 am

- **O121 - Advanta Sorghum Carbon Project in Argentina**
Tomas Sundblad (*Advanta Seeds, Benavidez, Buenos Aires, Argentina*)

11:22 am - 11:44 am

- **O122 - Micro dose soil ammendments effect on soil properties and performance of sorghum on legume-sorghum intercrop on smallholder farms vertisols in Homa Bay County, Kenya**
Peter Oloo Kisinyo (*School of Science, Agriculture and Environmental Studies, Rongo University, Rongo, Kenya*)

11:44 am - 12:06 pm

- **O123 - Assessment of Agroecological Diversification in Farming Systems among Smallholder Sorghum Farmers in Semi-Arid Eastern Kenya**
Carolyne Khalayi (*Kenya Agricultural and Livestock Organization, Rongo, Kenya*)

12:06 pm - 12:28 pm

- **O124 - Sorghum cultivation to reduce nitrogen loads into the environment by Biological Nitrification Inhibition (BNI) and enhance human nutrition**
Papa Saliou Sarr (*Crop Livestock and Environment, JIRCAS, Tsukuba, Ibaraki, Japan*)

... /...

11:00 am - 12:30 pm **C - Genetics and genomics of biotic constraints -3-** *Barthez Room - Level 2*

Chair: Ousmane Seyni Diakite

Selected oral presentations

- 11:00 am - 11:22 am • **O125 - Identification of sorghum aphid resistance loci and other related traits using cornerstone genomic resources**
Somashekhhar Punnuri (*Agricultural Research, Fort Valley State University, Fort Valley, GA, USA*)
- 11:22 am - 11:44 am • **O126 - Integrated analysis of sorghum transcriptome and metabolome provides new insights into the genetic mechanisms of host plant resistance to aphids**
Yinghua Huang (*USDA-ARS, Stillwater, OK, USA*)
- 11:44 am - 12:06 pm • **O127 - Molecular characterization of the mode of action of three anthracnose resistance genes in Sorghum bicolor**
Wilfred Vermerris (*Department of Microbiology & Cell Science, University of Florida, Gainesville, FL, USA*)
- 12:06 pm - 12:28 pm • **O128 - Exploiting Genetic Diversity to Achieve Sustainable Sorghum Anthracnose Disease Management**
Hugo Cuevas (*Tropical Agriculture Research Station, USDA-ARS, Mayaguez, Puerto Rico, Puerto Rico*)

11:00 am - 12:30 pm **D - Developing new products for human consumption -3-** *Rondelet Room - Level 2*

Chair: Reine Barbar

Selected oral presentations

- 11:00 am - 11:22 am • **O129 - Valorisation of natural bio-colorants from dye sorghum**
Polycarpe Kayodé (*Laboratory of Valorization and Quality Management of Food Bioingredients/FSA/UAC, University of Abomey-Calavi, Abomey-Calavi, Benin*)
- 11:22 am - 11:44 am • **O130 - Rural incubation of women millet and sorghum processors in Niger creates businesses with potential to improve nutrition**
Bruce Hamaker (*Food Science, Purdue University, West Lafayette, IN, USA*)
- 11:44 am - 12:06 pm • **O131 - Successful commercial demonstration of production of high value added food products from sorghum leading to development of new market and categories by Indian startup**
Shantanu Patil (*Sales and marketing, Meloop Foods Private Limited, Barshi, Maharashtra, India*)
- 12:06 pm - 12:28 pm • **O132 - Recent Advances in Sorghum Value Addition in Australia**
Rewati Raman Bhattarai (*Food Science, Curtin University, Perth, WA, Australia*)

12:30 pm - 2:00 pm **Lunch break - Visit of exhibition - Posters** *Antigone 1, 2 & 3 areas - Level 2*

PARALLEL SESSIONS 10

2:00 pm - 3:30 pm **A - Optimizing breeding programs to maximize genetic gains -3-** *Pasteur Auditorium - Level 1*

Chair: Cheikh Ndiaye

Selected oral presentations

- 2:00 pm - 2:22 pm • **O133 - It's MAGIC – challenges and opportunities in leveraging multi-parent population structure in sorghum improvement**
Melinda Yerka (*The University of Nevada, Reno, Reno, NV, USA*)
- 2:22 pm - 2:44 pm • **O134 - Screening of sorghum genotypes for resistance to striga**
Loyd Mbulwe (*Golden Valley Research Station, Zambia Agricultural Research Institution, Chisamba, Lusaka, Zambia*)
- 2:44 pm - 3:06 pm • **O135 - Genomic Prediction of Sweet Sorghum Agronomic Performance under Drought and Irrigated Environments in Haiti**
Jean-Rigaud Charles (*Chibas, Universite Quisqueya, Port au Prince, Haiti*)

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2:00 pm - 3:30 pm	B - Sorghum Idea Challenge	<i>Sully 1 Room - Level 1</i>
	<ul style="list-style-type: none"> • Special session Graeme Hamner, Baloua Nebie, Jurandir Vieira, Ephrem Habyarimana, Kirsten vom Brocken, Eva Weltzien, Timothy Dalton, Teferra Tadesse, Soren Knudsen, Kira Everhart-Valentin 	
2:00 pm - 3:30 pm	C - Genetics and genomics of biotic constraints -4-	<i>Barthez Room - Level 2</i>
	<p>Chair: Firew Mekib</p> <p><i>Selected oral presentations</i></p>	
2:00 pm - 2:22 pm	<ul style="list-style-type: none"> • 136 - The inner workings of the Australian Sorghum Midge Tested Scheme – how Midge Resistance ratings assigned and what they mean? Tracey Shatte (<i>Queensland Department of Agriculture & Fisheries, Warwick, Queensland, Australia</i>) 	
2:22 pm - 2:44 pm	<ul style="list-style-type: none"> • O137 - The role of phytochemicals in grain mold resistance in sorghum: opportunities and challenges Habte Nida (<i>Agronomy, Purdue University, West Lafayette, IN, USA</i>) 	
2:44 pm - 3:06 pm	<ul style="list-style-type: none"> • O138 - Genomes to genes to cultivars- a comprehensive approach towards adapted and fungal resistant sorghums Tesyfaye Mengiste (<i>Botany and plant pathology, Purdue University, West Lafayette, IN, USA</i>) 	
2:00 pm - 3:30 pm	D - Developing new products for human consumption -4-	<i>Rondelet Room - Level 2</i>
	<p>Chair: Paswel Marenya</p> <p><i>Selected oral presentations</i></p>	
2:00 pm - 2:22 pm	<ul style="list-style-type: none"> • O139 - Evaluating the performance of value-added Sorghum porridge in improving the diets of Pre-School Children in Migori County Evans Ouma (<i>Agronomy, Rongo University, Rongo, Kenya</i>) 	
2:44 pm - 3:06 pm	<ul style="list-style-type: none"> • O140 - Effect of malted sorghum-based porridge on the nutritional status of infants and young children diagnosed with moderate acute malnutrition in Uganda Richard Kajjura (<i>School of Public Health, Makerere University, Kampala, Uganda</i>) 	
3:30 pm - 4:00 pm	Coffee break - Visit of exhibition - Posters	<i>Antigone 1, 2 & 3 areas - Level 2</i>
PLENARY SESSION		
4:00 pm - 5:00 pm	Awards and Conference Closing	<i>Pasteur Auditorium - Level 1</i>
	<ul style="list-style-type: none"> • Special Announcement: Selected Host for the Next Global Sorghum Conference 	

FRIDAY 9 JUNE

SCIENTIFIC VISITS

9:20 am to 2:30 pm **Option 1 - Scientific facilities on Agropolis campus**

9:20 am **Bus departure from Hôtel Mercure Montpellier Centre Antigone**, bus parking avenue Jean Mermoz (Pre-registration and access badge required)

9:50 am **Visits**

- CAD: *Conserving and managing the genetic diversity of tropical and Mediterranean plants*
- AbioPhen: *Testing varieties adapted to future climate conditions*
- PHIV: *Histocytology and plant cell imaging platform*

1:00 pm **Lunch** at Restaurant du Cirad Lavalette (Access badge and voucher required)

2:30 pm **Return to Hôtel Mercure Montpellier Centre Antigone**

9:40 am to 2:30 pm **Option 2: Phenoarch phenotyping platform and the experimental vineyard on INRAE-Institut Agro La Gaillarde campus**

9:40 am **Bus departure from Hôtel Mercure Montpellier Centre Antigone**, bus parking avenue Jean Mermoz (Pre-registration and access badge required)

10:00 am **Visits**

- Phenoarch
- The Pierre Galet experimental vineyard

1:00 pm **Lunch** at Restaurant-self Campus La Gaillarde (Access badge and voucher required)

2:30 pm **Return to Hôtel Mercure Montpellier Centre Antigone**

SATELLITE MEETINGS

2:00 pm - 5:00 pm **Satellite meetings**



Sorghum in the 21st Century Global Sorghum Conference

Resiliency and Sustainability in the Face of Climate Change

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ABSTRACTS MONDAY 5 JUNE



In what climatic context does the evolution of agriculture take place?

Nathalie de Noblet-Ducoudré (nathalie.de-noblet@lscce.ipsl.fr)

Laboratoire des Sciences du Climat et de l'Environnement, CEA, Université Paris-Saclay, Gif-sur-Yvette, France

The IPCC has released, in march 2023, its 6th synthesis report¹. It shows that climate warming has reached 1.1°C during the decade 2011-2020 compared to pre-industrial times (1850-1900). The warming level is proportional to the cumulative anthropogenic emissions since 1850, and will only stop if we reach net zero emissions of this greenhouse gas (GHG). Projections show that 1.5°C of warming will likely be reached by 2030 and there are good chances that the warming level will exceed 2°C before the end of this century. Agriculture, forestry and other land uses have contributed 22% of the total GHG emissions in 2019, but also hold the potential to contribute significantly to mitigation.

Every increment of warming results in rapidly escalating hazards: more intense heatwaves and heavier precipitation everywhere on the globe, more frequent, intense and prolonged drought in many regions, and new compound events such as combined drought and heatwave. Those extremes are driving emerging risks for food production and accessibility.

Climate warming is also affecting production via the slower evolution of some climatic variables, e.g. mean temperature and evapotranspiration. Gradual warming lengthens the growing season for most natural ecosystems with earlier onset and later senescence. It displaces, geographically, some biotic stressors and sometimes desynchronizes the timing of phenological stages between pests/diseases and their hosts.

In this presentation I will give a quick overview of the present knowledge of climate change and its potential futures. I will also talk about observed and projected impacts on agriculture, at the global scale.

References:

1. <https://www.ipcc.ch/ar6-syr/>

The nexus between modelling and experimentation in understanding and predicting the ecophysiological basis of crop adaptation

Graeme Hammer (g.hammer@uq.edu.au)

Centre for Crop Science, QAAFI, University of Queensland, Brisbane, Qld, Australia

Functional plant traits and their interactions with the growing environment underpin crop adaptation. This has led to many simplistic views of the role of such traits in plant adaptive strategies. Surely more photosynthesis is better, and there must be an optimum level of tillering for a sorghum crop. But this is not the case, as the traits operate neither alone nor in isolation from their environment. While we might study trait variation and underpinning mechanisms in clever controlled experiments, the potential confounding effects of trait-trait and trait-environment dynamic interactions on plant growth and development over time remain obscure. There is a dynamic integration at play in generating the whole-organism phenotype. Hence, we face a paradox in predicting the consequences of trait variation across levels of biological organisation and time. This is the realm of predictive models: the central role of interactive dynamics is their hidden zeitgeist. Here I assert that harnessing the nexus of dynamic modelling and experimentation is necessary to better understand and predict crop adaptation. This has direct relevance to agronomy and plant breeding via the interpretation and prediction of G×M×E interactions. I will explore the potential value of this nexus in relation to enhanced understanding and prediction of the ecophysiological basis of crop adaptation in sorghum. Firstly, I will consider the interaction between high temperature and water limitation stresses on grain set and yield of sorghum. Secondly, I will consider the interactions among traits controlling tillering in sorghum. Both examples highlight the positive synergies from the nexus of modelling and experimentation.

Developing sorghum hybrids to meet market needs

[Laura Mayor](mailto:laura.mayor@corteva.com) (laura.mayor@corteva.com)

Corteva Agrisciences, Wamego, Kansas, United States

Over the last 60 years, the Corteva Sorghum research department has been providing elite commercial hybrids to growers. To this end, our research and commercial teams align objectives and breeding targets according to current markets and available resources. During the hybrid development process, the latest phenotyping and genotyping technologies are implemented to improve efficiency and productivity through the process. The implementation of these breeding technologies allows an increase in our genetic gain by developing superior parental lines and creating the best possible hybrid combinations among those parents. The result of this process is the delivery of hybrids with higher yield, improved resistance to diseases, better standability and enhanced drought tolerance.

An overview of sorghum research and development will be presented, as well as updates on collaborative projects currently underway.

The genomics of local adaptation in sorghum landraces

Aayudh Das¹ (azd6024@psu.edu), Geoffrey Morris², Jesse Lasky³

¹ Department of Biology, Pennsylvania State University, University Park, PA, United States ; ² Department of Soil and Crop Sciences, Colorado State University, Fort Collins, Colorado, United States ; ³ Department of Biology, Pennsylvania State University, University Park, PA, United States

Local adaptation is a fundamental source for the vast diversity within species, but the functional genetic basis still needs to be better resolved. As associations between SNPs and the environment of origin in sorghum landraces reflect local adaptation to some degree, we tested hypotheses about the functional genetic basis of local adaptation and its ability to predict phenotypic variation for adaptive traits. We performed a genome-wide scan characterizing 382 georeferenced landraces at 7,750,426 SNPs and quantifying allelic associations with *Striga* habitat suitability (HS), drought related bioclimatic variables and extractable soil aluminum. Finally, we evaluated whether these local adaptations are more likely to be: amino acid changing, located in putative promoter, located in open chromatin, potential gene loss of function mutations. Significant eGWAS candidates were further investigated for the possible signature of positive and/or divergent selection. Genetic variation is a prerequisite to evolutionary change and understanding what kinds of mutations are involved in local adaptation is essential to understand various adaptive traits vital for *Striga* and drought resistance in sorghum in Sub-Saharan Africa and South Asia.

Integration of sorghum genetics, human genetics, and environmental condition demystified tannin domestication

Xianran Li (xianran.li@usda.gov)

USDA-ARS, Pullman, WA, United States

Among five major cereal crops, only sorghum has half of cultivars with condensed tannins (potent bitter taste inducers) in grains. This counterintuition presents an evolutionary mystery. With a serendipity observation of sparrows decimated a sorghum field, we developed a coevolutionary model including sorghum, human, and birds to explain the mystery.

We uncovered that condensed tannins deterred sparrows from damage sorghum grains (birds don't like bitter taste) and identified two interacting genes (*Tannin1* and *Tannin2*) controlling for tannin presence. We found tannin sorghum cultivars predominantly grow in East & South Africa where the pressure from red-billed quelea (the world most abundant wild bird species) is severe, while non-tannin cultivars mainly grow in West Africa with mild bird pressure. This parallel distribution suggested that smallholders in East & South Africa selected tannins to fight against the severe herbivore threats. However, how African smallholders can take "bad taste" tannin sorghum as a staple food needed to be reconciled. As the bad taste is induced by bitter taster receptors (TAS2Rs), mutations in TAS2Rs may lead varied sensitivity for condensed tannins. We uncovered a parallel geographic distribution of a non-synonymous SNP in TAS2R5 to the tannin sorghum distribution. The ancestral tolerant allele is predominantly observed in East & South Africa, while the sensitive allele is observed mainly from West Africa.

Integrating domesticator (TAS2R alleles), domesticate (Tan1 and Tan2 alleles), and environment (bird pressure) together depicted harmonic interactions in African agroecosystems. In East & South Africa, smallholders (perceiving less bitterness from tannins because of tolerant TAS2R5 allele) selected tannin to fight against the pest bird; in West Africa with mild threats from birds, smallholders (carrying sensitive TAS2R5) selected non-tannin sorghum for better food. The matching sorghum genetics and human genetics illustrated the importance of the systems thinking in combating environmental challenges and personalized diet.

References:

1. Yuyue Wu, Tingting Guo, Qi Mu, Jinyu Wang, Xin Li, Yun Wu, Bin Tian, Ming Li Wang, Guihua Bai, Ramasamy Perumal, Harold Trick, Scott Bean, Ismail Dweikat, Mitchell Tuinstra, Geoffrey Morris, Tesfaye Tesso, Jianming Yu, and Xianran Li. Allelochemicals targeted to balance competing selections in African agroecosystems. *Nature Plants*. 2019, 5: 1229-1236.

Understanding sorghum race level diversity and development of sorghum genomic resources by using deep learning-based variant calling approach

Abhishek Rathore^{1,2} (abhishek.rathore@cgiar.org), Pradeep Ruperao³, Nepolean Thirunavukkarasu⁴, Roma Rani Das⁵, Baloua Nebie⁶, Harish Gandhi⁷

¹ CIMMYT, Medak, Telangana, India ; ² Excellence in Breeding, International Maize and Wheat Improvement Center (CIMMYT), Hyderabad, Telangana, India ; ³ ICRISAT, Hyderabad, Telangana, India ; ⁴ ICAR-IIMR, Hyderabad, Telangana, India ; ⁵ International Maize and Wheat Improvement Center (CIMMYT), Hyderabad, Telangana, India ; ⁶ International Maize and Wheat Improvement Center (CIMMYT), Dakar, Senegal ; ⁷ International Maize and Wheat Improvement Center (CIMMYT), Nairobi, India

Understanding sorghum race level diversity and development of sorghum genomic resources by using deep learning-based variant calling approach

Evolutionary divergence in sorghum race populations led to significant genetic and morphological variation. This study presents a k-mer-based sorghum race sequence comparison to discover the conserved k-mers of several accessions from sorghum. We further identified race-specific genetic signatures and the gene variability in 10,321 genes (PAVs). A deep learning-based variant calling methodology was used in a set of genotypic data derived from a diverse panel of 272 sorghum accessions with an objective to understand sorghum race structure, its diversity and domestication process. This analysis resulted in 1.7 million very high-quality genome-wide SNPs.

We further identified selective positive and negative signature regions through a deep genome-wide scan with different statistical methods including iHS and XP-EHH. This work identified a total of 2,370 genes associated with selection signatures which also included 179 selective sweep regions. These genes were randomly distributed over ten chromosomes.

Co-localization of these regions undergoing selective pressure with previously reported QTLs and genes revealed that the signatures of selection could be related to the domestication of important agronomic traits such as biomass and plant height.

This study and identified k-mer signatures will be extremely useful in future plant breeding programs aiming identifying the sorghum race and for trait and SNP markers.

A brief history of stay-green in sorghum: Has it made a difference?

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Stay-green in sorghum is largely an emergent consequence of constitutive physiological processes initiated during vegetative growth. In that sense, it is not a fundamental trait, but rather a consequence of the positive balance between water supply and demand, resulting in the retention of more green leaves and hence active photosynthesis during grain filling, ultimately leading to higher grain yield under end-of-season drought. We will present a brief history on the development of understanding around stay-green, beginning with its early selection in sorghum breeding programs more than 40 years ago in the US and Australia. A burst of activity around the turn of the century resulted in multiple groups worldwide mapping stay-green QTL in a range of genetic backgrounds. Serious physiological dissection of the trait commenced in the mid-90's and has continued to this day, first unravelling how nitrogen dynamics affect stay-green, followed by the development of a water supply/demand framework explaining stay-green at the whole-plant and crop levels. To some extent, our physiological understanding was driven by crop modelling, with a desire to understand how the phenotype emerged. Finding the key genes regulating stay-green eluded us for some time, with recent studies pointing to the *PIN* family of genes as potential candidates controlling tillering and leaf size (i.e. water demand) and root architecture (i.e. water supply). Many previous studies have also indicated enhanced lodging resistance in stay-green types, with more studies now underway in Australia to better understand this component. In particular, but not limited to, scientists in Africa, India, US and Australia have selected for stay-green in their sorghum breeding programs, generally noting a positive correlation between stay-green and grain yield during post-anthesis drought. Has stay-green made a difference? Yes – but the story is not finished yet.

Systems agronomy pathways for crop adaptation to heat stress and terminal droughts

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Sorghum is usually exposed to heat and terminal drought stresses during critical stages affecting yield and yield quality. The intensity and frequency of these stresses can only be expected to increase as our climate shifts. Systems agronomy can offer immediate solutions for crop adaptation, and as well as important insights into effective breeding pathways. Here we combined empirical research, crop modelling and data analytics to explore extreme sowing windows that minimise the likelihood of overlaps between abiotic stress events and sensitive crop stages, and answer How cold is too cold to sow sorghum? What are the implications of extreme sowing windows on the crop and cropping system? Empirical research included three years of multi-environment (n=37) genotype (G) by management (M) on-farm research, conducted across eastern Australia between 2018 and 2021. Homogeneous treatments across all trials included six commercial hybrids, sown at four plant populations, and three sowing times i.e., late winter, spring and summer. Data analytics involved the use of (a) Linear mixed models (ASReml-R) to identify main effects and interactions and to derive predicted means (BLUEs); (b) BLUEs were used to explore crop-ecophysiological relationships and validate crop models; (c) tested crop models were used to extrapolate results across sites and seasons, derive measures of downside risk, calculate environmental co-variates, and assess impacts at the cropping system level; and finally, (d) data mining techniques were used to untangle complex interactions and derive simple rules of thumbs for farmers. The inclusion of early sown sorghum in the crop sequence seems simple, though its implementation and consequences are not. Here we propose that in the race to increase crop adaptation to heat stresses plant breeding efforts should seriously consider cold tolerance traits during crop germination, emergence, and early vegetative stages as targets so that sorghum sowing windows could be significantly advanced.

Adapting to heat stresses by sowing summer grain crops in late-winter: Sorghum root growth, water use, and yield

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Water stress and extreme heat at flowering are common stresses limiting yields of summer crops globally. Here we explore the idea that crop adaptation to these stresses could be increased by sowing summer crops in late-winter, into cold soils, to avoid the overlap with critical flowering stage. However, little is known about the impacts of cold soils on crop root growth and function (i.e., water use), and final grain yield. Here we present results from two seasons of on-farm sorghum experimentation conducted at Nangwee, Queensland, Australia. Each trial consisted of a factorial combination of three times of sowing (TOS, late-winter, spring and summer), two levels of irrigation, four plant populations, and six genotypes. Crop roots were sampled at the flag leaf stage for each TOS. Crop water use was monitored using time-lapse electromagnetic induction surveys. Results showed that in the first season which was dry and had a large contrasting temperature between TOS, cold soils in the early sowing dates, lead to smaller crops with a smaller rooting systems and root-to-shoot ratios, and roots having a larger average root diameter. In contrast, in the second season which was much wetter and warmer, the effect of TOS on both shoot and root traits was insignificant. In both seasons, early sowing decreased the risk of extreme heat at flowering and increased yields by transferring water use from vegetative to reproductive stages. The larger yield of early sown sorghum was associated to larger grain numbers, particularly in tillers. Early sown crops also had larger values of water use efficiency, and left more water in the soil profile at maturity, particularly in irrigated conditions and small plant populations. We conclude that early sown sorghum is another option to increase crop adaptation to hotter and dryer environments.

Wide row configurations in sorghum reduce crop water use efficiency and yield in marginal rainfall environments in Australia

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In semi-arid environments of north-western New South Wales (NW NSW) and southwestern Queensland, Australia, farmers can vary plant density and row configuration to improve sorghum grain yields and mitigate climatic risks. Wide row configurations and low plant populations have been adopted to improve yield reliability by conserving soil water for the crop reproductive stages. However, the impact of these agronomic decisions on the water use efficiency of the sorghum and following crops are not considered. This paper uses on-farm experimentation to answer how plant density and row configuration affect yield, quality and water use efficiency at the crop and crop rotation levels. Four rainfed grain sorghum experiments were conducted at Gurley, NW NSW between 2010 - 2016. Experiments included four row configurations: solid (100 cm), super wide (150 cm), single skip and double skip, four target plant densities between 1.5 and 7.0 plants/m² and three sorghum hybrids.

Seasonal conditions were variable; spring planted experiments started with close to full soil water profiles and had average rainfall. Summer planted experiments started with a half full profile and had contrasting rainfall.

In general, grain yields declined as the row configuration widened. Plant densities equal to or greater than 3.0 plants/m² resulted in higher grain yields. Plant densities > 5.0 plants/m² gave no yield benefit.

Wide row configurations resulted in higher residual plant available water after harvest, particularly at deeper soil depths. In dry seasons, more water was retained in the mid row area, compared to under the crop row. In wet seasons, no difference was detected regardless of the sampling position. Generally, water use efficiency declined as row configuration widened.

We conclude that wide row configurations and low plant densities reduce sorghum grain yields and water use efficiency, in environments where water is the most limiting factor to crop yield.

Effect of soil treatment with Methionine on *Striga* infection and sorghum growth under field conditions in Ethiopia

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Decomposition of methionine in soil will result in the production of the sulfur-volatiles such as dimethyl disulfide and dimethyl trisulfide which inhibit *Striga* seed germination or even kill *Striga* seeds. Thus, the effect of DL-Methionine application on *Striga* infection, sorghum growth and yield was conducted at two locations on farmers' fields at Bisidimo and Qilee in the eastern Ethiopia. The objective of the study was to determine whether or not treating naturally *Striga* infested soil with and without methionine application to the soil before planting sorghum can affect *Striga* germination and attachment, emergence, sorghum biomass, yield components and grain yield. There were two treatments in six replication per field site. The amount of methionine applied to the soil was 0.5 g/kg soil (= 500kg/ha), assuming a soil density of 1 g/cm³ and a penetration-depth of 10 cm. The dissolved methionine was sprayed over the plot using a sprayer. After application, hand digging with forks to a depth of 10-15 cm was made in order to mix and obtain uniform distribution in the soil. Sorghum was planted about a month after application of methionine. The result showed statistically significant difference between the treated and untreated plots and this difference was vividly observed under field conditions on sorghum growth and subterranean *Striga* count at both sites. However, the drought has affected sorghum growth particularly after flowering of sorghum that hampered panicle exertion and grain filling at both sites. Thus, it can be concluded that the application of methionine has significantly reduced the number of *Striga* that germinate and attach to the sorghum roots as compared to the methionine untreated plots.

Flowering response to photoperiod combines the effect of the daylength with the effects of the daily changes in sunrise and sunset times and of temperature acclimation

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Sorghum bicolor was domesticated in African savannahs where it co-evolved with its pests and diseases. Consequently, in each place flowering date occurring at the mean date of the end of the rainy season when the global pressure of the pathogens is lower and available soil water reserve ensures grain filling was naturally selected. This synchronism appeared crucial for crop success and its determinism has been extensively studied.

Daylength determines flowering dates of photoperiod-sensitive plants. However, questions remain regarding flowering dates in the natural environment, such as the synchronous flowering of genotypes sown simultaneously at highly contrasting latitudes. The daily change in sunrise and sunset times is the cue for the synchronization of the flowering time of trees and the mating season of birds at the equator. Sunrise and sunset also synchronize the cell circadian clock, which is involved in the regulation of flowering. The photoperiodism model was consequently updated with knowledge acquired since its conception.

A large dataset of flowering records was gathered, including four 2-year series of monthly sowings of 28 sorghum varieties in Mali, a few simultaneous sowings in Mali and France, and data from breeding programs implemented in France, Nicaragua and Colombia.

A unique additive linear model combining daylength and daily changes in sunrise and sunset hours was accurately fitted for any type of response in the duration from sowing to panicle initiation to the sowing date without any temperature input. Simultaneous with the phyllochron, the duration to panicle initiation of field crops acclimated to the mean temperature at seedling emergence within the usual range of mean cropping temperatures. Once calibrated, the model accurately predicted the duration to panicle initiation of a broad set of varieties from the equatorial to the temperate zone.

Dissecting the genetic value and genetic variability for the limited transpiration trait in sorghum: from simulations to field phenomics

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Breeding sorghum for drought adaptation is pivotal to secure crop production in drought-prone regions. Limited transpiration (LT) is a putative trait that restricts plant water demand at a high vapor pressure deficit, saving water for use in critical periods later in the growing season. However, including LT in a breeding program relies on i) documenting its benefits in the sorghum belt of the United States and ii) identifying the trait in sorghum germplasm in field trials. First, we evaluated the plausibility of the LT trait in increasing grain yield in representative sites in Kansas, Texas, and Colorado. We used a process-based crop model, APSIM, which simulates interactions of genotype, environment, and management (G × E × M). *In silico* simulations demonstrated that the LT trait can increase grain yield by more than 5% in drought-prone environments predominant in western regions. Second, we tested that genetic variation for LT exists in sorghum germplasm, and canopy temperature (TC) is a surrogate method to discriminate this trait. In these experiments, we phenotyped transpiration via stomatal conductance (gs), canopy temperature (TC) from fixed IRT sensors (TCirt), and thermal imagery (TCimg) in 11 sorghum genotypes. Low gs and high TC confirmed that genotypes BTx2752 and SC979 carry the LT trait. Otherwise, high gs and low TC revealed that genotype DKS54-00 has the non-LT trait. The negative correlation between gs and TC, although non-significant, suggested TC as a potential approach to determine differences in transpiration. Nevertheless, dissecting LT via TCimg should consider leaf area and stand count as covariate variables. Overall, our findings state that breeding for LT would increase sorghum yield in drought-prone areas. Furthermore, variability in transpiration VPD response offers the opportunity to develop water-efficient hybrids for the sorghum belt of the United States.

Contrasts in leaf photosynthetic low-light response across temperatures generate differences in crop-scale radiation use efficiency

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A key crop adaptation trait is the radiation use efficiency, which quantifies the amount of biomass generated by the crop per unit of (total) solar energy intercepted on a per ground area basis (RUE, g above-ground biomass/MJ). Between C₄ crop species, maize has the potential to produce higher amounts of biomass and yield than grain sorghum in favourable moisture environments. This is attributed to a higher RUE in maize. Deepening the physiological basis of the contrasting maize and sorghum RUE would help to evaluate aspects of photosynthetic biology that are important for crop-scale RUE and yield improvement. Informed by a cross-scale trait network model of canopy photosynthesis, we designed a new photosynthetic response measurement procedure and generated cohesive sets of photosynthetic responses to combinations of CO₂, light, and temperature in maize and sorghum plants. A novel Bayesian model fitting methodology, incorporating a C₄ photosynthesis model, was developed and used for a simultaneous quantification of the photosynthetic responses. Differences in the response were quantified, revealing significant differences between sorghum and maize in: the Maximum Rubisco activity and the maximum PEP carboxylase activity at several leaf temperatures; and the fraction of photosynthetically active irradiance absorbed by PSII, which underpins the leaf-scale photosynthetic low-light response, across a broad range of leaf temperatures. Crop-scale RUE analysis using the cross-scale canopy photosynthesis model with fitted photosynthetic parameters predicts the importance of the photosynthetic low-light response and its temperature response for enhancing crop-scale RUE.

Plant response to a late heat stress can be modified by an earlier one: a case study on sorghum grain production

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Climate change is now a reality and observable effects include higher temperatures with successive periods of heat waves. These events have consequences in plant development and grain production. Sorghum is an African native cereal known for its robustness. However, in the context of climate change, sorghum production can be affected by heat stresses during reproductive stage. Even if the effects of single heat stress were already described as having an impact on sorghum grain production, the effects of recurrent heat waves were not studied until now.

A preliminary study was performed in 2021 with two contrasted genotypes grown under four heat stress scenarios in controlled conditions, combining single and recurrent heat waves. The aim of this study was to analyze i.) the effects of these stresses on plant production ii.) the eventual impact of an early heat stress on a later one. In addition to yield components analyses, morphological, spectral and biochemical measurements were performed on sorghum panicles.

Yield components, morphological traits and grain quality were differently affected depending on the stress scenario. Furthermore, our results show that an early heat stress can attenuate or amplify the response of a later one, depending on the considered variable, the genotype but also the position of the first stress compared to the second one.

New experiments are currently investigated in RICOCHETS project (2023-2026). Our original approach combines dynamics multiscale analyses with samplings at key times (early stress/recovery periods/late stress). These results will contribute to broaden our knowledge on the response of plants to recurrent heat waves, which can be used in future plant breeding programs.

Nutritional characterization and technological aptitude of twenty-nine ICRISAT Sorghum varieties in Burkina Faso

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Sorghum is the main source of nutrients for millions of people in Sub-Saharan Africa. Lack of information regarding the nutritional quality and functional properties of new sorghum varieties is a limitation to their adoption in rural diets. The present study aimed to determine the nutritional and functional properties of 29 sorghum varieties from ICRISAT. The varieties were characterized for Thousand Grain Weight (TGW), length and width of the grain, and flour colour. Standard methods according to the Association of Official Agricultural Chemists (AOAC) were used for the determination of macro- and micronutrient contents. Functional properties like solubility index, water and oil absorption capacity, and swelling rate were also determined. High variability was observed for TGW, with an average of $25.15 \text{ g} \pm 5 \text{ g}$. Seed size varied less, with an average length of $4.40 \pm 0.30 \text{ mm}$. The energy values of the sorghum varieties varied from 409 to 422 kcal/100 g. Jacumbè, Darrelken, Pitikala and Jiguikala varieties had protein contents above 15 g/100 g, with high solubility and swelling rates. These varieties are suitable for pastry and bread making. Soumba, Fambé, Sangatigui, Bogodjè, Grinkan and Tieblé varieties were characterised by high lipid contents of over 4 g/100 g with a high-water absorption capacity. They are suitable for the production of couscous. The iron and zinc contents remained low for all tested varieties, with averages of $5.71 \pm 0.9 \text{ mg/100 g}$ and $2.36 \pm 0.60 \text{ mg/100 g}$, respectively. The results are of great interest to breeders, processors and all those involved in the fight against malnutrition in sub-Saharan Africa. The McKnight Foundation-funded "Child nutrition" project uses the gained information to develop nutritious flours, for use in health centres targeting undernourished children. In these centres, the gained information is also shared with mothers seeking to reduce malnutrition levels in their children.

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Innovative food-to-food fortified sorghum flours to improve nutrition in rural West Africa

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Sorghum is the major cereal component in the diets of millions of people in West Africa where malnutrition and stunting in children continues to be a problem. There has been relatively little innovation in strategies that promote formulation and consumption of fortified sorghum foods in rural areas of West Africa. We hypothesize that a consumer-focused fortification strategy including macro- (protein, lipid) and micronutrients (provitamin A, iron and zinc) by selection of grain varieties combined with food-to-food (FtFF) fortification strategies that leverage local knowledge and sensory preferences would lead to nutrient-dense flour products preferred by children and be a sustainable market-driven approach to reduce malnutrition in West Africa. Furthermore, such products could serve as viable alternatives to imported fortified porridges formulas provided to children by local health centers. Formulations were done with five sorghum varieties with FtFF ingredients (cowpea, peanut, baobab, moringa, pumpkin, and/or carrot) that targeted energy and micronutrient (mineral and vitamin A) requirements of at-risk children (2-5 years). Formulations were optimized for flavor and hedonic preferences and assessed by consumer sensory testing of fortified porridges samples. Physicochemical characteristics were assessed by standard methods (AOAC). Formulations of thin porridges were consumer tested by mothers of young children for acceptability in Niamey at two government health centers and at four rural sites in Niger. In both urban and rural studies, FtFF sorghum porridges were compared to a local control (fortified sorghum porridge prepared at health centers). In Niamey and rural sites, overall acceptability scores showed higher acceptability of the FtFF sorghum porridge formulas compared to control porridges (Niamey: n=118, P<0.05; rural: n=251, P<0.05). These results suggest that FtFF sorghum products produced with improved varieties, based on local taste preferences, could be more widely adopted than traditional food aid products for local nutrition feeding programs. Supported by SMIL and McKnight Foundation programs.

Developing and marketing sorghum baked products: Acceptance of novel biscuits as influenced by sensory characteristics and information

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Sorghum is a traditional staple food in Lesotho. However, the consumption of sorghum products in Lesotho declines every year. The decrease is due to labour intensive and time-consuming processes, products perceived not tasty, outdated and associated with poverty. As a result, sorghum is currently underutilised. Sorghum biscuits are convenient and have health and nutritional advantages because they are gluten free and suitable for people with celiac disease. The aim of this study was to examine the influence of processing method on quality characteristics and acceptability of sorghum biscuits. Recipes for standardizing sorghum biscuits were developed from the basic steps of recipe verification, product evaluation and quantity adjustments. Sensory profiles of biscuits were produced using the generic descriptive method (Einstein, 1991). Fifteen panellists (6 males and 9 females), carried out evaluation. Samples were placed in individual transparent polyethylene zip-lock type bag (100 x 110 mm) labelled with a 3-digit random code and presented in individually randomized orders to the panellists. Evaluation was performed in 2 sessions, 2 h each, on 2 different days. The texture was described as crunchy, compact and fibrous. For consumer test, a total of 216 people were used in the survey. The questionnaire was completed by 171 males and 45 females, age range = <=25 - <=55 years old, mean = 32.06 years old for the informed category and 35.04 for the uninformed category. The informed and uninformed participants rated the sensory properties of sorghum biscuits for appearance, aroma, taste, texture and overall acceptability using five-point hedonic scale where 1 represents “extremely dislike” and 5 “extremely like”. All means were compared using the least significant difference (LSD) test at $p \leq 0.05$. There is a great need to educate the public about value added sorghum products to stimulate the innovations of products using sorghum.

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Supplementary Feeding on Soy-fortified cereal porridge improves the Nutritional Status of Pre-school Children aged 4-5 Years

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Poor quality diet is the most immediate factor responsible for malnutrition and ill health among school going children in many developing countries, including Kenya. A study was carried out to evaluate effect of soybean (soy) fortified porridge on nutritional status of pre-school children at Igero Primary School, Busia County. Three flour blends were formulated from maize-soy, sorghum-soy, maize (45%)-sorghum (25%)-soy to achieve the overall cereal-to soy ratio of 70 to 30 for each blend. A control treatment containing 100% maize without soy was included since this is normally provided by the school. The four treatments were used to make porridge for supplemental feeding. A longitudinal survey with Complete Randomized Design was employed. 235 pre-school children were randomly divided into four groups and the four types of porridge randomly assigned to the groups. Pre-school children were fed for six months with approximately 350 ml of porridge daily. The results showed a significant ($p < 0.05$) reduction in prevalence of underweight and wasting among children fed on soybean fortified porridges by the end of intervention. The underweight prevalence in the group fed on maize only, maize-soy, sorghum-soy and maize-sorghum-soy fortified porridges reduced from 14.5% to 13.8%, to 4.4%, 5.3%, and 5.8% respectively. The prevalence of wasting at baseline among groups of children fed on maize-soy, sorghum-soy, sorghum-maize-soy porridge was 10.8%, 10.7% and 12.5%, and these reduced significantly ($p < 0.05$) to 1.8%, 3.6% and 5.4% respectively by the 6th month compared to a 10.7% to 10.4% reduction from the control group fed on 100% maize porridge at the end of feeding trial. In conclusion, soybean fortified porridges improved the nutritional status of the children and therefore it is recommended that maize-soybean or sorghum-soybean blends be used in preparing porridge for supplemental feeding in schools to enhance nutritional status of pre-school children.

Sorghum wild relatives: The forgotten treasure-trove for unlocking the hidden hunger crises in Sudan

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Hidden hunger and/or micronutrient malnutrition is a major problem in Sudan. Sorghum for Sudan is more than a crop, it is named «elaish» an Arabic word meaning «living» for its high use in human food. Sudanese people who live in rural areas with predominantly sorghum-based diets are progressively obtruded by micronutrient deficiencies. To support the achievement of the 2030 Sustainable Development Goal of ending all forms of malnutrition (Goal 2.2), there must be an urgent need for improving the nutritional quality of sorghum plants. However, the limited genetic diversity in domesticated sorghum warrants exploring the wider variation present in sorghum wild relatives. Therefore, the objective of this study is to dissect the genetic basis of variability governing micronutrients and soluble protein concentrations among sorghum wild relatives. To this end, 200 weedy and/or wild sorghum accessions were screened for grain phytate, total and bioavailable Fe and Zn, and soluble protein contents. Three released domesticated sorghum cultivars were included as checks. Results indicated that there were significant variations for all grain nutritional values measured. Across the genotypes, the phytic acid content ranged between 205.0 and 382.4 (mg/100 g) with an overall average of 234.4. The total iron and zinc contents varied between 3.9 to 8.5 (mg/100g) and between 0.5 to 24.8 (mg/10g), respectively. The bioavailable iron and zinc varied between 43 to 95% and between 45 to 56%, respectively. The accessions HSD15147 and HSD12778 possessed over-the-top total iron (8.6 mg/100 g) and zinc contents (5.0 mg/100 g). In addition, the accessions Adar Abusabiba and Mohakera-red2 were found to possess low phytic acid contents. It is clear evidence that Sudanese wild sorghums hold huge potential merits for sorghum biofortification. In conclusion, the identification of the loci controlling the accumulations of micronutrients, and low phytic acid contents through genome-wide association studies are underway.

Crop diversity and West African farmers: agroecological perspectives

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Crop biodiversity is key in agroecological approaches to ensure food security and nutrition. However, in West Africa (WA) as elsewhere, global changes impose sometimes drastic choices, and the diversity of practical solutions experimented by farmers to adapt to these changes remains unknown. The aim of this study is to examine crop biodiversity-based options experimented by farmers in different ecological contexts across four countries, Senegal, Burkina Faso, Mali, and Niger. What species are grown by farmers' households and why? Which seed sources support this choice? And more specifically, what role does sorghum play in this strategy, as one of the main crops grown in WA. A collaborative survey developed in partnership with five academic institutions and four farmers' organizations was deployed in 144 villages among 285 people, men and women of different generations, using a uniform spatial sampling strategy in order to also consider the diversity of ecological contexts, from North to South and from East to West, across the four countries. The spatial organization of crop diversity varies between countries. Within countries, crop diversity increases from North to South, but it also depends on the number of languages spoken in villages and on the presence of farmers' organizations. Seed supply also varies between and within countries, and according to the species considered. For sorghum, 75% of farmers use their own seeds in Burkina, but only 50% in Senegal. 60% of farmers use market seeds for peanut in Niger, but only 15% in Senegal. Farmers' practices also vary for maize and cowpea. When attention is paid to one crop, the diversity of farmers practices cannot be captured. There is not one, but many crop biodiversity-based options, which differ according to contexts. As they are based on farmers' experiences, they would represent a promising agroecological perspective

Investigations on pollen-mediated gene flow between grain sorghum (*Sorghum bicolor*) and johnsongrass (*Sorghum halepense*)

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Gene flow between sorghum and johnsongrass can have ecological and environmental consequences. Herbicide resistance and other agronomic traits are being deployed in sorghum and potential transfer of these traits into johnsongrass may be a concern. However, the nature and dynamics of hybridization between the two species are not well understood. At Texas A&M University, USA, a team of researchers has been investigating gene flow between the two species under the controlled greenhouse as well as field experiments. Gene flow has been studied with sorghum as the female as well as the male parent. The F1 and BC1F1 progeny arising from these crosses have been studied for ploidy status and adaptive traits. Results indicate that 2n gamete production (male and female gametes) in sorghum is a key driver for viable hybrid seed production, and the frequency of 2n gamete production varies greatly among sorghum genotypes. Further, the environment and pollen load have a significant influence on the rate of outcrossing. Findings inform that gene flow between the two species can be greatly mitigated by the appropriate selection of sorghum cultivars for deploying novel traits. The knowledge generated from these experiments is helpful for developing robust technology stewardship protocols.

Sorghum diversity for sustainable cropping systems in marginal environments in the deep south of Madagascar

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For many specific marginal environments or cropping systems variety needs are not considered by national or international public programs or private seed companies because of resources limitations for the former or insufficient market for the latter. Nevertheless, farmers and other stakeholders are in demand of a new diversity in order to adapt to climate change and, or to move towards more sustainable cropping systems. The Androy region, in the south of Madagascar experiences extremely seasonal irregularity and recurrent famines. Maize is the dominant cereal but crop failures under the current conditions are recurrent. According to farmers traditional sorghum varieties were too late maturing to adapt to the changing climate. In this context, the CTAS and GRET (a Malagasy and French NGO) introduced new sorghum varieties from India and Sahelian countries, for their in-situ evaluation in locally designed agroecological cropping systems. The association of these two types of innovations provided impressive results for farmers and a large-scale adoption of an early sorghum variety (IRAT 204 "RASTA"). In the framework of a new rural development project supported by the EU, Cirad, together with the national Agricultural Research Institute FOFIFA is supporting these NGOs with the aim to broaden sorghum varietal diversity.

The main goal is to evaluate with farmers diverse varieties and segregating progenies bringing improved agronomic and/or quality traits. On-farm participatory evaluations allowed to identify new selection criteria and preferences, such as traits to reduce bird damage, tillering capacity, sweet stem. Preferred new ideotypes, are ranging from early guinea to bold-grain durra types, adopted by farmers with some documented seed exchange with neighbors.

The Sorghum international community needs to share and demonstrate more experiences of cases where targeted breeding has been limited but where access to appropriate diversity could greatly improve livelihoods for farmers managing specific cropping systems and environmental conditions.

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3D Computer Vision for High-throughput Phenotyping

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Computer vision, as part of artificial intelligence, has made remarkable progress in various areas of research, particularly in the recognition and segmentation of objects and their properties. Although computer vision for 2D is state-of-the-art, research for 3D data, such as point clouds, is still at an early stage.

The impact of climate change has made it crucial to explore new ways of crop production, which include not only breeding but also identifying and recommending new cultivation methods. Automated and high-throughput monitoring of plant development over time can be a useful approach in this regard. Outdoor 3D scanning provides an effective way to observe crops. In addition to existing methods that compute traits over the entire scan, there is a need to develop algorithms that can detect individual plants and their parts in complex canopies using 3D computer vision.

ICRISAT (India) and CZU Prague (Czech Republic) are collaborating on research aimed at developing algorithms for preprocessing input data with the later usage of 3D object detection and segmentation for plant phenotyping. The outdoor sensing device, built on top of Phenospex PlantEye, captures the necessary data, which we then process in several steps to prepare for the use of the algorithms. These steps include removing unrelated points (ground and flowerpots), splitting individual experiments, and applying data modifications such as voxelization and smoothing.

The preparation of the dataset for training AI models using the 3D computer vision algorithms poses another challenge. In addition to manual labeling, we are developing algorithms for semi-automatic labeling, data augmentation, and possibly artificial data generation. The goal of the research is to propose an automated data preparation pipeline for phenotyping tasks for different crops. Automation will enable the processing of large amounts of data from experiments and enable predicting more specific traits addressed on individual plants.

Evaluating variation in stem strength in response to artificial drought stress amongst sorghum genotypes

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Grain sorghum is a major summer cereal crop grown under dry-land conditions in Australia. Increasing demand for high quality sorghum grain for animal feed domestically and for human consumption and alcohol production overseas continues to boost market growth. However, stalk lodging remains a major constraint to yield advancement in sorghum. Lodging is a consequence of an imbalance in post-anthesis carbon supply in response to drought stress. Screening for lodging is challenging as this requires consistent levels of drought stress to be implemented in the field. Innovative screening protocols are therefore required to investigate lodging resistance in the field. An experiment was devised to assess variation in structural components governing stem strength (a component of lodging resistance) by simulating artificial drought-induced carbon stress at the Hermitage Research Facility near Warwick. The experiment included seven commercial sorghum hybrids and four levels of carbon stress: control, full defoliation (all leaves removed), half defoliation (leaves removed from one side) and half head (top half of the panicle cut off). Results indicated that removing leaves and panicles to generate varying levels of drought stress effectively mimicked the plant's response to *in-situ* drought stress in the field. Furthermore, genotypic variation existed in the extent of remobilisation from the stem and stem diameter. Overall, thicker stems and lower levels of stem remobilisation resulted in stronger stems. Interestingly, there were variations in stem strength for a given level of remobilisation, indicating the role of components that determine stalk strength in sorghum. These results establish that this method can be successfully applied in the field to screen genotypes that may vary in their stalk strength and lodging resistance in sorghum.

Quantifying effects of high temperature stress on seed set of sorghum

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High temperatures can adversely affect seed set% in sorghum, but application in breeding programs requires quantitative insights into these high temperature responses in order to develop suitable phenotyping methods. The objectives of this work were to quantify (1) the duration of the critical period during which seed set% is affected by high temperature, (2) the response of seed set to cumulative temperature stress, and (3) the use of grain number per unit rachis mass as a substitute for seed set%. Sorghum plants were grown in glasshouses in Brisbane, Australia in the absence of high temperature stress, and then moved to high temperature conditions at a range of temperatures and for different durations. Results indicated that in addition to the period around anthesis that was identified in earlier research, there was also a critical period around the flag leaf stage, when the panicle is exposed to high temperatures inside the boot. Seed set% generally declined linearly with cumulative temperature stress above a threshold, with genotypic differences observed for the threshold temperature, the tolerance above the threshold, and seed set% in the absence of temperature stress. Grain number per unit rachis mass can be used as a surrogate for seed set%, although genotypic effects on the relationship between these two traits mean that such a surrogate would require both a control and temperature stress treatment. Results provide the scientific insights to develop phenotyping strategies for adaptation to high temperature stress.

Deep learning pipeline for phenotyping sorghum panicles

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Head (panicle) density is a major component of sorghum yield with much research interest in manipulating this trait through management and genetics. High-throughput phenotyping techniques that utilize deep learning-based object detection models using RGB images have been developed to automate the laborious process of counting panicles [1]. However, these methods do not provide a general protocol for training deep learning-based panicle detection models and there is no proposal for a standard pipeline that discusses an end-to-end solution, i.e. from collection of new data through to model deployment. A robust model is essential for accurate panicle detection, as the target datasets in natural environments may differ from the training data (commonly known as domain shift). In this study, we present a comprehensive pipeline that outlines data collection, training data preparation, model training, model validation, and model deployment for accurate panicle detection and mapping panicle distribution across a commercial field. We present two experiments in our study. In the first experiment, we provide insights into a scenario where a pre-trained model, trained on a publicly available dataset is not suitable for the target domain, and then guide the preparation of new training data and evaluating the model's performance. The second experiment discusses a scenario where pre-trained models are suitable for the new target domain, and we demonstrate how to derive accurate head density estimates from the model detection results. Furthermore, we combine prior knowledge of row-spacing with detection results to calculate head density variation within individual rows. Our pipeline provides a high-resolution head density map that can aid in identifying agronomic variability within a field [2]. This work is progressing toward development of methods to combine proximal imaging and 3D models, generated from LiDAR scanners and mobile photogrammetry solutions, to estimate grain count per panicle.

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Effect of retraining on genomic prediction accuracy in sorghum

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The sorghum improvement program at Chibas started in 2012 with a recurrent selection strategy. Nowadays, genomic selection is mainly used for breeding sorghum varieties resistant to Sugarcane aphid (*melanaphis sacchari*). For certain conditions, simulation studies have shown that using new genotypes in the training population would improve the accuracy of genomic prediction. Re-training the training population in a genomic selection breeding program after a few cycles of selection could be necessary. The Chibas sorghum breeding program using genomic selection is already in its fourth cycle of genomic selection (GS4). The new training population is composed of genotypes from the base population and lines from four cycles of genomic selection (GS1, GS2, GS3 and GS4). Phenotyping data were generated at two different sites for two years (2021 and 2022). The hypotheses that will be tested with the data are; 1) Does re-training the training set population improve the predictive ability of the model for genomic prediction, 2) Adding GS-derived lines from recent selection cycles improve the accuracy of the prediction model? The results obtained from this work will make it possible to evaluate the genomic selection strategy used by Chibas for sorghum improvement in Haiti and also contribute to improving and optimizing our selection strategy.

Genetic gain from a rapid cycling genomic selection program for non photoperiodic dual use sorghum

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Novel approaches and technologies will bring an increase in the rate of genetic gain (rapid breeding) for contrasting environments with enhanced biotic and abiotic stresses in order to allow productivity to follow the future increase in demand for food and feed products that goes along with rapid population growth (rapid breeding to keep up with rapid population growth and demand for feed and food products)

We hypothesized that the comparison of measured genetic gain between advanced inbreds selected through phenotypic or genomic recurrent selection will show genomic assisted breeding to be more cost effective and to allow for faster genetic gain.

We will use the data for inbreds developed from 4 consecutive genomic selection cycles in two contrasting environments (one used for training and one that was not used for training).

We show that Genomic selection has allowed for increased gains, gains of over 125 kg per cycle and over 250 kg per year.

Improving rate of genetic gain through optimised breeding cycles

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The various production-related issues such as climate change, water resources, pests, and disease complex pose major challenges to sustaining and improving the grain and fodder yield of sorghum. The ever-increasing population and malnutrition demand improvement in the quantity and quality of sorghum productivity. On the other hand, the rate of genetic gain has become stable or reduced in most of the staple crops, including sorghum. To address these issues, new-generation concepts and approaches are required in sorghum improvement programs to breed superior varieties rapidly to achieve higher grain and nutritional productivity. The rate of GG is contributed by selection intensity, accuracy or heritability, genetic variance, and breeding cycle time. Modernizing sorghum breeding programs is the need of the hour to accelerate genetic gain, which can lead to the rapid development of superior varieties. A comprehensive breeding pipeline was developed in sorghum by capturing important elements such as genomic selection, breeding value-based crossing program, cost-effective mid-density SNP genotyping platforms, rapid breeding cycles for generation advancement, recycling of best lines, digital tools for phenotyping, efficient statistical designs in multi-location trials, and managing the entire breeding operation through breeding management systems. All these components were developed and implemented to deliver high-yielding varieties for various product profiles.



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ABSTRACTS TUESDAY 6 JUNE



Sorghum in Europe: State of play and prospects

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Sorghum ID is the inter-sector association, aiming to promote and develop sorghum production and genetics in Europe. Sorghum is the 5th most produced cereal globally, with steady production between 60 MMT and 70 MMT annually. Producing countries have distinct sorghum value creation profiles, including net exporters for feed production, auto-consumption for feed or local food consumption, and importers for food and feed. In Europe, sorghum cultivation has ranged between 500K and 560K hectares per year, with both grain and silage production. In Europe, sorghum offers many assets such as varieties very adapted to the European climate and climate change threats, easy cultivation practices, grain versatility for various industries, and healthy, gluten-free characteristics. These assets offer great prospects for seed breeders, farmers, industry, and customers. The main challenges lies in reaching a critical size and developing investments in R&D to generate a large product offer for a dynamic demand on the different sorghum uses.

Can the analysis of the genetic diversity of stress responses challenge the consensus on the relative performance of maize and sorghum under drought scenarios?

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After a record drought in summer 2022 in Europe, both the population and public authorities expect a strong response from agriculture to use less water in the very near future. In this context, increasing sorghum acreage appears to be an alternative to maize. Indeed, it is widely believed that maize is better suited to optimal conditions and sorghum to rainfed conditions. However, this reputation is based on few studies and few genotypes, which would ideally represent THE maize and THE sorghum as species. There is a great pool of genetic diversity in each species and thus potentially wide ranges of «drought or temperature resistance». It should therefore be possible to find sorghums and/or maize adapted to each specific environmental scenario. For example, there is a wide range of earliness available in each species. Earliness has a major role, positive in avoiding late drought but negative under moderate or chronic drought. It is therefore essential to identify in which specific scenarios a given combination of trait values (ideotype) results in a comparative advantage on plant production. In this talk, dealing here with maize, I will show how we have developed a conceptual framework to predict the impact of the genetic diversity, based on the coupling between phenotyping and crop modeling: (i) the development of a model of leaf development and expansion for which parameter values can be obtained in phenotyping platforms (ii) the parameterization of 254 hybrids that maximize the maize genetic diversity; (iii) and the determination of ideotypes of cycle length, leaf growth and sensitivity to water deficit and radiation, in current and future European environments. Overall, we provide evidence on «where and when» a combination of trait values can give a comparative yield advantage, as well as the limit of possibilities in current genetic diversity.

Breaking boundaries in sorghum value chains: the impact of Europe-Africa collaborations and future prospects

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Sorghum is a staple crop in semi-arid regions and its interest for diversifying the crop portfolio in Europe is increasing. While recognizing the regional differences in cropping practices, environmental conditions, and socio-economic contexts, both semi-arid and European regions face common challenges such as climate change adaptation and mitigation, development of new products and uses, and management of emerging biotic constraints. Collaborative efforts between European and African teams have played a crucial role in addressing these challenges.

This presentation will highlight various past and present collaborative actions between Africa and Europe across different scientific disciplines. These actions encompass the analysis of sorghum genetic diversity, developments of pre-breeding populations and phenotyping tools for breeding programs, multi-scale analyses of trait development for value chains stakeholders, and integrated approaches combining agronomy, ecophysiology, genetics, and breeding to support the development of customized crop production systems.

In addition to showcasing existing and ongoing collaborations between Europe and Africa, this presentation will aim to emphasize the need for a collaborative European-African framework that aligns with global actors in response to the rapidly evolving climatic and socio-economic conditions worldwide. Although significant progress has been made in knowledge and data sharing, further synergistic actions are necessary to foster innovation and facilitate their adaptations to diverse contexts. Establishing stronger connections within the sorghum research community and forging links with other plant communities, including cereals and beyond, would for instance greatly enhance sorghum research efficiency and impacts.

Novel strategies to mine the relevant biodiversity from genebanks to enhance crop adaptations for changing climate: case study-harnessing sorghum drought adaptations

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Sorghum is an important source of livelihood for semi-arid agricultural production regions and globally investigated drought-resilient crop option to stabilize the agri-systems for the upcoming climatic changes. ICRISAT genebank alone conserves large amount of global sorghum biodiversity (~40,000 sorghum accessions) which can be utilized in the breeding process to improve the existing sorghum-based systems and/or adapt and stabilize agri-systems in the future by introducing sorghum crop.

Nonetheless, utilization and systematic mining of this vast biodiversity for breeding imposes several major challenges; For example, understanding what are the crop features to be tapped on for enhancing its climate-adaptations and, consequently, the screening for those features through the gene-bank collections at the relevant scale.

In the presented work we demonstrated the approach to address the current challenges on the example of sorghum diversity panel (242 lines) where we first dissected the plant features underlying crop yield under the well-watered (WW) and water stress (WS) treatments using the lysimetric phenotyping system in two independent seasons (2017-18, 2018-2019). We found that crop capacity to effectively extract (amount of water extracted from the soil profile) and convert transpired water into the biomass (transpiration efficiency [biomass produced per unit of water transpired]) are some of the key features underlying the agronomic crop performance, especially under drought ($R^2 > 0.60$; $P < 0.001$ under WW&WS). We also demonstrated that the range of variability in these crop functions available in the diversity panel can be utilized to enhance drought adaptation of currently cultivated gene-pool. These potential donors of drought adaptations originated from the hot and dry geographies. Using this approach, we can develop specific collections that are enriched with traits specific for enhancing the adaptability of sorghum to hot and dry agro-ecologies.

Therefore, the paper delineates the novel approaches to 1) identify useful species variation to enhance production in drought-prone environments 2) evaluate that variation with relevant throughput 3) systematically mine the variation from the genebanks collections for utilization e.g. in breeding.

The genetics basis of sorghum adaptation to a changing climate

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Minimizing the negative impact of climate change on crop production, and hence world food security, is one of the most important challenges to our generation. Sorghum was domesticated in the northeastern quadrant of Africa (De Wet and Harlan, 1971), showing genetic diversity for adaptation to abiotic stresses, such as those caused by drought and high temperatures, which are becoming prevalent due to climate change. To look into the genetic basis of sorghum resilience to environments with abiotic stresses, we evaluated 245 sorghum lines for drought tolerance in two geographical locations showing distinct climates in Brazil, both under well-watered and under controlled drought stress conditions. To investigate possible causes of genotype-by-environment interaction (GxE), we performed multi-locus multiple-environment genome wide association mapping (GWAS) for grain yield and phenology traits and estimated the sensitivity of the associated marker effects to environmental variables. The variables, minimum, mean, and maximum temperatures, relative humidity, wind speed, solar irradiance and evapotranspiration, were assessed during the crop growth cycle. We found that drought stress reduced sorghum yield on average by 32%. Our results showed that grain yield was under strong environmental influence, with the GxE variance component surpassing the genetic component. Consistent with that, among loci significantly associated with grain yield by GWAS, five were main effect loci and ten showed significant GxE and, within those, seven had crossover-type behaviour, that is, showing environment-specific favorable alleles. Importantly, linear regression analyses between GxE marker effects and the mean of the environmental variables indicated that temperature increases between 29°C - 39°C can negatively impact sorghum grain yield. Projections indicate global temperature increases around 1.5°C above pre-industrial levels until 2040 (Pörtner et al, 2022). This indicates that breeding and research will need to include deliberate efforts to understand, harness and deploy strategies to enhance sorghum adaptation to environments with multiple stress.

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Breeding for reproductive cold tolerance in sorghum

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The sensitivity of sorghum to pre-flowering cold stress, resulting in reduced pollen viability and poor seed set, is a major constraint for expanding growing areas into higher altitudes and latitudes. Nevertheless, compared to juvenile cold tolerance, reproductive cold tolerance in sorghum has received much less attention so far.

Here we present first insights into the genetic architecture of this trait via GWAS in a broad diversity set (n= 330), and its inheritance in F1-hybrids using a *line x tester* design (n=49 factorial experimental hybrids). Phenotyping of crucial tolerance traits including spikelet fertility (*panicle harvest index*) and seed yield was conducted in multi-location field trials, including high-altitude tropical (Mexico) and high-latitude temperate (Germany) cold-stress environments.

We observed a high degree of phenotypic variation and identified several novel, temperate-adapted accessions of polyphyletic origin with superior and environmentally stable cold tolerance. Satisfying heritability estimates, a heterotic and mainly dominant inheritance in F1 hybrids and strong effects of general combining ability (GCA) indicate good prospects for breeding enhanced cultivars. Although GWAS revealed the trait to be strongly quantitative, promising genomic regions with multiple-trait associations were found, including hotspots on chromosomes 3 and 10 which contain candidate genes implicated in different developmental and survival processes under abiotic stress conditions. We expect that genomics-assisted crossing programmes aimed at combining multiple additive QTL from genetically diverse sources can help to rapidly advance tolerance to both juvenile and reproductive cold tolerance in elite sorghum breeding materials.

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Early-Stage Phenotyping of Root Angle Provides Insights into the Drought Tolerance Level of Sorghum (*Sorghum bicolor* L. Moench) Landraces

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Plant root system architecture plays an important adaptive role in drought-prone environments. Hence, a better understanding of root system architecture (RSA) traits and their association with yield and yield-related traits is critical for sorghum improvement in water-limited environments. Therefore, the objective of this study was to understand the association between RSA traits and agro-morphological traits. The study was conducted using 940 sorghum genotypes. Early-stage root traits, including root angle, were characterised in a poly-house, and data was collected at the 5th leaf stage. The field experiment was carried out at two locations (Mieso and Sheraro, Ethiopia) under water-stress environments. The results showed a moderate to low association between RSA and agro-morphological traits. Specifically, root angle showed a moderately negative association with grain yield, indicating that narrow root angle contributes to better grain yield under moisture stress conditions. Some specific genomic candidate regions associated with grain yield were also identified. Furthermore, the candidate regions co-located with genes described for drought-related resistance. Hence, based on this study, root angle should be a worthwhile selection criterion for sorghum genotypes grown under water-limited conditions. However, further analysis is required to identify the mechanisms and associated genes for enhanced root adaptation to water stress.

Keywords: Sorghum - Drought tolerance - Grain yield - Root system architecture - Root angle.

Identifying genotypic variation in transpiration efficiency (TE) among major sorghum races and examine their genetic association

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Drought is becoming a major sorghum production constrain in the face of changing climate. Targeting water efficient (TE) genotypes in water limited environments is considered to be the best approach to respond to these environments. The aims of this study were (1) to identify the phenotypic variation in TE among major sorghum races and, (2) to use genome wide association (GWAS) to map quantitative trait loci associated with the trait, and (3) to develop genomic predictive model for TE. A total of 300 key Ethiopian core germplasm/SMIL-core collection representing major races including durra, caudatum, kafir and guinea and intermediate races were grown in 16 L lysimeters in rain-out shelter in RCB design with 3 replications with the known checks at Melkassa, Ethiopia following a modified protocol developed by Chenu et al, 2016. At 4 fully expanded leaf stage, each pot was covered with black plastic to prevent water loss through evaporation and initial weight of the pot was measured to use as target weight. Experiments were harvested at 12 fully expanded leaf stage. Shoot TE was calculated as the ratio of dry mass at harvest to total water use. Preliminary result indicated a significant variation ($P < 5\%$) among the major races, durra showing a highest TE (5.1-6.6), while mixed races such as dura-caudatum, kafir-caudatum and dura-guinea showed intermediate result ranging from 3.8-4.9 As compared to, kafir, Guinea and caudatum that showed lowest TE (0-3.7). This result is in agreement with previously TE studies reported by Vadez et al. (2016). Samples for deep sequencing were sent to Purdue University for bioinformatics analysis and gene identification governing variation for TE. Although, TE has not been explored for immediate selection indexes in most breeding programs, the information generated will be a used as base for further selection criteria for complex drought adaption traits.

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Modeling adaptation of sorghum in Ethiopia with APSIM—opportunities with G×E×M

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Sorghum is an important food and feed crop in the dry lowland areas of Ethiopia. Farmers grow both early-sown long-duration landraces and late-sown short-duration improved varieties. Because timing and intensity of drought stress can vary in space and time, an understanding of major traits (G), environments (E), management (M), and their interactions (G×E×M) is needed to optimize grain and forage yield given the limited available resources. Crop simulation modeling can provide insights into these complex G×E×M interactions and be used to identify possible avenues for adaptation to prevalent drought patterns in Ethiopia. In a previous study predictive phenology models were developed for a range of Ethiopian germplasm. In this study, the aims were to (1) further parameterize and validate the APSIM-sorghum model for crop growth and yield of Ethiopian germplasm, and (2) quantify by simulation the productivity-risk trade-offs associated with early vs late sowing strategies in the dry lowlands of Ethiopia. Field experiments involving Ethiopian germplasm with contrasting phenology and height were conducted under well-watered (Melkassa) and water-limited (Miesso) conditions and crop development, growth and yield measured. Soil characterization and weather records at the experimental sites, combined with model parameterization, enabled testing of the APSIM-sorghum model, which showed good correspondence between simulated and observed data. The simulated productivity for the Ethiopian dry lowlands environments showed trade-offs between biomass and grain yield for early and late sowing strategies. The late sowing strategy tended to produce less biomass except in poor seasons, whereas it tended to produce greater grain yield except in very good seasons. This study exemplified the systems approach to identifying traits and management options needed to quantify the production-risk trade-offs associated with crop adaptation in the Ethiopian dry lowlands and further exemplifies the general robustness of the sorghum model in APSIM for this task.

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The need for local data for moving forward food assessments in Africa: a review using sorghum crop modeling as case study

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Crop growth models can be useful tools, yet data availability, accesibility, and quality compromises the usefulness of the outcomes. This review focused on compiling crop modeling efforts in Africa using Agricultural Production Systems Simulator (APSIM) as a case-study. Fourteen sorghum publications were collected, including 21 cultivars. The overall root mean square error (RMSE) for yield was 3600 kg/ha (relative RMSE = 20%). Most of the publications carried out their calibration process based on collected experimental data (n=10). Parameters related to plant phenology were most frequently modified. However, only 4 (out of 14) publications recorded crop phenology observations. Pointing out that studies based on limited field data might lead to unsupported agricultural interventions on smallholder agricultural systems. This research aims to highlight the need of investment in local level data and open sharing platforms to provide robust assessments addressing complex challenges of food, nutrition, and climate security.

Foresighting sorghum production through integrating general circulation and biophysical crop models with remote sensing at regional scales across north-eastern Australia

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The highly variable climate of Australia, combined with a strong influence of markets on grain price, and thus crop choice, impede accurate prediction of regional scale crop production. In addition, food producers are increasingly exposed to variability and change in world markets, commodity prices, accessibility to seeds and /or fertilizer and local weather. This increases their vulnerability and threatens resilience to cope economically as well as socially. To date, regional crop-modelling approaches have delivered relatively good estimates throughout the cropping season of the likely final crop yield for that season. However, accurate, timely and objective information on projected crop production, well before harvest, at farm, shire and region has been limited. This is further exacerbated by a recent increase in commodity market uncertainty and climate volatility within Australia and globally. Here we present (i) an integrated framework to estimate regional scale crop production and (ii) a preliminary analysis of the lead time and skill of a sorghum yield forecasting system driven by a dynamic general circulation model (GCM). In addition, we exemplify the likely utility of this approach to foresight the impact of climate on crop production estimates generated by integrating high-resolution satellite data for sorghum in north-eastern Australia. For example, having advance knowledge of the associated risk of crop production, well before sowing, will aid in changing a pre-determined decision and thus can mitigate some putative impacts. Finally, we propose that the application and integration of high-resolution satellite data with GCM-driven crop models will become increasingly accessible and thus valuable in decision-making for farmers, industry, government agencies and policy makers. This is likely to lead to more profitable and resilient sorghum farming systems.

CropGen: A new tool for optimising sorghum crop design for drought adaptation

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Sorghum is an important food and feed crop globally. Strategies to optimise its performance are needed to help meet rising demands in changing future environments. Typically, sorghum is grown as a dryland crop, with water availability being a major limitation for yield. Here we present a new tool, CropGen, for optimising sorghum design and yield. CropGen connects the APSIM sorghum model with an evolutionary optimisation algorithm to enable iterative exploration of genotype × environment × management (G×E×M) combinations to identify optimal crop improvement strategies based on several objectives, including yield, water use, and crop failure risk over diverse environments. Initial model testing was undertaken by exploring tillering × maturity combinations and predicting optimal sorghum designs in environment types (ETs) with contrasting seasonal crop water supply/demand trajectories. In the ET with minimal water stress around the critical flowering-grain fill period, yields were higher and optimised with high tillering and long maturity designs. Whilst such designs required more seasonal water use, there was little failure risk due to water abundance in these environments. In contrast, in the ET with significant water stress around the critical period, yield was optimised, and failure risk mitigated, with lower tillering and shorter maturity designs, due to a reduction in crop water use. Future work will expand this analysis to explore more complex G×E×M landscapes. The novel ability of CropGen to engender nuanced understanding of G×E×M interactions is key in exploring strategies for guiding research and plant breeding efforts to maximise crop performance across diverse environments.

Automated processing of GxExM parametrized simulations

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In order to maximize agricultural production yield, an optimal setup of GxExM parameters is required. By combining several parameters and their possible values, we can generate large number (up to hundreds of thousands) of simulations. Adding spatial (hundreds of locations) and temporal (decades of available historical weather data) component can result in billions of simulations that need to be generated and processed. Our aim is to show how such a task can be done by implementing custom automation tools developed at our university alongside existing simulation processing software (APSIM). We will present data from our ongoing research that deals with sorghum production in India and Africa, and use this case study to discuss benefits of this large-scale «big data» approach to simulation processing. Most notably how the resulting data can be statistically analyzed and visualized to serve as a decision support tool for both farmers (optimizing management practices) and breeders (trait selection for specific region / weather).

Our research team focuses on the topic of agricultural production simulation processing for several years now. Among others, we have published papers regarding the data preparation (Jarolimek, et al., 2019), the development of automation support tools (Pavlik et al., 2020) and evaluation of the output data (Ronanki, et al., 2022). In our presentation at the Global Sorghum Conference we would like to highlight our most recent progress which deals with high-performance computing optimization and also the current development of robust data platform to facilitate end user interaction with the calculated data sets.

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How farmer-breeder collaboration can increase functional sorghum diversity and reach larger-scale impact

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Participatory breeding has been criticized in terms of being too site-specific and unable to reach large-scale impact. The Farmer Research Network (FRN) approach^{1,2} can help to overcome these constraints. FRNs build on the infrastructure and social capital of farmer organizations, NGOs and/or development projects, and are guided by a set of principles, such as inclusion of marginalized groups, co-creation, engagement of farmers through the whole research process, rigorous research, and joint learning in the network. If FRN members want to engage with sorghum diversity and seed production, the first step would be to understand the diversity of farmers' needs. In West Africa, farmers' socio-ecological contexts and corresponding needs in terms of sorghum varieties differ largely. Different farmers may prefer early or late varieties, shorter or taller varieties, varieties adapted to low-input or intensified conditions, to mono- or intercrop systems, and to specific biotic or abiotic stresses. Also, specific varieties are suitable for different processed products such as porridge, couscous, or beer. No single variety can serve all the different purposes and needs, rather "best-fit" cultivars need to be identified, i.e. cultivars that explicitly serve specific functions in the production system. Breeders should then strive to co-develop a corresponding "Basket of variety options"³. Initially, the basket may be built from existing varieties or germplasm. In the longer term, these would be complemented by varieties derived from well-designed participatory breeding programs implemented in the FRN. The FRN infrastructure enables farmer-led variety testing under relevant on-farm conditions at scale. Combined with digital data collection and a typology of the FRN members, identification of varieties that fit best to specific farmers' contexts and needs is possible. Seed production of farmer-preferred cultivars can be coordinated in the same FRN. Due to the large-N variety testing and farmer learning, scaling is embedded in the process.

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The power of Farmer Research Network in technology promotion among smallholder farmers: The case of improved sorghum varieties in Eastern Uganda

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Smallholder farmers in eastern Uganda practice subsistence farming, primarily based on sorghum as their major staple food and income. Farms and farming practices are highly heterogeneous, characterized by low productivity and high yield gaps due to a multitude of biotic and abiotic factors coupled with poor adoption of improved technologies. To address these challenges, we initiated studies with an overall objective of generating farm context-based solutions towards addressing sorghum production challenges. Specifically, the study aimed at developing multi-stress tolerant sorghum varieties targeting Striga, drought and anthracnose and (ii) promote adoption of developed varieties through farmer research networks (FRNs). Using mixed participatory methods, focus group discussion and field experimentation, we engaged farmers to identify the production practices, challenges, and opportunities followed by a needs and gap analysis. From these engagements, lack of information, high cost of labour and inputs among others were identified as major challenges. In addition, new varieties are quite often not compatible with the current farming practices and require high inputs. Through on-farm participatory variety evaluation with 1200 farmers under FRN, 24 improved multi-stress lines were tested in 5 different locations and 6 lines were identified based on farmer-set selection criteria. The six lines were randomly distributed in tricrots to 1200 farmers for evaluation alongside 1 commercial and 1 farmer varieties in plots of 10m x 10m for 3 seasons using own management practices. Data on the agronomic performance and trait preference were collected by farmers. Using different statistical tools like direct-matrix and pair-wise ranking algorithms, the new varieties were ranked high and preferred over the check varieties. By the end of the third season, 3702 non-participating farmers had taken-up either one or two of the new varieties. In addition, internal markets for seed were created, and improved seed plus information sharing was readily available within communities.

Participatory Selection of Introgression Lines Derived from Wild and Exotic Sorghum with Farmers in Western Kenya

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Sorghum is an important food security crop in western Kenya. Its productivity is declining owing to low genetic diversity. Use of wild and weedy relatives offer new opportunities to create new genetic diversity and enhance adaptation. Low involvement of farmers from the early stages of breeding process has led to low adoption rates of the new varieties. The objective of this study was to identify and select preferred promising BC1F6 progenies derived from crosses between farmer preferred landrace grown in the Sahelian zones (CSM63E) and two wild parents (BBISS-08 and BBISS-09) that contain useful adaptation traits which can be used directly by farmers or as parental material in sorghum improvement. On-farm field experiments were planted in RCBD replicated 2 times in Migori and Sega sites in western Kenya. One hundred farmers from two farmer organizations, Aminyasa and Ugenya banana groups, participated in the selection progenies. Evaluation was based on various agronomic traits including earliness, grain yield, plant height, panicle size, overall farmer preference score, and resistance to pests and diseases. Based on farmer evaluation scores and other parameters, ten entries including 588, 534, 513, 591, 550, 465, 569, 563, 499 and 591 showed significant variation ($P < 0.05$) for various agronomic traits and compared well with some of the check varieties. The lines were selected as having high acceptability and considered as most suitable for growing in western Kenya. Most of them (63 %) exhibited good genetic potential and were early maturing. They also had large panicle size, high number of productive tillers and resistance to anthracnose disease while the rest had undesirable traits such as lodging, awns, excessive height, and were not selected by farmers. The identified useful progenies, germplasm enhancement, and involvement of farmers in the selection process are expected to accelerate breeding for adaptation to climate change in the region.

Sorghum Breeding for Agroecology: Biodiversity considerations in West Africa

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Agroecology as a movement and a science uses environmental and social principles for guiding food system transformation (Wezel et al. 2020). The biodiversity principle addresses the maintenance and enhancement of genetic resources for functional diversity in agroecosystems over time and space. The agroecological movement, while focusing on strengthening farmers' seed management options, rarely uses support from scientific breeding. This study seeks to understand how national breeding programs in West Africa address biodiversity issues relevant to agroecological transformation. Semi-structured interviews with sorghum breeders, farmer-organization and NGO representatives from Senegal, Mali, Burkina Faso and Niger provided the data for this study. All breeding programs are collaborating with farmers to identify preferred traits and set priorities for variety development for specific agroecologies or uses. All of these programs use local germplasm as the base for their breeding populations, and are thus contributing to conservation of these gene pools. They also introduce new genetic diversity for new uses, such as fodder quality, and resistances to biotic and abiotic stresses. All breeding programs evaluate their new selections in collaboration with farmer organizations, and thus support decentralized farmer decision making for seed production and dissemination. These findings show that breeding programs and agroecology activists share many concerns. Thus, there is a solid basis for enhancing biodiversity through more direct collaboration between farmers, activists and sorghum breeders. These opportunities will be discussed.

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Participatory sorghum development increased number of functional varieties and genetic diversity for climate resilience among smallholder farmers in Chirundu

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Community Technology Development Trust has collaborated with Zambia Agriculture Research Institute from 2019. The major goal has been to develop a portfolio of farmer-preferred sorghum varieties that address the diversity of farmer needs, contribute to climate change adaptation and enhance functional sorghum diversity in local communities. Farmers actively participate in variety development. Local and improved open-pollinated varieties are accessible in farmer-managed seed systems. Participatory Variety Development has increased the diversity of sorghum cultivars among smallholder farmers, with traits desired for local growing conditions and uses. Therefore, production and productivity is expected to increase. These cultivars have relatively big grains, high yielding, drought tolerant, short and early maturing. These traits are highly desired in this drought prone area, hence food security, genetic diversity and ability to adapt to reduced rainfall is being realised.

Farmers were interested in combining traits found in the cultivars 'Kuyuma' a short variety and 'Sima' a tall variety with big grain. The resulting preferred varieties 'Kuyuma/sima' are high-yielding, early maturing, short white sorghums with big grains and tolerant to drought. This was achieved by using simple but effective pollination techniques that could be implemented with farmers in their fields. 'Kuyuma' was crossed with 'Sima' under the guidance of the Sorghum Breeder. Head to row selections of preferred lines were done from a segregating population of 9000 F2 plants. The result was development of 7 distinct stable lines at F5 designated as ZSV-108, ZSV-110, ZSV-134, ZSV-199, ZSV-251, ZSV-208 and ZSV-261. The lines are undergoing variety testing and evaluation in replicated trials in farmer fields within the agro-ecology.

The lines qualify for formal variety release and fit into farmer contextual needs. The desired outcomes of the PVD process were; (i) enhanced involvement of farmers in variety development, (ii) increasing sorghum genetic diversity and (iii) creating opportunities for farmers.

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Nutritional and functional properties of infrared and microwave heat moisture-treated sorghum meals

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Starch is the main component of sorghum meals. The digestibility of a carbohydrate-rich product can be estimated by the glycaemic index (GI) using in vitro starch digestibility assay. Despite the statements in literature that, “sorghum foods are slowly digested starch and good for people with diabetes and obesity”, other researchers have proven sorghum foods to have a high and intermediate GI. Heat-moisture treatment (HMT) is one of the environmentally friendly physical modification methods that can be used to improve the physicochemical properties of starch without destroying its granular structure.

The nutritional and functional properties of infrared and microwave HMT sorghum meal were studied. Three types of sorghum meal (white and red non-tannin, red tannin) were treated by HMT at 25 % moisture by microwave (MW) and infrared energy (IR) (250 W) for 15 minutes.

All the microwave and Infrared HMT sorghum meal had significantly ($P < 0.05$) lower pasting peak viscosity as compared to the untreated samples. There was a reduction in the *in vitro* starch digestibility of the HMT samples with the red tannin sorghum type with the lowest estimated glycaemic index (eGI). HMT of starch changes the crystalline nature of the starch granule, which leads to the conversion of a fraction of amorphous lamella to a crystalline form. Tannins in tannin-type sorghum can also form complexes with starch and amylase enzymes through hydrogen bonds or hydrophobic interaction to reduce starch digestibility. This increases the amount of slowly digestible starch and resistant starch and further reduces the eGI.

The results of this study suggest that HMT by MW and IR energy changes the functional and nutritional properties of sorghum meals and has the potential to be used in the development of lower GI sorghum foods.

Sorghum grains milling: filling the technological gaps for new functional flours and semolina production

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Sorghum (*Sorghum bicolor*, L) is the 5th most cultivated cereal in the world for its grain. Sorghum is gluten-free and has interesting nutritional properties. Sorghum can provide farmers with diversification and an agronomic response to global warming due to its high photosynthetic capacity and drought tolerance [1]. The milling process is used to transform cereals, by combining different unitary milling operations and sorting of particles according to their size or aerodynamic properties. While this process has been widely optimized for wheat to separate the starchy albumen with low contamination of peripheral tissues and germ and produce flour or semolina in the case of durum wheat [2]. Yet this process has been scarcely studied for sorghum. The main challenge for sorghum is the buried location of the germ within the grain [3] that affects negatively the stability of flour. The aim of this study is to investigate the influence of pre-treatments (moisture, mechanical dehulling) to remove the peripheral envelopes; the different milling steps and settings associated with different granulometries to diversify the end products usages (semolina and flour). An experimental design was conducted considering these factors to optimize the extraction yield of flour/semolina using Bühler Mill. Specific conditions combining pretreatments and milling conditions were identified to produce high extraction yields of semolina and flour. These conditions were tested for hard (white) and soft (red) sorghum varieties to better rely the impact of intrinsic physical and biochemical properties of grain on extraction yield, granulometry and functionality of end products. Data were uploaded in knowledge-sharing tool on the production and characterization of vegetable powders called PowderLib. A focus was then made on flour stability through accelerated aging experiments in controlled temperatures. Biochemical and spectroscopic (FTIR) analyses were used to better assess these changes. Pretests in second transformation will be also highlighted.

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End-use quality driven sorghum improvement: new opportunities for high value food products

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Sorghum is a sustainable food crop with important and unique health promoting attributes. However, its use in modern food applications is relatively limited primarily due to reduced endosperm functionality compared to other major cereal grains. The reduced functionality is related to sorghum endosperm protein body structure, and often results in products that generally do not meet consumer sensory quality expectations. Process modifications are commonly required to enhance sorghum functionality in food products, which can add to manufacturing costs. New sorghum hybrids have been developed that incorporate a protein body mutation with high digestibility (HDP) trait. Evidence indicates that these new HDP sorghums perform better than normal hybrids during food processing, resulting in products with superior quality. The HDP sorghums could thus open opportunities for new applications of sorghum as a high value food ingredient to benefit producers and consumers in developing and developed nations alike. This presentation will cover new insights on the mechanisms behind the improved functionality of the HDP sorghum hybrids, specific food application technologies that could benefit from these sorghums, and the potential impact of the HDP sorghum use on global food security, poverty alleviation, human health, and environmental sustainability. Production challenges, and potential pitfalls of replacing traditional sorghum varieties with the new HDP sorghums in foods will also be addressed.

Extrusion processing of sorghum grain (whole and decorticated) used as ingredients for breads, biscuits and arraw

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Decorticated sorghum grain (DSG) and whole sorghum grain (WSG) are often used as thick and thin porridges. In order to add more value to products made from sorghum grains, an extrusion technology was developed using a single-screw extruder designed at Purdue University. Extruded DSG and WSG flours were tested as ingredients in breadmaking (15 to 30% incorporation), fast-cooking arraw (rolled flour) (87 to 93% extruded DSG), and biscuits (20 to 70% extruded WSG). Hydrocolloids were added to arraw formulations. No significant differences were found between the extruded DSG and WSG incorporated flours at 15 to 30% in breadmaking, and were comparable to 100% wheat flour bread. For arraw, extruded DSG with maltodextrin and gum Arabic gave high yield of granule formation (2 and 4 mm sieved) compared to traditional arraw. Cooking time for 4 mm granules was reduced from 37 to 10 min with extruded DSG. For 2 mm granules, reduction was from 25 to 6 min. Sensory data showed WSG-incorporated bread and fast-cooking arraw were highly acceptable by consumers. Biscuits made with 30% of extruded WSG showed good functional properties and sensory attributes compared to the control 100% wheat flour. Extruded sorghum flours have high potential for new innovative products.

Prioritizing sorghum value chain preferred traits : lessons learned from the field in Burkina Faso and way forward

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Investments in agricultural research to respond to the need to the end users have proven very unsuccessful at an aggregated level over the past decades in Burkina Faso. Prioritizing the different traits and cultivar/variety demands of farmers and other stakeholders in the cereal value chain has been the challenge faced by the breeding program in Sub-Saharan Africa . As such, the breeding program, face the tough question of how best to repond to the need of the end users across increasingly diverse actors from the value chain. Improved sorghum has been developed and diffuse through out the country but its adoption rate remain questionable and therefore requires investigation. Quantitative traits preferences assessment across two regions was with 400 farmers was conducted to understand the reason behind farmers decisions making on adopting new varieties. In-depth interviews were conducted with the value chain actors to unpect the adoption scenarios from their perspective. The results shows three main adoption scenarios that exist in sorghum diffusion. The results also suggest substantial differences from the value chain actors that do not necessarily use the same lenth to appreciate the improved variety making the prioritisation challenging for breeding programm. The findings have since informed the research portfolio development of participatory varietal developpement and lessons learned to strengthen future priority assessments in agricultural research.

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Panning for genetic gold: pan-genomics and other omics resource for crop improvement

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Genetic diversity is an essential building block for plant breeding programs. As new technologies dramatically increase capacity to characterise this diversity, effective new deployment strategies are required. Attempts to exploit natural genetic variation for more complex traits are hampered by difficulties in identifying useful genetic variants primarily due to confounding effects of context dependencies on phenotypic performance in elite genetic backgrounds. The increasing volume of sequence information being generated from diverse accessions in germplasm collections, combined with high throughput genotyping and phenotyping and crop modelling offer opportunities to better utilize this material to drive forward breeding. In this presentation, the development and deployment of a range of genomics resources to support sorghum crop improvement will be detailed, including a pan-genome which identifies and catalogues thousands of novel genes from crop wild relatives not previously identified in cultivated sorghum. Such resources are powerful tools to bridge the gap between genomics and applied breeding.

Editing the way to resilient high value cereals

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We have developed efficient and effective CRISPR/Cas9 gene editing methodologies for sorghum. We have demonstrated that gRNAs driven by sorghum U6 promoters have been shown to deliver more efficient editing in both sorghum and barley than other promoters tested, such as rice U6 or U3. We have targeted traits such as grain size, grain number, grain protein content and digestibility as well as a number of developmental traits which play important roles in shoot and root architecture, panicle and inflorescence branching, lignin content and stem thickness. Previous work in the group on RNAi techniques in sorghum to downregulate G-protein γ -subunits and protein foldases have produced grain with larger grain, protein contents up to 16% and improved digestibility. Field grown RNAi lines have shown significant gains in productivity and feed conversion in poultry feeding diets. Two years of poultry feeding trails have shown that considerable savings (>25 cents in feed costs per chicken) can be achieved. Gene editing of the same genes has generated similar phenotypes, with the exception of foldase knockouts with severe impediments to plant growth. Gamma-kafirin knockouts have higher protein content, increase digestibility and reduced methane gas production in ruminant animals. Knockouts of various PIN and VRN gene family members cause significant changes in root biomass, branching and angle of seminar roots. Reduced root angle and deeper rooting phenotypes have significant advantages in deep soils with water at depth, delivering more drought and heat resilience in sorghum.

Sorghum Mutation Breeding in the Age of Next-Generation Sequencing

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Mutation Breeding is a classical and effective approach to generate diversity and create novel traits. Advances in sequencing technologies and genome editing tools have advanced mutation breeding beyond release of new varieties. In Sorghum we have established a Pedigreed Mutant Library in the sorghum inbred line BTx623 by mutagenizing the seeds with ethyl methane sulfonate (EMS). The BTx623 we used to make the mutant library was purified by single seed descent for six generations to achieve near uniform background. The library has 6,400 M4seed pools and possesses a great diversity of mutant phenotypes. Over 1000 sorghum mutants with altered agronomic traits have been isolated from the mutant library. Using next-generation sequencing (NGS), we have established an effective bioinformatic pipeline to identify the causal mutations through bulk-segregant-analysis (BSA) of the whole genome sequencing data of the pooled mutants selected from F2 populations. Once an F2 backcrossed population is established, the cost to identify the causal mutation is under \$200 in NGS sequencing. On the other hand, we have sequenced 1256 lines from the mutant library and generated >10 million EMS-induced mutations. All genes in BTx623 genome, except for 517 short genes, have at least one mutation that results in either an amino acid change or knockout mutation. The mutation data will be available for public search on Sorghumbase (<https://www.sorghumbase.org/>). The mutant library has a high mutation frequency, which enable the selection of desired traits in a manageable number of lines but also make the direct use for breeding difficult.

Genotype–environment associations to reveal the molecular basis of environmental adaptation in sorghum

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A fundamental goal in plant biology is to identify and understand the variation underlying plants' adaptation to their environment. Climate change has given new urgency to this goal, as society aims to accelerate adaptation of crops to hotter, less predictable climates. In the pre-genomic era, identifying adaptive alleles was painstaking work, leveraging genetics, molecular biology, physiology, and ecology. Now, the rise of genomics and new computational approaches may facilitate this research. Genotype–environment associations (GEAs) use statistical associations between allele frequency and environment of origin to test the hypothesis that allelic variation at a given gene is adapted to local environments. Researchers may scan the genome for GEAs to generate hypotheses on adaptive genetic variants (environmental genome-wide association studies). Despite the rapid adoption of these methods, many important questions remain about the interpretation of GEA findings, which arise from fundamental unanswered questions on the genetic architecture of adaptation and limitations inherent to association-based analyses. We outline strategies to ground GEAs in the underlying hypotheses of genetic architecture and better test GEA-generated hypotheses using genetics and ecophysiology. We provide recommendations for new users who seek to learn about the molecular basis of adaptation. When combined with a rigorous hypothesis testing framework, GEAs may facilitate our understanding of the molecular basis of climate adaptation for plant improvement.

OGA (Fermented human urine) fertilizer an auto-innovation among women farmers in Niger

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Sahelian pearl millet production is often associated with low panicle yield due to poor soil chemical fertility. Options such as NPK micro-dosing, seed priming and coating can increase pearl millet panicle yield. However, these options are barely available to the Sahelian women farmers in particular due to high cost and lack of skills. *Oga* (fermented-human-urine) was developed as an innovation to ameliorate soil chemical fertility and, in turn, increase pearl millet panicle yield. In large-N trials at women's fields in Maradi and Tillabery region of Niger (2014 – 2018), *Oga* (diluted at 1:1 ratio with water) was applied twice (15 and 30 days after sowing) as a fertilizer innovation at the rate of 0.2 liter per planting pocket. Results showed a consistent panicle yield increase between +200 to +300kg per hectare in general. *Oga* increased panicle yield in different soil types, social classes (*young, elderly with help and elderly without help*) and villages. *Oga* is effective, economical/affordable, socially accepted, simple to apply, and sustainable. *Oga* improves soil chemical fertility. Since sorghum and pearl millet are the two major staple crops produced in the Sahel, transferring the *Oga* pearl millet innovation to sorghum might increase yield and benefit the Sahelian women producers.

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Can low-input agriculture in semi-arid Burkina Faso feed its soil, livestock and people?

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In Burkina Faso, farmers optimize available resources based on principles of agroecology to compensate their limited investment capacity in production factors. We investigated farm-level management of resources to assess farms capacity to fulfil their food and feed requirements. We monitored for one year 22 households representing the diversity of the farming system in our study area. We quantified inputs and outputs in the cropping system (177 fields), along with crop residue dynamics. Moreover, resource flows at farm level were quantified weekly. Cropping systems were characterized by a negative nitrogen balance of about 12 kg N/ha/year, with market-oriented farms and large livestock owners having the most negative balance. Legumes grown (sole and intercropping) contributed to alleviate the nitrogen depletion by adding 15 kg N/ha/year to the nitrogen inputs through atmospheric fixation, but cereal-legume intercropping benefits were limited because of the small proportion of legumes (8%) in intercropped fields. Livestock grazed crop residues left on the soil (739 kg dry matter/ha) at a rate of 26 -76 kg/ha/week, thus strongly reducing the potential for mulching in the region. Livestock protein requirements were rarely met from farm-produced feed with average feed gaps ranging between 40 and 89% of the daily requirements for small and large herd keepers respectively. Large livestock owners relied on transhumance during the rainy season, grazing (73 and 58% of metabolizable energy and protein respectively), and frequent purchase of crop residues and concentrates to feed their livestock. The amount of grain produced was generally enough to fulfil household energy requirements (89-175% of kcal required); except for household under land scarcity. Current farm management provides enough food for the majority of farms, but results in soil fertility mining and poor crop livestock production. More legume crops, associated to improved manure and forage management, are needed to sustain crop and livestock production.

Co-designing sorghum-based cropping systems with rotations to improve soil fertility and yield in Burkina Faso

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Farm households in Burkina Faso face many challenges including poor soil fertility, climate variation and land constraint due to migrants arrived from the North of the country. Low soil fertility prevents farmers from achieving food self-sufficiency and food security. The present study aims at co-designing and testing in a participatory setting, sorghum-based cropping systems to improve soil fertility and yield as soil infertility was mentioned by farmers as their main constraint. Researchers and farmers suggested three rotations which were tested in on-station trials in two contrasted communities. The experiment was designed following a fisher block with four repetitions. In the first year, cowpea, mucuna and crotalaria were grown in sole crop system. In Tanvousse, all the plots received organic manure 2.5t/ha and in Nagreankoudogo all the plots received NPK, 75kg/ha with localized application. Cowpea and mucuna biomass were harvested but crotalaria biomass was left in the plot. For the second year, sorghum was grown in all plots with the same conditions of fertilization, therefore, we had sorghum preceded by cowpea (T1), sorghum preceded by mucuna (T2), sorghum preceded by crotalaria (T3). During the growing season, two participatory evaluations were conducted. Results showed that T1, T2 and T3 produced respectively 900 kg/ha, 900 kg/ha and 800kg/ha of sorghum grains in Tanvousse and 2100 kg/ha, 1900 kg/ha, and 2100 kg/ha in Nagreankoudogo. Striga impact was recorded because farmers consider it as fertility indicator. For striga impact in "striga/100 sorghum plants", T1, T2 and T3 got respectively 72, 140, 55 in Tanvousse and 180, 60, 65 in Nagreankoudogo. At the flowering stage, farmers first choice was T2 in Tanvousse and T1 in Nagreankoudogo. At the maturity of sorghum, farmers first choice was T1 in both communities which also got the highest yield in both communities. Farmers opinion seems to be context dependent.

Exploration of sorghum genetic variability for adaptation to intercropping with cowpea - case study in Burkina Faso -

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The ecosystem services provided by intercropping have been clearly demonstrated. The association of two or more crops in a same field allows to produce more grain per unit area than the component crops grown in pure stand. In particular, sorghum-cowpea intercropping is both a traditional and a promising way for the intensification of smallholder's fields in soudano-sahelian conditions. In the present study, we aimed to explore prospects of dedicated breeding for improvement of sorghum adaptation to intercropping through the characterization of genotype by cropping system interactions within sorghum germplasm and of specific adaptation traits.

From a larger collection, 30 sorghum varieties were selected based on 2-year data with the aim of retaining the greatest possible diversity while selecting the most adapted varieties to pedoclimatic conditions. The experimental design was a split plot with three replications evaluated over two cropping seasons in 2020 and 2021 in Gampela experimental station near Ouagadougou. For each variety, the elementary plot was divided into one subplot where the variety was cultivated in pure stand and one subplot where the variety was cultivated in a substitutive intercrop alternating one row of sorghum with one row of cowpea. A unique cowpea tester variety was used. Overall, thirty agro-morphological traits were measured.

Genotypic effects were highly significant for most traits. Year and genotype x year effects were highly significant. In both years, a significant correlation was observed between yield in intercrop and in pure stand ($R^2= 0.36$ in 2020 and $R^2=0.57$ in 2021), very few occurrences of significant genotype x cropping system interactions among all studied traits and no significant effects of sorghum genotypes on cowpea grain yield were observed. However, the behavior of some varieties that depart from this global trend will be analyzed. Implications for the implementation of breeding strategies targeting intercropping systems will be discussed.

Dual-purpose sorghum in Mali : adoption factors and producer perceptions

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Dual-purpose sorghum varieties appear as a viable option for better agriculture-livestock integration in the context of declining soil fertility affecting sub-Saharan Africa.

The objective of this study carried out in 8 villages in the Sudanian zone of Mali was to determine the factors of adoption of dual-purpose sorghum varieties and identify the perceptions of producers. The methodology was based on individual surveys of 165 farms.

Results indicated that ethnicity ($P=0.000$), ownership of livestock ($P=0.017$) and agricultural area ($P=0.003$) have a strong correlation with the adoption of dual purpose varieties. The Bambaras ethnic with an average of 13 ha and 16.7 Tropical Livestock Units appear to be the biggest adopters of dual purpose varieties (56.6%).

The dual-purpose varieties are generally well perceived by producers; 80% of them observed that they have a higher level of yield than their old varieties and are more resistant to drought; the results of trials conducted in stations and on farms confirmed this with 1700 kg per ha for the dual-purpose variety against 836 kg for the local one. but some producers (42%) found that they have a shorter shelf life due to pest attack.

According to 85% of respondents, the sweet and tender fodder of these varieties is highly appreciated by animals and children, which causes losses when the crop is still in the field and has led to the abandonment of dual-purpose sorghum varieties in some localities.

The results of this study show that the adoption decision of the producers does not depend only on the yield but on other factors such as the aptitude for conservation and the risks of losses by animals or children. The fact that children appreciated the dual purpose sorghum varieties (they eat them like sugarcane) could also open up new uses, for example in school gardens, and new markets.

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Brown midrib sorghum forages create new opportunities for animal producers in West Africa

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Feed shortages was identified to be one of main constraints limiting animal production for milk and meat in Niger. Stover from cereal crops are a significant source of feed during the long and dry season with producers showing preference for sorghum stovers. *Brown midrib (bmr)* sorghums are well known for improved forage quality around the world; however, farmers in Niger do not have access to *bmr* sorghum cultivars. To address this limitation, a new forages sorghum breeding program was initiated in Niger to introduce the *bmr6* and *bmr12* into elite Nigerien sorghum varieties. Agronomic studies were performed to determine the most efficient forage production systems. A double-cut technical package was developed and optimized that increased forage production. This system was evaluated using the most promising new *bmr* lines deployed on 107 farmers' fields in three agroecological zones. The results showed stover production increased by 1.4 to 2 using the double cut technique. Of the lines evaluated in these trials, farmers expressed interest in Sepon-82 *bmr6* (29%), MR732 *bmr6* (21%), Wassa *bmr6*(18%), Macia *bmr6* (16%), Irat 204 *bmr6* (8%), Check (VL) 5%. Animal performance trials were conducted using these lines using a set of 24 white Sahelian goats that included 12 males and 12 females. Goats fed the *brown midrib* lines performed significantly better than goats fed the local sorghum check showing daily weight gains of 4.23g/d and 2.24g/d, respectively. The use of *bmr6* and 12 genes into elites sorghum varieties genetic background may provide new opportunities for farmers in Niger and West Africa.

Keywords: Sorghum - Brown midrib - Technical package - Farmers - Nutritional value.

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Variability and Character Association among Forage Biomass and Nutritional Quality Traits of Sorghum Collections in Ethiopia

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A study was conducted to investigate variability and traits association on 166 sorghum collections prescreened from 2010 core collections planted in three replications in Ethiopia. Data were collected at booting stage of plant growth and development for several traits. The results revealed large variation in all traits. Among others, the *Invitro Organic Matter Digestibility* (IVOMD) of the genotypes were found significantly ($P < 0.05$) and positively correlated with Leaf to Stem ratio (LS), Crude Protein (CP) ($r = 0.81$) and Metabolizable Energy (ME) ($r = 0.99$), and negatively associated ($P < 0.05$) with Days to Booting (DCH), plant height (PLH), Brix, Stem Dry Weight (SDW), Total Dry Weight (TDW), Neutral Detergent Fiber (NDF) Acid Detergent Fiber (ADF) ($r = 0.86$), and Acid Detergent Lignin (ADL) ($r = 0.92$) concentrations. It can be concluded that sorghum genotypes of Ethiopian collection, possessing characters of earliness with more proportion of leaf to stem ratio have more CP, ME and IVOMD concentrations, whereas those having character of late maturity and tall plant height with less proportion of leaf to stem ratio have more dry matter accumulation, and sweetness - dominated by fibers (NDF, ADF, and ADL) and hence have less CP, ME and IVOMD concentrations. The implication is that there is considerable potential for selection and improvement among Ethiopian collections and land races for forage/fodder.

Enhancing the sustainable production of sorghum by exploiting biological nitrogen fixation by microbial symbionts associated with aerial roots

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Biological nitrogen fixation (BNF) by crop plants via microbial symbiosis decreases fertilizer dependence and is an effective approach to lowering the economic and environmental costs of crop production. BNF is commonly associated with legumes, but indigenous landraces of maize (*Zea mays* L.) in Oaxaca, Mexico can support nitrogen-fixing bacteria in the mucilage of their aerial roots (adventitious nodal roots) that supply 29-82% of the plant's nitrogen [1]. A similar phenomenon has been identified in select sorghum accessions. We are using a systems biology approach to investigate the mechanisms enabling these symbiotic interactions in sorghum. A genome-wide association study of the sorghum minicore [2] and the sorghum association panel (SAP) [3] in Florida and Wisconsin revealed that the proportion of genotypes forming aerial roots was 12-fold greater in the minicore than in the SAP, suggesting the presence of aerial roots has been under negative selection in modern breeding programs. The GWAS resulted in several candidate loci associated with the number of nodes forming aerial roots that are being validated through genetic analysis of segregating populations derived from crosses between bioenergy sorghums developed at the University of Florida and landraces that form aerial roots. In addition, we are using transgenic validation approaches relying on an improved sorghum leaf-whorl transformation system we developed. In parallel, a single-cell RNA-seq approach is being used to identify both the mucilage-producing cells in the aerial roots and the gene regulatory networks responsible for mucilage production. Analysis of the aerial root microbiome has identified several species of nitrogen-fixing microbes, and variations in species composition on different genotypes grown at different geographic locations. This multipronged approach is expected to enhance the sustainability of sorghum cultivation by reducing the dependence on chemical fertilizers. Funded by the U.S. Department of Energy Office of Biological and Environmental Research grant no. DE-SC0021052.

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Understanding the spatiotemporal regulation of biosynthesis of sorgoleone, an inhibitor of nitrification secreted from sorghum root hair cells

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Modern crop production heavily relies on N fertilizer. Fertilizer-derived NH₄⁺ is converted to NO₂⁻, then to NO₃⁻ in the process termed nitrification. Nitrification and subsequent denitrification (microbial reduction of NO₃⁻ and NO₂⁻ to gaseous forms of N, mainly N₂ and N₂O) promote massive loss of N from the soil, which typically accounts for more than half of N fertilizer applied to the soil. Some plant species are capable of inhibiting nitrification in the root zone, (termed Biological Nitrification Inhibition, BNI), which increases the N retention and availability. However, agriculture in 20th century largely ignored BNI, because it was easier to simply add more N fertilizer to compensate for the loss. Such over-application, however, caused multiple problems in the environment, including the emission of the powerful greenhouse gas N₂O and groundwater contamination by NO₃⁻. Previous studies have shown that N losses from the field as N₂O and NO₃⁻ are reduced around the rhizosphere of BNI-positive crops. Therefore, integrating BNI back into the major crop plants will provide a path to more sustainable agriculture.

Sorghum is special among the commonly cultivated crops in that BNI activity is found even in elite varieties. We are interested in increasing the amount of sorgoleone, the major BNI compound in sorghum. In this work, we have analyzed the spatiotemporal expression patterns of sorgoleone biosynthesis enzymes, and discovered that the synthesis is highly developmentally regulated. We also identified the endoplasmic reticulum (ER) as the likely site of sorgoleone biosynthesis, on which multiple enzymes within the pathway form a protein complex. We also obtained pharmacological evidence suggesting that an active transporter is involved in sorgoleone secretion. The results we obtained will serve as a basis for increasing sorgoleone secretion in sorghum or transferring the ability to other crop plants.

Harnessing root biology for sorghum adaptation to tropical environments with abiotic stresses

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Acidic soils with low-pH are prevalent in the tropical and sub-tropical world, encompassing many countries with strategic importance for world food security. The clay fraction of these highly weathered soils is enriched for aluminum (Al) and iron (Fe) oxides, which are the central chemical basis for important abiotic stress factors that limit crop yields on acidic soils. Under low soil pH, ionic Al damages the root system, restricting water and nutrient uptake. Phosphorus (P) on tropical soils is fixed to Al and Fe oxides, being highly unavailable for uptake by the plants. Hence, sorghum adaptation to tropical regions involves tolerance to multiple abiotic stresses, including drought. We approach this problem by investigating root biology as a source of adaptive traits for sustainable sorghum production on acidic soils. Using different types of sorghum populations, bi-parental and random mating populations, as well as diverse association panels, we detected genomic regions jointly associated with performance traits on a tropical soil, also showing the importance of overdominance for grain yield under stress. These populations with complementary genetic properties are being used as an important integrative resource to identify adaptive QTL and the underlying genes. Enhanced recombination in a random mating population, coupled with selection, has proven to be efficient for positional cloning of otherwise rare alleles underlying Al tolerance in sorghum. In addition, allele frequency shifts in selected progeny contrasting for grain yield on a low-P soil reinforces the role of *phosphorus starvation tolerance1* genes, which encode receptor kinases, on root morphology and sorghum grain yield under low-P availability. Finally, we will explore genomic selection approaches including both dominance effects and pre-detected QTLs as fixed effects for predicting grain yield and other traits assessed on acidic soils, as a way to connect gene discovery and molecular breeding targeting abiotic stress tolerance in sorghum.

Transcription factor nuclear trafficking elicited by aluminum sensing in the plasma membrane plays a role in the regulation of the sorghum *SbMATE* transporter

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Aluminum (Al) toxicity is a major constraint for crop production on acidic soils, which are widespread worldwide¹. In sorghum, the root citrate transporter, *SbMATE*, confers Al tolerance via Al-activated citrate release to the rhizosphere, where citrate binds and detoxifies Al³⁺². Previous findings revealed that *SbMATE* is transcriptionally regulated by a WRKY and a zinc finger-DHHC transcription factors (TF), *SbWRKY1* and *SbZNF1*, respectively, which bind to tandem repeats in the *SbMATE* promoter region to synergistically *trans*-activate *SbMATE*³. The present study aimed at elucidating the cellular mechanisms whereby *SbWRKY1* and *SbZNF1* transcriptionally regulate *SbMATE*. A phylogenetic tree for each protein family was inferred to explore the relationship of *SbWRKY1* and *SbZNF1* with WRKY and zf-DHHC proteins from other plant species. Electrophoretic Mobility Shift Assays were performed to finely map TF binding elements in the *SbMATE* promoter. Lastly, tobacco and Arabidopsis overexpressing *SbZNF1* and *SbWRKY1* fused to fluorescent tags were exposed to Al³⁺ to understand their localization dynamics under Al stress. We found that *SbWRKY1*, which is a member of the WRKY group III proteins, contains a rare heptapeptide variant in a key region for DNA recognition, and recognizes a novel *cis*-element for WRKY proteins. We established that *SbZNF1* localizes in the plasma membrane, consistent with its four predicted transmembrane domains, whereas *SbWRKY1* is located in the nucleus. Using Bimolecular Fluorescence Complementation assays, *SbZNF1* and *SbWRKY1* were found to physically interact in the plasma membrane and, in response to Al³⁺, *SbZNF1* is mobilized to the nucleus in a *SbWRKY1*-dependent manner. This study suggests that coordinated TF tracking in root apical cells in response to Al³⁺ may contribute to the previously observed synergistic action of *SbZNF1* and *SbWRKY1* on *SbMATE* expression.

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Sorghum aphid host plant resistance: Implications for global durability

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Genetic improvement of host plant resistance (HPR) to insects is a sustainable avenue for improving global sorghum productivity, however, biotype shifts can erase progress under high selection pressure. Sorghum breeding for HPR to the recent outbreak of sorghum aphid (*Melanaphis sorghi*) in the Americas has focused on *Resistance to Melanaphis sorghi 1 (RMES1)*. Using near-isogenic lines, we found that *RMES1* is reducing aphid reproduction and therefore vulnerable to a biotype shift. Pan-genome references with the *RMES1* allele contain a large insertion, harboring several immunity related receptor genes, relative to susceptible genotypes. This supports transcriptome and metabolome evidence of an induced HPR mechanism mounted in response to aphids. To provide sorghum breeders with a second source of HPR, association analyses in global landraces and Haitian breeding germplasm were performed. We identified *RMES2* on Chr09 which is likely already in use where aphid resistance is a breeding target. In contrast to the globally rare *RMES1* allele, *RMES2* is globally common and putatively encodes a WRKY transcription factor acting as a hub for defense gene induction. Marker development for *RMES2* is under way which will allow breeders to develop multigenic aphid resistance, enhancing the durability of individual HPR sources and sorghum sustainability.

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IMPACT OF HERBICIDE IMIDAZOLINONE-RESISTANCE TRAIT INTROGRESSION IN GRAIN SORGHUM (*SORGHUM BICOLOR* L. MOENCH)

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The development of sorghum crop's weed-control technologies is widely required for reducing significant yield losses that are registered due to the competition of weeds in different growing stages. A new herbicide tolerance technology was commercially launched in Argentina, Australia, USA, Brazil and other countries that confers herbicide imidazolinone resistance in sorghum and provides the possibility of weed control in pre and post-emergent herbicide applications¹. This technology is known and registered as "igrowth™ weed control". There were reported that when herbicide resistance trait is introgressed in crops, almost always has an effect in the crop adaptation that can have a direct impact on its productive capacity. The purpose of this research was to study the impact of herbicide imidazolinone resistance trait on yield and other attributes of interest on grain sorghum. The incorporation of the Igrowth gene on different genetic backgrounds was evaluated in experiments with and without herbicide application in different environments. The genotypes used in trials consisted of five conventional hybrids and their Igrowth™ iso-hybrids generated through conventional backcross method. No significant effects of the character were detected on yield in any of the evaluated iso-hybrids, leading to the conclusion that there is no loss of grain yield due to the trait introgression of the character. In contrast, the phenotypic variables studied had showed effects of the trait introgression. No significant differences were observed in aerial biomass with the herbicide application in igrowth™ hybrids. The trait-by-environment interaction was not significant and there were no significant effects of herbicide treatment-by-environment. These results would lead us to the conclusion that the mutation that gives resistance to the imidazolinone-herbicide chemical family is safe to develop commercial hybrids using trait introgression conventional methods.

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Population genomics of *Low Germination Stimulant 1* enabled molecular breeding of *Striga* resistant sorghum varieties

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Striga hermonthica is a devastating obligate parasite of staple crops in West Africa (WA). This parasite requires signals from the host for its germination. One of the mechanisms of *Striga* resistance is low germination stimulant production by the host due to loss of function of the *LGS1* gene. The development of resistant varieties through phenotypic selection is challenged by *Striga*'s spatial variability. Diagnostic markers targeting *LGS1* loss of function alleles could accelerate the development of *Striga*-resistant sorghum. The deletion of the cloned *LGS1* is hypothesized to confer resistance in WA *Striga* using breeder-friendly markers. The objectives of this study are to (i) identify single nucleotide polymorphisms (SNPs) that are linked and in linkage disequilibrium (LD) with *LGS1* deletion in diverse sorghum germplasm, (ii) develop Kompetitive Allele-Specific PCR (KASP) markers that accurately genotype these SNPs, and (iii) test the markers for *Striga* resistance in sorghum biparental population. Genotyping-by-sequencing polymorphism data for WA germplasm was analyzed to identify SNPs in LD with deletion alleles at *LGS1*. Eight SNPs that are linked and in LD with *LGS1* deletion were converted into KASP markers. Putative resistance and susceptible classes in inbred lines and F3 progeny of SRN39 (resistant) and Mota Maradi (susceptible) were differentiated through KASP genotyping. Root exudates from progenies with putative deletion of *LGS1* based on KASP assay were tested for laboratory germination assay of *Striga* seeds and in pot assay confirming the KASP results. Our findings confirm that these new KASP markers will be suitable for marker-assisted selection for *Striga* resistance in multiple genetic backgrounds of WA germplasm.

PP37 multi-parent advanced generation inter-cross (MAGIC) population – a resource for *Striga* research

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Striga (*Striga hermonthica*), a hemiparasitic plant, is a major threat to sorghum production in arid and semi-arid parts of the world where sorghum is a staple food crop for millions. Genetic resistance is considered the most effective control strategy against the parasite. Because of the unique and complex biological interactions between the parasite and the host plant, it is plausible that multiple genes for *Striga* resistance could be found. However, to-date, the only gene identified in sorghum that confers resistance to *Striga* is the low germination stimulant (*LGS1*) locus, when it is missing or altered in some resistant lines. The objective of this study was to identify new *Striga* resistant genes through a genome-wide association analysis (GWAS) conducted on a multi-parent advanced generation inter-cross (MAGIC) population, PP37. The population was constructed by crossing 25 founder lines known to be resistant or tolerant to *Striga* with 10 random male sterile (*ms3ms3*) plants in a population, allowing these crosses to randomly mate, each time advancing only seed produced on tagged sterile (*ms3ms3*) plants. After multiple generations of random mating, 1000 random recombinant fertile plants were subjected to five generations of selfing through single seed descent (SSD) to generate 1000 recombinant MAGIC inbred lines. The PP37 MAGIC inbred lines were then phenotyped for *Striga* resistance and agronomic traits for two seasons in Northwestern Ethiopia. The population showed a wide range in resistance with several lines exhibiting very strong *Striga* resistance. GWAS indicated a few new loci associated with *Striga* emergence counts that appear to be strong and independent of *lgs1*-based resistance. Moreover, GWAS for plant architecture traits resulted in prominent peaks indicating suitability of the population for mapping QTLs for several traits. With validation and characterization currently underway, MAGIC PP37 lines would be valuable germplasm resource for *Striga* research, breeding, and mapping.

The IAVAO crop network: a NARS led regional platform for germplasm exchange and multi-environment trials

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Tremendous progress has been made in terms of crop breeding in West-Africa. However, National breeding programs in West-Africa still have limited resources and are generally too isolated to access significant fundings allowing to develop more innovative breeding approaches. A regional network that brings together breeding programs on several crops including sorghum was initiated in 2018. It gathers 5 different countries in West-Africa (Burkina Faso, Mali, Niger, Senegal, and Togo) and creates the conditions of germplasm exchange as well as data and information sharing. The network is supported by a charter that establishes the rules and responsibilities of its members, covers intellectual property issues related to the exchange and use of germplasm and data, while ensuring a network as functional as possible, and confidence and trust among partners. Measurement variables and methods as well as experimental protocols have been collectively harmonized around common ontologies. Experimental data are stored and analyzed in a shared instance of the Breeding Management System (BMS) and accessible to the members of the network. Globally, since 2018, 61 sorghum varieties have been evaluated through experimental trials conducted in 21 different environments in West-Africa. Between 28 and 45 varieties were evaluated each year in 9 to 13 locations. The data produced so far provides a valuable database on the adaptation of a large set of sorghum varieties and breeding lines representative of the elite material that currently forms the core of national breeding programs in West-Africa. Germplasm exchange allowed breeders to test varieties from other countries and revealed them some interesting material for registration or as trait donors. The multi environment trials also provided valuable data to progress on characterization of photoperiod sensitivity and modeling of target environments. Perspectives to link and extend this network to on-farm testing networks and farmers' germplasm is also under development.

Characterization of adaptation mechanisms in sorghum using a multi-reference back-cross nested association mapping design and envirotyping

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The development of climate-smart varieties requires the identification of haplotypes influencing traits of agronomic interest with well-defined effects across environments. For that we need advanced crossing schemes, multi-environment characterization, and state of the art statistical methodology. In this contribution, we present a sorghum multi-reference back-cross nested association mapping population composed of 3901 lines produced by crossing 24 diverse parents to three elite parents from West and Central Africa (WCA-BCNAM). This population is potentially one of the most relevant sorghum resources for research and breeding purposes in that region. The population was characterized in environments contrasting for photoperiod, rainfall, temperature, and soil fertility. To analyse this multi-parental, multi-environment design, we developed a new statistical methodology for QTL detection and parental effect estimation. In addition, envirotyping data were integrated in our models to determine the influence of environmental covariables on the genetic effects. We used this strategy to analyse the genetic architecture of flowering time and plant height, which represent key adaptation mechanisms. Our results allowed a better characterisation of well-known genomic regions impacting flowering time concerning their response to photoperiod with Ma6 and Ma1 being photoperiod sensitive and candidate gene Elf3 being insensitive. We also accessed a better understanding of plant height genetic determinism with the combined effects of phenology dependent (Ma6) and independent (qHT7.1 and Dw3) genomic regions. The strategy implemented in this work illustrates the need of synergy between genetics, breeding, and statistical genetics to harness the potential of sorghum in a changing climate. The resources and tools developed in this project should serve the whole sorghum community, for example by providing relevant elite parents for breeding programs.

Performance of phenomic selection in sorghum : Exploring population structure and GXE effects on prediction accuracy

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The concept of phenomic selection has been formalized by Rincent et al. (2018) based on the idea that spectral information (Near Infra Red Spectroscopy (NIRS), Hyperspectral Imaging...) acquired from animal or plant tissues contains genetic information that can be used to predict the genetic values of candidates to selection. Together with this genetic information, spectra also captures information linked to the environment and genotype by environment interaction effects, that can also prove to be useful to optimize the prediction of individual's performances in different environmental contexts. Furthermore, because spectral information corresponds to intermediate phenotype (endophenotypes) located between the genome and phenotypes of interest, it can also capture interaction effects between genes that are typically difficult to obtain from DNA polymorphism information. This novel approach of phenomic prediction has proven to be relevant in several plant species, achieving higher genetic gains in a variety of contexts than with classical phenotypic or genomic selection approaches. In this study, we explored the relevance of phenomic selection to predict various traits of agronomic interest in two sorghum population's types. First, a broad-based population (GWAS) that has been evaluated across more than ten environments on which near infrared spectra were acquired on grains (1 environment) and stems (5 environments) was used. In addition, a large multi-reference Back-Cross Nested Association Mapping population, based on 3 recurrent parents and more than 20 donor parents (Garin et al., 2023), including more than 3900 BC1F4 families characterized in diverse conditions and for which NIRS spectra have been acquired on grains (1 to 2 sites maximum depending on the families) was also mobilized. Based on these populations, two questions were addressed, the effect of population structure on the prediction accuracies of genomic and phenomic selection and the definition of strategies to capture GXE effects to maximize prediction accuracies.

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Sorghum in the 21st Century Global Sorghum Conference

Resiliency and Sustainability in the Face of Climate Change

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ABSTRACTS WEDNESDAY 7 JUNE



ADVANTA Championing Future R&D Strategies in Genetic Improvement and Seed Treatment Technologies of Sorghum for Global Food, Feed, Fodder, Biofuel and Nutrition Security

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Advanta Seeds with its vast global presence is addressing crop improvement of climate resilient sorghum [*Sorghum bicolor*(L.) Moench] for green energy, human food, livestock feed and for industrial use. Advanta has made significant contribution in Sorghum improvement, and deployed novel technologies of Advanta across sorghum ecosystems. Our alignment with SDG goals aims at health and wellness to transform food and feed system, and diversification of agriculture with climate resilient Sorghums. Advanta Seeds – world leader in Sorghum have a systematic roadmap and plan of action to build credible future footprint leading to business plans in line with climate resilient agriculture.

Our drought tolerant productive grain sorghum hybrids, nutritive forages with Sweet stalks (Sugargraze, Megasweet) for juice based 1G ethanol production, High biomass sorghums for and 2G ethanol production, Brachy sorgho for Silage, High yield Brown Mid Rib SSG (BMR) Rocket and new generation fodder crops with high protein, palatability, digestibility have created successful value chains and markets in Indian subcontinent contributing to productivity gains, green energy, lower methane emissions, higher milk yields and enhanced health and bodyweight of the animals.

Sorghum hybrids with tolerance to sugarcane aphid marketed under the Advanta US, Inc. APHIX™ brand has been a success story also in Argentina, Brazil and Central America. We have also launched global proprietary technology IMI tolerant sorghum under iGrowth™ brand in Argentina, Uruguay, Australia, Brazil, Bolivia, and USA, which is a non-GMO trait from a specific recessive, single gene mutation. These technologies being tested in India is expected to provide greater productivity gains upon its registration and release in the next three years. This has been possible because of holistic partnerships and collaborations for the projects between Advanta and Public/Private institutes leading to fast-track technology generation, testing and uptake enabling livelihood security and economic profitability of small holder famers across globe.

Dutch bred Dusormil sorghums HD100 and HD7, were found suitable for harvest with a dual purpose harvester unlocking a multipurpose crop and its applications.

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In the Netherlands in 2022, two Dutch bred sorghums were tested by Farm Balance Cooperative and project partners. This was executed as part of an EU project for regenerative agriculture in the province Noord-Brabant: **Multipurpose Crops for Soil, Farmer and Construction. Supply chain development for food and construction materials with sorghum.** The Sorghums were tested for harvestability with a dual purpose harvester and found well suited. The grain was threshed and the straw was cut in pieces of 20 and 60 cm. HD7 grain was used for buffalo's feed while the HD100 was dried and milled. The flour was highly attractive for food products. The leaves were stripped and consumed by buffalo's leaving cleaned stems. The stems were dried and pre-processed in a hammer mill. The pre-processed fibres and cellulose were tested as insulation material, fibre board and bio composite. The stubble and roots enriched soil structure and organic matter. The Farm Balance Cooperative obtained proof of concept shows that Sorghum can be utilized as a multipurpose crop with a low nitrogen input and a high biomass output. Embracing both environmental as economical aspects for soil, farmer and Construction Stored Carbon (CSC). The project team worked with professionals and officials to develop this new use of sorghum in the Netherlands and possibly throughout Europe.

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Genotype by Environment Interaction and Stability analysis of Sorghum [*Sorghum bicolor* (L.) Moench] Genotypes in Western Ethiopia

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Sorghum is an important cereal crop used as a staple food in Sub-Saharan African countries. However, its productivity is still low due to the unavailability of high-yielding and stable improved varieties, compounded by the increasing impact of climate change on agricultural systems. Genotype performance depends on the genetic makeup of the genotype and the environment where it is grown, and climate change is expected to exacerbate the challenges of identifying stable and high-yielding genotypes. In this study, eighteen sorghum genotypes, including standard checks (Bonsa and Gemedi), were evaluated across three locations for two consecutive years in Western Ethiopia. The objective was to identify stable, adaptable, and high-yielding genotypes that can withstand the changing climate and be released in the study areas and other similar agroecologies of Ethiopia. Combined analysis of variance showed highly significant ($P < 0.01$) differences among tested genotypes for grain yield. The study also used advanced statistical techniques, including AMMI and GGE biplot analyses, to identify the most stable and high-yielding genotypes across the different environments. The result of AMMI showed that genotype and genotype-environment interaction were also highly significant ($P < 0.01$) for grain yield. The $G \times E$ term was partitioned into five significant Interaction Principal Component Axes, with only the first two capturing 63.4% of the $G \times E$ variance. Similarly, the GGE biplot analysis revealed that the first two PCAs explained 75.1% of the GGE variance. The results identified genotypes, ETSL 100124-1 and Baji X Lalo/ (16)-5-1/01, with yields of 2.74 ton/ha and 2.35 ton/ha, respectively, were not only high yielding but also stable across the different environments, indicating their potential for resilience to changing climatic conditions. Overall, the finding highlights the importance of developing crop varieties that can adapt to changing climatic conditions to improve productivity and food security in Ethiopia.

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Development of energy sorghum cultivars for bioenergy in Brazil

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Embrapa Maize and Sorghum develops cultivars for bioenergy involving the biomass and sweet types. This sorghums are characterized for their high biomass productivity, production of soluble sugars in the stem and high grain production as well as having a relative short growing cycle of four to six months (Castro et al, 2022; Pereira et al., 2022; Parrella et al. 2018). Also, in the current climate change scenario, sorghum becomes even more strategic as it is a water efficient species and is adapted to high temperatures and water deficits. Sweet and biomass sorghum cultivars can be divided into four categories based on the industrial transformation vehicle and photoperiod sensitivity. Photo-insensitive (PI) hybrids can produce 50 – 70 t ha⁻¹ fresh biomass and photosensitive (PS) hybrids can produce 120 – 150 t ha⁻¹ fresh biomass during the long days of summer in Brazil, making sorghum highly competitive with other bioenergy alternatives. Sweet sorghum is the traditional feedstock with juice extraction rich in sucrose for fermentation (G1-technology). We have developed a “Period of Industrialization – PIU” protocol for selecting sweet sorghum cultivars with high sucrose extraction for a minimum period of 30 days, facilitating “Industrial Planning”. Biomass photosensitive sorghum hybrids with dry stems and low sugar content are burned to generate vapor or electricity. Embrapa has also developed biomass sorghum hybrids with reduced lignin using the brown midrib mutant for Second Generation Technology G2 to transform cellulose and hemicellulose into fermentable sugars. In addition to this. All of these sorghum cultivars also have the potential to be used as a feedstock to produce biogas and biomethane. Genes for both biotic and abiotic stress tolerances have been introgressed into breeding lines and hybrids using both molecular and traditional breeding methods.

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Development of sorghum hybrids with good response to synthetic fertilizers to improve yield in Mali

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Sorghum [*Sorghum bicolor* (L.) Moench] is a very important food crop for many rural communities in Mali (Kergna et al., 2016). Several improved varieties and hybrids have been released in Mali over several years. However, sorghum yields in farmers' fields remain stagnant at less than 1 t ha⁻¹ on average. There are several factors attributed to low yields and major ones include; poor soil fertility, stress due to frequent droughts, pests and diseases. Another important factor affecting production of sorghum on farm is low use of farm inputs such as synthetic fertilizers. Some farmers have applied recommended good agricultural practices (GAPs) but the majority of varieties being grown by farmers, especially local varieties, do not respond well to application of synthetic fertilizers. To address this problem, ICRISAT and its partners are developing hybrids with good response to fertilizer application. Selected sorghum hybrids and varieties were evaluated for their response to synthetic fertilizers applied using varying fertilizer application rates in alpha lattice experimental design. Preliminary on-farm trial results observed led to the identification of 3 hybrids with good response to synthetic fertilizers with grain yield of about 3-4 t ha⁻¹ compared to varieties (checks) which had about 1 t ha⁻¹. These hybrids had higher yields compared to varieties which were included in the evaluation as checks. Some of these hybrids evaluated have since been released. Although many farmers are reluctant to apply fertilizers, the yield advantage observed from these hybrids with good response to fertilizers justify the need for use of synthetic fertilizers and improve yields.

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Sorghum Seed System Security situation among Smallholders in Semi-Arid Eastern Kenya

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Sorghum is an important food crop in many rural households in arid and semi-arid areas of Eastern Kenya. However, its production is limited by inaccessibility of adequate quantities of quality seeds adapted to the local prevailing agroecological and socio-economic conditions at planting time. The objective of the study was to determine factors influencing choice of sorghum seed sources and sorghum seed security situation in Makueni and Kitui counties of Eastern Kenya. Fifty sorghum growing households were randomly sampled and interviewed using a structured questionnaire. The sorghum seed security assessment approach focussed mainly on the functioning of seed channels. Result from Kitui County showed that 56% of farmers utilize seeds from Research Institutes while 36% use recycled seeds and 8% from their friend/ neighbours. In Makueni, 80% of farmers preferred using recycled seeds as their sorghum seed source. There was no significant difference ($P > 0.05$) in the quantity of sorghum seeds shared among neighbours/friends in both Counties. Factors such as level of education, age, and farm size significantly influenced the choice of sorghum seed sources. Farmers with different typologies considered issues such as seed quality, seed cost and influence from friends based on their contexts. Delayed supply of sorghum seed was highly mentioned by 60% and 32% of farmers in Makueni and Kitui, respectively, as the major problem when procuring seed. Other factors of concern included affordability at 28% and 32% in Makueni and Kitui respectively, and fake seeds at 12% in both counties. The informal seed sector was found to be the most important source, followed by informal sources. Thus, there is a need for deliberate effort to support the informal/formal seed sectors to benefit majority of smallholder farmers to ensure adequate and affordable supply of sorghum seed to reduce seed insecurity at planting time to support reliable food system.

Dissemination process of new seed variety in Senegal: analysis of the interactions of the actors of the millet and sorghum sectors

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One of the determinants of the low productivity of the millet and sorghum sectors in Senegal is the low use of improved varieties in rural areas. On average, the yields obtained on the farm are four to five times lower than those of the improved varieties obtained on the station (Diallo and Ndiaye, 2022). This low adoption is however attributable to a dysfunction of the seed system. This article aims to diagnose the level of collaboration and interaction of actors in order to find the bottlenecks that prevent the evolution of the seed system. A qualitative analysis of the survey data, based on the innovation spiral model of Wielinga (2016) and the Agricultural Innovation System (AIS) approach, was made. This analysis has shown that, in parallel with the hypothesis put forward at the start, the poor performance of the Senegalese seed system is attributable to the lack of interaction of the various actors that make up the system. Indeed, the analysis shows five major flaws that block the process :

- A linear diffusion process
- Weak synergy between ISRA and ANCAR
- Late notifications from the State for seed orders to be subsidized
- Insufficient pre-bases produced by ISRA
- The presence of non-professional actors in seed multiplication activities

The proper functioning of the seed system would then suppose the simultaneous application of policies on these five bottlenecks. Thus, the article proposes a retroactive dissemination model that makes it possible to simultaneously correct the shortcomings of the current system.

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Scaling the pearl millet and sorghum seedball technology in the Sahel

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In search of a simple effective innovation to increase the yield of pearl millet and sorghum for Sahelian smallholder farmers, seedball technology was developed. Seedball is a cheap *seed-pelleting* technology that combines sand, loam, and seed, with additives (woodash or NPK) to improve seedlings establishment in poor chemical fertile soil. Seedball is simple to produce, affordable, and based on indigenous-local materials; it saves seeds, reduces re-sowing and seedlings thinning time. Seedball was tested on pearl millet and sorghum in >5,000 field trials (2015-2018) in Maradi region of Niger Republic. For pearl millet, two seedball types were produced from a mixture of 80g sand + 50g loam + 2.5g seeds + 25ml water, which contained either 1g NPK or 3g woodash as nutrient additives. About 2.0cm diameter-sized seedballs were produced. For sorghum, the mixture was 80g sand + 50g loam + 1.5gNPK + 25ml water; 3.5 cm seedball which contained about 8 seeds each, were produced. Results showed seedball increased the yield of pearl millet between 12-33% across years, and about 32% in sorghum, depending on soil-type and nutrient content. Since seedball yield increase is more visible in sandy-soil, contextualize scaling is recommended to remote fields with sandy-soils of low fertility.

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Analysis of Macro-Institutional Determinants of the adoption of new sorghum/millet varieties in Burkina Faso

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Sorghum/millet yields have been on a downward trend since 2006 despite the development of new varieties. This paper identifies the macro-institutional determinants that govern the adoption of new varieties of these crops. It mobilizes the institutional economics approach and operationalizes it through descriptive and content analysis and ordered multinomial Probit regression. Qualitative and quantitative data were collected and combined with secondary quantitative data. The analytical results show a social willingness to adopt the new sorghum/millet varieties. However, economic and social incentives result in a scaling down of adoption compared to maize. This neglect, which is motivated by funding approaches, has led to the implementation of the community-based improved seed system, which is not subject to regulation. The specificity of these crops requires the support of a transitional seed access system.

Keywords: Institution - Sorghum/millet - Adoption - Ordered multinomial probit - Burkina Faso.

From demo plot to sorghum seed system construction: a journey with the tribal farmers of Adilabad District, India

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In this contribution we present the milestones and results of an ongoing long-term farmer-participatory project. The project supports tribal farmer communities in Adilabad District, India, by increasing their access to high quality- and diverse sorghum seeds. A large set of approaches and methods has been applied to meet the specific requirements of the target population. During the initial phase of the project, extensive surveys including a specific emphasize on cultural dimensions, allowed us to define the socio-economic-, cultural-, and environmental context of the farmers and identify specific needs in terms of dual-purpose (suitable for human consumption and animal feed) sorghum varieties. Subsequently, on-station experiments and demo-plots in farmers' fields were implemented to select a set of suitable varieties. Afterwards, those varieties were evaluated by 200 farmers from 20 villages during a Tricot (Triadic Comparison of Technologies) experiment, which is a first attempt to apply this citizen science approach to select sorghum varieties. The Tricot experiment was successful because 90% of the farmers decided to increase the surface of their most appreciated variety. We extended this study by performing a randomized control trial (RCT) to evaluate the ability of the farmers to produce their own seeds, following guidelines similar to the ones used for certification. The intervention was composed of a training and a motivational exercise, centred around the cultural importance of sorghum. During the RCT we identified important challenges, like the difficulty to teach new management practices and physical constraints to cultivate sorghum in isolated fields, to multiply open-pollinated varieties. However, we could identify a group of farmers with enough resources and abilities to become the basis of a decentralized multiplication system. Thus, our overall approach constitutes a promising strategy to implement concrete solutions for sorghum seed supply in challenging environments.

Environment characterisation of sorghum (*Sorghum bicolor* L.) crops using climate, satellite imagery, and crop simulation modelling in Australia

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Over the last decades, high-throughput phenotyping technologies have become increasingly important to measure environmental stress parameters at the canopy level in crops. The linkage of satellite imagery, sensors, and crop growth models have been proposed here to improve the characterization of sorghum crop environments in terms of genotype x environment (GxE) interactions. This study presents an attempt to evaluate the performance of sorghum crops based on climatic, remote sensing, and modelled stress indices experienced during specific developmental phases. Using historical data from the National Variety Trials (NVTs) in Australia, we integrated meteorological and satellite imagery data with crop growth models to generate biologically integrated environmental indices that can be incorporated into statistical prediction models. The key environmental covariables related to genotype specific responses were first identified for inclusion in the environmental characterizations. Functional clustering techniques considering the longitudinal character of the covariables were taken into account for the identification of sorghum agricultural zones. In addition, we evaluate the use of digital and model technologies to remotely track crop growth and development, and to quantify seasonal stresses in an efficient manner on sorghum NVTs. We discuss the deployment of these technologies to analyse how GxE effects can be related to environmental covariates derived from climatic and crop model assessments.

Environment characterization in sorghum by modeling water-deficit and heat patterns in the US Great Plains region

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The definition of target population of environments is critical to improve the efficiency of breeding programs in staple crops such as sorghum (*Sorghum bicolor* L.). The aim of this study was to characterize the target population of environments for sorghum within the United States (US) sorghum belt. The APSIM-sorghum crop growth model and ~35 years of historical weather data were employed to identify water-deficit (WSP) and heat patterns (HSP) for 15 sites spread across Kansas, Texas, and Oklahoma. Four WSP were identified with large differences in the timing of onset, intensity, and duration of the stress. In the western region, the most frequent WSP (~35%) was stress during grain filling with late recovery. Three HSP were defined, with the low HSP being most frequent (~68%). Field data from Kansas State University sorghum hybrid yield performance trials (2006-2013 period, 6 hybrids, 10 sites, 46 site x year combinations) were classified into the previously defined water and heat clusters. Both simulated and observed yield data showed that as the intensity of the stress increased, grain yield was reduced. The patterns were regrouped into four categories to generate a simple classification to be implemented in a breeding program. This new classification accounted for the observed genotype by environment (GxE) interaction. A better definition of target population of environments to improve predictability of GxE interaction could accelerate genetic gains.

Field-scale greenhouse gas fluxes from sorghum in the U.S. Great Plains using eddy covariance

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The current contribution of sorghum as a feedstock for commercial ethanol production in the U.S. is less than 5%. As a drought-tolerant, low-input crop with a comparable ethanol yield to corn, grain sorghum has the potential to make an increasing contribution to the ethanol market. However, this may require providing new market incentives for sorghum producers for carbon capture and reduced greenhouse gas (GHG) emissions. In this project, we continuously measured GHG emissions (in g CO₂e/acre) at the field level from a 100-acre sorghum field in the Texas High Plains Plains region for two years. We used the eddy covariance method to continuously measure CO₂, N₂O, and CH₄ fluxes. The field was managed with minimum tillage and nitrogen fertilizer was not applied during the growing season. Our results indicate that soil, plant, and environmental conditions strongly affected diurnal and growing season CO₂ exchange and respiration from the field. During the growing season, the field was a net carbon sink with uptake of approximately 4,200 kg ha⁻¹. The N₂O and CH₄ emissions in carbon equivalents were approximately 300 kg ha⁻¹. In addition, we found a significant correlation between diurnal N₂O emissions and soil heat flux during high emission periods in the growing season. Incorporating results from our study with modeling can improve our understanding of the GHG budget of sorghum cropping systems and its impact on the overall carbon intensity of sorghum ethanol production.

Sorghum in France: climate-related yield and its perspectives

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France is the first European sorghum producer, cultivating grain and fodder sorghum, single or multi-cut, mainly intended to feed livestock. French sorghum cultivated areas tend to rise, especially trusting the fact that sorghum is a resilient crop to face the warmer and drier summer caused by climate change. From 2003, Arvalis along with GEVES and UFS Sorgho lead and contribute to a field trials network to assess grain sorghum cultivars performances in various climates. This data base, representing a total of 6753 location-cultivar-year combinations (with a mean of 30 locations and 52 cultivars per year), allows us to monitor grain yield potential according to production areas and phenology evolutions throughout the years. Other specific trials were led to assess sorghum production response to water availability along sorghum cycle. With that in mind, we developed a function to predict yield under water deficit, considering the potential yield without water constraint, the real evapotranspiration (RET) and the maximal evapotranspiration (MET). This function paired with a water balance (in this case Irré-LIS®) allows us to evaluate water deficit impact on sorghum production. In the near future, sorghum in France and abroad will undergo numerous water deficit scenarios. Our work at Arvalis, combining cultivar x environment trials and specific water response field experiments, is helpful to guide farmers choices to optimize and secure their yield.

Composts from two invasive species (*Hyptis suaveolens* and *Chromolaena odorata*) enhance stem sugar and grain production in photoperiodic sweet sorghum

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Moving towards more sustainable agricultural production requires gradual decrease of mineral fertilizers use in the cropping system. The present study was undertaken to improve the cropping practices on sweet sorghum. It aimed at assessing the impact of compost from two invasive species, on agro-morphological performance of sweet sorghum grown under optimal water conditions. A field experiment was conducted during three different growing seasons (one in 2020 and two in 2021) at Abomey-Calavi (Benin) under rainfall conditions supplemented by drip irrigation. A split split plot design was used to study three factors. The first was the source of compost produced using two invasive species: *Hyptis suaveolens* (S1) and *Chromolaena odorata* (S2). The second factor was the dose of fertilizer with five modalities: 100% compost (D1), 25% Mineral + 75% compost (D2), 50% Mineral + 50% compost (D3), 100% Mineral (D4) and 0% Mineral + 0% compost (D5). Three sweet photoperiodic sorghum genotypes were studied (G1, G2 and G3). Our results showed that the growing season has significantly affected all the studied variables. Compost from S2 has better improved leaf and stem biomass, stem sugar related traits and grain production in the first two seasons while S1 improved better these traits in the third season. The dose of 100% compost showed the best performance for sugar and grain production in the first and third seasons. On the overall experiments, genotype G2 showed the best performance for sugar and grain production with compost S2. Significant correlations were found between stem dry weight (DW) and sugar content and also between panicle DW and sugar concentration at maturity, showing a good ability for dual purpose for these genotypes. These results will help to improve the practices regarding the use of organic fertilizer in sorghum cropping as an alternative to inorganic fertilizers.

Characterization of genetic variants in carotenoid biosynthesis pathway, a hub for sorghum crop improvement

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Crop breeding must develop nutrient dense varieties resilient to environmental stressors and pests. In sorghum, carotenoid biosynthesis could be a major target for breeding as important metabolites involved in striga tolerance, drought response and pro-vitamin A are derived from this pathway. Despite its potential, breeding for carotenoids is challenging as the phenotyping often relies on high-performance liquid chromatography (HPLC) which is expensive, time-consuming, and highly technical. Marker assisted selection could provide a cost-effective and breeder friendly alternative however, allelic variants correlated with carotenoids must be identified. Given the essential role of carotenoids in plants, we hypothesize that functional domains of carotenoid biosynthesis genes are conserved across plant species. To test this hypothesis, protein sequence alignment of 64 genes involved in carotenoid biosynthesis will be done for homologs in sorghum, maize, rice, and arabidopsis. We expect to identify regions with high conservation at the amino acid level across species for the gene families. The conserved regions identified will be used to identify functional variants in sorghum pan-genome using snpEff. We hypothesize that among the functional variants identified, there will be some correlated with the genotypes' carotenoid content, drought response and striga tolerance. Variants that show high effect on these traits will be used to develop breeder friendly KASP markers. The outcome of this study will be a toolkit of markers and donor lines that can be used to quickly introduce higher beta carotene concentration, higher striga resistance and higher drought tolerance in sorghum breeding programs.

Genomics of Sorghum Grain Carotenoid Bioavailability

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Carotenoids are a group of plant compounds that are a major dietary source of vitamin A globally. Consumption of higher levels of carotenoids are associated with health benefits such as improved immunity, visual health function and a reduced risk of age-related macular degeneration. Regions experiencing the most food insecurity and vitamin deficiencies rely on cereal based diets, such as sorghum, that are generally low in carotenoids. Molecular breeding can be used to increase carotenoid concentrations to biologically relevant levels, however, the carotenoid bioavailability must also be considered during the breeding process. We hypothesized that sorghum grain carotenoid bioaccessibility is an oligogenic trait that is correlated with other grain composition traits. To test these hypotheses, we 1) conducted Pearson's correlations between grain composition traits and carotenoid bioaccessibility ($n=62$), 2) measured carotenoid levels and relative bioaccessibility in a diverse panel of sorghum accessions ($n=128$) via HPLC and in vitro digestion, and 3) conducted genome-wide association studies (GWAS) to identify marker-trait associations between carotenoid bioaccessibility and single nucleotide polymorphisms (SNPs). Significant correlations were identified between carotenoid bioaccessibility and starch, fat, and protein content. GWAS identified significant SNPs associated with carotenoid bioaccessibility. There was also a strong peak on chromosome 6 with an association with provitamin A carotenoid bioaccessibility. These results identified for the first time in sorghum, markers underlying variation in carotenoid bioaccessibility, and with further research these markers can contribute to efforts aimed at carotenoid biofortification.

Analysis of polysaccharide composition during sorghum grain development

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Sorghum (*Sorghum bicolor* (L.) is the fifth most important grain produced in the world. Native to Africa, sorghum is now cultivated all over the world. In a context of climate change, its cultivation is increasing in Europe due to its low input and water requirements. The attractiveness of sorghum grain is also explained by its nutritional qualities, in particular its gluten-free and relatively high content of polysaccharides and proteins.

In sorghum grains, polysaccharides are of two types: storage and parietal polysaccharides. Storage polysaccharides are composed of starch (60-75% of grain) accumulated in the endosperm. Cell wall polysaccharides, representing 2 to 7 % of grain weight, are mainly arabinoxylans and mixed β -glucans. Beside their structural role, cell wall polysaccharides impact the nutritional and technological qualities of grains as they represent the vast majority of dietary fibers.

While the composition of cell walls in mature grains has been well studied, less is known about the polysaccharide deposition during grain development and the mechanisms that drive their assembly within the cell wall, even though they are key factors in determining the physico-chemical properties of cell walls and the end use of grain.

In this purpose, polysaccharides in the endosperm and outer layers of grains were analyzed at different stages of grain development. Mixed β -glucan and starch contents were also determined. By specific stainings and immunolabellings, polysaccharides were monitored in the different tissue layers. To go further, transcriptomic analyses were carried out after laser microdissection of grains to separate endosperm from outer layers. This analysis led to the determination of genes involved in the biosynthesis and remodelling of cell wall polysaccharides.

These overall results provide new knowledges on polysaccharide assembly during the development of sorghum grain.

Sorghum grain germination reveals new opportunities to improve kafirin digestibility: biochemical insights and Mass-spectrometry label-free based quantitative proteomics

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Sorghum (*Sorghum bicolor* L.) is the 5th most produced and consumed cereal over the world. In Europe its cultivation is on the rise as the summer drought and *heat* stress are becoming common. However, kafirin, the sorghum grain storage protein presents lower digestibility compared to their main cereals counterparts. Germination has been proposed to be a suitable bioprocessing method to improve the protein digestibility of cereal and legume seed proteins. Here and for the first time, the *in vitro* protein digestibility from sorghum germinated seeds was connected with the dynamic changes of the proteome and biochemical markers. Germination was rationalized so as to evenly sample the grains from the dry state to the radicle emergence. Flour free sulfhydryl groups increased during germination and *in vitro* protein digestibility improved even though kafirin proteolysis remained a late event. Several proteins harboring oxidoreductases, chaperones and/or enzymatic activities were found differently abundant during germination. The dynamics in relative abundance of several hydrolytic enzymes was found to coincide with appearance of water/salt soluble kafirin derived peptides. We identified several proteases candidates whose abundance were increased at boot time of kafirin degradation. The present study provides the first deep information about the molecular and cellular events occurring during sorghum seed germination and reveals potential biomarkers of the kafirin proteolytic breakdown by endoproteases proteases. It uncovers new opportunities to improve sorghum nutritional value through the use of driven germination.

Keywords: Sorghum seed - Germination - proteomics - Endoproteases - Kafirin - In vitro digestibility.

Grain filling duration in sorghum: Opportunities for yield improvement

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Yield increases in sorghum have been achieved primarily by increasing grain number. Scope exists to increase yield by increasing grain size, however this has been limited by the negative correlation between grain size and grain number. The duration of the grain filling period has the potential to enable increased grain size without a trade-off with reduced grain number. In this study we explored grain filling duration (GFD) in a diverse panel of 904 sorghum lines, in three environments across two years. Significant variation in GFD was observed, ranging from 400 to 750 thermal units including significantly longer GFD than current commercial hybrids. Longer GFD was shown to result in larger grain size. Additionally, no significant association was observed between GFD and grain number per panicle, flowering time, or plant height, indicating that GFD can be manipulated without penalty to these traits. A simulation study to estimate the benefit of an increased GFD across sorghum growing environments over 60 years revealed positive impacts on yields when GFD was increased by either 10% or 20% respectively. These results reveal opportunities to exploit GFD for improved genetic gains for yield in sorghum especially in environments or seasons where water is not limiting post anthesis.

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What doesn't kill you makes you stronger: the benefits of being cyanogenic in a changing world

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Sorghum contains the cyanogenic glucoside, dhurrin, which breaks down to release hydrogen cyanide (HCN, prussic acid). Plants that are young, stressed or have been heavily fertilised are toxic to grazing animals and can cause death. This has always been considered a problem, representing a diversion of valuable resources that could otherwise have been used for growth, in addition to the dangers of toxicity to stock. Here, three lines of evidence are used to analyse the costs and benefits of producing dhurrin: comparison of the growth and stress tolerance of cultivated sorghums with EMS mutants lacking dhurrin (*tcd1*); analysis of the expression of dhurrin pathway genes using RNAseq at different stages of development; and genomic and phenomic analyses of the wild relatives of sorghum native to northern Australia, representing all the different subgenera. Considered together, the results support the hypothesis that in cultivated sorghum dhurrin is primarily used a defence against herbivores in young tissues but plays important roles in stress tolerance and optimising nitrogen management. in older plants. The Australian sorghums display completely different patterns of allocation. For example, they have very low concentrations of dhurrin in the leaves and stems and, in some species, show little response to drought and fertilisers. This tertiary gene pool may provide alternatives ways to develop low toxic forage sorghum that do not compromise the benefits from cyanogenesis detected in cultivated species particularly under conditions of high temperature and drought.

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Modulating brassinosteroid signaling to confer drought tolerance in Sorghum

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Sorghum (*Sorghum bicolor* (L.) Moench) is a cereal ranked among the five main cereal crops in the world and a staple food of billions of people in Asia and Africa. However, drought is a limiting factor in areas where it is cultivated, compromising its productivity and hence grain yield and quality. Our group discovered that by modulating brassinosteroid (BR) signaling it is possible to confer drought resistance in the plant model system *Arabidopsis thaliana* (Fàbregas et al., 2018).

In the current work, we found that Sorghum BRI1 receptor controls osmotic and drought stress responses by heterologous complementation of *bri1* mutants in *Arabidopsis* with Sorghum BRI1 protein. Moreover, a weak mutation in the Sorghum BRI1 receptor conferred osmotic stress and drought tolerance without compromising growth in Sorghum 'BTx623' inbred variety. Transcriptional studies by RNA-Seq and metabolic studies by LC-MS, uncoupled the drought tolerance of *bri1* mutants and growth penalization, suggesting a direct regulation of drought key genes and metabolites. In conclusion, we have proved that BRI1 is not only a positive regulator of growth but also a negative regulator of drought stress. Current efforts are being made to generate BR receptors overexpressors and CRISPR/Cas9-based mutants, by *Agrobacterium tumefaciens*-mediated Sorghum transformation using morphogenic regulators. Fine-tuning BR signaling can confer drought tolerance without penalizing overall growth, ensuring the current needs of food security.

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Differential responses of antioxidant enzymes in two sorghum lines contrasting in water deficit and salt tolerance

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Sorghum bicolor (L.) Moench is an African indigenous crop used as human food for at least 500 million people. Drought and salinity reduce yield in sorghum, despite sorghum having better tolerance to drought than other staple food crops such as maize and rice. Oxidative stress is among the many mechanisms by which drought and salinity cause damage to plants. Therefore, identification of sorghum genotypes in which the extent of oxidative stress is restrained during drought and salinity conditions is useful in understanding some of the biochemical machinery mediating sorghum tolerance to drought and salinity. We thus used differences in period to leaf rolling under water deficit stress or leaf browning under salinity stress as indicators of differences in drought tolerance or salinity tolerance, respectively, between two contrasting sorghum genotypes. The Alisto genotype showed leaf rolling much later than the Wbk genotype under water deficit conditions but showed leaf browning earlier than the Wbk genotype under NaCl-induced salinity stress. Biomass loss was less pronounced in Alisto in response to water deficit than in Wbk, whereas the biomass loss was less pronounced in Wbk than Alisto in response to salinity stress. These contrasting responses corresponded to differences in lipid peroxidation and distinct differences in the responses of specific isoforms of superoxide dismutase, ascorbate peroxidase and catalase between Alisto and Wbk in response to water deficit or salinity. These findings suggest that Alisto is more drought tolerant than Wbk, whereas Wbk is more salinity tolerant than Alisto. Furthermore, we conclude that the differences in the level of induction or attenuation of the activity of specific isoforms of antioxidant enzymes contributes to the observed differences in responses to drought or salinity between Alisto and Wbk.

Virus-induced gene silencing facilitated the discovery of a new gene affecting the photosynthetic capacity of sorghum under cold stress

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Manipulating the photosynthetic capacity of plant species will be required to meet the future global demands for food, feed, fiber, and fuel. This strategy would be particularly relevant under the predicted future climate scenarios of more frequent and intense abiotic stress events because any environmental stress limits the amount of fixed CO₂ and triggers photoprotection mechanisms. We have dissected the genetic architecture that controls the photosynthetic capacity of sorghum (*Sorghum bicolor* L. Moench) under non-stress, cold and drought stress, and discovered several polymorphisms that explained variation in the carbon fixation capacity. A 4kb region on chromosome 7 containing three candidate genes was consistently associated with variation in gas exchange and chlorophyll fluorescence parameters under cold stress. After sequencing these candidates, an uncharacterized *lipoate protein ligase* (*LPL*) gene emerged as the most promising target for further validation. Therefore, we utilized foxtail mosaic virus (FoMV) to implement a virus-induced gene silencing (VIGS) method and investigate the function of LPL on the carbon fixation capacity of sorghum during cold stress (16°C/16°C) and a recovery period (28°C/24°C). *LPL* silencing caused a significant reduction in leaf carbon assimilation rate, concomitant reductions in several chlorophyll fluorescence parameters, and a lower rate of lipoylation of two known *LPL* substrates (pyruvate dehydrogenase and α -ketoglutarate dehydrogenase). This study demonstrates the effectiveness of FoMV VIGS to characterize gene function in sorghum and reveals *LPL* as a new photosynthesis-related gene that could be exploited to manipulate carbon fixation under cold stress conditions.

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Brown Midrib brachytic dwarf sorghum silage as a high-quality forage alternative

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Brown midrib (BMR) brachytic dwarf sorghum silage is an important alternative to high-quality forage and produces better nutritional value than non-BMR sorghum. The main objective of this study was to measure the effects of sorghum variety type (grain sorghum versus brachytic dwarf forage sorghum), trait [brown midrib (BMR) vs. non-BMR], and harvest time on dry matter yield (DMY), nutrient composition, and fiber quality, of whole-plant sorghum grown in 5 locations in Argentina from 2021 to 2022. A total of 4 grain sorghum, 3 non-BMR brachytic dwarf forage sorghum, and 2 BMR brachytic dwarf forage sorghum hybrids were tested for a total of 9 hybrids. The experimental design was a randomized complete block design (RCBD) with 2 repetitions. Whole-plant sorghum silage was harvested at 3 different times: Before optimal harvest time (25-28% of dry matter (%DM)), optimal harvest time (32-35%DM), and after optimal harvest time (>38%DM). Dry Matter yield was greater for non-BMR brachytic dwarf forage sorghum than BMR brachytic dwarf forage sorghum. Significant differences were observed between BMR hybrids and non-BMR hybrids for predicted 30-h neutral detergent fiber digestibility (NDFD30h) (as % of NDF). Additionally, this greater predicted NDFD30h in BMR sorghums versus non-BMR was maintained throughout the different moments of harvesting. There was about 8 to 14 points difference of NDFD30h in favor of BMR sorghum versus non-BMR sorghum. At later harvest moments, the content of DM and starch were increased, while NDF was decreased, with a slight decrease in predicted %NDFD30h. Harvesting around 32 to 35%DM, allows obtaining a higher starch content, without significantly reducing fiber digestibility. Currently Advanta has a collaboration agreement with the Córdoba University to measure gas methane emissions in beef cattle fed with BMR sorghum compared to non-BMR materials.

The brown midrib (*bmr*) mutants prevent stalk rots under drought conditions and improve sorghum biomass quality

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Lignin provides rigidity to cell walls and a barrier against pathogens but decreases biomass digestibility. Sorghum *bmr* increases digestibility for livestock and bioenergy uses. Loss-of-function mutations in *Bmr2*, *Bmr6*, and *Bmr12* encoding monolignol biosynthetic enzymes 4-coumarate:CoA ligase, cinnamyl alcohol dehydrogenase, and a caffeic acid O-methyltransferase, respectively, result in reduced lignin levels and increased digestibility. Surprisingly, near-isogenic *bmr2*, *bmr6* and *bmr12* well-watered greenhouse-grown plants were equally or more resistant to *Fusarium* stalk rot (*Fusarium thapsinum*) and charcoal rot (*Macrophomina phaseolina*) than their corresponding wild-type. Because sorghum is vulnerable to stalk rots during drought, we developed a greenhouse protocol to evaluate lines for disease responses under water-deficit conditions. Under water deficit, near-isogenic *bmr2*, *bmr6* and *bmr12* lines were equally or more resistant to the two stalk pathogens than their corresponding wild-type. Three alleles of *Bmr19* that encodes a folylpolyglutamate synthase in 1-carbon metabolism, one allele of *Bmr30* that encodes chalcone isomerase in flavonoid biosynthesis, and two alleles from unidentified genes (*Bmr29* and *Bmr31*) were incorporated into three parental lines to develop near-isogenic lines. Most *bmr* lines were as resistant to the stalk pathogens as their corresponding wild-type. Under water-deficit condition, wild-type BTx623 was highly susceptible to *M. phaseolina*, while near-isogenic *bmr29-1* and *bmr31-1* lines were as resistant as counterparts grown under well-watered conditions. Following *F. thapsinum* and *M. phaseolina* inoculations, *bmr12* showed increased salicylic and jasmonic acids, phytohormones involved in defense signaling, than the wild-type, using targeted metabolomics; *bmr12* also showed increased induction of defense genes under water deficit, using RNA-sequencing, indicating that drought conditions primed *bmr12* for pathogen defense. These studies provide evidence that impairing lignin synthesis does not weaken sorghum defenses against fungal pathogens, and *bmr* mutants may be valuable for development of hybrids with increased resistance to pathogens and drought for improved stover quality and usability.

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The *brown midrib (bmr)* mutants: a tool to tailor lignin synthesis in sorghum for forage end uses

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Our goal is to tailor sorghum biomass composition for forage and renewable products. The *brown midrib (bmr)* mutants of sorghum and other C4 grasses have a visible red to brown leaf midrib in contrast to green or white midribs observed in wildtype plants. This phenotype, more importantly, is associated with reduced lignin content and altered lignin composition, which has led to its use to increase forage digestibility for ruminant livestock and potential applications for conversion of biomass to biofuels and renewable chemicals. The sorghum *bmr* mutants were generated through chemical mutagenesis (EMS and DES). *Bmr2*, *6* and *12* encode enzymes in monolignol biosynthesis (4-coumarate-CoA ligase, 4CL; cinnamyl alcohol dehydrogenase, CAD; caffeic acid-O-methyltransferase, COMT), which synthesizes hydroxycinnamoyl alcohols polymerized into lignin within cell walls. *Bmr19* encodes folypolyglutamate synthase (FPGS), an enzyme required for regeneration of the cofactor SAM, which is the methyl donor for many biochemical pathways. *Bmr30* encodes a chalcone isomerase required for flavonoid synthesis, and the flavonoid triclin is part of the lignin polymer in grass cell walls. *Bmr29* and *Bmr31* are being identified through a mapping by next-generation DNA sequencing approach. Progress to date indicates that neither locus encodes an enzyme directly involved in the synthesis of monolignols. These characterized *bmr* mutants have reduced lignin concentration in biomass compared to their wild-type counterparts, even though lignin concentrations are less impacted in *bmr* mutants not directly affecting monolignol synthesis (*bmr19*, *bmr29*, *bmr30* and *bmr31*). The *bmr* mutants represent potentially valuable tools to manipulate lignin synthesis beyond what has been previously observed in sorghum and to enhance biomass composition for forages and bioenergy feedstocks. We are currently combining alleles from different *bmr* loci together to further reduce lignin levels and alter its composition within sorghum cell walls.

Prussic-acid Free Sorghum Creates New Opportunities for Hay and Silage Production

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Sorghum is well-adapted to low-input, drought-prone environments. The crop generally requires less water to grow compared to maize and exhibits excellent performance in diverse agricultural production systems. Forage sorghums are of great interest to farmers in semi-arid environments because of their high biomass potential; however, the accumulation of dhurrin in leaves and stems can create risk for HCN toxicity in livestock feed. Recent studies have shown that dhurrin is stable in dry sorghum tissue samples and can be readily released as HCN when rehydrated with water or rumen fluid. Dhurrin-free sorghums are being developed by mutagenesis as tools to eliminate the risk of HCN toxicity. Greenhouse and field trials have shown that dhurrin-free plants exhibit higher growth rates than wild-type plants but these plants also have greater susceptibility to FAW feeding at the seedling stage. Comparisons of near-isogenic lines (NILs) and near isogenic hybrids (NIHs) with contrasting dhurrin accumulation patterns have demonstrated few differences in leaf greenness or plant productivity characteristics between wild-type and dhurrin-free genotypes. Animal feeding trials demonstrated favorable feeding preference for dhurrin-free sorghum genotypes with no reduction in nutritional quality. Taken together, these studies suggest that dhurrin-free sorghums may provide a new tool for managing the risk of HCN toxicity in livestock.

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The Impact of Collaboration on Sorghum Research and Development System in Africa: The Case of Ethiopia

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Ethiopia is an agrarian country with 50% of GDP, 85% of employment (the rural population of Ethiopia), 90% of earnings from export, and 70% of raw material required for agroprocessing industries contributed by Agriculture. Ethiopia is rich in crop diversity of which sorghum is one. Annually 1.8 million ha of land is allotted for sorghum production for production of 3.6 million metric tons of grain. It ranks third in both total area coverage next to tef and maize. Despite the strategic importance of sorghum, its productivity is very low.. The major reasons for low productivity have been human resource, physical, financial and technical capacities in research and development. In order to alleviate these challenges, collaborative projects have been implemented, of which iMashilla, SMIL, HOPE and ISC are some of the few. Key performance indicators have been used to assess the impact. In view of the collaboration, Ethiopia is now the third largest sorghum producing countries in the world after USA and Nigeria. The productivity of sorghum has increased from 2 to 2.9 tons/ha. In addition, these collaborative projects have enhanced technical, human resource, physical and financial capacity of sorghum in Ethiopia. As a result the Ethiopian sorghum research and development have been enhanced through these collaborative programs and has become one of the best in Ethiopia and sub-Saharan Africa. These model collaboration schemes have to be scaled up to other crops research programs both in Ethiopia and Africa.

Communicating Research Effectively and Timely to Non-Research Audiences in Agriculture

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Where do researchers excel: doing the research, analyzing the results and sharing the information with their fellow researchers. Where do many struggle: communicating effectively and timely their research and results to research sponsors and non-research audiences. This session will help you identify your target audience, understand what they need to hear and give tips for presenting your information. We know you know your data; that's why you've submitted academic papers, and your audience also knows this. But to demonstrate your expertise, we don't need to hear all the technical details; we need you to be able to explain it to your audience with their needs in mind. Your research maybe be groundbreaking, but if you can't get the industry or research sponsors to get behind you, the research is not effective. Storytelling is a key strategy for communicating a story successfully and one we will explore in the workshop. Storytelling has three main aspects making it effective. First, we remember stories with events presented in order, making the overall information memorable. Second, we can connect and remember things more easily when we can relate our results with previous knowledge or experience. Lastly, making an emotional connection can help with memory retention and provides a more impactful experience for your target audience.

As a presenter team, Dr. Ignacio Ciampitti, Kansas State University, has experience presenting to audiences globally and his co-presenter Stacy Mayo-Martinez, Martinez Media & Marketing Group, has sat in the seat of checkoff investor advisor and sold ideas and initiatives to Fortune 500 executives. The presenters will prepare you to walk away with three tactics you can use immediately to understand your audience, scale your message to use their keywords and present engagingly.

Overcoming Aspiration Failures in Sorghum Consumption in Africa

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The potential of sorghum to contribute to nutritional impacts among other welfare outcomes depends on its widespread consumption. In some ways, sorghum and millets are strategic crops as they have been historically widely consumed staples in many parts of Africa for millennia. However, over the past several decades, the production and consumption of sorghum have shown declining or stagnating trends due to production and climatic challenges, lack of intensification and declining public investments. Importantly, changing consumer preferences driven, partly by competition from other cereals such as maize, rice, and wheat have also contributed to declining consumption. To reverse these trends may require social innovations to harness emerging consumer interest in healthy grains. Such social innovations will likely include strategies to overcome low consumer aspirations for sorghum consumption, thus opening potentially large but hitherto latent consumer markets. This paper provides guidance on several areas of focus to achieve these ends. The strategies identified begin with investments in breeding and food technology for grain characteristics and products aimed at attracting cohorts of modern sorghum consumers. An equally important strategy include capitalising on strong cultural consumption preferences in some geographies and using consumer education in other areas of low or declining consumption. Finally, investment scenarios in the scaling and adaptation of successful models of sorghum sector growth and development are suggested.

O101

Potential contribution of sorghum to sustainable food systems in southern Africa: A case for Zimbabwe

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Most diets of the population in sub-Saharan Africa are dominated by cereals, especially maize that is consumed at an average rate of 100kg per capita per year. Demand of the cereal grains is increasing due to rapid population growth coupled to huge demand for usage as biofuels and feed. However, productivity of many crops is greatly being affected by climate change effect that has greatly caused spatial and temporal variations in yields. Unfortunately, most of the resource limited communities in sub-Saharan Africa have limited capacity to adapt to these adverse climate effects. Traditional crops such as sorghum are highly resilient to climate change effects and could provide alternative solutions in buffering the food systems in sub-Saharan Africa. In Zimbabwe, the government is supporting the development of sustainable value chains of traditional crops such as sorghum since they are nutritious and resilient. The objective of this report is to highlight the current efforts on sorghum value chains development in Zimbabwe, supportive researches, and to map potential areas that require interventions in future. There has been efforts by the University of Zimbabwe to produce food, feeds and beverages from sorghum and a number of products have been showcased at various platforms. Research on sorghum genetics was mainly done by the national and international research institutes as well as the private sector. To date a total of five varieties of sorghum are on the market, however, seed supply is limited and unable to meet the government of Zimbabwe input scheme. In terms of agronomic practices there has been a few reports on sustainable intensification approaches such as conservation agriculture application to sorghum. Harnessing the sorghum value chain raises huge possibilities of increasing resilience in Zimbabwe, and also with great capacity of upscaling the livelihoods of people through income and sustainable food systems.

O102

High-resolution spatiotemporal transcriptome landscape of sorghum seed development

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Seed development is an dynamic process of grain maturation and directly affects the yield and quality of cereal crops. Improving grain quality has been an important goal for sorghum breeding. To obtain a foundational understanding of sorghum seed development, we developed a spatiotemporal transcriptome atlas of sorghum seed development from fertilization to maturity with physiological characterization and metabolomics analysis. Our preliminary data analysis showed that about 24,000 genes were expressed during the endosperm and embryo development. The functional annotation of tissue-specific (embryo and endosperm) and stage-specific genes highlighted the fundamental transcriptomic reprogramming during sorghum seed development. Combined analysis of the metabolomics and transcriptomics data will reveal key genes related to the biosynthesis of nutrition in the sorghum grain. Cereal yield and grain quality can be impaired by environmental factors associated with climate change such as heat stress. To understand the impact of heat stress (HS) on sorghum seed development, we imposed a moderate (35°C), and a severe (40°C) HS for 3 days at eight distinct seed development stages. It was observed that HS negatively impacts key genes in starch and protein biosynthetic pathways more during the early phase of seed development than the late stages. The observed reduced seed size from the HS was a result of the downregulation of starch-related metabolism, kafirins, fatty acid, and lipid biosynthesis. The results of these projects will provide essential knowledge for understanding the dynamic regulations of seed development under normal and HS condition in sorghum.

Digging into the transcriptome of a developing sorghum grain to find the culprits of protein content and low digestibility

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The potential of sorghum to cope with biotic and abiotic constraints could enable it to contribute to global food security in the context of climate change. However, the low digestibility of the grain reserve proteins (called kafirins) by gastrointestinal proteases is hampering its wider use for food and feed. The structure of the protein bodies in which are stored the kafirins is potentially responsible of this defect. The molecular mechanisms underlying the development and modification of kafirin-containing protein bodies are still largely unknown. In this context, our objective is to decipher the molecular mechanisms involved in the regulation of the content and digestibility of sorghum grain reserve proteins. The evolution of the transcriptome was monitored during the grain development of the Macia genotype, and supplemented by an analysis of gene co-expression networks (GCN). In parallel, the protein content of the grains and their *in vitro* digestibility were measured. Analyses of GCN allowed the identification of transcription factors (TFs) potentially regulating the mechanisms of protein reserve establishment. We identified co-expression modules involving kafirin genes and genes orthologs to TFs already known in maize, rice and arabidopsis. In those modules, we also identified not yet identified TFs. In the future, we plan to evaluate the role of these TFs by a simplified cellular overexpression system in sorghum protoplasts. We will also investigate variability of protein content and digestibility in a panel representing sorghum worldwide genetic diversity and European commercial offer, in order to perform GWAS analyses and phenomic and genomic predictions.

Keywords : Sorghum - Grain - Protein digestibility - Gene co-expression network - Transcription factor.

Exploring Natural and Induced Genetic Variation for Protein Digestibility in Sorghum Grain

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Sorghum (*Sorghum bicolor* L. Moench) is a staple crop and a major source of food and energy for the World's developing countries; however, its consumers are constrained by the post-cooking low digestibility of its grain proteins. Limited natural variation for protein digestibility was found in local landraces and improved sorghum varieties in West Africa. Chemical mutagenesis was used to create two mutants with highly digestible proteins, SbEMS1613 and SbEMS3324, with 50% and 100% increased lysine and tryptophane contents (g/100g samples) respectively compared to their wild-type parent, BTx623. These mutations map to new alleles of *Sobic.005G074400* (*hdp*) coding for a protein disulfide isomerase, and *Sobic.005G189000* (*hl2*) for a Kafirin precursor protein. The high lysine-high digestible alleles were introgressed into the background of elite, white-grain, tannin-free, Senegalese sorghum varieties. These BC3F7 sorghum lines exhibited an average protein content of 13% with 20% improved protein digestibility compared to the local varieties. Three of these lines are proposed for registration. Molecular markers for each mutation were developed to support rapid introgression into local varieties through marker assisted selection.

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Transforming grain sorghum's yield potential and grain quality through trait-based ideotype breeding

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Sorghum has an inherent ability to adapt to harsh environmental conditions; further improvements are needed to keep sorghum production feasible under future changing climate. The proposed project addresses this need through the development of trait-based ideotype sorghum hybrids specifically targeted for water-deficit and favorable environments. The knowledge and germplasm resulting from this project will help enhance water-deficit tolerance and productivity in harsh conditions and regain acres under relatively favorable environments. To achieve this result, a multi-disciplinary integrated approach is assembled to (i) Increase radiation use efficiency through erect leaf architecture and increased plant height; (ii) Modulating stomatal density to increase water use efficiency under water-deficit conditions and enhance carbon gain under favorable environments; (iii) Optimizing stay green trait for improved source-sink relationships to enhance yield and grain protein; and (iv) Explore opportunities to increase seed number and sink strength by altering panicle architecture. All these objectives will be integrated through crop modeling to fully assess the interactions between target traits and environments. As such, crop-climate modeling will be used to determine effective trait combinations for specific environments, i.e., for water-limited (low stomatal density, stay green, tillering, higher primary rachis branches in panicle) and favorable (erect leaves with increased height, higher plant density, higher stomatal density, improved assimilate translocating hybrids, larger sink size and strength) environments. Preliminary evidence generated by the group include (i) phenotypic and molecular markers for leaf erectness and plant height; (ii) machine learning tool developed and standardized for breeding hybrids with differential stomatal density; and (iii) phenotypes and markers for different levels of stay green. Utilizing a large grant funded by USCP, the multi-disciplinary and multi-institutional team along with industry partners aim to develop sorghum hybrids targeted to thrive under harsh environments and enhance yield potential under relatively favorable environments.

Does ecotypic variation in *Striga hermonthica* alter efficacy of *LOW GERMINATION STIMULANT 1*-based resistance in sorghum?

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Cereal crop yields across sub-Saharan Africa are negatively affected by *Striga hermonthica* Del. Benth, a hemiparasite that infects host roots and siphons its water, and photoassimilates. Sorghum (*Sorghum bicolor*) genotypes exhibit pre-germination resistance to *Striga*, due to natural mutations on the *LOW GERMINATION STIMULANT 1* (*LGS1*) locus. We interrogated whether ecotypic variations in *Striga* could complicate development and deployment of *lgs1*-based resistance technologies across infested regions. We first tested phenotypic diversity among *Striga* ecotypes collected across African ecosystems with regards to response to host-derived chemical cues that induce germination of parasite seeds (strigolactones). We found some with stronger response to orobanchol relative to 5-deoxystrigol – major strigolactones in sorghum and pearl millet – suggesting limits to the value of any allele-based resistance. Next, we evaluated whether root exudates from sorghum genotypes carrying different *lgs1* deletion mutations display differential response to *Striga* ecotypes *in vitro*. We also assayed lines carrying the frameshift allele, a 2-bp insertion at the start of *LGS1* coding region, for *Striga* resistance. Results revealed that mutants stimulated different rates of *Striga* germination compared to genetically similar non-mutant pairs. Finally, we generated near isogenic lines (NILs) by introgressing loss-of-function *LGS1* from SRN39 (a *Striga*-resistant genotype that possesses the *lgs1-1* variant) into elite farmer-preferred backgrounds from Niger, namely Mota Maradi, Sepon82 and MR732. We found that the NILs displayed marked resistance to *Striga* collected from one geographical region, evidenced by significantly lower numbers of germinated *Striga* seeds compared to unimproved parents. In this talk, I will highlight the patterns of response of these improved materials to different *Striga* ecotypes and discuss the far-reaching implications of the observed ecotypic parasite variations on development and deployment of *LGS1*-based technologies for broad-spectrum resistance to the noxious weed.

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Count the cost: Trade-offs associated with *LOW GERMINATION STIMULANT 1* resistance in *Sorghum bicolor*

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Sorghum bicolor production in sub-Saharan Africa is greatly impacted by the devastating parasitic plant *Striga hermonthica*. Certain ecotypes of *S. bicolor* traditional varieties have evolved a defense strategy against the parasite, exploiting that *Striga* germination is sensitive to structural variation in host exuded strigolactones. Naturally occurring mutations at the *LOW GERMINATION STIMULANT 1* (*LGS1*) locus alter strigolactone stereochemistry, resulting in reduced parasite germination¹. Loss-of-function at the *LGS1* locus has the highest frequency in landscapes where *S. hermonthica* is the most abundant, indicating *LGS1* loss-of-function as a local adaptation strategy for hosts in regions with high parasite load². However, functional *LGS1* is fixed where the parasite is absent, alluding to potential fitness trade-offs coupled with the mutation. As hormones, strigolactones are involved in numerous aspects of plant growth and development, including the regulation of above ground architecture, root growth, photosynthetic processes, and establishment of symbiotic relationships with mycorrhizae. The changes to strigolactone stereochemistry caused by loss-of-function at *LGS1* may have pleiotropic effects on other host biological functions, but this remains poorly understood. Here, we use gene-edited *S. bicolor* to investigate the fitness costs of maintaining loss-of-function at *LGS1* in two separate genetic backgrounds. Informed by previously generated transcriptome data, plants were tested for differences in light harvesting processes and disruptions to establishment of mycorrhizae. We find *lgs1* plants to have a developmental delay, reduced rates of photosynthesis, and lower rates of colonization by arbuscular mycorrhizal fungi. Thus, we find support for loss-of-function at *LGS1* to be coupled with pleiotropic effects on multiple biological functions. By considering the trade-offs associated with *lgs1*-based resistance, we characterize and give context to the associated fitness costs of a locally adapted host resistance strategy.

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The sorghum mutant *LOW GERMINATION STIMULANT 1 (lgs1)* at the nexus of food security in Africa

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Sorghum is a food staple for millions of people in sub-Saharan Africa, but parasitic weeds of the *Striga* genus greatly diminish its production. *Striga* leads to significant crop losses and can wipe out entire harvests. Damage to agriculture in Africa is estimated at approximately US\$7 billion a year, with infestations affecting lives of over 100 million people in 25 countries¹. An efficient and cost-effective way of managing *Striga* in smallholder farms in Africa is to deploy early maturing resistant varieties. We leveraged genomics and the vast genetic diversity of sorghum – evolutionarily adapted to cope with *Striga* parasitism in Africa² – to identify new *Striga*-resistant sorghum. We exploited a *Striga* resistance mechanism that hinges on essential communication molecules – strigolactones exuded by hosts to trigger parasite seed germination. We used the Sorghum Association Panel (SAP) to search for sorghum genotypes with a mutation on the *LOW GERMINATION STIMULANT 1 (LGS1)* locus that makes them ineffective in inducing *Striga* germination³. We identified new *lgs1* sorghum genotypes designated as SAP *lgs1*. SAP *lgs1* had the SL exudation profile of known *lgs1* sorghum whose hallmark is production of the low inducer of germination, orobanchol. Laboratory and field resistance screens showed that the SAP *lgs1* genotypes also exhibited remarkable resistance against *Striga*. Field evaluation provided a further opportunity to study flowering time and all the accessions were within the time considered as early maturity in sorghum. This is important because early maturity helps cope with *Striga* by reducing infestation and it is imperative as a drought coping mechanism. Incorporating this early maturing material into breeding programs can potentially alleviate losses caused by *Striga* parasitism and positively impact food security in smallholder farms of Africa in wake of climate change.

Keywords: Food security - Low germination stimulant 1 locus - *Striga* resistance - Strigolactone - Sub-Saharan Africa - Early maturing.

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Sorghum in Senegal: overview of work on pathology in the past five years

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In Senegal, sorghum is the second most important rainfed cereal crop after millet, with an estimated total area of more than 200,737 ha for a national production of 188,500 tons and an average yield of 939 kg/ha; what is below the crop's potential. These low yields are explained by inappropriate production practices, damage caused by diseases (fungal, bacterial), insects, weeds and drought. Among these diseases we have leaf blight, anthracnose, grain molds and others. The objective of this study is to synthesize the activities done in sorghum pathology in Senegal during 05 years. Surveys were done to identify main diseases and hot spots. Also, varieties from the national sorghum collection were evaluated for their resistance to two major sorghum diseases: anthracnose and grain mold. Mycoflora diversity on seed infected with grain mold were also determined. Field trials were installed in hot spots at farmer's fields in a randomized completed block with 03 repetition. Mycoflora diversity was determined using the blotting paper method. Hots spots and sorghum main diseases are known. One variety of the national collection was identified as tolerant to anthracnose and grain mold. We also found 04 accessions resistant anthracnose with high yield. For pathogen diversity, 04 genus were more frequent in analyzed samples: *Curvularia*, *Fusarium*, *Alternaria*, *Aspergillus*. All these results contribute to improve sorghum productivity.

Keywords: Sorghum - Senegal - Anthracnose - Grain mold - Overview.

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Designing an e-platform for promoting sorghum value chain networking arrangements and countering climate change induced food insecurity

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Agriculture is one of the strategic sectors in Zimbabwe's economy and it has immense potential for providing food security and poverty alleviation. Though sorghum is ranked as a second staple cereal crop after maize, the former has comparative advantages in the semi-arid areas. The crop has manifested its resilience in the face of climate change. The study traces sorghum's potential as a livelihood security bridge in semi-arid areas and presents evidence for the need to design electronic marketing platforms. The main objective of this review is therefore to map the scope of stakeholder networking arrangements in sorghum production and strengthening marketing channels. Key insights show that the adoption of e-platforms focusing on generating value of agricultural stakeholders is important for rural development and industrialization as guided by the Zimbabwe national development agenda. However, strategies implemented to improve networking among agricultural stakeholders in Zimbabwe are not cross cutting and have sustained the inefficiency in the sector. Using a participatory demand driven approach, a low-cost web-based application was designed for the sorghum value chain. This targets to create an interactive one-stop platform for producers, traders, processors, and consumers among other strategic stakeholders. This platform will promote sorghum production through the provision of a virtual interface that will enhance binding relationships among stakeholders. In doing this, numerous bottlenecks will be broken where consumers' access to information on sorghum products to enhance food security and nutrition is supported. Additionally, farmers who lacked market information and modern agronomic practices will benefit through increased production volumes. In as much as the application focused on the primary pillars of the sorghum value chain, there will be spill over effects to postharvest technology management, plant breeding, and consumer behaviour. This will expand the interfaces of the sorghum value chain web-based application and expand opportunities for the various actors.

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Diagnostics on sorghum value chain challenges, market opportunities, and potential solutions for Ethiopia

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According to FAO, Sorghum is the 5th most-produced grain in the world with Ethiopia being one of the top 10 sorghum producing countries. In the past 5 years, total sorghum production in Ethiopia has shown minimal decrease but this could further dwindle due to the attention given to other commodities especially for wheat and maize in the country. There are multiple challenges across the sorghum production value chain in Ethiopia. There is limited agricultural input availability and utilization, limited drive to provide technical support to farmers on sorghum production, and limited value addition activities. Overall, these challenges across the value chain are primarily caused by underdeveloped market for the commodity. Increasing the market potential of sorghum in Ethiopia would be the right place to start to fix these issues. Worldwide, there are multiple use cases that can be adopted to stimulate sorghum's industrial use in Ethiopia. Based on existing and potential market demand, supply, and sorghum price in Ethiopia, feed, processed food, and beverages are viable options to increase Sorghum's market potential in the next 5 years. Clustering, grouping farmers together based on similarities such as location, production, and farming activities, should be used as a vehicle to boost production through productivity increase, land expansion, and market linkages to address the demand that would be created from the market opportunities. This can be helpful in identifying patterns and providing information to farmers through extension agents to improve farming practices and hence their production and productivity.

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Lessons from the impacts of a sorghum participatory breeding program addressing the needs of resource poor farmers in marginal areas of Nicaragua

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White-grain sorghum is an important food crop for resource-poor farmers of the dry belt of Central America. From 2002 to 2008, a participatory breeding program (PB) was implemented with local farmer groups in the Northern region of Nicaragua, aiming to develop sorghum varieties adapted to local cropping systems and farmers' needs.

From 2020 to 2022 an *ex post* impact evaluation of this program was carried out by Cirad and the farmer Union FECODESA using the "ImpresS" method. A detailed impact pathway and timeline of the innovation process were developed. Participatory workshops with farmers and institutional actors allowed to identify 20 impact descriptors and to refine the links between outputs, outcomes and impacts in the impact pathway. Translated into indicators, these impacts were assessed through a household survey with 127 farmers, focus-group interviews as well as secondary data. We found that 90% of interviewed farmers growing sorghum were still using varieties from this program. Among these varieties, one photoperiod-insensitive and one photoperiod-sensitive are cultivated by 76% and 29% of farmers respectively. The program enabled farmers access and evaluate directly in their own farming conditions a broad genetic diversity and thereby identify those varieties most resilient to the extreme climatic events and suited to local cropping systems as well as bringing resistance to sugarcane aphid that local cultivars do not have. Further the new varieties have improved grain quality for local food preparations. Major impacts perceived by respondents include better availability and access to quality seed, changes in sorghum production towards agroecological practices, and improved food security. This program also contributed to strengthen the local farmer organizations.

Comparing these results to those of sorghum PB programs implemented in Burkina Faso during the decade 2002-2012 enables us to understand internal and external factors driving the innovation process and its major outcomes and impacts.

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O113

High protein sorghums for improved health and productivity for smallholder communities

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Cereals contribute over fifty percent to the total dietary protein supply in Africa, and the share may be even higher in the rural areas. Because they are lower in protein and are particularly short in certain essential amino acids, protein deficiency is widespread among communities dependent on cereals as main food source. Thus future research must address the increase in demand for novel cereal proteins both for food and feed applications. Improvement of protein expression and quality along the spectrum of food and agriculture has significant economic and health implications in both the developed and developing world. The current research was initiated as a small-scale collaborative effort with USDA-ARS grain quality research lab to characterize sorghum breeding lines for protein traits. With support of an international food company Kellogg and the US grower community, the initiative was transitioned into breeding for improved protein content and essential amino acids lysine and leucine for human food and animal feed. Through near infrared (NIR) spectroscopy and wet chemistry screening, genotypes with higher protein content were identified among the global sorghum collection. These sources were used as parents to initiate new breeding populations, and evaluation of families and individuals derived from these populations resulted in novel lines that combine a high protein profile with desirable agronomic characteristics. These lines and their hybrids consistently expressed superior agronomic performance and 20-50% higher protein, lysine and leucine than commercial checks. Adoption of such varieties/hybrids or their use as breeding parents to develop locally adapted varieties in developing countries should reduce protein malnutrition and contribute to better health and economic outcomes. However, selection for high protein varieties need to take into consideration potential tradeoffs of yield and yield stability, and needs to link basic cereal and crop improvement sciences to identify the ideal variety.

O114

Digestibility, biochemical changes and Kafirins polymerization analysis during sorghum grain development

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Sorghum is the 5th most produced cereal worldwide. It has many advantages e.g., drought tolerance and its safety for coeliac and gluten allergic people. Kafirins, sorghum seed storage proteins accumulate during grain development in spherical organelles called protein bodies (PBs) and provide nutrients (nitrogen) during germination. They are more hydrophobic and resistant to digestibility by the gastrointestinal proteases, when compared with their counterparts in maize and wheat. Kafirins low digestibility would result from the molecular and supramolecular assembly of kafirin within the PBs. In sorghum, the links between the evolution of the redox state of kafirins and their assembly is scarcely documented. Therefore, our objective is to probe the pattern of kafirin accumulation and *in vitro* protein digestibility during grain development. These investigations were implemented with grains from two genotypes (with and without tannins) harvested at selected intervals from the 7th to the 40th days after flowering (DAF). The dynamics of grain dry mass, water content, redox state, kafirin solubility and polymerization status, during grain development were determined. The grain dry mass and protein content increased continuously during grain development to reach a maximum at 29DAF that plateaued until grain maturity. With scanning electron microscopy, PBs were detected early during grain development (7DAF). Relative amounts between kafirin complexes and monomers were obtained from a sequential extraction followed by size exclusion chromatography analysis. The complexes and monomers accumulation were negatively correlated with a crossover point at 29DAF. The *in vitro* protein digestibility declined a few days after achieving the maximum of kafirin disulfide crosslinking (33DAF), at a time coinciding to the onset of grain dehydration. This contribution brings new insights on kafirin assembly in relationship with protein digestibility during grain development. It validates the prominent role of kafirin complexation and sorghum protein digestibility.

Keywords: Sorghum; grain development; redox state; kafirin; digestibility.

Evaluation of genotype and growing season impacts on the synthesis of phenolic compounds during sorghum (*Sorghum bicolor* (L.) Moench) grain development

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Sorghum is grown for millennia on African continent. More recently, its use for the world's food supply has been boosted due not only to its agronomic and environmental advantages, but mainly to its bioactive potential, attributed to phenolic compounds (PC). Sorghum phenolic content and profile are influenced by the genotype and growing season (GS). However, information about the synthesis of PC and the impact of these factors on grain development are scarce. Therefore, the aim of this study was to analyze how genotype and GS influence the synthesis of PC during sorghum grain growth. This study was carried out with grains from two genotypes (IS15752 and Macia; red and white pericarp, respectively) harvested in two GS (2017/2018) and at five selected intervals from the 7th to the 40th days after flowering (DAF). Free (FPC) and bound (BPC) PC were sequentially extracted and analyzed by a high-resolution metabolomics tool (UPLC-ESI-QTOF/MS). Globally, 97 PC were annotated, being 36 PC found in common to both genotypes. Red pericarp sorghum showed the highest number of exclusive compounds (43 PC) and the lowest FPC/BPC ratio, indicating a greater phenolic diversity with the most part of PC complexed to the cell matrix. The phenolic profile also varied, flavonoids (59%) and phenolic acids (41%) were the major classes in red pericarp and in white pericarp sorghum, respectively. Throughout the sorghum grain development, white pericarp sorghum presented higher ion abundance of FPC, with a decrease (60%) from 25DAF to mature stage; while red pericarp sorghum showed a sharp increase by 15-fold times from 25DAF. There was a low variability in the phenolic profile between the studied GS, so the genetic effect was more evident. This work can input open databases of phenolic compounds and stimulate the selection of sorghum genotype based on their bioactive potential.

O116

Genetic enhancement to improve productivity, resilience and nutrition of sorghum in Sub-Saharan AfricaMacDonald Jumbo (jumbo.mcdonald@gmail.com)*Accelerated Crop Improvement, International Crops Research Institute for the Semi-Arid Tropics, Bamako, Mali*

Sorghum [*Sorghum bicolor* (L.) Moench] is an indigenous crop to Africa and is a basic staple food for many rural communities. Sorghum ranks second among cereal crops in Sub Saharan Africa (SSA) in terms of area of cultivation. World annual sorghum production is over 60 million tonnes, of which Africa produces about 20 million tonnes. More than 35% of sorghum is grown for grain for human consumption while the rest is used for animal feed, fodder, and alcohol production. Sorghum is grown on 24.8 million hectares in SSA (FAOSTAT, 2021); however, on-farm grain yields remain poor with reported average of about 1 t ha⁻¹ but this can improve if farmers use current improved varieties and hybrids combined with application of good agricultural practices (GAP). Sorghum has wide adaptation and is grown in diverse environments but being a hardy crop has more advantage in drier areas compared to most cereal crops such as maize and rice, therefore; sorghum, is considered as best suited crop for ensuring food security in the face of climate change. Sorghum grain is rich in bioactive phenolic compounds, such as ferulic acid, gallic acid, vanillic acid, luteolin, and apigenin, 3-deoxyanthocyanidins (3-DXA), known to provide many health benefits, including antioxidant, anti-inflammatory, anti-proliferative, anti-diabetic, and anti-atherogenic activities. Some new varieties screened for Iron and Zinc, have shown high levels for these two micronutrients. Considering rising demand for grain for human food, animal feed, brewery and biomass for fodder; our research focus has been on developing high yielding, dual purpose, climate resilient sorghum varieties and hybrids with enhanced grain iron and zinc. Newly developed hybrids and varieties have shown yield potential of up to 6-8 t ha⁻¹, and some of these have since been released in many countries through collaboration with agricultural research and extension systems (NARES), private sector and farmers.

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ABSTRACTS THURSDAY 8 JUNE



The Potential Hidden Within Sorghum Diversity Populations

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In this talk, we will explore the power of new genomics and phenotyping resources to unravel the complex genetic architecture underlying multiple traits of interest in sorghum. The foundation of this research lies in the sorghum association panel, a population assembled over fifteen years ago to represent global sorghum genetic and phenotyping diversity. To date the sorghum association panel has been phenotyped for over 200 traits across diverse environments. Generating a new and high-density genetic marker dataset containing more than 40 million SNPs enabled the identification of novel significant associations from previously collected field experiment phenotypes. Using image analysis based phenotyping, we successfully mapped the locations of genes, including the cloned genes *tan1* and *y1*, responsible for regulating variation in the production of specialized metabolites within sorghum grain. A novel high throughput assay for testing the impact of grain samples on the human gut microbiome in vitro established a link between the composition of human gut microbiomes and the consumption of sorghum varieties, mediated by the abundance of metabolites within the sorghum grain. The relationship between sorghum genetic variation and the abundance of bacterial taxa associated with human health was validated via a QTL mapping study. Our study demonstrates the potential to link specific alleles in crop genetics to human health via the food-gut-health axis as well as how new genomic and phenotyping resources can extract fresh insights from existing sorghum field studies.

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Resilience and Sustainability of Sorghum productivity in the face of Climate Change: Case of West Africa

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Sorghum is the 5th most important cereal crop globally and Africa's second most important grain crop. West Africa contributes close to 50% of its production on the continent and about 27% of global production. Despite its importance to food security and the livelihoods of many, especially those in the semi-arid zones of the sub-region, its cultivation is largely at the subsistence level and under rain-fed conditions, making it vulnerable to the ever-changing climate. Additionally, there is increasing industrial demand for the crop in the brewery and other food industries. While its production in the sub-region has been increasing, the increase is attributable to expansion of the area under cultivation rather than increased productivity. Thus, its yield (about 1 t/ha) is still way below the potential of the varieties cultivated, suggesting the need to intensify its production sustainably to meet the growing demand from the increasing population and industrial requirements. In this presentation, we discuss (i) the major production constraints (biophysical environment, pests and diseases), (ii) the effect of socio-economic factors (inadequate capital and access to credit, limited access to production inputs such as improved seeds, inorganic fertilizers, and chemicals required for crop protection) on sustainable intensification and the need to address them to enable effective use of resources, and (iii) the influence of management practices on the productivity of sorghum under current and future climate. It is concluded that, sustainable intensification of sorghum production in West Africa requires aggressive promotion of sustainable intensification practices (SIP) given the fragile resource base and increasing demand. Sustainable intensification practices needs to be tailored to specific locations in the landscape due to the heterogeneity of the soils, weather, and socio-economic factors that influence management practices. The design of SIP must consider the pillars of sustainability and requires the deployment of co-learning strategies to enhance adoption.

O117

The genetic control and consequences of heat induced partial fertility in CMS in sorghum

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The A1 cytoplasmic male sterility (CMS) system is used almost exclusively for the commercial production of F1 hybrids in sorghum. When high temperatures occur around flowering, A1 cytoplasmic male sterility can break down in some genotypes, allowing normally male sterile female parents to produce viable pollen. In commercial seed fields partial fertility has significant commercial consequences, as it can result in the production of a mixture of inbred and hybrid seed which may render the hybrid seed unsalable. While the genetic control of fertility restoration in F1 hybrids is well known, the genetic control of partial fertility is largely unknown. In this study we screened a panel consisting of 2042 male sterile parent lines genotyped with 21,000 SNP markers at six locations, with the trait being scored on individual panicles flowering on a particular day. This resulted in a total of 19,995 plot x day observations. GWAS analysis of this data identified 43 regions of the genome associated with the trait indicating that it is under complex multigenic control involving nuclear genes from a range of different networks influencing a variety of biological processes, which are distinct from the major restorer genes. We provide evidence that partial fertility is a major contributor to the low levels of genetic diversity in the elite female parent pools, potentially constraining genetic gain for yield. With increases in temperature, it is likely that partial fertility will become an increasing constraint on hybrid seed production.

O118

Integrating molecular genetics and precision phenotyping to elucidate gene function contributing to sorghum drought resilience

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Drought is a complex trait and identifying the genes underlying sorghum's innate drought tolerance and how they are regulated in the broader context of the whole plant and its environment requires advanced approaches in genetics, genomics, and phenotyping. In a collaborative project funded by the US Department of Energy (DOE), we leverage a field-based phenotyping infrastructure at Maricopa, Arizona, which provides an exceptional capability for managed stress trials in a hot and arid environment through controlled irrigation. An automated field scanner system collects high-resolution phenotyping data using a variety of sensors throughout the growing season, from seedling establishment to harvest. An EMS-mutagenized sorghum population (BTx623 background) was phenotyped under the field scanner to compare drought-stressed and well-watered plants. Each mutant's genome has been sequenced so that sequence variants can be linked with multi-dimensional phenotypes. Being able to assess the genotype-to-phenotype link in response to drought over the life cycle of the plant will facilitate discovery of genes and their functions. State-of-the-art phenotyping data analytics pipelines are being extended to define stress-related phenotypes at multiple scales. To accelerate mapping of causal loci that underlie several mutants of interest, we are using bulked segregant analysis (BSA)-seq.

In parallel, we've generated regulatory and network maps (transcriptome, co-expression, accessible chromatin) from several diverse sorghum lines in response to controlled-environment drought stress and are using these data to identify genetic loci and transcription factor-DNA interactions that associate with drought response. Ultimately, these integrated data can identify control points for enhancing the productivity of bioenergy sorghum in marginal environments through precision breeding or engineering, and thus accelerate the development of improved varieties that are high-yielding with limited water resources.

O119

Identification of molecular basis of drought adaptation strategies in *Sorghum bicolor*

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Drought adaptation strategies comprise avoidance, tolerance and escape mechanisms. Plants use these mechanisms and synchronize their physiological and developmental processes in response to drought. Plants avoid drought by maximizing the water uptake and minimizing the water loss via increasing the root length and stomatal closure, respectively. Also, an active accumulation of solute in the cell, detoxification of ROS, and rapid changes in the mRNA and protein level lead to the tolerant state of the plants. Although the physiological and molecular basis of drought resistance mechanisms are well studied in maize and other cereal crops, it is less studied in sorghum. Therefore, we are aiming to dissect the molecular mechanisms of drought resilience strategies in *Sorghum bicolor*. Sorghum, a C4 grass, is one of the most drought tolerant crops grown in the semiarid regions. We hypothesized that genetic variations in the candidate genes VPP1 and NAC080308, DRO1, and P5CS1, identified in maize, rice and barley, respectively underlie drought adaptation in sorghum. Under this hypothesis, we expect to see synonymous and nonsynonymous mutations in the 5' UTR, 3' UTR, CDS, and promoter regions of these candidates across the sorghum accessions. These mutations lead to developing drought adaptation traits for a particular sorghum variety. We identified the orthologs of these candidates and currently, we are analyzing causative variants in the orthologs across the sorghum germplasms. Moreover, we generated a list of apriori candidates involved in drought signaling mechanisms in plants based on the existing literature. We identified ortholog of each apriori candidate in sorghum and then performed colocalization analysis via envGWAS. We found that CKA2 and HAB1 are potential candidates for drought. These findings will facilitate targeting of specific genes that can be included in a breeding pipeline for developing a climate resilient sorghum variety to ensure food security in the future.

O120

A new insight into proteomic responses of sorghum to combined drought and heat stress

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Drought and heat stress have detrimental effects on crop growth and productivity, which compromise global food security. Plant responses to independent and combined effects of these stresses differ significantly. Consequently, the combination of different stresses does not necessarily lead to an additive response, instead a unique response may occur due to the synergistic or antagonistic effect of both stressors. For example, under drought, plants reduce water loss by closing the stomata, while under heat, plants open the stomata to release heat through transpiration. When these stresses occur simultaneously, the plant must maintain a balance between preventing water loss and achieving canopy cooling.

Sorghum is an important cereal crop and possesses better drought and heat tolerance than some major cereals. Although much progress has been made in identifying proteins involved in some crop responses to drought or heat stress, knowledge on such responses in sorghum is limited and in fact does not exist for combined drought and heat stress in sorghum lines that respond differently to these stresses. Therefore, we used label-free quantitative proteomic analyses to identify key proteins that determine tolerance to the combined stress in two sorghum genotypes with contrasting responses to drought and heat. Experimental treatments consisted of a control, drought stress alone, heat stress alone, and a combination of drought and heat stress.

Analysis of differentially expressed proteins revealed some common and unique responses to the single and/or combined drought and heat stresses. KEGG annotation uncovered proteins associated with key molecular pathways that provide insight into underlying mechanisms of sorghum adaptation to combined drought and heat stress. The candidate proteins include peroxidase 5-like, chitinase, saccharopine dehydrogenase (NAD(+), L-glutamate-forming), isopentenylidiphosphate delta-isomerase, NAD(P)H dehydrogenase (quinone) and 24-methylenesterol C-methyltransferase. These proteins represent potential molecular targets for genetic improvement of sorghum tolerance to combined drought and heat stress.

Advanta Sorghum Carbon Project in Argentina

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In 2021, ADVANTA Argentina started a carbon footprint evaluation program based on our grain and forage sorghums, with the intention to deliver value and support the assembly of new value chains focused on this important aspect of sustainability. The research initiative started to generate the first results that allow proposing concrete and measurable alternatives to improve the sustainability of agriculture and livestock. First, we analyzed footprint resultant of the seed production in Argentina, and it turned out to be 0.77 kg CO₂eq/kg seed, less than half the global reference value 1,79 kg CO₂eq/kg seed (Agri-footprint 4.0). We are currently working on further reducing this footprint, to later offset the rest with carbon credits, and thus, be able to offer a carbon-neutral seed bag to the grower.

Secondly, we seek to offer improved hybrids, that allows to reduce this footprint at the grower field level. Thousands of hectares of grain production have been analyzed, in two growing seasons with rainfed conditions and with different agricultural practices including cover crops with legumes and the use of biological inputs, looking for combinations that help reduce the footprint. The results show the performance of sorghum in critical years and suggest alternatives to obtain the highest grain production with lower carbon footprint.

We also calculated the carbon footprint of the forage sorghum silo, showing a favorable result in terms of footprint per kg of dry matter, soluble protein or metabolizable energy compared to corn silos.

We believe that sorghum could play a key role integrating carbon reduced value chains, expanding its value and to different verticalized industries like meat, dairy and biofuels (bioethanol and biogas).

O122

Micro dose soil amendments effect on soil properties and performance of sorghum on legume-sorghum intercrop on smallholder farms vertisols in Homa Bay County, Kenya

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High cost of the inorganic inputs has made smallholder farmers fields (SHFs) unable to apply the recommended rates to address low crop yields such as sorghum in Kenya. Micro dosing, which involves application of small, affordable quantities of fertilizers was tested on selected SHFs in vertisols of Homa Bay County, Kenya. Treatments were; control (no treatment), 2 tons farm yard manure (FYM)/ha, micro dose (13 kg P +37.5 kg N/ha), micro dose + FYM and recommended fertilizer rates (26 kg P +75 kg N/ha) in RCBD. The study was conducted in two farmers' field in Homa Bay Town and Rachuonyo North sub-counties, Homa Bay County. Initial soil analytical results revealed that the pH was 7.8- 8.2 with low carbon (2.3 -2.5%) and total N (0.09%) levels at both sites. Soil available P (16.98–20.65 mg/kg soil) and base cations (Ca; 6.2-7.5, Mg; 3.4 -7.3 and K; 2.9-5.5 cmol/kg) were adequate for sorghum production. Microdose and recommended fertilizer rate increased soil N and P levels while FYM increased soil organic carbon. Both organic and inorganic fertilizer sources had significant effects on sorghum yields at both sites. At Homa Bay Town sub-county sorghum grain followed the increasing order of control; 0.74 tons/ha < FYM; 1.02 ton/ha < micro dose; 1.32 tons/ha < recommended rate; 1.40 tons/ha < micro doze + FYM 1.46 tons/ha. At Rachuonyo North sub-countiey sorghum grain yields were control; 0.97 tons/ha< FYM ; 1.17ton/ha < micro doze; 1.47 tons/ha< recommended rate; 1.54 tons/ha < micro doze + FYM; 1.74 tons/ha. There were no significant differences between micro dose, micro dose + FYM and recommended fertilizer rates, meaning that farmers can use micro dose to increase sorghum yield in vertisols of Homa Bay County.

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O123

Assessment of Agroecological Diversification in Farming Systems among Smallholder Sorghum Farmers in Semi-Arid Eastern Kenya

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The current agricultural systems are producing huge volumes of food for the world's population using high external inputs. This has greatly contributed to destruction of forests, diminishing water resources, biodiversity, soil depletion, and high levels of greenhouse gases, yet food/nutritional insecurity remains a critical global challenge. To reverse this trend and restore environmental sustainability, especially on marginal agricultural systems like Eastern Kenya, agroecological approaches using ecological and social principles of food production have been strongly recommended. The approaches promote biological diversity within and among crops, microbial diversity, wild relatives/wild edible plant species which all provide biological foundation for food/nutrition security and contribute towards economic development. This study was carried out to assess the level of agroecological diversity which exists in the semi-arid region of Tharaka Nithi County, Eastern Kenya characterized by sorghum growing, agroforestry/crops/livestock farming systems. Thirty households were randomly sampled and interviewed using a structured questionnaire. Descriptive analyses and diversity index, Shannon–Wiener diversity index (H') and Simpson's index (D) was utilized to analyze diversity, richness, and distribution of crop species in the study region. Thirteen crop species, forty-two tree types and nine livestock types were identified. High relative densities of sorghum, cowpea, green grams, pearl millet and maize with 13.6, 13.6, 11.0, 9.6 and 8.6 indices were determined respectively. The study region had a slightly low index difference between the long rains and short rains because farmers tend to manage high level of crop diversity in the long rains. There was a strong and significant positive correlation ($r= 0.828^{**}$) between crops and trees and moderate positive correlation ($r= + 0.514^{**}$) both at $p < 0.01$) between farm size and livestock. The study concludes that the level of functional diversity in smallholder farms in this County is useful and could contribute significantly towards food security, nutrition, and income generation.

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Sorghum cultivation to reduce nitrogen loads into the environment by Biological Nitrification Inhibition (BNI) and enhance human nutrition

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The cultivation of sorghum, the 5th widely cultivated cereal worldwide, is gaining more importance in the actual context of fertilizer soaring. High inputs of nitrogen fertilizers have adverse effects to the environment due to the nitrification process led by Ammonia-oxidizing archaea (AOA) and bacteria (AOB). Their abundance in soil strictly affects the distribution of nitrogen. Slowing down soil nitrification helps reduce nitrogen loss via denitrification and NO₃-leaching. A naturally known-strategy developed in some plants is to inhibit the activity of microbial nitrifiers by synthesising and releasing in the rhizosphere soil, specific secondary metabolites playing the role of inhibitors. Among these metabolites, is sorgoleone released from sorghum roots. We conducted greenhouse and field experiments using different sorghum genotypes with contrasting sorgoleone-releasing capacity, and determined the soil nitrification, and the effect of sorghum growth on soil microbial population. The results of both trials showed that the sorghum genotypes which release higher sorgoleone significantly reduce the population of nitrifiers, mainly the AOA, in the rhizosphere soil. Subsequently, the nitrification was further reduced where AOA and AOB decreased, demonstrating the active nitrification inhibitory factor of sorgoleone.

The breeding of sorghum lines with the ability to release higher concentrations of sorgoleone is a strategic way to improve the biological nitrification inhibition in sorghum cropping systems, increase crop production and human nutrition, and reduce the negative environmental impact caused by the high application of chemical fertilizers.

O125

Identification of sorghum aphid resistance loci and other related traits using cornerstone genomic resources

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The sorghum association panel has been extensively used by the sorghum research community to provide a wealth of information for crop improvement. Recently, extensive genomic resources were generated as a result of significant progress in high-throughput sequencing technologies and bioinformatics methods. We used whole-genome sequencing resources to identify QTL relevant to sorghum aphid resistance traits and other related agronomic traits. The high-density genomic marker set of nearly 7 million variants included 5,420,745 single-nucleotide polymorphisms (SNPs), 1,349,015 insertions/deletions (indels), and 171,907 copy number variants (CNVs). The phenotypic data set generated from a set of 287 accessions of SAP panel planted in 2019 and 2020 in Tifton, Georgia was used in genome wide association studies (GWAS). Some of the phenotypic data such as plant height and stem thickness were generated using high-throughput phenotyping methodologies (drone and ground-based robots). GWAS analysis was performed using both MLM and FarmCPU models in rMVP on the quality filtered markers of all types. We identified numerous markers located within previously identified QTLs for these traits. This study allowed us to compare how a wealth of genomic information can enhance our ability to tag markers to different traits. The density of these genomic resources has enhanced the resolution at which QTL may be identified and improve the dissection of the genetic pathways underlying these agronomically important traits.

Integrated analysis of sorghum transcriptome and metabolome provides new insights into the genetic mechanisms of host plant resistance to aphids

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Sorghum is a staple food crop grown worldwide but aphids (greenbug and sugarcane aphid) are the major constraint of sorghum production. Particularly sugarcane aphid (SCA) has emerged as a key pest of sorghum since its outbreak in the U.S. in 2013. Use of resistant sorghum hybrids/cultivars for aphid management is an excellent solution. Several sorghum genotypes have shown resistance to SCA, yet the genetic basis of plant resistance is poorly understood. Thus, our recent research focuses on identification of resistance sources and analysis of resistance mechanism using the emerging technologies (OMICS such as genomics, transcriptomics and metabolomics). Transcriptional studies were conducted in resistant and susceptible genotypes infested with SCA to evaluate differential gene expression between resistant and susceptible lines. Principal component analysis revealed a difference in transcriptomic profiles between the two genotypes. The differentially expressed genes (DEGs) identified from the expression profiles were used for gene ontology and pathway analysis, which reveals upregulation of a suite of genes related to the defense pathway in the resistant genotype compared to the susceptible genotype. These DEGs are related to R genes (NBS-LRR), signal transduction (MAPK, SA and JA), transcription factors (WRKY and MYB), and defense metabolites (flavonoids and terpenoids). Expression of 36 DEGs was confirmed by the RT-PCR data performed with the same genotypes (infested vs. non-infested). Furthermore, LC-MS analysis of the two genotypes demonstrated higher levels of JA and SA in the resistant genotype infested by SCA. The phytohormone bioassay in the susceptible genotype treated with JA and SA showed a decrease in both aphid population on plant and plant damage. Together, these comparative analyses of two genotypes indicate these genes related to SA and JA pathways were involved in host plant resistance. Our findings provide new insight into the genetic and molecular mechanisms of host plant defense against sugarcane aphids.

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Molecular characterization of the mode of action of three anthracnose resistance genes in *Sorghum bicolor*

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Sorghum's ability to withstand periods of drought, flooding and fluctuations in temperature make it an attractive crop for production areas that will be impacted by global climate change. To enable the expansion of sorghum cultivation in warm and humid climates around the world, anthracnose resistance is of paramount importance. This disease is caused by the hemibiotrophic fungal pathogen *Colletotrichum sublineola* and affects all above-ground parts of susceptible plants, causing yield losses of up to 50%. The cost of fungicides, the health and environmental hazards associated with their use, and the observed regional variation in pathotypes make the use of sorghum genotypes harboring multiple anthracnose resistance genes the most successful strategy to safeguard yield in an environmentally and economically sustainable manner. We have been working on the molecular characterization of three anthracnose resistance genes, one on chromosome 9 identified through QTL mapping [1] and two on chromosome 5 identified through a genome-wide association study of the sorghum association panel [2]. The locus on chromosome 9, validated via virus-induced gene silencing, induces local cell death to prevent the pathogen from spreading. The roles of the loci on chromosome 5 were investigated via transcriptome profiling of resistant and susceptible genotypes using multiple timepoints post infection. The expression data were subjected to a weighted gene co-expression network analysis (WCGNA) [3] and a gene regulatory network analysis. This led to the identification of a signaling cascade that culminates in the production of reactive oxygen species intended to kill the pathogen. This research was funded by the U.S. Department of Energy Office of Biological and Environmental Research grant nos. DE-SC0014439 and DE-SC0019097.

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Exploiting Genetic Diversity to Achieve Sustainable Sorghum Anthracnose Disease Management

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The resilience and sustainability of sorghum is determined by the effective use of its large genetic diversity for tolerance to biotic and abiotic stresses. Host plant disease resistance offers the most sustainable control mechanism against biotic stresses. Anthracnose caused by *Colletotrichum sublineolais* one of the most damaging sorghum fungal diseases worldwide, because it affects all aerial tissues of the plant, resulting in substantial yield losses. The identification of host plant resistance sources in genetically diverse sorghum germplasm is imperative to establish a long-term management control that increases the resilience and sustainability of sorghum. A subset of ~1,700 tropical accessions from the USDA-NPGS sorghum core collection were genetically characterized through genotyping-by-sequencing (GBS) to study its genetic diversity and population structure. The data are publicly accessible as a genomic resource. The anthracnose resistance response was evaluated in accessions from Ethiopia, Sudan, Yemen, West and Central Africa and sweet sorghums and identified many genetically diverse resistant accessions. Genome-wide association studies (GWAS) associated multiple genomic regions with the observed resistance response, but genomic regions on chromosomes 4, 5, 8 and 9 were controlling most of the phenotypic variation. In parallel, the sorghum association panel (SAP) and three recombinant inbred lines populations from the nested association mapping population (SC1103, SC265 and SC1345) were screened for anthracnose resistance. The GWAS and QTL studies identified multiple anthracnose resistance loci in this temperate-adapted germplasm. Comparative genome mapping analysis revealed that some of the resistance loci identified in tropical germplasm were introgressed into temperate-adapted germplasm. Therefore, the introgressions of new resistance sources from tropical germplasm must be strategically selected based on population structure and genetic profile. The combination of these different resistance sources will be the most effective strategies to manage anthracnose disease, thus making an important contribution to the resilience of sorghum exposed to new environmental conditions.

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Valorisation of natural bio-colorants from dye sorghum

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Dye sorghum (*Sorghum bicolor*) as a distinct crop was only recently «discovered» by scientists in Benin. It is specifically grown for the red pigments in its leaf sheaths, which are used to colour foods and in traditional medicine. Apart from producing dye-containing leaf sheaths, dye sorghum also produces grain. Sorghum is the only plant known to contain the specific 3-deoxyanthocyanins in significant quantities. The 3-deoxyanthocyanidins are recognized as health-promoting phytochemicals, as they are more cytotoxic to human cancer cells than their 3-hydroxylated anthocyanidin analogs. Recently, researchers from Benin and The Netherlands studied the diversity of dye sorghum, its chemical composition and extraction; and to develop methods for its cultivation and processing. Interestingly, very high levels of 3-deoxyanthocyanidins (apigeninidin and luteolinidin) were found. The amount of apigeninidin was 30 times higher than in cereal bran and the total anthocyanin content 5 times higher than in fruits and vegetables. The concentration of 3-deoxyanthocyanidin is mostly linked to environmental conditions during crop growth. A fertilization trial showed clear differences in leaf sheath size between treatments. Cultivation practices were optimized and subsequently the yields of both bio-colorant and grain increased by a factor of 2 and 3, respectively. Farmers successfully cultivated the dye sorghum crop on a commercial basis. A Beninese company regularly purchases tons of fresh leaves for local and international trade thereby supporting livelihood of farmers. Improved practices for post-harvest handling of leaf sheaths were developed to facilitate the export of dry leaf sheaths abroad. Extraction methods for bio-colorants were also developed. Innovative food processing of grain allowed to produce (un)fermented porridges and beer, which are highly appreciated by consumers. Efforts are still needed in the legislation domain in view to allow the introduction of the dye sorghum leaf sheath to EU market.

O130

Rural incubation of women millet and sorghum processors in Niger creates businesses with potential to improve nutrition

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Through the Feed the Future Sorghum and Millet Innovation Lab and its predecessor INTSORMIL, a food processing incubator (Hub-and-Spoke system) was developed in Niger that, in partnership with the McKnight Foundation, supported rural women processing of millet and sorghum products. A range of food products, differing by site, were developed and sold in local markets with fortified products becoming the highest selling. These food-to-food fortified (FtFF) products formulated to deliver ~20-30% DV for shortfall micronutrients (iron, zinc, pro-vitamin A) and a good source of protein were designed for local taste preferences with high acceptability by children. In the 2020-2022 period, at four different rural Nigerien sites, total sale of the fortified flour was ~25,000 USD representing ~40,000 units (500 g) and ~20 MT of flour purchased mostly for children. Linkages at each site with local government health centers has resulted in documentation of numerous cases of improvement from undernourished states of children. Spoke processing sites have naturally expanded through women training. In spring 2023, a diet assessment retrospective study was begun to determine the extent to which FtFF millet and sorghum flours has improved diet quality of children in these sites.

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Successful commercial demonstration of production of high value added food products from sorghum leading to development of new market and categories by Indian startup

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The decline in white sorghum (Dagdi jowar) area in region of Barshi, reason being farmers switch to other cash crops, post harvest losses, unseasonal rain, customers switching from traditional flatbread made from Sorghum resulting in low demand. The challenge of low shelf life, lack of quality convenience food products from sorghum and current market filled with corn/wheat based ingredients for high value products. Lack of consumer awareness, volatile sorghum prices, consumers habit with wheat, corn, rice based food products makes more challenge to make sorghum based food product mainstream. Social enterprise Meloop foods state of the art facility with its R&D capability, multi stakeholder engagement have managed to develop the retail products, commercial ingredients and developed dry supply chain for sorghum. The Gluten-free cookies, breakfast cereals, premixes, roasted snacks, Sorghum flakes, premix as ingredient to substitute corn flakes ready to fry, plant based, malnutrition program created new market space. Meloop foods has redefine the buyer group with sorghum ingredients options that is superior in taste, texture and consumer acceptability. The Pregelatinization, thermal treatment, parboiling, roasting, baking and milling are the process worked to make it commercially viable products and paring with right ingredients for celiac, gut, weight loss customer segments.

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Recent Advances in Sorghum Value Addition in Australia

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Sorghum is Australia's third largest cereal crop, with 2 million tonnes per annum compared to the 58 million tonnes produced worldwide. This makes Australia the ninth-largest sorghum producer globally, but we are the second-largest exporter, with a gap in local value addition to the crop. Commercial production is mainly limited to a small number of red and white varieties, most of which are exported for animal feed. However, there has been recent interest in the supply of specific genotypes for value-added food applications. Our current research focuses on identifying specific genotypes best suited for food applications, including popping, decorticated flour, bread dough, and antioxidant ingredients. This presentation will highlight recent advances in the development of these applications with the aim of increasing the use of Australian sorghum grains in mainstream food products.

Studies of popping ability using seven genotypes showed that sorghum with medium grain size, bulk density, and high grain hardness showed a higher popping yield and expansion ratio than others. Furthermore, popping quality was positively correlated with in vitro starch and protein digestibility. Pre-treatment of whole sorghum grains with polysaccharide degrading enzymes showed that enzyme combination synergistically removed the pericarp non-starch polysaccharides giving a decorticated grain with potential for improved nutritional quality. In another study, bread dough was prepared from a combination (1:1) of different sorghum genotypes with wheat flour using our standard microdoughLAB method for understanding dough quality. We identified a specific sorghum genotype that demonstrated higher extensibility, shorter dough development time, longer stability and satisfactory softening degree compared to the other genotypes indicating its better suitability for bread dough. We have studied the antioxidant properties of diverse sorghum genotypes under different environmental conditions and identified G×E combinations that give high antioxidant sorghum flour having potential as a healthy food ingredient.

It's MAGIC – challenges and opportunities in leveraging multi-parent population structure in sorghum improvement

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In 2017 a new sorghum breeding program was established in northern Nevada, USA, focusing on grain quality for end-uses in the food sciences. A sorghum grain quality Multiparent Advanced Generation InterCross (MAGIC) population was developed from eight parents (trait donors) with the aim of combining the waxy (low-amylose) trait with a wide range of other traits known to impact food and alcoholic beverage quality. This presentation will cover the genetic and phenotypic development of the population with an emphasis on observations of transgressive segregation for protein, lysine, starch, amylose, and oil content; starch and protein digestibility, grain color, seed size, kernel hardness, and vitreosity. Results will be related to genomic and agronomic data, causal alleles, and malting and brewing quality. The benefits of using MAGIC populations for genetic mapping versus adaptation breeding will be highlighted. Challenges inherent in developing and leveraging the MAGIC design will provide a roadmap that can enhance the adoption of this powerful tool in sorghum breeding and genetics to fill value-added, gluten-free food and beverage markets.

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Screening of sorghum genotypes for resistance to striga

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Sorghum (*Sorghum bicolor*) is an important staple crop in Sub Sahara Africa. In Zambia due to lower annual rainfall especially in southern part, sorghum has been a major source of cereal grain plant with starchy seeds due to its good tolerance to drought stress.

However its production has been very constrained with parasitic “witch” weed (*striga asiastica*) that attaches to the roots of sorghum causing harmful allelopathy effects causing severe stunting and loss of yield.

To mitigate this challenge, Sorghum breeders in Zambia have been focusing on identifying wild sorghum accessions which grow as weedy plants and use the as source of *striga* resistance gene source introgression to cultivated sorghum in order to improve immunity to *striga*.

This breeding however has been very slow such that to date only ZSV-12 and ZSV-13 has shown some good level of tolerance to *striga* depending on planting timing as avoidance and escape IPM strategies adds more value in reducing yield loss of these two varieties.

There is an urgent need in capacity building involving Marker assisted breeding and its build up techniques like phenotyping so that all the released sorghum varieties and elite lines can be grouped according to its similar value for cultivation and improve them towards developing resistance *striga*.

The objective of attending the orghum in the 21st century global sorghum conference is to build capacity through not only during conference sessions but through networking as there will be more interaction with difference resource persons, breeders, agronomists, pathologists. Geneticist, entomologists etc. so that the knowledge and guidance acquired will be immediately applied in order to help improve sorghum production to improve food security and income generation especially among rural households in Zambia.

Keywords: Sorghum bicolor - Striga asiastica.

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O135

Genomic Prediction of Sweet Sorghum Agronomic Performance under Drought and Irrigated Environments in Haiti

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Over the last decade, genomic selection has gained momentum as a tool for predicting phenotypic performance in plant breeding populations and accelerating the development of new cultivars. Different statistical models and approaches have been developed to implement genomic selection in plant breeding, and strategies that promote accurate and resource-efficient prediction are of increasing interest. Since its establishment in 2010, the sweet sorghum breeding program at “CHIBAS” has led efforts to develop and release cultivars resilient to abiotic and biotic stress. Among the abiotic constraints, drought stress is the most limiting since growers depend on erratic rainfall for sorghum production. The goal of the present study was to evaluate the predictive ability of genomic prediction models across contrasting environments in Haiti using two statistical methods (Bayes B, and BRR). We evaluated twelve sorghum traits and performed genomic predictions within and across irrigated and water stress treatments planted at two different dates. Overall, the two methods showed similar results. Prediction accuracy was higher for within-environment (0.31 to 0.70) than across-environment (0.06 to 0.70) involving “water stress 1” scenarios. Additionally, prediction accuracy varied substantially for all traits, with total green leaf showing the highest mean value (0.70), and grain yield showing the least (0.49). Accuracies of genomic prediction obtained here are encouraging for implementation of genomic selection in small breeding programs for drought tolerance.

Keywords: Sorghum - Genomic prediction - Water Stress - Phenotypic performance.

O136

The inner workings of the Australian Sorghum Midge Tested Scheme – how Midge Resistance ratings assigned and what they mean?

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Sorghum midge (*Stenodiplosis sorghicola*) is one of the most damaging insect pests of grain sorghum worldwide. In Australia, the most effective method of combating this pest has been the incorporation of sorghum midge resistance into commercial grain sorghum hybrids. This has not only reduced the yield impact of this pest, but also significantly decreased the use of insecticides in midge control.

To provide accurate and independent information about midge resistance (MR) levels in commercial hybrids in Australia, the Midge Tested Scheme was developed and has been operating since 1993. The Scheme incorporates an annual experiment where test hybrids are grown alongside a set of standard lines (of known resistance ratings) and high midge pressures are applied during the flowering period. These higher pressures allow for more accurate discrimination between higher and lower levels of MR across hybrids. The experiment is performed inside a large plastic tunnel which helps maintain ideal temperature and humidity conditions to encourage high levels of infestation whilst minimizing the influence of external factors such as: weather, other insect pests, birds and potential visiting non-preference interactions that can occur in field situations. The number of female egg-laying midge are counted daily during flowering and at maturity, heads are assessed for percentage midge damage. This damage is analysed in combination with total midge number, head size and flowering date to find a prediction for each test hybrid that corresponds with head damage per midge. These predictions are then statistically compared to the standard lines to find the most appropriate MR ratings.

These MR ratings in turn provide agronomists and growers with important decision making tools. Higher ratings afford more flexibility in planting times and the ratings can also be used to calculate Economic Thresholds, which can in turn lead to fewer, more targeted insecticide applications.

The role of phytochemicals in grain mold resistance in sorghum: opportunities and challenges

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Sorghum grain mold resulting from concurrent infection by multiple fungal species is the most important disease of the crop. Host resistance is considered the most effective and feasible approach to control the disease. However, genetic resistance against the disease is complex. Some of the resistance mechanisms have implications on grain functional properties and agronomic traits which require an in-depth study of the genetic architecture of resistance. Over the past few years, we have conducted a series of studies to dissect the genetics, molecular, and biochemical components of grain mold resistance. Genome-wide association analysis of diverse sets of natural variants and transcriptome analysis of developing sorghum grain identified genes and loci that may contribute to resistance. Two sets of landrace collections, one with a large set of 1425, and a second set with 635 landraces were studied for association of resistance and SNPs across the genome while sorghum lines with known reaction to the disease were used for transcriptome analysis. The GWAS on the two sets of landraces identified the sorghum *Y1* locus a MYB transcription factor that regulates seed color and biosynthesis of 3-deoxyanthocyanidin, and a known SNP in the *Tan1* gene, a regulator of tannin accumulation in sorghum grain. We also identified a locus containing a *Kafirin* gene to be associated with grain mold resistance. These results highlight the critical roles of sorghum phytochemicals as well as the seed's physical characteristics in grain mold resistance. The sorghum *Y1* and the *Tan1* genes are known to regulate the biosynthesis of pathogen inducible phytochemicals particularly the 3-deoxyanthocyanidin phytoalexins as well as tannins. The transcriptome analysis provided evidence on the molecular link between pathogen perception and biosynthesis of the phytochemicals. The roles of the phytochemicals and kafirins in relation to human nutrition, health benefits and disease and pest tolerance will be discussed.

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Genomes to genes to cultivars- a comprehensive approach towards adapted and fungal resistant sorghums

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Crop production is facing challenges that are likely to worsen due to climate change. Increased frequency of drought, disease epidemics and expanding ecological niche of pathogens are consequences of climate change. Production of sorghum may be pushed to higher rainfall or irrigated regions which have the potential for better productivity if diseases are managed. The design of smarter diseases management strategies is crucial to manage current and emerging pathogens. As part of the USAID supported Sorghum and Millet Innovation lab, multidisciplinary research was conducted with an ultimate goal of developing disease resistant and adapted sorghum cultivars. Fungal diseases anthracnose and grain mold are challenges to sorghum production worldwide and are targets of our studies. Whole genome resequencing combined with classical genetic mapping using biparental segregating or Recombinant Inbred Lines (RILs) pinpointed broad-spectrum or race specific disease resistance genes. Four of these resistance genes encode canonical NLRs (nucleotide-binding leucine-rich repeat immune sensors), and two are non-canonical resistance genes. In addition, Ethiopian landrace sorghums were studied for disease resistance and agromorphological traits to lay the foundation for sorghum improvement. This population harbor unique genes and alleles that can benefit sorghum breeding. Consistently, association genetic analyses defined genomic regions and loci for fungal resistance and other traits. About 400 of these landrace sorghums are being sequenced to better understand the genetics of key traits and develop a genome enabled breeding program. In parallel, exploiting the landrace population for disease resistance, adaptation, and high yield resulted in the release of two varieties 'Jabaa', and 'Merera'. The serendipitous isolation of 'Merera' which appears to display unique features provided opportunities for blending 'Merera' flour with other local food making processes. As we review successes and challenges, the prospect of developing resilient sorghums that can thrive in a changing environment and pathogen dynamics will be discussed.

Evaluating the performance of value-added Sorghum porridge in improving the diets of Pre-School Children in Migori County

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More than a quarter of children under five years, have stunted growth indicating a heavy burden of undernutrition in Kenya including Migori County where 26.4 percent of children are stunted, with boys recording a higher prevalence than girls. The national and county governments have recommended interventions targeting counties with a high burden of chronic malnutrition such as Migori in order to minimize the negative impact of malnutrition in young children. This study therefore evaluated effect of sorghum value-added porridge on nutritional status of 150 pre-school children at Kasembo Primary School in Migori County. The Objective was to test the effect of sorghum porridge fortified with soybean on nutritional status of pre-school going children. A Complete Randomized Design with two experimental sorghum porridge formulations comprising sorghum-maize-soybean (SMS) at 45%, 25% and 30 % respectively; sorghum-soybean (SS) at 70% and 30%, and a control treatment (MM) with 100% maize were prepared and fed to children, divided into two groups for each treatment, daily for four months. Anthropometric measurements including weight, height, and mid upper arm circumference (MUAC) were taken monthly for each child. At the end of 4 months, children fed on SMS blended porridge had the highest gains in weight (2.0 kg), height (2.2cm) and MUAC (10.9 mm). The SS gave the second-best gains in weight (1.4 kg), height (1.5 cm), MUAC (8.5 mm). MM porridge alone without soybean fortification gave the least gains in weight (0.9 kg), height (1.3 cm) and MUAC (8.0 mm). The differences in mean weight, height and MUAC among the three treatments were statistically significant ($p \leq 0.05$). The study concluded that soybean fortified sorghum porridge formulation improved the nutritional status of the pre-school children and recommends feeding it to school children to address the problem of malnutrition in Migori County.

Effect of malted sorghum-based porridge on the nutritional status of infants and young children diagnosed with moderate acute malnutrition in Uganda

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Background: Moderate acute malnutrition (MAM) and anaemia are prevalent among infants and young children (IYC) in Uganda. A lack of consensus regarding the most effective strategy for managing MAM among IYC resulted in the present study comparing the effect of malted sorghum-based porridge (MSBP) (an active malt, extruded maize and soy sorghum supplementary porridge developed for the purpose of the present study) as an intervention versus an extruded maize and soy micronutrient fortified blend (CSB+) as a control and current standard care. Outcome measures were anthropometric status and haemoglobin levels.

Methods: The study comprised a double-blind cluster randomised control trial with eight to 10 conveniently sampled consenting mother–IYC pairs per cluster who were randomly assigned to the intervention ($n = 110$) or control ($n = 110$) for 3 months. Weekly anthropometric measurements were taken. Haemoglobin levels were measured at baseline and end line. Mean length-for-age, weight-for-age, length-for-weight and mean haemoglobin levels of the treatment and control groups were compared using an independent t -test. The Z-test was used to compare proportions of the outcome indicators between the treatment and control groups.

Results: Difference in mean weight-for-age Z-scores in the treatment group improved compared to control ($P = 0.010$). The change in mean haemoglobin levels was lower in the treatment versus the control group ($P = 0.010$). The proportion of IYC recovering from MAM between treatment and control did not differ significantly ($P = 0.055$).

Conclusions: Recovery rates after supplementation with MSBP versus CSB+ resulted in similar weight-for-length and haemoglobin levels. Therefore, MSBP has the potential for being scaled up in the management of IYC with MAM in Uganda.

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ZEWDU	Solomon	Understanding the phenotypic and genotypic variation among key Ethiopian core collections and introduced forage sorghum genotypes	P158
DERESE	Assefa Solomon	The impact of drought on sorghum production, and farmer's varietal and trait preferences, in the north eastern Ethiopia: implications for breeding	P159

ADDITIONAL POSTERS

S1 - Capturing sorghum's genetic potential in responding to climatic and environmental challenges

Last name	First name	Title of poster	# poster
PERUMAL	Ramasamy	Pilot-scale genome-wide association mapping in a diverse sorghum germplasms identified novel genetic loci linked to major agronomic, stomatal and root traits	P160

S2 - Optimizing sorghum production techniques to minimize loss and maximize on-farm returns

Last name	First name	Title of poster	# poster
TIRFESSA	Alemu	Exploring Sorghum Forage Technologies in Ethiopia: a Comprehensive Package for Impact	P161

Sorghum Wild Relatives: Underutilized Genetic Resources for Enhancing Post-Flowering Drought tolerance in Sorghum

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The stay-green (SG) is an important trait that enables sorghum plants to maintain their green leaves and photosynthesis capacity for a longer time after anthesis, especially under drought-stress conditions. Thus, elucidating the molecular and physiological mechanisms associated with the SG trait is maybe the key to overcoming the stagnation in sorghum productivity. To do so, a total of 255 Sudanese wild and/or weedy accessions were screened for their SG trait using SSR molecular markers. The domesticated sorghum cultivars B35, and Tabat were included to represent resistant and susceptible checks, respectively. Cluster analysis revealed that 21 wild sorghum accessions were situated within the same cluster along with the universal drought-tolerant donor cultivar B35. Out of 21, 8 accessions were cultivated in the field along with the domesticated checks (Tabat and B35). A split plot trial in a randomized completely block design was employed. Water intervals (7, 14, and 21 days) were assigned as main-plot treatments, whereas the genotypes were assigned as sub-plot treatments. Each treatment was repeated three times. Days to 1st flowering, days to 50% flowering, SPAD chlorophyll, Chlorophyll a, b, and total chlorophyll and Proline contents were measured. In the biplot, the axes of the principal components (PC1 and PC2) accounted for 72.13 % of the variation. The component PC1 explained 40 % and PC2 explained 24.13% of the total variation. The partial least squares regression indicated that the wild sorghum accession Elteboan-3 was a most valid potential donor for post-flowering drought tolerance.

Stability Analysis of Dwarf Sorghum Varieties for Grain Yield in Northern Nigeria Using GGE Biplot Analysis

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The cultivation of sorghum for food and feed to livestock in Nigeria is threatened due to current security challenges. As an important staple, it is necessary to introduce new, suitable sorghum varieties to help meet their household requirements. The study was conducted to i) determine the interaction between the genotype and environment for grain yield and plant height and ii) identify stable and adaptable high yielding varieties for target environments using GGE biplot analysis. Fourteen (14) dwarf sorghum varieties were evaluated in a randomized complete block design across nine locations in Northern Nigeria in 2020 and 2021. The combined analysis of variance indicated that the genotype x environment interaction (GEI) was significant ($P < 0.01$) for grain yield and plant height. Grain yield of the varieties ranged from 3367kg ha⁻¹ for 12KNICSV-252 to 1683 kg ha⁻¹ for 12KNICSV-107 with an average of 2388kg ha⁻¹. The total variation in grain yield was 83.65%, composed of PC1 and PC2 values at 73.81% and 9.84%, respectively. The GGE biplot analysis of the grain yield at each location indicated that 12KNICSV-260 was the ideal variety, with a high yield potential and the most stability at multi-locations, followed by 12KNICSV- 297 and 12KNICSV-252. The varieties 12KNICSV-260, 12KNICSV-252 and 12KNICSV-297 were adapted and performed better at Dadin Kowa, Gambawa, Minjibir, Samaru, Birnin kudu and BUK. Farmers prefer early maturing and high grain yielding varieties. The area prone to banditry is placing a premium on dwarf sorghum varieties to keep up areas of sorghum production. The identified high yielding and stable varieties are recommended for promotion for greater adoption and commercialization to contribute to food insecurity in Nigeria.

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Advances in sorghum breeding in East Africa: A case of East African Centre of Innovation for Finger Millet and Sorghum

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Food and nutritional insecurity coupled with high poverty index are the major challenges faced by communities living in the arid and semi-arid regions of East Africa. Sorghum is a dominant cereal crops deeply rooted in the agri-food systems of semi-arid communities, accounting for 80% of drylands grain production in the region. Their productivity however is very low. The low yields are mainly due to less adapted varieties susceptible to drought, stem borers, fungal diseases such as turicum leaf blight and anthracnose, and striga weed. This is further compounded by limited availability and access to quality seed as well as poor institutional and market linkages. The East African Centre of Innovation for Finger millet and Sorghum uses integrated crop improvement approaches to address the above challenges through; i) engaging and envisioning with the beneficiaries using a system approach in product profile development to ensure demand articulation and practical actions by beneficiaries, ii) learning, optimizing and adapting modern tools, technologies and methods for discovery and integration of targeted market traits using both phenomics and genomic tools and iii) proper data management for informed decision making hence increased genetic gain. This therefore enhances timely release of impactful varieties along with good agronomic practices that enables smallholder farmers to transit from substance existence to commercial farming hence improving food, nutrition and income security, and resilience to climate change.

Sorghum Wild Relatives in Sudan: An Unopened Treasure for Durable *Striga hermonthica* Resistance

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Striga hermonthica is the most devastating biotic factor affecting sorghum in sub-Saharan Africa. Although several *Striga*-resistant sorghum varieties have been developed in the past, *Striga* species are also co-evolving with the plants, and are therefore continuously breaking the resistance. Under such circumstances, Sudanese sorghum wild relatives might serve as useful genetic material to find resistance genes. Therefore, the objective of the current study is to mine the Sudanese sorghum wild relatives' gene pool for post-attachment *Striga* resistance namely mechanical barrier and hypersensitive-like using SSR molecular markers. To this end, a total of 255 wild and/or weedy species of Sudanese sorghums were used in this study. These wild sorghum accessions represented five taxon names; verticilliflorum, aethiopicum, purpureosericeum, virgatum, and halepense. The domesticated sorghum cultivars Tabat, Framida, and N13 were included to represent resistant and susceptible checks. Two SSR primers were used to detect HR1 and HR2 genes underpinning the hypersensitive resistance mechanism. Out of 14 SSR markers used, 9 markers were shown to be polymorphic for the mechanical barrier mechanism to *Striga* resistance in sorghum. Results indicated there were at least 22 wild sorghum accessions situated within the same cluster along with the universal Indian-resistant donor cultivar N13. While for hypersensitive, 83 accessions gave bands similar to that of the universal resistant donor Framida. Apart from that 17 accessions have HR1, 61 accessions have HR2, and 5 accessions have both resistance genes. Candidate SNPs within Sobic.006G009400 and Sobic.009G056400 were identified and converted to KASP markers for both hypersensitive-alike and mechanical barrier resistance mechanisms, pending validation. In conclusion, 5 accessions namely Abusabiba, Ab-Areeif-10, W.S160S, HSD15143, and HSD15156 were proved to possess both targeted resistance mechanisms which can be served as potential donors for the *Striga* resistance breeding program.

New striga resistant lines for the Sahelian zones of West Africa

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Sorghum is the second most produced cereal in Togo after maize with an annual production of around 300,000 tons in 2021. Although yields have improved slightly in recent years, sorghum is still subject to constraints including *striga*, ranked as the main biotic constraint by growers in 2019. To address this constraint and provide smallholder farmers with tolerant varieties, a molecular marker-assisted backcrossing program involving the donor SRN39 and the recurrent elite variety sorvato1 was initiated. On the basis of genotypic and agro morphological data, 21 lines in the BC1F3 generation containing the resistant allele *lgs1* were selected and tested on two sites in farmers fields with high natural infestation and two control sites including one on the station and the another in the farmer field environment. Statistical analysis showed a significant difference between the different lines for the number of *striga* plants/m². Seven (7) lines were then identified as *striga* resistant promising varieties to be confirm during the next trials. In addition a yield reduction ranking from 15 to 90 % was observed.

Correlation and Path Coefficient Analysis for Yield and Other Traits of Sorghum (*Sorghum bicolor* L. Moench) Land Races at Intermediate agro-ecology of Ethiopia

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This Experiment was conducted to study the association among the yield contributing traits and their direct and indirect effects on the yield of sorghum. Knowing the association and path analysis of yield related traits is essential for breeders. So, this activity was conducted with the objectives of investigating the relationship among yield, yield related traits and their effect on yield. A total of 42 late and medium maturing sorghum genotypes were evaluated by using 7x6 triple lattice designs with three replications at Assosa in 2020 cropping season. For most of the investigated traits, the magnitudes of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients. This implies that there was inherent relationship between these traits. Grain yield showed significant and positive phenotypic and genotypic correlation with days to flowering, days to maturity, thousand grain weight and plant height. The strongest phenotypic association of grain yield was observed with thousand grain weight ($r=0.82$) followed by days to maturity ($r=0.63^{**}$) and days to flowering ($r=0.53^{**}$). Apart from yield greater association was recorded between days to maturity and thousand grain weight ($r=0.65$) followed by disease score with insect score ($r=0.59$). The strongest positive genotypic association was observed between grain yield and thousand grain weight ($r=0.87^{**}$) followed by days to flowering and days to maturity ($r=0.78^{**}$) and thousand grain weight and days to maturity ($r=0.78$). Thousand grain weight has the highest positive direct (0.57) effect on grain yield while overall plant aspect has higher negative (-0.21) direct effect on grain yield.

Sorghum cultivation limiting factors and farmer's criteria traits identification in Niger

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Sorghum is one of the most important cereal crops well adapted to Niger harsh and dry environmental condition. In Niger, there are biotic and abiotic factors impacting sorghum cultivation. The objectives of this study were to determine production limiting factors and preferred traits of sorghum farmers in Niger. Twenty sorghum growing villages in Tahoua and Maradi region were surveyed. The villages were selected based on sorghum production volumes recorded in the various regions as documented by the National Institute of Statistics of Niger database. Limiting factors affecting sorghum cultivation which include, rainfall scarcity, water logging, midge, migratory bird, striga, animal straying, soil fertility, non-adaptative and non-productive varieties utilization were identified. Among the factors, water scarcity and Striga impact were identified as the main sorghum limiting factor in the two regions. In addition, early maturing planting and taller and high yielding Striga resistant varieties with white pericarp and good taste are preferred by farmer. Insertion of farmer's views in the breeding process is the best improvement strategies for developing an easiest and acceptable variety by smallholder's farmers.

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Screening sorghum genotypes for *Striga* Resistance in Niger

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In Niger, sorghum (*Sorghum bicolor*) is one of the most important staple crop for food and money. The crop is confronted to striga (*Striga hermonthica*), a plant parasite, which drastically hinders the productivity and causing yield loss between 20% to 80%. The best and easiest way to control and improve sorghum productivity is through the development of novel Striga resistance sorghum genotypes. The purpose of this study was to assess 20 sorghum genotypes from diverse country for striga resistance and grain yield capacity. Varieties with high yield average, medium size and resistance to Striga were found.

Modelling phyllochron-plastochron relationship in sorghum in order to predict panicle initiation date

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When the rates of leaf initiation and leaf emergence are identical, as in rice, the rank of the last initiated leaf can be directly determined by the last emerged leaf ranking. Oppositely, when plastochron is shorter than phyllochron, as in maize and sorghum, the number of growing leaves inside the whorl increases with time and prevents estimating the panicle initiation date on simple visual observation.

The objective of this work was to quantify the relationships between leaf initiation, leaf appearance and leaf ligulation in three contrasted sorghum genotypes (two parents and their hybrid) in order to 1) estimate the date of panicle initiation based on the number of appeared leaves and 2) investigate the potential heterosis effect.

The appearance rate in thermal time varied according to the genotype, with the hybrid having a faster rate than its two parents. Leaf initiation rate also presented a variability within the three lines, the hybrid having an intermediate position. The shorter phyllochron in the hybrid corresponded to its higher growth rate, expression of an heterosis effect.

The relationships between leaf initiation and appearance were highly significant and genotype-specific. Nevertheless, the slopes of the regressions were close, leading to small differences in the prediction: thus when the 12th leaf just emerges, between the 19th or 20th leaf is initiated according to the genotype. Therefore, using a single model across the three lines does not increase the rank error and can be applied in breeding programs to estimate the date of panicle initiation.

The result needs to be confirmed on a larger panel of sorghum genotype in order to test the model robustness. The main limitation for field application remains the estimation in a genotype of the total number of leaves to be developed before panicle initiation, trait that can vary in photoperiod sensitive cultivars.

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Identification of multiple diseases resistance among key Ethiopian sorghum core collections

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Sorghum (*Sorghum bicolor*) is an important source of food and animal feed in Ethiopia. It is produced in diverse agro-ecologies. The intermediate and low altitude areas in the Western parts of Ethiopia provide sufficient moisture and other climatic conditions for optimal sorghum production but productivity is severely challenged by different diseases caused by different fungal pathogens. The aim of this study was to explore the potential traits of Ethiopia sorghum core collections for their resistance to major sorghum foliar disease mainly anthracnose caused by *Colletotrichum sublineolum*, Leaf blight caused by *Exserhilum turcicum*, Zonate leaf spot caused by *Gloeocercospora sorghi* and Rust caused by *Puccinia purpurea*. A subset of 80 sorghum accessions were systematically selected from 2010 Ethiopian sorghum core collections described as SMIL core collections. The study conducted at three hotspot sites for stated sorghum foliar diseases in Western Ethiopia under natural conditions during 2020 and 2021 cropping season using row- column design. The occurrences of more than three foliar diseases were recorded during the study periods. Data on disease severity of different foliar diseases was recorded at various stages (Vegetative, flowering and post flowering) on 1-9 scale. Severity scores were converted to percent severity index for the analysis of variances. Four genotypes consistently recorded for significantly lower severity scale and conversely lower percent severity index for at least three foliar diseases (anthracnose, leaf blight and rust) across all tested locations and years. This indicates the existence of sorghum genotypes possessing multiple diseases resistances. These genotypes are useful in sorghum disease resistance breeding and recommended to be used in both conventional and molecular breeding program in Ethiopia.

Harnessing African Sorghum Biodiversity

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Ethiopia is a key center of genetic origin for sorghum. A collection of over 10,000 sorghum lines were curated at the Ethiopian Biodiversity Institute providing the basis for a panel of 2,200 lines to be assembled within the Ethiopian Institute of Agricultural Research (EIAR) national sorghum program collaborating with other researchers of a global network supported by the Kansas State University led Sorghum and Millet Innovation Lab (SMIL).

A core working collection of 300 lines was then phenotyped in multiple locations in Ethiopia and also fully genotyped by the EIAR national sorghum program team in collaboration with Purdue University. This global collaboration and core working collection enabled unique gene discovery by multiple teams. In the case of host plant resistance against fungal pathogens, genes responsible for anthracnose resistance were identified and a rapid effort to translate those genes into farmer appreciated local produced sorghum varieties in western Ethiopia was realized.

The national registration and release of an improved sorghum variety 'Merera' with up to 40% yield gain under high disease pressure was realized. Over 14 metric tons of this improved seed has been multiplied and is being scaled and commercialized in Ethiopia. A second disease resistant sorghum variety with white color has also been released and will be further scaled into the national seed system through public, private and community based pathways.

The potential of sorghum hybrids in enhancing productivity in the dry lands of Ethiopia

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Hybrid cultivars generally yield higher and tolerate environmental stresses better than inbred varieties and are thought to enhance resilience to climate change. Moreover, hybrids can strengthen seed supply value chain and encourage the development of commercial seed supply system. The use of hybrid cultivars particularly sorghum hybrids in Ethiopia is very limited. Lack of superior hybrids adapted to the local situation is one of the major reasons for the limited utilization of hybrids. As part of the Sorghum and Millet Innovation Lab (SMIL) project, a range of activities including introduction and testing of parental lines and hybrids from public breeding programs in the US and other sources have been conducted in Ethiopian dry lowlands over the past years. With an ultimate goal of developing parental lines for a hybrid program based on native germplasm, these activities were implemented as a short-term intervention that include evaluation of a set of drought tolerant hybrids that were introduced from Purdue University. Candidate drought tolerant hybrids selected for release showed about a 30% grain yield advantage over recently released open-pollinated cultivars.

Adaptation and farmers' participatory selection of sorghum varieties in moisture stressed lowland areas of East Hararghe, Oromia, Ethiopia

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Sorghum [*Sorghum bicolor* (L.) Moench] is an indigenous and second most important cereal crop in Africa (Elkhalifa and El-Tinay, 2002), and serves as a staple food for millions in Africa and Asia (Ejeta and Grenier 2005). In Ethiopia, it is primarily used for making different kinds of foods such as Injera, Porridge, "Nefro", infant food, syrup, and beverages like "Tella" and "Arekie". In eastern Hararghe Zone of Oromia region, sorghum ranks first in area coverage and production (CSA 2020/21). However, the lowland agro-pastoral districts of the Zone (the study area ranging altitude of 1457 to 1471masl) such as Qumbi, Gola Oda, Midhaga Tola and Mayu Mulluqe are characterized by frequent drought episodes due to insufficient amount and erratic distribution of rainfall. In consequence, crop failure and death of livestock are common phenomena in these areas; leaving the households chronically food insecure. Moreover, farmers in these districts have limited access to improved crop and livestock production technologies. As sorghum is the best alternative crop to introduce in to such drought prone areas compared to other cereals, adaptation of ten early maturing sorghum varieties were tested at six locations using randomized complete block design (RCBD) with three replications in 2021/22 growing season with the objective of identifying adapted and productive varieties for the target moisture stressed lowland areas. Pertinent data (plant vigour, days to physiological maturity, tolerance to insect (stalk borer) infestation, tolerance to striga infestation, plant height, stay green characteristics, overall field performance, and yield were collected and analyzed. Farmers have also evaluated the varieties and selected their suitable varieties based on their own criteria. The future plan will be developing appropriate agronomic practices for the selected varieties based on agronomic performance and farmers' selection.

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Plant response to a late heat stress can be modified by an earlier one: a case study on sorghum grain production

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Climate change is now a reality and observable effects include higher temperatures with successive periods of heat waves. These events have consequences in plant development and grain production. Sorghum is an African native cereal known for its robustness. However, in the context of climate change, sorghum production can be affected by heat stresses during reproductive stage. Even if the effects of single heat stress were already described as having an impact on sorghum grain production, the effects of recurrent heat waves were not studied until now.

A preliminary study was performed in 2021 with two contrasted genotypes grown under four heat stress scenarios in controlled conditions, combining single and recurrent heat waves. The aim of this study was to analyze i.) the effects of these stresses on plant production ii.) the eventual impact of an early heat stress on a later one. In addition to yield components analyses, morphological, spectral and biochemical measurements were performed on sorghum panicles.

Yield components, morphological traits and grain quality were differently affected depending on the stress scenario. Furthermore, our results show that an early heat stress can attenuate or amplify the response of a later one, depending on the considered variable, the genotype but also the position of the first stress compared to the second one.

New experiments are currently investigated in RICOCHETS project (2023-2026). Our original approach combines dynamics multiscale analyses with samplings at key times (early stress/recovery periods/late stress). These results will contribute to broaden our knowledge on the response of plants to recurrent heat waves, which can be used in future plant breeding programs.

Exploring the genetic basis of anthracnose resistance and major agronomic traits in Ethiopian sorghum landraces through genome-wide association study

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Sorghum bicolor is an important food security crop globally. Despite its importance, the productivity of the crop is challenged by various biotic and abiotic stresses. Sorghum anthracnose, caused by the fungal pathogen *Colletotrichum sublineola*, is a major disease that reduces sorghum productivity. Developing anthracnose-resistant and high-yielding sorghum cultivars is critical for enhancing productivity. Here, we conducted field experiments on 329 diverse Ethiopia sorghum landraces across two locations in Ethiopia for two consecutive years where disease responses were scored under natural infestation. Genome-wide association analysis (GWAS) was conducted using multi-locus models to identify genomic regions and candidate genes associated with anthracnose resistance and major agronomic traits. Using 107,377 SNPs generated through the GBS method followed by quality control of the data, we identified SNPs significantly associated with anthracnose resistance and other agronomic traits. For instance, sequence polymorphisms on chromosome 4 (S04_66140995) and 2 (S02_75784037) were strongly associated with anthracnose resistance and contained receptor-like kinases and stress-induced-antifungal tyrosine kinase that were previously implicated in disease resistance. The GWAS for key agronomic traits revealed significant loci and genomic regions associated with complex traits. Significant SNPs that explained phenotypic variation of up to 79% were associated with complex traits. The genomic region marked with S03_60681608 annotated to the *dehydrin* gene, encoding proteins that accumulate during seed maturation and in response to stresses, was associated with thousand-grain weight. Similarly, significant SNPs were identified on chromosome 4 for days to flowering, days to maturity, plant height, panicle length, panicle weight and grain yield. Our study opens avenues for molecular breeding of sorghum; the identified SNPs and candidate genes can be used to design molecular markers to improve different traits, including anthracnose resistance and other agronomic traits.

Keywords: Anthracnose - Agronomic traits - Candidate genes - *Colletotrichum sublineola* - *Sorghum bicolor*, Genome-wide association study.

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Disease-resistant, adapted and high-yielding sorghums for the disease prone intermediate altitudes in Ethiopia

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Sorghum is a staple food crop for millions of subsistence small-scale farmers in Ethiopia. However, the productivity of sorghum has been limited by several factors such as biotic and abiotic stresses, limited access to improved varieties, traditional farming practices, and poor extension and value chain systems. In Western Ethiopia, sorghum is grown in intermediate-altitude regions where plant diseases are major bottlenecks. Plant diseases such as anthracnose and grain mold pose significant challenges to sorghum production in this region, resulting in considerable yield losses. To address these challenges, Bako Agricultural Research Center in collaboration with the USAID-supported SMIL project made an effort to develop disease-resistant, adapted, and high-yielding sorghum varieties for intermediate altitudes, utilizing the Ethiopian sorghum landraces core collection. Two sorghum varieties 'Merera' and 'Jabaa' were released for intermediate altitude areas to boost productivity and food security. The varieties showed strong resistance to pathogens, as well as the potential to increase yields by up to 46% and 39% compared to local varieties. Efforts have been made to demonstrate and scale out the 'Merera' variety in potential sorghum-growing parts of Western Ethiopia. We distributed high-quality 'Merera' seeds to farmers, provided training on improved farming techniques, and established demonstration plots to showcase the benefits of improved technologies with the goal to scale out these practices and scaling outs to reach more farmers in the region. It is expected that with strong extension services reaching more farmers and the deployment of these varieties, increased sorghum productivity, food security, and increased income will be achieved for farmers. In conclusion, the development of disease-resistant and high-yielding sorghum varieties with strong extension services has provided a promising solution to the challenges faced by small-scale farmers in the intermediate altitudes of Western Ethiopia.

Keywords: Disease resistant - Jabaa - Merera - Plant disease - Variety - Yield.

Generation of sorghum EMS mutant library facilitating high through-put mutant identification using FIND-IT

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Sorghum is a genetically diverse crop adapted for growth in semiarid regions across the world where it successfully competes with other crop plants especially under drought conditions. However, development of sorghum grain yield during the past 50 years has been limited compared to wheat, rice, maize and barley. To increase grain yield and quality, new genetic variation can be induced by applying gene editing or classical mutagenesis induced by e.g. chemicals.

We have built an EMS sorghum mutant library consisting of progeny grains harvested from 150,000 M1 plants grown from mutagenized BTx623 seeds. The mutant frequency has been estimated in the range of 50-400 non-synonymous mutations per plant in gene coding sequences equivalent to 3-21 mutations per million base pairs.

The large mutant library in combination with the FIND-IT mutation detection platform allows identification of the full spectrum of amino acid substitutions deriving from the EMS induced nucleotide transitions including gene knockouts. Specific mutants can be identified from the library and planted into soil within one week supporting trait development in breeding new sorghum varieties. Since the FIND-IT methodology is GMO free, the newly identified genetic variants can directly be used in breeding programs, thereby rapidly improving sorghum grain yield or quality for animal and human consumption.

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Genetic variability of sorghum [*Sorghum bicolor* (L.) Moench] inbred lines for transpiration efficiency (TE)

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Sorghum [*Sorghum bicolor* (L.) Moench] is the king of cereal crops in the arid and semiarid tropics, where drought is a recurrent problem affecting crop production because of erratic amount and distribution of rainfall. Although sorghum has a genetic potential to withstand the effect of drought, it is being affected by the current climate change scenarios. The present experiment was conducted with the view of assessing sorghum variability to transpiration efficiency, and association among traits using 101 sorghum genotypes in greenhouse facility at Melkassa Agricultural Research Center during 2021/22. The design of the experiment was RCBD with two replications. Data analyses were computed using SAS 9.4. The analysis of variance showed significant difference among genotypes for all traits considered, indicating the presence of considerable genetic variability among tested genotypes. High heritability coupled with high genetic advance as percentage of the mean (GAM) was recorded for plant transpiration efficiency and shoot transpiration efficiency. Moderate heritability coupled with high GAM were recorded for total dry biomass, shoot dry biomass, root dry biomass, shoot fresh biomass, water use, and leaf area, suggesting the possibility of improving these traits through direct selection. Correlation analysis revealed that plant transpiration efficiency had positively significant genotypic and phenotypic correlations with shoot transpiration efficiency, total dry biomass, shoot fresh biomass, root dry biomass, shoot fresh biomass and leaf chlorophyll content. Cluster analysis grouped genotypes into six clusters. The maximum inter-cluster distance was between cluster II and cluster V, suggesting the possibility of improving genotypes through hybridization. Overall, the present study indicates the presence of considerable genetic variability to improve transpiration efficiency of sorghum and to develop adaptable and heigh yielder sorghum varieties for drought stress environment.

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Developing functional genomics tools for sorghum, by transient or stable transformation

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*The poster will be presented by both co-first-authors

Sorghum is the fifth most important cereal grown across the world in terms of grain production. Grain and flour are used as a staple food in many low-income countries and grains and vegetative parts can also be used for animal feed, energy production or engineering of bio-based product. However, improvements are still needed to adapt varieties to specific uses and various biotic and abiotic stresses.

In order to identify molecular mechanisms that could be required for those improvements, numerous transcriptomic and genetic studies are performed and increasingly available in the literature and databases. Many candidate genes have been identified and need to be validated. However, the low rate of genetic transformation efficiency for this recalcitrant species still remains an obstacle for functional genomics studies.

We will present here a transient transfection protocol based protoplast using PEG-mediated method. We have overexpressed transcription factors of interest to validate their function and identified their target genes through transcriptomic studies.

The aim is now to optimize a protocol of stable transformation either with immature embryos, leaf whorls or other organs. We are investing the main share of our efforts on *Agrobacterium* mediated transformation using immature embryos from sorghum variety Texas 430 and reporter genes, *GFP* and *GUS*.

Protein content evaluation of the Chibas sorghum panel and QTLs detection

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Sorghum is the main crop in the drylands of Haiti, and its consumption is increasing due to the rising prices of imported products for human consumption. The well-being of the population and the nutritional situation can be improved by disseminating sorghum lines with high grain yields and high protein contents. 270 sorghum lines were evaluated for protein content using a FOSS NIRS DS2500 near infrared spectrometer. The results of this study showed a high phenotypic variability in protein content (10%-15%). The genomic heritability calculated for this trait is 0.79. Some lines of this panel have protein contents that are close to soybean. We are currently performing association analysis to identify QTLs within this sorghum population. Sorghum is the main crop in the drylands of Haiti, and its consumption is increasing due to the rising prices of imported products for human consumption. The well-being of the population and the nutritional situation can be improved by disseminating sorghum lines with high grain yields and high protein contents; a high protein sorghum could also be used to make chicken feed without having to add much soy meal. 270 sorghum lines were evaluated for protein content using a FOSS NIRS DS2500 near infrared spectrometer. The results of this study showed a high phenotypic variability in protein content (10%-15%). The genomic heritability calculated for this trait is 0.79. We will present the results on the genetic characterization of protein content and prediction models for protein content and the implication of our work to breed for high protein sorghum lines.

Keywords: Sorghum - Genomic heritability - Protein content of Chibas.

Factors affecting accuracy for genomic prediction in sorghum

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252 sorghum *Melanaphis sacchari* resistant inbred lines developed by Chibas in Haiti have been genotyped by genotyping by sequencing (GBS) and 102 990 SNPs were detected. After imputation with the A.mat function in the RRBLUP package a total of 44 985 SNPs were selected to make prediction and calculate genomic heritability. Prediction model RRBLUP is used as a model of prediction for two contrasting traits (grain yield and brix). The genotypes were planted in 2017 in a randomized complete block design (RCBD) with four blocks across three different environments. The experimental field was located in Haiti at Croix des bouquets (N18, 64526°; W72, 9985°).

The main objective of this study is to evaluate, using empirical data, the effects of the following factors on genomic prediction; number of replication, level of relatedness between individuals, statistical models and training set size. Our results showed that all factors affect genomic prediction accuracy differently. The retraining effect on genomic prediction accuracy will be also evaluated and in this poster we will discuss the implication of our results for genomic selection.

Keywords: Sorghum - Genomic prediction - Training set - Replicates - Relatedness - Empirical data.

Lignin level as a contributor in aphid resistant in *Sorghum bicolor*

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Lignin serves as a physical barrier to invading pathogens in plants. Recent research shows that lignin level can be a contributor to insect and pathogens resistance and enhancing aphid resistance.

Towards developing isogenic lines of aphid resistant sorghum bicolor, lignin analysis can be one of the key parameters that can be followed as well as by traditional chemistry analysis which is time consuming and expensive or by Near InfraRed Spectrometry (NIRS) using an appropriate calibration model.

For this purpose, we will report on analysis of lignin for 165 genotypes using the Klason method (hydrolysis and hot extraction). These samples will be used to establish the prediction model by NIRS calibration.

Genetic correlation between lignin content and aphid resistance will be investigated and we will also test if selection for aphid resistance has selected high lignin inbreds.

Keywords: aphid resistance - Insect and pathogens resistance - Sorghum bicolor - NIRS - prediction model - Klason Method.

Development sorghum hybrids adaptable to Canadian climate and their utilization for food, forage, biofuel and bioenergy products leading to sustainable farming systems

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The sorghum breeding program is generally followed in arid and semi-arid tropic climate throughout the world. AERC Inc. has developed breeding programs in temperate climate at 45.4.degree North latitude in Ottawa, Ontario, Canada where none else has initiated in the world. AERC Inc. has introduced sorghum in Canada and after more than three decades of research, released five hybrids which performs well under temperate climate. Being a C4 crop, sorghum has better water and nitrogen use efficiency as compared to traditional crops in Canada, along with better adaptability and stability in yield to a wide range of soil types. Canada has a large area of unused marginal lands which has low or little suitability for other crops. Sorghum hybrids developed by AERC Inc. have been tested and optimized for grain and biomass production which could provide a better option to utilize the marginal lands on which the traditional biofuel crops like corn and soybean are not suitable to grow efficiently thereby making better use of the available resources without significant extra input costs. In addition, it would not only lead to the diversification in the energy production sector, but at the same time it will also help in diversifying the food and feed industry using sorghum grains and silage as animal food/feed including gluten free alternatives for human consumption. The roots of biomass sorghum can capture and store atmospheric carbon thereby replenishing the soil carbon content as well as sequestering CO₂ from the atmosphere. This would help in replenishing the soil carbon content of the marginal lands and storing the atmospheric carbon in the root biomass for longer period of time leading to reduction in GHG. The presentation will cover overall growing aspect of developed hybrid seed and its use in Canada and abroad.

Evaluation of the new Senegalese sorghum [*Sorghum bicolor* (L.) Moench] collection identifies new sources of resistance to grain mold and anthracnose resistance

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Sorghum is an important cereal crop in arid areas of Asia and Africa. It is mainly used for human consumption or as fodder for livestock. However, anthracnose and grain molds, whose extent depend on temperature and moisture, are among the major constraints that affect yield but also sorghum grains quality. They cause production losses for up to 100%. Although several methods such as crop rotation, use of fungicides, and shifting of sowing dates... have been proposed by farmers to fight against these constraints, none of them has been effective. Thus, the most suitable strategy remains the development of varieties resistant to these constraints. Understanding genetic variability would be useful to develop much more appropriate breeding strategies. An experiment on a sorghum collection of 256 genotypes was conducted in eastern Senegal and the lower Casamance during the winter of 2020 as an incomplete randomized block design (16x16 alpha lattice design), to identify new sources of resistance to anthracnose and grain mold. The analysis of variance revealed a genetic variability within our plant material for all the traits considered. The Pearson pairwise correlation showed that grain yield and its components were negatively affected by grain mold and anthracnose diseases. These three variables were into two principal components each having eigenvalues greater than 1.00 and explaining 78.3% of the variability. The hierarchical cluster analysis identified group one as the best containing genotypes with higher yield and resistance to mold and anthracnose. Out of these genotypes, twenty-two combine good yield, good resistance to grain mold and anthracnose. Thus, these genotypes can be used as parents in future programs to improve our elite varieties.

Keywords: Sorghum - Senegal - Constraints biotic - Grains Yield - Grain mold - Anthracnose.

Sorghum Yield under Intercropping System in Sahel Zone Climate Condition of Mali

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Cereal-leguminous cropping system is part of logic of sustainable intensification. However, in Sahel zones of Mali, the yields of this cropping system are generally low due to the inadequate practice of this system. To minimize the negative effects of climate variability, it is important to assess sorghum yield variation under different intercropping system.

In this purpose, a precipitation data from 59 years were analyzed and two experiments were carried out in the 2017 and 2018 season on two sowing dates. Analysis of the precipitation data indicates that the average rainfall in the study area is 700.30 mm and the rainy season is June to October.

The results of the experiment show that a slight variation in the diameter of the stem, the height of the plant and these are only significantly affected by the genotype. The highest grain yield (2193 and 1842 kg / ha) and biomass yield (4570 and 4637) were recorded with 1 row of Jacumbe sorghum alternated with 1 row of Korobalen cowpea (2Jac1Kor) in the two sowing dates. The best cereal yield was obtained with 1Kor2Tiand in the second sowing (1377 kg / ha) and the best biomass yield (2378 kg / ha) with 2Kor1Jac in the first sowing.

LER values greater than 1.0 were obtained for all cross-crop treatments. The result confirms that a higher total yield can be obtained from sorghum-legume intercropping than sole sorghum cropping. This technology therefore makes it possible to produce more on less sown area.

The study allowed us to understand that the season (year) strongly affected the yield of sorghum grains and biomass. This can be explained by the reduction in the amount of precipitation (725.1mm) during the rainy season 2018 compared to 2017 (882.7mm).

Keywords: Climate Variability - Sorghum - Cowpea - Yield.

Generic model of the leaf size distribution for sorghum and related C4 species

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Crop growth models (CGM) are a valuable tool to study and interpret crop responses to future scenarios and to predict crop performances in contrasting growing conditions. Canopy architecture plays an important role in the simulation of crop growth, biomass accumulation and ultimately in grain yield predictions. Hence, inaccuracies in the simulation of leaf area dynamics will directly impact intercepted radiation, biomass production and transpiration demand by the crop, especially during the early stages when the canopy is not yet fully covering the soil. This can adversely affect CGM performance. An empirical bell-shaped function of individual leaf size versus leaf position, combined with the response of leaf appearance to thermal time, is frequently used to simulate total leaf area per axis in many CGM to represent the leaf area index. This study proposes that an individual leaf area approach, based on leaf length and leaf width of successive leaves can make modelling of leaf area dynamics less empirical, thus potentially offering the flexibility to simulate genotypic, and genotypic x environment differences in sorghum (*Sorghum bicolor* (L.) Moench), maize (*Zea mays* L.), and pearl millet (*Pennisetum americanum* L.). A generic model of leaf area by leaf position is being developed using leaf length and width data from individual sizes compiled from multiple experiments from 1990-2022 and involves a broad range of genotypes of sorghum, maize, and pearl millet. Improvements in CGM parametrization for Genotypic x Management x Environmental interactions to enhance yields, help point the way forward to concrete strategies for identifying future targets of breeding and sustainable management practices in agriculture.

Root system architecture and its association with grain yield for stay green introgressed sorghum genotypes

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The study was conducted on forty-three stay green introgressed traits of sorghum genotypes to ascertain the relationship of root system architecture, particularly root angle trait with grain yield under moisture-stressed conditions. The root system architecture of the sorghum genotypes was phenotyped using a row-column design with two replications at Jimma University. To evaluate the grain yield performance an experiment was conducted in a controlled environment and at the field condition using a complete block design with two replications and a row-column design with two replications at Melkassa and Mieso respectively. The analysis of the phenotyped genotypes was computed after using the Anderson-Darling normality test and Levene homogeneity test. The result indicated that there were large variations in root system architecture traits of sorghum genotypes and for instance, there was a highly significant variation (0.001 %) for leaf area and shoot fresh weight. Similarly, leaf area and root angle, showed a highly significant variation. Result of correlation analysis indicated that there was a strong and positive correlation between shoot dry weights and shoot fresh weight. Strong and negative correlations were observed between root vigor and leaf length. Root angle and root length correlated negatively. A regression analysis was computed to evaluate the association between root angle and grain yield traits and a consistent result was found for the experiment conducted in a greenhouse and at field conditions. As a result, in terms of grain yield narrow root angle genotypes performed better than wider root angle genotypes in moisture-stressed conditions. Hence, in summary, the root system architecture trait particularly the root angle trait is relevant to sorghum grain yield improvement and has to be considered as a selection criterion in sorghum breeding programs for moisture-stressed environments.

Keywords: Root System Architecture - Root Angle - Narrow Root Angle - Wider Root Angle - Stay green.

Sorghum inbred lines combining high yield and grain mold resistance ready for deployment to seed system in Senegal

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In Senegal, during these past ten years, important attempts in the improvement of short and medium duration high yielding sorghum have been made leading to the release of several varieties. However, combining resistance to grain mold with high grain yield in tannin-free white grained and photo insensitive sorghum remain one of the major challenges of the sorghum breeding program. In this study, 25 Mini-NAM inbred lines having grain mold resistant QTL were evaluated in multi-location environments across the country during the 2019, 2020 and 2021 rainy seasons. The objective was to identify high yielding inbred lines that are resistant to grain mold and preferred by farmers. Data were collected for grain yield and resistance to grain mold. Participatory varietal selection (PVS) has been held in three locations in order to able farmers to select lines that meet their preferences. The multi-environment field evaluations results identified the inbred line ISRA-S-692-400 as the best grain mold resistant and yield performing followed by ISRA-S-692-300-1; ISRA-S-692-270 1; and ISRA-S-692-269. The line ISRA-S-692-269 was the most stable followed by ISRA-S-692-270 2; ISRA-S-692-400; and ISRA-S-692-300 1. PVS results indicated that farmers best preferred inbred lines are ISRA-S-692-319, ISRA-S-692-269, ISRA-S-692-300-2, ISRA-S-692-300-1, and ISRA-S-692-400. Majors' men farmers criteria prior to adoption are high grain yield, short maturity cycle, grain suitability for local dishes and forage yield; while for women, whitish grain, grain suitability for local dishes, big and open panicles are preferred. Based on agronomic performance and PVS the five inbred lines ISRA-S-692-400; ISRA-S-692-300-1, ISRA-S-692-269, ISRA-S-692-300-2, and ISRA-S-692-319 have been selected. The grain of these fives best inbred lines will be tested for grain suitability for local food and the best three will be registered and push to the seed system before the end of 2023.

Keywords: Sorghum - Inbred line - Resistance - Yield - Grain mold - Senegal.

Farmers' Production Constraints, Preferred Varietal Traits and Perceptions on Sorghum Grain Mold in Senegal

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Improving sorghum adoption rate by developing adapted varieties that meet end-user preferences and uses is a major challenge for most National Agricultural Research System breeding programs. In this study, a participatory rural appraisal was undertaken to identify the main sorghum production constraints, the farmers' preferred traits and their perceptions on sorghum grain mold in Senegal. The study was conducted in four representative rural communities of Senegal namely Bagadadji, Malicounda, Missirah and Sagna located in the administrative regions of Kolda, Thies, Tambacounda and Kaffrine respectively. A total of 260 farmers were surveyed and data were collected through focus group discussions and individual questionnaires. The results indicated that striga is the most important sorghum production constraints, followed by insects, poor soil fertility and drought. Grain mold was identified as the second most important sorghum disease. Discoloration on grain surface was the most important criteria farmers used to recognize the disease. The most important sorghum plant traits farmers desired in improved varieties are medium to short plant maturity cycle, medium plant height, large open or semi-compact panicle, big and white grain that are suitable for local dishes, and variety adaptation for local growing conditions. The results indicated also that the sorghum cropping system is dominated by male farmers who mainly grow local landraces. The survey revealed also that fertilizer and pesticide are fewer used by farmers. Further studies on sorghum value chain are needed to better define the breeding products profile meeting the end-user preferences in Senegal.

Keywords: Sorghum - PRA - Focus group discussion - Grain mold - Preferences - Constraints - Senegal.

Genome-wide association studies revealed quantitative trait loci associated with sorghum drought resistance in the national sorghum collection of Senegal

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Combining resistance to drought with high grain yield is of major interest for farmers in Senegal where sorghum is mainly cultivated during the rainy season. However, breeding for drought resistance is difficult because most of the known donor parents are exotic, non-adapted to growing environments and have poor grain quality that are not suitable for food. In this study, 321 cultivars of the national sorghum collection of Senegal were used to identify new local sources of resistance to drought, adapted to growing environments and suitable for food. These accessions were phenotyped for drought using well-watered and water-limited field plots during the 2018 and 2020 off-seasons. Data were collected for time to flowering, panicle weight, grain weight and grain yield. Using genotyping-by-sequencing, 145 235 SNP markers were obtained across 321 accessions of the Senegalese collection were genotyped for genome-wide association studies (GWAS). GWAS results showed 35 QTL associated with flowering time, panicle weight, seed weight and grain yield. Of these QTL, 9 were specific to the 2018 trial and 26 for the 2020 trial. The combined data analysis using BLUP method revealed 9 QTL with 6 associated with flowering and 3 with grain weight. This study demonstrates the potential value of using locally adapted sorghum cultivars that are resistant to drought as donor parents for the improvement of elite sorghum varieties in Senegal.

Keywords: Drought resistance - National collection - GWAS - QTL - Sorghum - Senegal.

Multi-Location Evaluation of Highly Digestible Sorghum Mini-NAM Lines for Yield and Resistance to Grain Mold in Senegal

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Sorghum [*Sorghum bicolor* (L) Moench] is cultivated in several tropical and temperate regions of the world where it is used for human and animal consumption and as a raw material in industry. In West Africa, more precisely in Senegal, its grains are used for human consumption and its fodder is used for animals. From a nutritional point of view, sorghum proteins are not very digestible after wet cooking compared to corn, wheat and rice proteins. The Senegalese' project to improve protein digestibility of elite sorghum varieties has resulted in the creation of 23 recombinant sorghum lines with highly digestible protein from various crosses between the P721Q mutant and elite Senegalese varieties such as Nguinthe, Nganda and Darou. This study focuses on the multi-local evaluation of these 23 lines in the ISRA stations of Bambey, Tissé kaymor, Sinthiou Maléme and Séfa. The 7×4 Alpha lattice incomplete block design was used. The data were collected in tablets with the Fieldlab application, processed by Excel and analyzed by the R software. The analysis of variance showed high genetic variability within the studied material (P<0.001) for the variables grain yield and grain mold resistance. The more grain mold tolerant lines were L13-2, L21-2, L42-3 and L48-1. The best performing lines for grain yield were L24-10, L12-4, L12-9-1 and L48-1100-1 with yields ranging from 2192.4 to 1874.1442 kg/ha. The lines that combined good yield with good mold tolerance were L48-1100-2, L24-10 and L36-5-2. These lines will be re-evaluated during the raining season 2023 and a participatory varietal selection will be organized to allow producers to choose the best lines according to their preferences.

Keywords : Sorghum - Digestibility - Yield - Mold - Senegal.

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Genome-Wide Association Study of a Sorghum Collection from Niger and Senegal for its response to Anthracnose and Grain Mold

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Grain Mold and Anthracnose are part of the most devastating diseases affecting sorghum production. To identify potential molecular traits associated with these diseases, we screened over one hundred sorghum genotypes from Senegal and Niger. The experiment was conducted under different environments and, in both countries during the growing season of 2022. In parallel, we identified Single Nucleotide Polymorphisms (SNPs) within the genomic sequences of a collection to which belongs the tested plant material. Combining the generated SNP dataset and the recorded disease severity scores, we will conduct a Genome Wide Association Study (GWAS). We expect to identify genomic regions associated with disease responses, specifically resistance.

Keywords: SNPs - Disease Resistance - Marker-Assisted Selection.

Development of elite gene pools for more efficient integration of trait genetics into the breeding pipeline to accelerate delivery of sorghum varieties

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Breeding pipelines aim to rapidly introduce favorable alleles into desired elite backgrounds to achieve an Acceptable Range of Values (ARV) for a combination of target traits. To enable this, the concept of elite-by-elite breeding has been adopted by most public breeding programs. However, no standard strategy exists for building elite gene pools, resulting in inefficient cross designs that hinder genetic gain and trait delivery in many sorghum and millet programs. Elite lines with similar performance for a given trait possess the same or different allelic combinations (haplotypes) at key loci; these lines are referred here as *cis* and *trans*-elites, respectively. Data collected from Senegalese sorghum and millet breeding programs revealed that crossing between *trans*-elite lines of equivalent performance leads up to 70% of progeny to fall outside the ARV for the flowering period. Therefore, we have defined two categories of traits: «acquired traits» (both parental lines perform within the AVR) versus «desired traits» (AVR is targeted in at least one parental line) for which we described different mating strategies using elite gene pools. It makes it possible to simultaneously increase the probability of obtaining superior offspring for desired traits and the probability of retaining individuals in the acceptable range for acquired traits. We simulated different genetic architecture and gene action scenarios to show that the more complex the trait genetics, the lower the probability of recovering preferable parental haplotypes with *trans*-elite crosses. Finally, we proposed three approaches that could be used to rapidly develop elite gene pools and incorporate them into current phenotypic and genomic selection pipelines. This study provides a framework for breeders to answer with the greatest confidence the most important question of which parental lines to cross for best use of genetic variation in sorghum and millet programs to accelerate genetic gain and trait delivery.

Genomics-assisted breeding for drought adaptation of sorghum in the Sahelian region

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Drought and unpredictable rainfall decrease sorghum (*Sorghum bicolor*, L. Moench) productivity in semiarid regions of West Africa. Understanding the genetic architecture of drought tolerance of sorghum germplasm from breeding programs could contribute to efficient molecular breeding in West Africa. This study aimed to dissect the genetic architecture of drought adaptation to develop high-throughput and breeder-friendly markers for rapid introgression of favorable trait-associated alleles into farmers' preferred varieties. First, we used genotyping-by sequencing to characterize 159,101 SNPs across 756 accessions of the West African sorghum association panel assembled from breeding programs of Senegal, Niger, Mali, and Togo. The genetic diversity structured by botanical types and subpopulations within botanical types across countries. Large-effect quantitative trait loci (QTL) for photoperiodic flowering indicate an oligogenic architecture of flowering time in West African sorghum. Secondly, we applied genome-wide association studies using pre- and post-flowering drought response variables from ten managed water stress environments to identify genomic regions associated with drought responses. Significantly positive pleiotropic associations contributed to high phenotypic variance and colocalized with known staygreen (*Stg*) loci. Results suggest the existence of *Stg* alleles in West African sorghum. Three marker loci associated with large-effect alleles were converted into breeder-friendly markers and used in marker-assisted selection for drought tolerance. These resources combined with discoveries from the global scientific community are used to accelerate the development of locally-adapted varieties through efficient genomics-assisted breeding to meet global food demand in semiarid regions of West Africa.

STRAIT: Delivering Sorghum Trait Packages from the Seed Bank to the Seed Bag

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The sorghum industry sector faces many challenges and opportunities (e.g. stress tolerance, grain quality, herbicide resistance, grain quality) that could be addressed most rapidly and cost-effectively by marker-assisted selection (MAS) for targeted traits. However, developing and deploying trait-associated markers requires dedicated resources for trait discovery that is not available to all sorghum seed companies. Molecular markers are a powerful tool which can reveal genetic information and genomic structure which is unobtainable through traditional phenotypic observation. Here we present our work to implement an integrated marker assisted breeding program for sorghum: STRAIT. The project aims to 1) develop molecular markers for traits of interest from exotic sources which are applicable in a broad spectrum of breeding populations, 2) generate elite germplasm with the introgressed trait of interest for the transfer of the trait into different breeding populations, and 3) provide knowledge of the underlying genetic structure and genetic effects. The program has been successful thus far in implementing this platform for three traits: sugarcane aphid tolerance, striga tolerance, and chilling tolerance. Currently, STRAIT is working on implementation of the pipeline for other traits of interest, such as staygreen, stable height, and additional sources of SCA resistance.

Shedding light on the evolutionary history of wild and cultivated african sorghum : “the guinea margaritifera case”

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Throughout their domestication process, the evolution of cultivated plants has been in part driven by their intimate relationships with humans, resulting in strong directional selection and short and long-range dispersal movements due to the farmers' practices and their social organization. Beside these anthropic effects, gene flow with wild relatives remained highly active, leading to introgression events in both compartments. African sorghum constitutes a relevant case study as it is grown close to its wild relatives and its diversity is modelled by specific anthropic drivers.

To unravel the origin and evolutionary history of sorghum, an adequate sampling of the cultivated and wild compartments as well as the correct classification of each analyzed accession is a prerequisite. However, as sorghum is cultivated in sympatry with its wild relatives and as gene flow between the two compartments may occur, unambiguous assignments of accessions in these 2 compartments is far from obvious. Here, we used a combination of grain morphological and genomic data to validate the status of the accessions (wild vs cultivated) and investigate their evolutionary relationships. In addition, the guinea margaritifera sub-race which has been suggested as a second potential domestication event in Western Africa has been more intensively sampled. We genotyped 139 wild samples and 243 cultivated accessions representative of the worldwide diversity, among which 50 guinea margaritifera. We identified two margaritifera groups that are genetically close to a group of wild accessions from Mali and bear signals of introgression with wild accessions from out of Western Africa but also with cultivated guinea from Western Africa. Our results indicate a complex history of the sorghum domestication, especially in Western Africa where gene flow between wild and cultivated sorghums might have led to the emergence of a peculiar group of sorghum.

Greenhouse screening of sorghum recombinant inbred lines varying for pre- and post-attachment resistance mechanisms to the parasitic weed *Striga hermonthica*

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Striga hermonthica is one of the major sorghum production constraints causing a yield loss up from 40 up to 100% in a Sevier infestation particularly in low input production system in Sub-Saharan African countries. Several efforts have been made to combat/reduce the impact of striga on sorghum and one of the best controlling strategies is believed to be host plant resistance mechanisms. Low germination stimulant (LGS1) is one of that mechanism controlling strigolactone production in sorghum before striga attachment. In addition, another resistance mechanism is post-attachment incompatibility. The objective of this study was to evaluate recombinant inbred lines (RILs) for their reaction to pre- and post- striga attachment mechanisms. A total of 15 RILs developed from crosses between two known striga resistant (SRN39) and susceptible (P954063) lines were screened in greenhouse facility at the National Agricultural Biotechnology Research Center at Holeta, Ethiopia using CRD in 6 replications. Data on periodic *Striga* emergence counts, number of emerged *Striga* at harvest, total number of attached striga on roots and their total dry weight were recorded. Our result revealed that, RILs showed a significant variation both for pre- and post-attachment resistant mechanisms. The pot study showed that *lgs1* mutant plants had fewer emerged *Striga* as a group than those without this mutation. The lines as a group carrying the *lgs1* mutation had only about half the number of emerged *Striga* as the wildtype group. Some lines also appear to have incompatibility, reducing the number of successful parasites. Incompatibility protects sorghum from *Striga* and segregates independently from *lgs1*. Some RI lines have both *Striga* resistance traits as reflected by the low area under their *Striga* progress curves. The *Striga* resistance of incompatibility may be stronger than *lgs1* as suggested by the low area under the curve in certain *LGS1* lines.

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Possibility of using wild sorghum to improve agroecological properties, nitrogen use efficiency, and adaptation to low nitrogen production systems in cultivated sorghum

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Sorghum (*Sorghum bicolor* (L.) Moench) is the world's fifth economically most important cereal and is a staple particularly in the semi-arid tropics of Africa and Asia. Its uses in western countries is steadily increasing due particularly to its climate change resilience and health promoting properties. Genetic gains in this crop can benefit from wild relatives such as *Sorghum halepense*. Hybridization of *Sorghum bicolor* with wild *Sorghum halepense* can help meet agroecological requirements of generating high-yields in an environment friendly way. In this work, we present the Resource Use Efficiency results from a whole-genome resequenced diversity panel made up of *S. bicolor* and an advanced population derived from *S. bicolor* × *S. halepense* multi-parent crosses. Agronomic, physiological, primary productivity, nitrogen use efficiency metrics, and norms of reaction results are discussed.

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Assessment of the viral disease threats on sorghum in Africa

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Viruses are responsible for half of the cases of disease emergences on the cultivated plants. This predominance of emergent viruses can be explained by their broad genetic diversity, their high multiplication level and their rapid adaptation. The sorghum cultivation has been recently intensified worldwide in response to climate change and in a view to agro-diversification. While several virus species have been reported on sorghum, up to now, the viral prevalence and the emergence risks on sorghum in Africa have never been investigated.

We will present here the methodology used for an exploratory analysis of sorghum-infecting viruses in Togo. A sampling survey was conducted across the country, 154 and 257 symptomatic leaf samples were collected on sorghum and maize, respectively. All the samples were analyzed using the virion-associated nucleic acid (VANA) metagenomics approach and HiSeq Illumina sequencing. Overall, 75% and 7% of the VANA reads and contigs respectively obtained from maize and sorghum samples shared identity with plant viruses.

Specifically, we detected sequences of five previously described virus species: *Maize streak virus* (*Geminiviridae*), *Maize yellow mosaic virus* (*Solemoviridae*), *Sugarcane mosaic virus* (*Potiviridae*), *Zea mays chrysovirus* and *Zea mays chrysovirus 1* (*Chrysoviridae*), *Maize-associated totivirus*, *Maize-associated totivirus 1*, *Maize-associated totivirus 2* and *Maize-associated totivirus 3* (*Totiviridae*) and original sequences of five undescribed virus species: Badna-like, Gemini-like, Mito-like, Endorna-like and Partiti-like virus on sorghum and maize. Maize streak virus (MSV), maize-associated totivirus species and maize yellow mosaic virus (MaYMV), were the most frequent viruses on maize with respectively prevalence of 58%, 30% and 24%. On sorghum, endorna-like virus, partiti-like virus and MSV were the most prevalent viruses with 14.9%, 6.5% and 1.3%, respectively. These high throughput sequencing and metagenomics technologies will allow the development of inexpensive, fast, standardized and effective molecular diagnostic methods for all currently known or unknown viral diseases on sorghum.

The genetic basis of phenotypic plasticity in sorghum: Dissection with an environmental profiling

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Identifying the environmental and genetic drivers that occur in phenotype's expression can help to dissect complex traits. This study aims to identify the critical sorghum growth period sensitive to environmental stimuli and to assess genetic loci's effects along the environmental gradient. We evaluated a mapping population of 253 recombinant inbred lines (RIL) in five natural environments focusing on two photoperiod sensitivity traits: flag leaf ligulation and plant height as proxies for assessing grain mold resistance. Grain mold severity scores have been rated and yield components (panicle and grain weight per plant) have been measured. From initial results, variance component analysis attributed 21.50% of the flag leaf ligulation to the environment, and 41.22% of the variation to the genotype. For the plant height, environmental effects accounted for 51.16 % of the phenotypic variance, followed by the genotype effect (24.96%). Using environmental means, we applied the joint regression analysis to unravel the pattern underneath the trait variation. Further, we will implement the CERIS (Critical Environmental Regressor through Informed Search) framework to replace environmental means with an environmental index biologically informing. The combination of environmental parameters: photoperiod (daylength), growing degree day (GDD, °C), diurnal temperature range (DTR, °C), photothermal time (PTT, °C), precipitation (PR, mm); and growth windows with the strongest correlation will be chosen as the environmental index. By regressing again the phenotypes of each RIL on the environment index, two reaction-norm parameters (intercept and slope) will be obtained. The genetic map will then be built using reaction-norm values (as phenotypes) with 952 SNP markers from 3495 SNPs generated by DArTag technology, to identify the genetic loci underlying phenotypic plasticity along environment gradient.

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Review: Favorable traits for breeding pearl millet top cross hybrids with long spike using Senegalese and Nigerien early to medium maturity groups

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Pearl millet is the only reliable food crop in the arid zones of India and Africa. Top cross hybrid is the most practicable cultivar to sustain food security of the rapid growing population in the region. There is great potential to improve millet production through hybridization between Senegalese and Nigerien clusters, where farmers preferred varieties with long spikes. Spike parameters can provide genetic difference between parents for hybrid vigor. Senegal material like Souna-3 and Thialack are of thin and compact panicle whereas Nigerien varieties HKB, H80-10Gr, Gamoji, and Tchinin-Bijini have large spike girth. Large panicle diameter showed good combining ability for grain yield beyond being easy to convert into A4 CMS carrier. Both clusters showed long panicles while Souna-3 had a good GCA for spike length. It also combined well with Gamoji for increased downy mildew resistance, the most disastrous disease of millet in Asia and Africa. The best yielding entry was derived from H80-10Gr and Thialack 2. Their offspring were tall and had long panicles and a positive SCA regarding panicle yield. Positive correlation existed between grain yield and spike length. Both clusters are of same maturity cycle, thus making it possible to identify parents of synchronous hybrids.

Genomic analysis and phenotypic characterization of Sorghum for the development of Striga resistant varieties in Niger

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Sorghum (*Sorghum bicolor*) is a major cereal crop in Africa. However, this crop is facing critical yield reduction (up to 70% yield loss) due to the plant parasite (*Striga hermonthica*). Among breeding programs goals of Niger (West Africa) is the development of Striga resistant varieties that are adapted and appreciated by smallholder farmers. Low germination stimulant is one of the mechanisms of Striga resistant in sorghum. In this study, populations derived from crosses with Mota Maradi and MR732 (susceptible local varieties) and SRN39 (resistant variety) were genotyped with KASP markers in outsourced laboratory and evaluated in controlled environments (artificial infestation). In total, 18 genotypes were tested including local varieties, resistant varieties, susceptible varieties and their progenies. For genotypes KASP markers for *Lgs1* (snpSB00246 and snpSB00487) were selected to identify hypothetical susceptible and resistant varieties. No differentiation among the replicates (n³) within genotype. The genotyping result revealed the status of each genotype with 44.44% resistant (n=8) and 55.56% susceptible (n=10). For the controlled environment, Striga seed were sowed with sorghum seeds for the first inoculation in low fertility soil. The second inoculation was done 11 days after sowing with pre-conditioned striga seed in distilled water and ambient temperature.

The evaluation under natural infestation showed seven hypothetical resistant genotypes (in terms of the emerged Striga plants and sorghum performance) that have the favorable allele for low germination stimulant production. These genotypes (once confirmed in natural infested farmer's fields) could be potential candidates for Striga resistant varieties in Niger.

Anatomical traits at stem level of sorghum could you help optimize the selection of performing genotypes targeted to biomass applications

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The presence and structure of lignins have an important impact on the quality of a wide range of different plant-based resources. The mechanical and degradability properties of the different tissues of the plant material largely depends on the lignification of the cell walls, the histological features such as the cellular morphology or the relative amount of each tissue fraction, the composition and the spatial distribution of tissues within plant organs. Many studies, in particular devoted to increase the degradability of plant cell walls, showed a wide range of techniques for studying lignin and polysaccharides.

By combining staining, microscopic methodologies and imagery we reached a high level of cellular resolution. Large scale studies of anatomical features (Zhang *et al.* (2013), Legland *et al.* (2017), El Hage (2018)) on maize showed links between anatomical traits in stalk and the detection of candidate genes, the biomass stalk anatomical traits and the biochemical or physical properties of the biomass and led to the identification of candidate genes.

Recent studies on sorghum mobilized quantitative anatomical internode analysis to better understand response to water availability (Perrier *et al.* (2017), Luquet *et al.* (2018)) and biogas production (Thomas *et al.* 2021). However most of these studies focused on a single internode level of the stem. In this presentation we highlight the intra stem variability of a set of morphological, anatomical and biochemical traits analyzed in successive elongated internodes along the stem of two contrasted genotypes for composition and hydrolysis yield over 3 years.

Two approaches of anatomical studies are presented: colorimetric information and multispectral autofluorescence imaging to focus on phenolic compounds.

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Interpreting genetic variation in plant transpiration efficiency from leaves

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Transpiration efficiency (TE) quantifies the accumulated biomass per unit of water transpired at the whole-plant level and is an important adaptation trait for dryland cropping in drought-prone environments. Differences in TE have been observed within and across C₄ crop species, but a deeper physiological understanding to connect this variation in underlying traits can help identify new avenues for crop improvement. A cross-scale canopy photosynthetic network model suggests that leaf photosynthetic CO₂ assimilation rate, stomatal conductance, and their diurnal patterns can influence whole-plant TE. Here, we investigate trait variation at both the leaf and whole-plant levels in a panel of C₄ crop species known to have different drought responses: eight sorghum, one maize and one pearl millet. During the vegetative stage, leaf photosynthetic response to intercellular CO₂ and light, diurnal stomatal conductance was measured. Whole-plant water use was obtained using a lysimetry platform and plant shoot biomass was measured at anthesis and used to calculate plant-level TE.

Results showed genotypic differences in TE of sorghum were consistent with previous experiments and genotypes with high TE tended to have low stomatal conductance diurnally. This work provides valuable data across biological scales, which can be used in further modelling analysis to understand the implications of photosynthetic responses and diurnal stomatal conductance on whole-plant TE.

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Variability for agronomic and yield traits for Uganda's sorghum germplasm, and their implications for sorghum improvement

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Sorghum (*sorghum bicolor*) is the third most important cereal crop after maize and rice in Uganda. Sorghum is widely grown in the drier short grass areas of northern, eastern and western parts of the country by the resource poor farmers. Typically, there are many cultivars of sorghum grown in Uganda for a variety of purposes including food, porridge, beer and fodder as well as cash income indicating variable target production environments and product range. An experiment was conducted to characterize a collection of 742 genotypes assembled from the sorghum breeding program including breeding lines, released varieties, introductions and gene bank materials for end-user traits using an augmented design with 14 blocks each holding 53 lines for two seasons Preliminary analysis showed significant differences for plant height, disease incidence and grain weight ($P \leq 0.001$). The differences in season were significant ($P \leq 0.001$) for all traits measured. Differences among interaction effects of genotype x season were significant only for shoot fly damage counts, Seedling vigour and grain weight ($P \leq 0.002$ to $P \leq 0.001$). A wide range in values of agronomic and yield traits revealed in this study confirm the existence of genetic variability in Uganda's sorghum collection. Information generated from this study will be very useful for future breeding and prediction of genetic gains from selections in the national sorghum breeding program.

SorgEnloS: Sorghum for grain use: Establishment of new, locally adapted varieties

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To adapt to climate change and increase biodiversity, it is necessary to establish new, robust crops in local agriculture. Grain sorghum can represent a risk protection for farmers during drought conditions and enable the establishment of new regional value chains. At present, however, no locally adapted varieties to Hesse and comparable agroecological regions in Germany are available. Further, there is a lack of information regarding the optimal agronomical practices (sowing densities, fertilization etc.) under local conditions.

Therefore, the aim of the project is to develop stress-tolerant and locally adapted grain sorghum varieties in view of climate change. These varieties will help to increase biodiversity in agriculture and represent an important innovation, both as a new (in Germany) high quality animal feed and as a gluten-free 'superfood'. Since grain sorghum is a novel crop in Hesse, progress in breeding needs to be accompanied by knowledge extension of plant production measurements to farmers, and building of value chains. With this joint effort, the establishment of grain sorghum as a new robust crop seems feasible.

The project partners are institutions covering the aspects of breeding and agronomy on the one hand, and farmers conducting on-farm variety trials on the other hand.

- Breeding of grain sorghum for animal feed and as a gluten-free food (development and testing of new, locally adapted grain sorghum breeding material with enhanced cold tolerance)

- Optimization of agronomical practices in local grain sorghum production, including sowing density, row spacing and N-fertilization trials

- On-farm variety trials, including both commercial grain sorghum hybrids from other European countries and experimental hybrids of the University Giessen breeding program. Evaluation regarding their suitability under practical farming, and involvement of farmers in selection process.

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Heat induced brassinosteroid signaling affects growth, metabolomic networks and yield in *Sorghum bicolor*

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Plant responses to adverse climate conditions are orchestrated by plant hormone signaling wherein brassinosteroids (BRs) play a crucial role, as recent discoveries in BR signaling have shown^{1,2,3}. Gupta et al. (2023)² demonstrated the role of BR receptors in thermosensing and -morphogenesis in *Arabidopsis* and show an impact on the plants' metabolism. To cope with abiotic stress, metabolomic networks within in the plant are important to protect plants against environmental pressures without impairing growth and are regulated by specific BR signaling pathways³. To further elucidate the role of metabolite networks upon high temperature stress and the consequences for nutrient accumulation and yield in crop species, we obtained BR receptor mutants from an EMS of the resilient cereal *Sorghum bicolor*. Phenotypic analysis of the plants revealed differences in grain production and growth. Moreover, experiments upon elevated temperature point towards a different growth response and metabolite accumulation between wildtype and BR receptor mutants. These insights on BR signaling upon climate change in cereals and experimental set-ups will be used for upcoming research under modelled climate change conditions to further elucidate 1) the role of BR signaling in climate change in sorghum 2) to link climate-change related metabolism to sorghum nutritional capacity 3) to extract meaningful data to improve cereal breeding in climate change conditions.

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Assessing Genomic Prediction for Agronomic and Grain Quality Traits in Elite Texas Grain Sorghum Hybrids

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Grain sorghum is an important cereal crop in Texas, USA, with growing needs for improved agronomic and grain quality traits to meet environmental and market demands. Implementation of genomic selection (GS) into the breeding pipeline has the potential to enhance breeding efficiency and precision in the development of elite sorghum hybrids. In this study, we aimed to develop GS models for agronomic and grain quality traits to compare the efficacy of GS for various traits in Texas elite grain germplasm.

We evaluated 94 inbred lines via a partial factorial mating scheme and observed 399 hybrid combinations across four environments for agronomic traits: grain yield, plant height, days to flowering, exertion, panicle weight, testweight; and grain quality traits: ash, protein, moisture, fat, fiber, and starch content. Genotyping-by-sequencing was used to obtain high-density single nucleotide polymorphism markers for the inbred lines. We employed genomic best linear unbiased prediction (GBLUP) methods to construct GS models. The GS models were validated using 5-fold cross validation, and the results showed varying prediction accuracy across traits. The accuracy of the GBLUP models ranged from low to high ($r = 0.14$ to 0.74) across all traits. Grain yield ($r = 0.18$) and panicle weight ($r = 0.14$) had the lowest accuracies. The highest accuracy was achieved for fiber content ($r = 0.74$).

Our results demonstrate the potential of GS to enhance the breeding of elite Texas grain sorghum hybrids for improved agronomic and grain quality traits, with each trait requiring its own considerations for successful implementation into the breeding pipeline.

Evaluation of some new dual purpose sorghum varieties using GGE-Biplot and AMMI Analysis across multi Agro-ecological zones in Niger

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In the SSA region, the pressing demand for fodder coupled with the importance of the grain of sorghum for people, makes imperative to reconsider the present mono-commodity breeding strategy of sorghum. In Niger, farmers grow sorghum as a dual-purpose crop therefore, breeding for dual-purpose sorghum lines which combine high grain yield with reasonable dry stover yield is a strategic way in improving the livelihood of rural farmers. Thirty sorghum elite lines were evaluated for the dual-purpose stability. The GGE Biplot and AMMI analysis were performed in order to identify the most stable lines across environments. The results showed two megaenvironments namely Tarna and Bengou with Tarna being the discriminant and ideal environment for evaluating dual purpose sorghum varieties in Niger. G28 (Seguifa) was the most stable sorghum across the two megaenvironments. G20 (ICSX14 018 BCJP-14-1-SB6) and G28 (Seguifa) were the selected varieties for the first megaenvironment; whereas, G1 (014-SB-EPDU-1004) and G3 (BC1F6-11) were selected as the best varieties for the second megaenvironment. The high-yielding and stable sorghum varieties (Seguifa with 2143 kg/ha) selected in this study should be broadly evaluated on-farm in order to disseminate for small holder farmers in southern Sudan and Sahelian regions of Niger republic.

Keywords: Sorghum - Dual purpose - GGE-biplot - AMMI - Megaenvironment.

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Putative natural genetic variation contribute to grain mold resistance in sorghum germplasm of Senegal

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Grain mold, a major disease of sorghum, occurs at the beginning of grain formation and is due to infection by several fungal species. To date, the genetic control of resistance to this disease is still poorly understood. To identify genomic regions related to this complex trait, a diversity panel of 340 accessions from the Senegalese Sorghum Germplasm was screened in two locations in Senegal during the rainy season of 2020. A GWAS study was performed using 145,234 SNPs and two models (GLM + Q and BLINK) for grain mold resistance at physiological maturity (ScMMP) and after threshing (ScMAB). Six (6) and ten (10) QTLs were identified for ScMMP and ScMAB, respectively. Two new loci were found to be linked to genes associated with tolerance to biotic and abiotic stresses in crops such as rice and sugarcane. These are the gene *Atox1* (Chromosome 1, S1_62720835, 44% of proportion of variance explained (PVE)), which is involved in copper storage, modulation of transcription, and oxidative defense and the MYB Transcription Factor (Chromosome 2, S2_32084488, 36% PVE), which is involved in growth, development and response to various stresses. The identification of these loci, associated with new resistance mechanisms allows a better understanding of the genetic control of this trait. The highly resistant accessions that carry the favorable allele at QTLs can serve as donor parents for breeding.

Adaptation of bio-fortified sorghum hybrids (*Sorghum bicolor*) to drought resilience in Mali

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Sorghum is a staple food in Mali, yet grain yields are low and do not contain high lysine, threonine, iron and zinc content. Drought is the most significant cause of crop yield loss, especially in water limited areas where most of the world's poorest farmers live. Development of drought tolerant bio-fortified sorghum hybrids will enhance food production and the livelihood of farmers in these areas. To assess the adaptation, yield potential, and to identify the traits contributing directly and indirectly to drought resilience, a study was conducted in two locations. Thus, a total of 49 F1 hybrids were developed and used in this study along with three commercial hybrids. Ten (10) bio fortified hybrids were identified with grain yield ranging from 3774 to 5068 kg ha⁻¹ with an average heading date of 74-83 days. The new bio-fortified sorghum hybrids in this study yielded three times as much as the local varieties, which yielded 1 to 1.5 tons. The index of varietal sensitivity varied 253.43 to 81.12 %. For drought resilience, a significant correlation was identified with index of varietal sensitivity through mibrid, stay green and leaf senescence. A positive and negative correlation among grain yield, stay green and mibrid were observed. This study identified bio fortified sorghum hybrids with high grain yield and tolerant to drought stresses. These ten hybrids are worthy to be utilized in participatory trials for their registration in the seed catalog.

Population genomics of *Low Germination Stimulant 1* enabled molecular breeding of *Striga* resistant sorghum varieties

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Striga hermonthica is a devastating obligate parasite of staple crops in West Africa (WA). This parasite requires signals from the host for its germination. One of the mechanisms of *Striga* resistance is low germination stimulant production by the host due to loss of function of the *LGS1* gene. The development of resistant varieties through phenotypic selection is challenged by *Striga*'s spatial variability. Diagnostic markers targeting *LGS1* loss of function alleles could accelerate the development of *Striga*-resistant sorghum. The deletion of the cloned *LGS1* is hypothesized to confer resistance in WA *Striga* using breeder-friendly markers. The objectives of this study are to (i) identify single nucleotide polymorphisms (SNPs) that are linked and in linkage disequilibrium (LD) with *LGS1* deletion in diverse sorghum germplasm, (ii) develop Kompetitive Allele-Specific PCR (KASP) markers that accurately genotype these SNPs, and (iii) test the markers for *Striga* resistance in sorghum biparental population. Genotyping-by-sequencing polymorphism data for WA germplasm was analyzed to identify SNPs in LD with deletion alleles at *LGS1*. Eight SNPs that are linked and in LD with *LGS1* deletion were converted into KASP markers. Putative resistance and susceptible classes in inbred lines and F3 progeny of SRN39 (resistant) and Mota Maradi (susceptible) were differentiated through KASP genotyping. Root exudates from progenies with putative deletion of *LGS1* based on KASP assay were tested for laboratory germination assay of *Striga* seeds and in pot assay confirming the KASP results. Our findings confirm that these new KASP markers will be suitable for marker-assisted selection for *Striga* resistance in multiple genetic backgrounds of WA germplasm.

Mapping race differentiation along the cultivated sorghum genome

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Sorghum genetic diversity features morphological races such as Bicolor, Caudatum, Durra, Kafir and Guinea, as well as geographical origins throughout Africa and Asia. Among the different genetic groups, the Guinea margaritifera subrace receives a particular status suggesting a secondary domestication event. Whole genome sequencing data provide new ground to better understand sorghum genetic diversity. We have access to the wealth of sequencing data produced by the Sorghum Genomics Toolbox (SGT) project. We have complemented the SGT sample with 37 accessions that have extended the coverage of the margaritifera subrace. After a new SNP call, we recovered a dataset of 972, mostly cultivated, accessions characterised with 31 million SNP loci. We performed principal component analyses (PCAs) after applying different thresholds for minimum allele frequency and for missing data. Overall, we obtained high-level components that differentiate Guinea margaritifera materials, confirming the special status of this subrace. On this basis, we are characterising the distribution of this differentiation along the genome and the extent of genetic exchange between the margaritifera subrace and the other cultivated forms. The data is ready to be accessed on our South Green platform using the Gigwa data management tool and various analytical options that will make it an excellent resource for data mining by researchers and students interested in germplasm management and improvement.

Agronomic performance of grain sorghum hybrids under water stress and its correlation to seedling phenotyping

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Drought-tolerant sorghum cultivars is essential for cultivation in semiarid areas or uneven rainfall distribution. In this sense, seedling phenotyping methods to evaluate the performance of genotypes under drought stress is crucial to reduce time and labor. The objective of this work was to evaluate the agronomic performance of grain sorghum hybrids under water stress, and to correlate them to root traits in seedlings stage. Twenty-six grain sorghum hybrids were grown in field trials, under post-flowering water stress and non-stress. The same hybrids were grown in cone-tainers, under water stress from ten days after germination to the stage of five leaves, when root morphology traits were taken using Winrhizo Pro 2007a system. Under water stress, the hybrids with the best performances were BRS310, 1516057, 1719034, 1719026, 1716041, 1G282, 1516059, 1720052, 1716049, 1718036 and 1716045. The seedling traits total root volume, total area of the root surface, surface area of very fine roots between 0 and 1 mm in diameter and root dry mass/shoot dry mass ratio showed positive correlation to grain yield in field.

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Sorghum [*Sorghum bicolor*, (L.) Moench.] root system architecture unveils new genetic resources under low Phosphorus condition

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Sorghum is a climate-smart crop, highly adaptable to different climatic regions of the world. However, phosphorus (P) deficiency and finite phosphate reserves for fertilizer production pose a threat for future global sorghum production. Understanding root system architecture (RSA) plasticity is central towards breeding for P-efficient crops. This study aimed at detecting early genetic responses of sorghum RSA to P deficiency and selecting genotypes with interesting root phenotypes under low P. Diverse sorghum lines (n=297) genotyped using DArTSeq generated over 12K quality genome wide single-nucleotide polymorphisms (SNPs). Root phenotyping was performed in a paper-based hydroponic rhizotron system under low and normal P nutrition in controlled greenhouse conditions. A total of 23 root morphology traits were used to describe genetic and phenotypic variability at two time points. Genotypic and P-response variation were observed for multiple root-related traits as early as 21 days after germination (DAG). This was confirmed after 42 DAG, with correspondingly high broad sense heritability, in traits such as number of roots, maximum root system width and volume, root surface area, root network area, solidity, root dry weight, and total root/shoot dry weight. Although multi-variate analysis revealed three major clusters defining distinct sorghum RSA types, genotypes nevertheless clustered separately under low and normal P conditions. Association studies identified many quantitative trait loci (QTL) and genes potentially involved in P transport, DNA repair and stress responses. Several pleiotropic QTL for RSA were found on different chromosomes at the two time-points, providing a starting point for gene identification and/or genomic selection of beneficial RSA trait for low-P conditions. The genetic determination of key factors underlying RSA and P efficiency will enable selection at earlier growth stages, hence reducing phenotyping costs and time. Selected elite lines with interesting RSA traits for low P environments will be incorporated into current sorghum breeding programs.

Functional characterization of the nine cytochrome CYP79A encoding genes in *Sorghum bicolor*

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Plants produce a plethora of specialized metabolites (bio-active natural products) to adapt to abiotic and biotic stresses. Sorghum produces the cyanogenic glucoside dhurrin. Cyanogenic glucosides are chemical defense compounds able to detonate a hydrogen cyanide bomb upon cell disruption by herbivores or pests¹. The biosynthesis of dhurrin in sorghum is catalyzed by two membrane bound cytochromes P450, CYP79A1 and CYP71E1, and a soluble UDPG-glucosyltransferase, UGT85B1, forming an enzyme complex (metabolon) channeling conversion of the tyrosine precursor into dhurrin. CYP79A1 catalyzes the conversion of tyrosine to the corresponding *E*-oxime and CYP71E1 catalyzes the conversion of the *E*-oxime into a cyanohydrin which upon UGT85B1-mediated glucosylation is converted into dhurrin. Both cytochromes catalyze multistep reactions. A *tdc1* mutant plant obtained in a sorghum TILLING population following EMS mutagenesis was found to harbor a CYP79A1 P414L variant with no catalytic activity².

The genome sequence of sorghum (cultivar BTx623) harbors nine different CYP79A encoding genes. Because the single P414L mutation in CYP79A1 resulted in sorghum plants not producing any dhurrin², we wanted to know the functionality of the other eight CYP79A genes. Transient expression in *Nicotiana benthamiana* showed that these all catalyzed conversion of an amino acid into the corresponding oxime although with different specificities, including valine, leucine, isoleucine and phenylalanine as substrates. Transcriptome analyses showed expression of these genes at specific stages of plant ontogeny and in specific tissues. To more directly analyze the physiological functions of the nine CYP79A genes, knock-out mutants of each of these genes are currently being identified using the FIND-IT screening technology platform on an EMS sorghum mutant library consisting of progeny grains harvested from 150,000 M1 plants grown from mutagenized BTx623 seeds³. The FIND-IT methodology is GMO-free. Identified genetic variants with improved characteristics may be directly used in breeding programs.

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Addressing genetic and management options for resistance to *Striga hermonthica* in sorghum plant genetic resources from East Africa

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Sorghum (*Sorghum bicolor* L.) is a crucial staple cereal crop in East Africa, which is cultivated by millions of smallholder farmers striving for drought tolerance and high yield potential. Despite its potential for local adaptation, sorghum production is hampered by a plethora of abiotic and biotic stresses, including the root hemiparasite witchweed (*Striga hermonthica*). Witchweed is responsible for devastating yield losses in sorghum, reducing the potential of sustainable regional production. Several options exist to improve sorghum resistance to witchweed, including agronomic practices and host plant genetic resistance. Here we present a project, in its initial steps, in which we set out to evaluate management and genetic options to improve sorghum resistance to *Striga hermonthica*. We assembled a panel of approximately 300 sorghum farmer varieties sampled across East Africa, which will be evaluated for their genetic and phenotypic diversity. We devised a joint garden characterisation of the sorghum farmer varieties in combination with two factors: intercropping with beans (+I) and the presence of witchweed (+W), for a total of four combinations: -I-W, -I+W, +I-W, +I+W. Genotyping-by-sequencing methods will be used to characterise the collection towards identifying genomic regions associated with *Striga* resistance using a genome-wide association study (GWAS). At the same time, we want to characterise the value of intercropping in contributing to sorghum performance and the impact of witchweed. Our objective is to identify genetic factors existing in untapped diversity of genetic resources, which may support the development of sorghum varieties with the potential for intercropping and durable resistance to *Striga hermonthica* in an attempt to boost food security *vis-à-vis* adaptation to climate change.

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Breeding diploid perennial grain sorghum for multiple harvests

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Annual agriculture is responsible for several local, regional, and global ecosystem disservices, including soil erosion, soil degradation, aquatic eutrophication, and greenhouse gas emissions. Perennial grain crops have the potential to transform annual agriculture from a destructive to a beneficial provider of ecosystem services while simultaneously enhancing food production. Perennial cover, according to estimates, reduces nitrogen losses¹ and maintains topsoil² 30-50 times better than annual crops. It is also attractive for both mechanized and smallholder agriculture. In terms of utilization, perennial grains are very similar to annual grains, but they still need some agronomic modifications. We breed perennial sorghums to combine the high yield of elite sorghums, achieved through a century of scientific breeding, with the economic and environmental benefits of obtaining multiple harvests from a single planting. We recently discovered a method for producing diploid offspring of annual sorghum crossed with tetraploid perennials³, allowing us to combine perenniality, yield, and quality alleles at the diploid level. In 2021, we examined the perenniality-related traits and winter survival of S3011-D F_{2:3} diploid families in Salina, Kansas, and Tifton, Georgia. S3011-D is a diploid population derived from S3011-A1, a triploid plant created by crossing perennial sorghum (accession G9N) with *S. bicolor*(cytoplasmic male sterile KS105A). We phenotyped 171 S3011-D F_{3:4} diploid families in Tifton, Georgia, in 2022, analyzing days to 50% flowering, rhizome growth, grain yield, and grain size. DNA was extracted from leaf tissue from each plant. As we await 2022 winter survival data, genotyping is underway. This study will identify quantitative trait loci (QTLs), diagnostic DNA markers for early generation selection, and genetic mechanisms underlying perenniality and seed yield in diploid perennial grain sorghum. We are also investigating additional novel traits that could be derived from tetraploids to improve conventional grain and/or forage sorghum, such as disease resistance.

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Crop improvement network approach to co-develop market required products and strengthen partners' capacities in Africa

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CIMMYT, under the OneCGIAR, has initiated new crop improvement programs for dryland cereals (sorghum, pearl millet) and legumes (groundnut, chickpea, pigeon pea) to complement National Research Programs (NARS). The network involves 10 NARs in West and Central Africa (CSIR-SARI/Ghana, IAR/Nigeria, IER/Mali, INERA/Burkina Faso, INRAN/Niger, IRAD/Cameroon, ISRA/Senegal, ITRA/Togo, ITRAD/Chad, LCRI/Nigeria) and 7 in East and South Africa (ARC/Sudan, EIAR/Ethiopia, KALRO/Kenya, NARO/Uganda, TARI/Tanzania, ZARI/Zambia, NRCM/Malawi). The purpose of this initiative is to develop a truly collaborative CGIAR-NARS breeding program, where CIMMYT is playing a role of facilitator within the network. Partnership and multi-disciplinary approach are central in the designing and the implementation of these programs. Thus, consultative regional workshops were organized for each crop with major stakeholders. During these workshops, the regional and country market segments (MS) and target product profiles (TPP) were reviewed and traits per crop prioritized for regional consideration in new population development plans. In addition, national Product Design Team (PDT) meetings have been organized for over 10 different countries to review national MS and TPP and align them with country priorities and market requirements. Partners research stations facilities/equipment and breeding programs have been evaluated using the "ABI Transform Breeding Program Questionnaire", available on the Excelling in Breeding platform (<http://www.excellenceinbreeding.org/toolbox/form/narssmes>). The data from these assessments present the comparative advantages of each partner, constituting the basis for the assignment of network activities among partners and helping resource mobilization. Assessment results are also used to develop and implement improvement plans for partner breeding programs to align with quantitative genetics theory and practice, deploy molecular breeding, and implement regional and national field trials utilizing advanced designs. These networks build on existing ones with more emphasis on efficiency of breeding operations to increase genetic gain and are also open to private companies and other major stakeholders working on the different value chains.

The sixth important locus for hybrid vigor in a Japanese F₁ variety of sorghum

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Energy and biomass sorghums show significant hybrid vigor. For example, F₁ variety is ~4 meters, although the parental lines have short statures of ~1.2 meters. In our previous studies, this hybrid vigor observed in Tentaka was mainly explained by five genes, *i.e.*, two flowering date (FD) genes, *Ma3/SbPhyB* and *Ma6/SbGhd7*, and three internode-elongating genes, *Dw1*, *Dw3*, and *Dw7a*¹. The dominant and/or epistatic models for heterosis fitted to this result.

To confirm this, pyramided inbred lines containing the dominant alleles of these five genes were established. These plants reached approximately 90% in culm length, and 85% in wet weight compared to the F₁. Although hybrid vigor was almost revealed in this manner, the reasons for why these were less than 100% were unclear. Two hypotheses were thus considered. First, there are many minor quantitative trait loci with weak effects. Second, there is a sixth gene, which is not detected in the initial analysis using the F₂ population.

During the pyramiding process, we coincidentally found a line segregating FD, which resulted in different culm lengths, even though the two FD genes were fixed to homozygous dominant alleles. According to the segregation ratio, the corresponding gene was single.

Molecular genetic analysis revealed that the two heterozygous loci remained and were segregated. One locus was associated with the segregated FD. As the late-flowering allele is dominant, the corresponding gene also contributes to the above dominant and/or epistatic models. Overall, six loci are important for hybrid vigor in the F₁ variety, Tentaka. The reason indicating why the genes were not detected in the initial analysis is also discussed.

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Identification of Anthracnose Resistance Gene in *Sorghum bicolor*

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Anthracnose disease, caused by *Colletotrichum sublineola*, results in considerable yield loss of sorghum crops globally, especially in regions where wet and humid conditions prevail. The use of fungicides poses health and environmental concerns and is not economically feasible in many sorghum-growing regions, and can result in fungicide resistance, making chemical control ineffective. Genetic resistance provides the most sustainable disease control strategy. By exploring the natural variation in sorghum, many resistant variants were identified. In this investigation, we aim to identify the resistance gene underlying broad-spectrum resistance to different strains of *C. sublineola* in one of these resistant lines. The investigation will use the F4:5 recombinant inbred lines (RILs) obtained by crossing PML981488 and a susceptible genotype, TAM428, to define the resistance genes/loci. To identify the resistant and susceptible RILs, four-week-old plants of 212 RILs were inoculated with 2×10^6 spores/mL of a mixture of five different strains of *C. sublineola* and screened for disease symptoms on a quantitative scale. The RILs showed a 1:1 ratio of resistant to susceptible plants, indicating that the alleles have segregated with minimal variation. Furthermore, the RILs were categorized into those showing no disease symptoms, hypersensitive reaction, or necrotic lesions. Genomic DNA will be extracted from 50 RILs each in the three disease response categories, and DNA pooled from each phenotypic category will be sequenced. Bulked segregant analysis will be conducted after whole-genome resequencing to map the genomic regions that carry the resistance gene. Genetic mapping based on recombination analysis will identify the specific resistance gene. Successfully identifying this broad-spectrum resistance gene will help in developing broad-spectrum anthracnose-resistant sorghum cultivars.

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Impact of midge damage on new guinea sorghum lines performance in eastern part of Burkina Faso

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Sorghum is the most grown cereal crop in Burkina Faso, however, its production is low due to biotic constraints. This investigation was conducted in a midge hot-spot site (Fada) and a not hot-spot site (Kamboinse). The study objective was to determine impact of midge on the performance of newly developed guinea sorghum lines. Field trials were conducted over two years and twenty sorghum lines including checks were evaluated in a randomized complete bloc design. Agro-morphological parameters and midge damage were evaluated in all sites with emphasis on grain yield and midge damage in order of importance to determine lines' performance and level of tolerance to midge. According to heading characteristics, seven lines (Kouria, PR3009B, ICSB176003, Fambe B, Lata//Grin-9-14-1-1, ICSB176008, 12B) were well adapted to the sudano-sahelian zone and majority of tested lines were susceptible to midge with a yield loss ranged from 50% to 80% compared to yield in not hot spot site. Only, five lines (ICSB 176002, Kapelga, Kouria, Lata//DouaG-4-27-1-1 and Lata//Grin-9-14-1-1) performed well in a midge hot-spot site. These lines exhibited a high level of tolerance to midge damage and could be promoted for large cultivation in the eastern part of the country to mitigate midge impact.

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Phenotyping for resistance to pre-harvest sprouting in grain sorghum (*Sorghum bicolor* L. Moench)

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Pre-harvest sprouting (PHS) is a common threat to cereal crops in which the grain maturation phase takes place under rainy, moist conditions. Susceptibility to PHS is higher in sorghum genotypes displaying low levels of seed dormancy before harvest maturity. Other attributes such as glume or panicle morphology may also affect susceptibility to PHS. Breeding for resistance to PHS in grain sorghum requires the identification of grain physiological and morphological attributes affecting this trait, and a protocol for phenotyping and rating genotypes according to their susceptibility to PHS. In this work, we tested germination under laboratory conditions using detached grains and intact panicles for a panel of 20 sorghum genotypes including 11 parental lines, 6 hybrids and 3 reference inbred lines with contrasting PHS response. Records for natural sprouting in the field for these genotypes were also included in the analysis. Multivariate analyses of germination data allowed separation of genotypes into two major categories (resistant and susceptible to PHS). Laboratory germination data correlated significantly with PHS in the field. In most genotypes, the glumes had a significant, inhibitory effect on germination. The low levels of grain dormancy were observed among high tannin backgrounds, and vice versa, indicating that a pigmented testa alone does not provide resistance to PHS. Altogether, the phenotyping protocol allowed the classification of sorghum genotypes according to their susceptibility to PHS and the identification of different attributes useful for breeding for PHS resistance in this crop.

A new source of diversity for sorghum improvement?

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Sorghum is considered like a rainfed crop but it is also grown in the dry season: direct sowing in northern Senegal and transplanted after approximately 45 days of growth in the nursery in the Lake Chad Basin. The genetic diversity of these varieties of sorghum is not well known, the objective of this study is therefore to evaluate this diversity of rainfed sorghum and dry season sorghum collected in Senegal and in the Lake Chad Basin and to understand its organization.

The plant material studied includes 153 accessions covering 4 eco-seasonal types of sorghum defined on the basis of seasonality (rainy season, dry season) and eco-geographical zone (Senegal and Lake Chad Basin). High-throughput sequencing data (GBS) made it possible, on the basis of approximately 120,000 SNPs covering the sorghum genome, to describe the genetic diversity of the collection studied in relation to the 4 eco-seasonal types. The genetic diversity of each population was estimated by evaluating its number of total alleles, its number of private alleles and its allelic richness. Principal component analysis was carried out to study the organization of the genetic diversity of the global population.

The genomic analysis showed that the diversity of the 153 sorghum accessions is structured into 3 genetic groups. This organization of the diversity reflects the influence of seasonality and geographical origin of sorghum accessions. Two-thirds of dry season sorghum accessions in the Lake Chad Basin form a well-differentiated group from rainfed sorghum accessions. These experimental results provide new directions for integrating dry season sorghum diversity into sorghum improvement programs.

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Stay green, brix and dhurrin effects on yield stability in sorghum

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Haiti has a great variability in terms of nature of soils and microclimates. This pedoclimatic variability changes the relative ranking of genotype performances when they are growing from one environment to another, which makes selection of broadly adapted genotypes difficult. Thus, choosing efficient and stable lines and identifying the physiological mechanisms and/or the genetic architecture associated with stability and agronomic performance are crucial for breeding programs. A first trial evaluating 250 sorghum lines (developed by Chibas) in 16 contrasting environments was conducted. Here, we will report on modeling the contribution of stem sugars, stay green and dhurrin content as predictors of yield stability in sorghum. The hypotheses to be tested are: 1) Does yield stability correlate with these variables?, 2) Is genomic prediction a good predictor of yield stability in sorghum?, 3) Do the brix, stay green and dhurrin rate have sufficient heritability that they could be used simultaneously in a selection index with (or without) a genomic predictor to predict yield stability? The results obtained from this study will help to develop a better prediction index for new genotype performance.

Keywords: Genomic prediction - GXE - Stability - Stay green - Sorghum - Brix - Dhurrin.

Increasing Sorghum cold tolerance for cultivation in Germany

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Sorghum is the fifth most important cereal crop worldwide and is characterised by a deep root system, high photosynthetic efficiency and wax coated leaves. These characteristics make Sorghum more drought tolerant and led to substitution of other cereals in Africa, South America and Australia. Sorghum cultivation in Germany has been increasing over the past years but is still on a low level.

The SORGHUM project aims to investigate its potential as an alternative C4 plant in Germany and to evaluate the respective climate change mitigation potential. Since the major challenges of larger Sorghum cultivation in Germany are insufficient cold tolerance and non-adapted maturation, the project focuses on the genetic base of these two traits towards identification of desirable allelic variants and development of molecular breeding tools. Moreover, we will test whether an increased humus reproduction and respective active carbon sequestration supports an improved greenhouse gas balance of crop production.

Hybrids are produced from 50 preselected restorer and four mother lines. The selection based on previous phenotypic data of recombinant inbred lines populations that had already been adapted to the photoperiodic conditions in Germany. Field experiments at different locations along a north-south-axis in two subsequent years will be performed to study the cold tolerance of the test hybrids and identify lines with superior performance. In addition, germination assays in a controlled environment will be carried out on the parental lines and test hybrids. Selected hybrids will be studied under drought conditions to assess the soil carbon fixation under current and changing climate conditions. Finally, with the help of training populations and genome wide marker information, genomic prediction models for cold tolerance, early maturity, yield, carbon fixation and biomass of crop residues will be developed. Here we present first results of the germination assays and the field phenotyping for cold tolerance.

Genetic improvement of sorghum for post-flowering drought tolerance

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Sorghum bicolor is one of the most important crops around the world. It is grown chiefly as food, fodder and for bioethanol in Africa, America, and Asia. Sorghum is typically adapted in arid and semi-arid area due to its hardiness. Notwithstanding its high adaptability, climate change effects continue to affect sorghum production. Among them, drought is one of the biggest challenges. Many studies have been done, but it remains a lot to understand the genetics basis of drought. In Senegal, sorghum breeding programs have developed in the past several varieties characterized by an early maturity, reduction of plant height, high yield and tolerant to grain mold. However, these varieties are susceptible to drought. The objective of this study is to develop sorghum drought tolerant varieties through stay green QTLs and elucidate the mechanisms that control post-flowering drought tolerance. Stay green populations developed from a Nested Association Mapping with B35 as the donor parent, NGANDA, GOLOBE and DAROU as recurrent parents will be used for QTLs mapping. These stay green populations will be assessed for dhurrin and proline content, nitrogen use efficiency and other agronomical traits under different water treatments in three locations (Bambey, Niore and Sinthiou Maleme) in Senegal. SNP markers will be used and GWAS performed to detect significant association between phenotypes and genotypes. From these activities, we expect at the end of the work establish a genetic correlation between dhurrin and proline content, soil nitrogen availability and stay green trait. Likewise, identify QTLs for post-flowering drought tolerance. Drought tolerant varieties will assist sorghum improvement programs in the identification of drought tolerance sources and will contribute to the development of high yielding varieties with good fodder quality.

Keywords: Sorghum bicolor - Stay green - SNP - QTL - GWAS - Drought - Dhurrin - Proline - Nitrogen.

Building a sorghum grain : a transcriptome roadmap targeting protein content and digestibility

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Sorghum is the world's 5th most important grain crop. Its ability to cope with biotic and abiotic constraints could allow it to contribute to global food security in the context of climate change. However, the low digestibility of the grain reserve proteins (called kafirins) by gastrointestinal proteases is hampering its wider use for food and feed. The structure of the protein bodies in which are stored the kafirins is potentially responsible of this defect. The molecular mechanisms underlying the development and modification of kafirin-containing protein bodies are still largely unknown. In this context, our objective is to decipher the molecular mechanisms involved in the regulation of the content and digestibility of sorghum grain reserve proteins. The evolution of the transcriptome was monitored during the grain development of the Macia genotype, and supplemented by an analysis of gene co-expression networks (GCN). In parallel, the protein content of the grains and their *in vitro* digestibility were measured. Analyses allowed the identification of transcription factors (TFs) potentially regulating the mechanisms of protein reserve establishment. We identified co-expression modules involving kafirin genes and genes orthologs to TFs already known in maize, rice and arabidopsis. In those modules, we also identified not yet identified TFs. In the future, we plan to evaluate the role of these TFs by a simplified cellular overexpression system in sorghum protoplasts.

Keywords: Sorghum - Grain - Protein digestibility - Gene co-expression network - Transcription factor.

Combining abilities and heterosis for biomass yield and quality related traits in single-cut forage sorghum adapted to temperate climates

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Sorghum is among the most important cereals in the world in terms of human and animal nutrition and contributes to several bio-based value chains, including bioenergy production. The development of varieties fitting the expectations of these different end-products requires a better understanding of the genetic determinism of the traits contributing to the targeted ideotypes. In this context, the objectives of this study were to estimate the general and specific combining abilities of biomass quality and production related traits, explore their correlations and assess the heterosis levels achieved. To reach, these goals a factorial design based on 10 female and 16 male parents that were selected for their General Combining Abilities (GCA) for biomass production has been developed. One hundred and forty seven hybrids were evaluated on 3 sites together with their parental lines in 2014. Heritability of 0.69, 0.79 and 0.90 were observed respectively for the dry matter yield, lodging at maturity and biomass digestibility. Correlations' analysis between hybrid genetic values and combining ability components showed that hybrid performance is mainly correlated with the male parents GCA and depends only weakly of the female GCA. Higher best parent relative heterosis (up to 49%) was observed for biomass yield compared to biomass digestibility (up to 9%) and a negative genetic correlation (-0.54 for the blup values and -0.6 for the GCA values) was observed between biomass yield and digestibility in the factorial design. The best hybrids were selected and evaluated on 4 and 3 sites respectively in 2015 and 2016. In addition to allow the identification of elite parental lines that will be used in future crosses, this study underlined the negative correlations between biomass production and quality that will need to be tackled and the lack of strategies to accurately predict heterosis in single cut forage sorghum.

Utilization of electron-beam mutagenesis for sorghum crop improvement

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Sorghum (*S. bicolor*) is one of the most important cereal crops in the world and ranks fifth in terms of grain production and harvested area. Sorghum is widely grown for multiple uses, including human food, animal feed, and biofuels. Enhancing the genetic diversity of sorghum can be valuable for sorghum improvement, and induced mutagenesis can be a tool in this respect. Mutagens such as electron beam (e-beam) radiation are safer, more convenient, and more environmentally benign compared to radioisotopes and chemical mutagens. The present study investigated the effectiveness and efficiency of induced mutation by e-beam radiation in sorghum. Varying doses of high-energy e-beam radiation viz., 200Gy, 400Gy, 600Gy, 800Gy, 1000Gy, and 1200Gy were tested on three different sorghum genotypes, R.08306, R.Tx436, and R.Tx437. The treated M1 seeds along with the non- treated seeds were planted in the field, and data on plant emergence, fertility, and plant height were recorded. It was observed that the three sorghum genotypes used in the study varied in their sensitivity to e-beam radiation, with R.Tx436 showing the most sensitivity. There was no plant emergence at 200Gy and 400GY for R.Tx436 and R.Tx437, respectively. Furthermore, the seedset in R.08306 was reduced with increasing doses of e-beam. We are currently testing low doses of high-energy e-beam in the range of 30-200Gy to further optimize the dose. Further, we are also evaluating low-energy e-beam for mutagenesis in sorghum. Ongoing efforts include the determination of LD₅₀ values based on plant emergence and fertility for both high and low-energy e-beams. Traits of interest include herbicide resistance and adaptation to abiotic and biotic stresses. Findings are expected to favor the utilization of e-beam as an alternative mutagen for sorghum improvement.

Agro-physiological responses of sorghum to the combined effects of aphid pressure and drought stress in Haiti

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Melanaphis sorghi is among the major constraints impairing sorghum cultivation in Haiti and combined aphid infestation and drought stress could decrease yield further. The present study aims at assessing the impact of aphid attack and drought stress on agro-physiological performances of sorghum. A field experiment is underway and testing three factors. The first is the water regime with two modalities: droughted treatment and well-watered one, the control. The second factor is aphid exposure with two modalities: high aphid pressure and a treatment with imidacloprid application to control the aphid. Twelve sorghum genotypes with contrasting behaviors to aphid attack and drought stress are tested using three replications in two locations with different altitudes (Mirebalais and Saint Raphael). Many hypotheses including the increase of cuticular wax deposition in sorghum leaf, dhurrin and soluble sugars content, stay green and leaf stomata regulation are under test to identify drought adaptation mechanisms used by these genotypes. Similarly, HCN, lignin, osmolytes (trans aconic acid, salicylic acid and jasmonic acid) contents, the presence of trichome under leaves and trichome density are also being assessed to identify the genotypic responses to aphid infestation and the mechanisms underlying sorghum tolerance. G×E interactions will be assessed on these traits to understand yield stability and adaptation of these genotypes depending on the growing environment. All these results will serve in the breeding program for genetic improvement of local sorghum cultivars to aphid pressure and drought stress.

Development of dual-purpose sorghum in Mali provide agroecological intensification of livestock farming

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Context: Rural community land saturation and intensive livestock farming lead to new fodder demands no longer satisfied by the current systems. Livestock and crop farmers satisfy currently their fodder demand by growing maize which is rapidly expanding over traditional cereals resulting in a significant agricultural biodiversity decline. Breeding innovative novel double purpose sorghum varieties sorghum will help develop value chains around fodder production. This new fodder will bear a positive impact on farmers' incomes, particularly around urban centers where fodder shortages are a brake on intensive cattle farming.

Material and Method: Sorghum varieties with improved fodder quality and higher biomass yield, integrating the bmr gene (better digestibility) were developed. Phenology and above ground biomass establishment were carried out to calibrate crop models to predict novel varieties adaptation. Feeding value was determined using near-infrared spectroscopy while productivity was confirmed through a multi-location trial network.

Results and Discussion: Similar to landraces, new varieties, sensitive to photoperiod, adjust maturity according to the end of rainy season. Photoperiodic varieties are therefore naturally adapted to climate variability, which is the main expected effect of climate change. Biomass produced by new sorghum varieties exceeds that of maize. Using dwarf plants or late planting increases stover quality but also reduces biomass production while bmr trait introgression allows us to reduce stem lignin content without affecting yield potential. Many traits inherited from landraces (photoperiod, tillering, plant height and grain quality) that have long often been overlooked are now important stakes in breeding programs. Sorghum is known for its good water and mineral use efficiency, but crop models must be adapted to specific case of photoperiodic sorghums.

Conclusion: This research, which reconciles science and local knowledge, will lead to the co-construction with farmers of new cropping systems compatible with an agro-ecological intensification fodder production.

Comparative effects of bmr-12 and D genes on sorghum stover quality

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Background: Rapidly increasing forage requirements of West African production systems prompted sorghum breeding programs to develop dual-purpose varieties that produce grain for food and fodder as a feed. Recessive alleles of two genes are known to improve sorghum forage value by reducing stem lignin content: the Dry gene (D) which controls stem juiciness and the brown midrib gene (bmr-12). This work evaluates the effects of introgression of these two alleles in Kalla Kéné, a photoperiod-sensitive variety from Mali with dry stem and white midrib.

Material and method: three near-isogenic lines (ISOJ, ISOB, and ISOJB) were developed from five successive backcrosses between the recurrent parent Kalla Kéné and Redlan (bmr-12) a bmr juicy sorghum as donor parent. Line ISOJ has juicy allele, ISOB the brown midrib and ISOJB both alleles (juicy stem and brown midrib). Stem quality of the isogenic lines was studied in interaction with sowing dates using a split-plot design repeated over three years. Measurements were focused on phenology, morphology and stem chemical composition.

Results and discussion: Genotype and sowing date effects are highly significant. Genotype x sowing date interaction is not significant. Delay in sowing leads to a decrease in lignin content, a later maturity, followed by a highly reduced biomass production. Lines with bmr-12 trait have a more strongly reduced lignin content compared to the one with only juicy allele. For all sowing dates, the decrease in lignin content does not lead to lodging.

Conclusion: bmr trait is the best way to improve forage quality of photoperiod-sensitive sorghums. Innovative dual-purpose varieties will help develop value chains around fodder production. This result will have a positive impact on farmers' incomes, especially around urban centers where fodder deficits are a brake on livestock intensive farming. Conversion of malian elite sorghum varieties to bmr lines is underway.

Adaptation of bio-fortified sorghum hybrids (*sorghum bicolor*) to drought resilience in Mali

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Sorghum is a staple food in Mali, yet grain yields are low and do not contain high lysine, threonine, iron and zinc content. Drought is the most significant cause of crop yield loss, especially in water limited areas where most of the world's poorest farmers live. Development of drought tolerant bio-fortified sorghum hybrids will enhance food production and the livelihood of farmers in these areas. To assess the adaptation, yield potential, and to identify the traits contributing directly and indirectly to sorghum drought resilience, a study was conducted in two locations. Thus, a total of 49 F1 new hybrids were developed and used in this study along with three commercial hybrids. Ten bio fortified hybrids were identified with grain yield ranging from 3774 to 5068 kg ha⁻¹ with an average heading date of 74-83 days. The new bio-fortified sorghum hybrids yielded three times as much as the local varieties, which yielded 1 to 1.5 tons. The index of varietal drought sensitivity varied 253.43 to 81.12 %. For drought resilience, a significant correlation was identified with index of varietal sensitivity through green mibrid, stay green and leaf senescence. A positive and negative correlation among grain yield, stay green and mibrid were observed. This study identified bio fortified sorghum hybrids with high grain yield and tolerant to drought stresses. These ten hybrids are worthy to be utilized in participatory trials for their registration in the seed catalog.

Climate change impacts on sorghum adaptation in Mali

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Introduction: Climate models are foreseen the future distribution of rainfall in Africa differently. However, an increase in climate variability and a succession of droughts and floods are unanimously expected. Climate variability is an inherent feature in Sub-Saharan environments where farmers acquired expertise to mitigate climate change impacts by developing climate smart varieties over generations. The objective of this work is to determine the impacts of climate change on sorghum adaptation in Mali using the CERES crop model under future climate scenarios.

Material and Method: Data predicted by 6 climate models following the medium scenario (RCP4.5) were extracted for 16 rainfall stations in Mali from 2023 to 2052. Predicted values were corrected for biases against historical data. Phenological module of CERES crop model was calibrated for two Malian sorghum varieties. One corresponds to research ideotype (early maturing type) and the other one is photoperiod-sensitive, late maturing inspired by landraces. CERES model was used to predict flowering time of the two varieties, which permitted to delimit their upcoming growing areas.

Results and Discussion: Climate models predict differently the upcoming rainfall evolution. Most climate models used do not respect the current structure of rainy season in sub-Saharan Africa, which can be considered as bias calculations. The CCCma model was used because it better respects the known structure of rainy season.

Climate change impacts differ according to sorghum varieties photoperiod sensitivity thresholds. The most photoperiodic sorghums are less affected by climate change with a slight shift from North to South for growing areas. Photoperiodism will always be an essential factor in climate change adaptation.

Conclusion: Currently, climate models must be used cautiously to accurately predict crop adaptation, which depends primarily on the start and end dates of the rainy season.

Introgression of QTLs for anthracnose resistance (*Colletotrichum sublineolum*) in an elite sorghum variety from Mali

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Sorghum (*Sorghum bicolor*), the fifth most cultivated cereal in the world, ensures food security for millions of people in Africa. Anthracnose (*Colletotrichum sublineolum*) is one of the most important disease in sorghum production areas in Mali. Anthracnose causes premature drying and defoliation resulting in low grain yield. The objective of this study is to improve sorghum resistance to anthracnose by introgressing resistance QTLs into an elite Malian sorghum variety. Study was conducted at the Sotuba station. Pathogen source consisted of *C. sublineolum* strains collected in the major sorghum production zones in Mali (Kita, Bougouni, Longorola, Farako, N'tarla, Signé, sirakelé, Bla and Cinzana). Tiandougou Coura, a highly susceptible to anthracnose Malian elite variety was used as a recurrent parent and three varieties (B35, Grinkan and E36-1) were use as donor for resistance to anthracnose. The QTLs were introgressed by molecular marker-assisted backcrossing method in order to obtain three BC3F3 populations (one population per donor parent). Population development was also accelerated by forcing floral initiation to allow the development of three generations per year. The BC3F4 plants are currently being phenotyped for anthracnose resistance, yield traits, stover and grain quality.

Population Genomic Structure of Sorghum across Landscape, Environment and Culture

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Domesticated sorghum has served as a staple crop across Africa and Asia for thousands of years and has adapted to a wide range of environments. As domesticators, people have played a large role in the dispersal and selection of sorghum subspecies as traits are selected according to preference and ability to adapt locally. However, the factors and extent of these variables leading to genetic differences among populations and geographic regions remain to be studied. In my current study, we examine the ecological context of population-genomic structure in sorghum to assess the relative importance of several potentially important factors. These factors include spatial connectivity, environment, human movement, and culture. We build models of human movement across heterogeneous environments (e.g. seas or deserts) to estimate potential patterns of sorghum gene flow. We use variance partitioning with redundancy analysis to estimate the portion of genome wide variation explained for ~1800 global landraces. For example, I find that human language families across Eurasia and Africa explain 17% of genomic variation among landraces. Wavelet analyses show strong heterogeneity in patterns of isolation by distance, e.g. with very slow accumulation of genetic differences across geographic distance in more recent Chinese landrace populations. This research may provide a historical and background framework for sorghum geneticists and further understanding of evolutionary drivers of sorghum diversity.

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Thermal suitability maps to support sorghum cultivation in Switzerland

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In Switzerland, sorghum still represents a niche crop, and its cultivation area is of only about 300 ha. Yet the interest for sorghum is increasing, not least because of the challenges imposed to other crops by climate change. As a plant adapted to dry conditions, sorghum is well equipped for facing increasingly frequent periods of drought, as projected by climate change scenarios for our country. Moreover, it has a high biomass potential, and is suitable both as animal feed as well as for human nutrition.

Contributing to ongoing efforts to promote sorghum cultivation in Switzerland, we present the development of thermal suitability maps that aim at illustrating the potential extension of the cultivation area under current climatic conditions, separately for silage and grain sorghum. Behind the maps is an assessment of growing degree-days based on gridded daily temperature fields for 2001-2020. We used growing degree-days requirements obtained from field trials conducted during 2009-2011 (grain sorghum) and 2018-2022 (silage sorghum) as thresholds for gauging the average date of maturity and the probability that the harvest can take place before the end of October, which we considered as a latest harvest date for the sorghum types under examination.

The maps clearly show the different extent of areas suitable for growing silage and grain sorghum in relation to temperature. The former account for the largest part, the latter are limited to only about a quarter of the current arable land in Switzerland. Due to the simplicity of the approach, the development of maps for other sorghum types is conceivable to support both agronomic research and agricultural practice.

SorghumBase 2023: Building Partnerships and Integrating Genetic Knowledge for the Sorghum Community

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SorghumBase (<https://www.sorghumbase.org>) is a USDA-ARS funded resource released in 2020. The Sorghumbase team works closely with the community to support stewardship of sorghum genomics data, establish best-practices on managing the data and provide opportunities for networking and capacity building within the community. We maintain a database of scientific publications, genome sequences, gene structure annotations, and comparative genomic analyses integrated with curated data from the gene Expression Atlas at EBI, Plant Reactome pathway database, and QTL Atlas at OZ Sorghum. Release 5, includes 28 sorghum genomes, and 7 additional species, including Arabidopsis, rice, maize, which serve as sources for curated gene function and phylogenetic analyses. Protein-coding gene trees are built using the community annotations. The resulting gene trees support information on orthology, paralogy, and candidate copy numbers variation (CNVs). The information on CNVs can be observed within the gene neighborhood views available from the search interface. The gene trees are also used to identify potential annotation artifacts, and can support future community curation efforts. SorghumBase hosts over 61 million genetic variants including natural variants, as well as novel EMS-induced point mutations. These can be visualized in context to gene-based views for their impact on a transcript, capturing functional effects in over 48.1K BTx623 transcripts. In addition to the genomic resources, SorghumBase provides weekly updates of news items, conferences, and community events. In the last six months, our publications database has grown to over 600 papers, 40 of which have been highlighted in recent [News](#) posts. News items on are indexed and searchable, and include information on how to access data related to the articles from the site. A user guide is available from the site and feedback may be provided via a contact form. Individual training sessions may be scheduled upon request.

Contribution to the knowledge of insects from imported foodstuffs in markets of Niger

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In Niger, storage insects reduce the grain quantity and quality during storage period. Worldwide, these insects damage 5 to 35% of stored grains; and cause $\geq 40\%$ of damages in tropical countries. Samples of imported commodities were collected from markets to collect and identify insects infesting the grains, and control methods were identified. The results indicated that grains of millet, sorghum, maize, cowpea, and soybean (Nigeria) and maize (Benin and Burkina), rice (Asia) are sold in the markets. The imported commodities were attacked by storage insects that cause significant losses. From sampled insects, 6 species including *Tribolium confusum*, *Tribolium castaneum*, *Sitophilus oryzae*, *Sitophilus granarius* and *Acanthoscelides obtectus* attack cereal grains and *Callosobruchus maculatus* on cowpea grain. To control these insects, traders use expensive and toxic insecticides. It was recommended the application of biopesticides for stock treatments and the use of triple bagging to ensure the better storage of grain products in markets. Also, upgrade phytosanitary control stations with modern devices for detecting storage insects to prevent their introduction into grain products found in the markets.

Keywords: Storage insects - Imported commodities - Damages - Biopesticides and triple bagging.

Site-specific N and P fertilizer for improving the productivity of the smallholder sorghum systems in semi-arid Ethiopia

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In the dry lowlands of Ethiopia, the current agronomic recommendations, including plant populations and nitrogen and phosphorus fertilizer application rates for sorghum, were developed more than three decades ago with little consideration for the soil type and fertility. Nor do they take into account input costs relative to the output value. Field experiments at on-station and on-farm sites were conducted at different locations in the north, northeast, and eastern Ethiopian semi-arid areas from 2019 to 2022. In 2019, the treatment factors consisted of two plant densities, two improved early maturing varieties and three nitrogen (N) and phosphorus (P) fertilizer rates, laid out in a randomized block design. The trials in 2020–2022 did not include the plant density treatment because there was no response at any of the locations. The treatment was also modified to include more N and P rates, including the previous rates used in 2019. The interaction effect of location and N and P fertilizer had a highly significant ($P < 0.05$) influence on sorghum grain and stover yields. Generally, the study did not support the blanket recommendation of a higher level of 20 kg P ha⁻¹. Applying up to 10 kg P ha⁻¹ was enough to maintain the soil P status after the harvested crop. While applying 23 to 46 kg N ha⁻¹ in northern and north-eastern Ethiopia and 23 kg N ha⁻¹ in eastern Ethiopia can be more attractive options for resource-constrained farmers. A long-term simulation was also conducted using a crop model to identify a low-risk strategy from the various N management options that can be more feasible according to the risk preferences of smallholder farmers in the face of a variable climate. The identified strategies could be a stepping stone to the sustainable intensification of smallholder sorghum systems in semi-arid Ethiopia.

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Survey of the Prevalence and Incidence of Foliar and Panicle Diseases of Sorghum Across Production Fields in Niger

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In Niger, sorghum ranks second as the most important cereal after pearl millet and is used primarily as a staple food and fodder. In 2019, an extensive survey of the occurrence and distribution of foliar and panicle diseases affecting sorghum in farmers' fields from major production regions of Niger was conducted.

A total of 121 fields in the regions of Tillabéri, Tahoua, Dosso and Maradi along paved and unpaved roads, including National and Secondary (RN1, RN2, RN3) were surveyed. In each field, 60 plants at late flowering to hard dough stages of development were assessed using a W-shaped pattern.

The study documented 21 different sorghum diseases, including anthracnose, long smut, oval leaf spot, leaf blight, head smut and zonate leaf spot. The most prevalent diseases were anthracnose, leaf blight, oval leaf spot, rough leaf spot and long smut. The highest mean incidence of anthracnose, leaf blight and rough leaf spot was recorded from Maradi, whereas, the regions of Dosso and Tahoua exhibited the highest mean oval leaf spot incidence. The highest incidence of long smut and zonate leaf spot was recorded in fields in Dosso region. Locations with highest incidence of these diseases can be considered 'hot spots' for resistance evaluations.

This study is significant because for the 1st time it provides researchers, funding and governmental agencies in Niger a guide on the occurrence, distribution, prevalence and 'hot spots' for sorghum diseases. the occurrence, distribution, prevalence and 'hot spots' for sorghum diseases.

Keywords: Sorghum - Disease incidence - Fungal diseases - dwarf mosaic virus - Anthracnose.

Genetic Variability, Heritability and Genetic Advance for Agronomic Traits of Ethiopian Sorghum [*Sorghum bicolor* (L.) Moench] Landraces

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Sorghum (*Sorghum bicolor* L. Moench) is an important food security crop mainly in semi-arid and tropical parts of the African countries. Even though it is believed to be originated and domesticated in Ethiopia, sorghum production is inhibited by limited number of high yielding varieties. A field experiment was conducted at Assosa and Pawe Agricultural Research Centers during the 2019/20 cropping season with the objective of identifying sorghum landraces and breeding lines with high grain yield, study phenotypic and genotypic variability, heritability and genetic advance for yield and yield contributing traits. Forty two (42) sorghum landraces and breeding lines were planted in RCBD design in row column arrangement with two replications. The result of analysis of variance revealed that there is a significant variation among the tested landraces and breeding lines for all the evaluated characters. The highest yield of 3297Kg/ha was recorded for AScol19-Krm 124 followed by Ya036/1 with the mean yield of 3146kg/ha while the lowest grain yield of 817kg/ha was recorded for ETSCAs 10002-2-13-1 breeding line. Higher Phenotypic Coefficient of Variation and Genotypic Coefficient of Variation values were scored for grain yield. High estimates of broad sense heritability were found in all plant characters under study. Highest heritability estimates (97.8) were found in grain yield. Values of genetic advance ranged between 21.94 for days to physiological maturity to 1934.46 for grain yield and the genetic gain (of the mean percent) was ranged from 11.48 for days to physiological maturity to 99.41 for grain yield. The greater extent of broad sense heritability together with higher genetic advance in characters studied showed the evidence that these traits were under the control of additive genetic effects which means undertaking selection in these landraces and breeding lines should lead to a rapid enhancement of the traits studied.

Sesame (*Sesamum indicum* L.) seeds and di ammonium phosphate (dap) potential for controlling Striga seed germination, sorghum growth and grain yield

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Sorghum is important staple food for feeding humans and animals in sub-Saharan African country. Nowadays, with the advent of climate change couple to the population growth, the crop is faced to new challenges which are gradually affecting the productivity. In Niger, a dry land country where farmers are growing sorghum at a small scale for family subsistence, the crop is confronted to biotic and abiotic constraints including nutrient deficiency in the soil. Among those constraint, Striga is the one that causes huge damage to sorghum cultivation through yield reduction. In addition, nutrient depletion in the soil are causing weed progresses in farmer's field at a large scale. In fact, to overcome Striga problem several control methods have been successfully tested, but some of them are efficient but not accessible to farmers. It is important to control the weed by using effective and accessible way for smallholder farmer in Niger. The main objective of this study was to assess the effectiveness of different doses of sesame (0, 0.5 and 1.5 g) and DAP (0, 2 and 5 g) on Striga impact and sorghum grain yield. Two (2) grammes micro dosing utilization of DAP shows good result in Striga plant emergency and distribution along sorghum field. Concerning the three doses of sesame seed involve in this experiment, the micro dosing two (1.5 g) positively affect Striga effect. The combination sesame seed and DAP can significantly reduce Striga impact on sorghum cultivation and increased sorghum grain yield.

Agricultural Mechanization Indices, Productivity and Profitability for Sorghum Value Chain in Busia County, Kenya

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The use of agricultural Mechanization technologies in Sorghum value chain is limited as compared to other value chains such as maize. A study on the agricultural mechanization indices, productivity and profitability was undertaken in Sorghum value chain Busia-County. The overall goal of the study was to contribute to the understanding of the agricultural mechanization indices, productivity and profitability for the sorghum value chain for purposes of recommending research and policy interventions in Kenya. A survey was undertaken to collect data from four sub counties of Busia County with a focus on the sorghum value chain. A multistage sampling procedure was adopted with the first stage being the county, second, sub-county, third, the ward and finally the respondents. While the random sampling procedure was preferred this was combined with purposive sampling in order to get the correct and appropriate sampling unit. Both descriptive and analytical models were used to analyze and report the data collected. Descriptive statistics used included graphs, tables and histograms, while the models included multiple regression models, Mechanization index (MI), productive and profitability functions. The results indicate that mechanization of sorghum value chain was limited with overall MI of 0.18, without oxen but increases to 0.4 when draught power (oxen) was included. Low MI maybe associated with relatively small sizes of plots under sorghum cultivation. The sorghum productivity was estimated using a Cobb Douglas production function, which indicated that investment on machinery, and draught power were positive and significant in influencing sorghum productivity. Thus a shift in policy is recommended to empower farmers afford small-scale machinery either through purchase or service distribution model. While use of draught power was positive, this would eventually be replaced by investing in affordable small-scale machinery.

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Response of the Set of Anthracnose Differentials to other Foliar and Panicle Diseases in Niger

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This study was conducted to determine the reactions of 19 sorghum lines, of which 18 had been used for *Colletotrichum sublineola* pathotype determination to other foliar and panicle diseases in two agroecological zones in Niger. The anthracnose resistant check SC748-5 was infected with leaf blight, oval leaf spot, and zonate leaf spot but free of long smut, rough leaf spot, and target leaf spot. BTx623 and TAM428 which are susceptible to anthracnose were infected with leaf blight, long smut, oval leaf spot and zonate leaf spot. Across locations, all the lines tested were infected with leaf blight, caused by *Exserohilum turcicum*. PI570726, an accession from Sudan was infected with only leaf blight but free of all the other diseases observed in both locations. This work showed that some of the sorghum anthracnose differentials, especially PI570726 may possess genes for resistance to multiple sorghum diseases and can be utilized as parents in breeding programs in Niger.

Keywords: Sorghum - Fungal diseases - *Colletotrichum sublineola* - *Exserohilum turcicum*.

Sorghum crop comparison to assess stability of food production in Senegal

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Sorghum is a key component for food security in Africa, grown extensively accounting for 28 M ha in the continent, with half of those located in the western region. Sorghum resiliency to climatic constraints positions this crop as a key element to ensure food supply. However, its adaptability compared to other field crops have not been previously reported. In this context, the use of crop growth models allows the evaluation of the effect of weather variability (different growing seasons) and the overall impact on different field crops. Therefore, this study employed a modeling approach aiming to i) target crop selection (sorghum, peanut, millet, and mungbean) to climatic vulnerabilities, ii) calculate the potential improvement on food production driven by crop selection. For this propose, field studies were conducted in five locations in Senegal (Bambey, Niore du Rip, Saint-Louis, Sefa, and Sinthiou Maleme) and two planting dates during the 2022 growing season. The outcomes of all trials were employed to characterize the most common crop choices and calibrate/validate the APSIM model for these field crops and environments. This study highlights the importance of field data collection and crop choice to provide significant insights to support smallholders.

Sorghum Producer Yield Contest: A synthesis-analysis of major management and environmental drivers

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To reverse the negative trend in sorghum (*Sorghum bicolor* L.) planted area across the United States (US), it is critical to identify the best management practices within the target environments. This study aims to provide new insights of the effects of environment (E) and management (M) on sorghum yields. The objectives of this study were: i) describe the relevance of E factors (mainly heat and drought), and ii) explore the effect of M component on yield variability across different US sorghum producing regions. The US National Sorghum Producer (NSP) Yield Contest self-reported farmer-based dataset, spanning 24 states from 2013 to 2017 period (n=782) was split in yield terciles (low < 7.6; intermediate 7.6-9.7; high > 9.7 Mg ha⁻¹). Three different approaches were applied independently to each yield tercile independently: i) crop modeling simulation, ii) conditional inference tree, iii) fuzzy C means spatial clustering. The E component accounted for nearly half of the sorghum yield variation for the low-yielding tercile, while the M factor was the most relevant for the high-yielding tercile. Geographically relevant yield clusters identified two regions within the US region, i) east (with early planting dates and high N fertilization rates), and ii) west (with irrigation as the main management factor). A third region was defined in the south coastal zone (with planting dates before April 1). This study provides insights on the major E and M factors limiting attainable yields across the main US sorghum producing regions.

Participatory evaluation of local biopesticides against sorghum and cowpea pests in conservation in Sudanian zone of Mali

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In Mali, sorghum and cowpea grow occupies an important place in agriculture-livestock integration. These dual purpose crops are threatened by pests (insects). Farmers use a lot of chemicals to control that have a negative impact on the environment and human health. The objective is to improve the more agro-ecological sorghum and cowpea protection system. After the identification of biopesticide plants (Zarama, Neem, Benefindjon) with farmers, a conservation trial for sorghum and cowpea based on biopesticide treatments was set up in Sotuba. Three doses (7.5g; 15g; 30g) were tested on Sankaraka, Djiguifa, Ghana shoba and Tiandougoucouira against *Callosobruchus maculatus*. The results showed that the number of *Callosobruchus maculatus* decreases with biopesticides compared to the untreated control. The attack rate decreases with Neem by up to 2%. The dose (30g) was better with all plant biopesticide tested.

Keywords: Biopesticides - Pests - Conservation - Cowpea - Sorghum.

Cultivation of sorghum in Poland and the content of selected bioactive compounds in harvested sorghum grain

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The research on sorghum in Poland began with cultivars harvested for biomass production, as they were characterized by rapid growth, high straw yield and did not produce generative organs in the soil and climatic conditions of Poland. However, intensive breeding work provided to study the possibilities of cultivating varieties that give fully mature seeds every year in temperate climate conditions. Five prospective varieties of sorghum were selected for field research. The average grain yield was 3-4 t/ha at 15% moisture. The yield was not high compared to sub-tropical area of cultivation. Nevertheless, it indicates that with the ongoing climate change, it is possible to grow sorghum above 50 degrees north latitude. In addition, the research carried out so far in Poland has shown the high nutritional potential of this plant and the richness of active substances contained in sorghum grain from domestic crops. It has been shown that the tested material is a rich source of bioactive compounds with antioxidant properties. Among the carotenoids, lutein was the most found, and in the case of sterols, sorghum grain contained the most beta-sitosterol. Catechin is a flavonoid present in the highest concentration in the analyzed grain samples. Among the phenolic acids, the highest content in sorghum seeds was found for ferulic, p-coumaric and protocatechuic acids. Currently, research on the possibility of sorghum cultivation in Poland and its nutritional potential has been supported by the Ministry of Agriculture and Rural Development as part of research on biological progress in plant production.

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Potential of cereal-legume intercropping systems in future climates: a modelling study in Burkina Faso

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In the semi-arid zone of Burkina Faso, farmers practice intercropping to minimize climatic risk by ensuring at least one crop in case of particular stress. Crop models are useful tools for evaluating the effect of abiotic stresses on crop performances. Our study aimed to evaluate the contribution of intercropping to the resilience to climate change. An experiment was conducted in 2017 and 2018 at the Saria research station. Two pairs of varieties of sorghum and cowpea were evaluated in intercropping and sole crop. The STICS model was used and calibrated on the 2018 sole crop experimental data, which represented the most optimal cropping situation. Two CO₂ pathway emission scenarios and five probable future climate models were used to analyze the climate impact for the middle of the century. The results showed that the model satisfactorily simulated the phenology and grain yield of both crops with NRMSE values within the observation errors. Consistent with observed data, simulated yields were higher in sole crop systems, followed by the ones in intercropping systems. Climate analysis showed that crop yields were more sensitive to changes in rainfall and temperature than CO₂. The relatively cold-dry (+0.83°C and -12.5% by 2050) future climate was most favorable to grain yields with yield increases averaging from +3.6% to +7.8% for cowpea when intercropped, and from +7% to +107% in both cropping systems for sorghum. In contrast, the relatively cold-wet (-0.21°C and +30.2% by 2050) future climate was the most unfavorable with grain yield reductions averaging from 0.4 to 29% for both crops. Furthermore, our study showed that intercropping systems stabilized grain yields for most varieties with lower coefficients of variation than in sole crops systems. Overall, the results suggested that intercropping can contribute to the resilience of crops to climate change in the semi-arid zones of Burkina Faso.

***Melanaphis sorghi* (Hemiptera: Aphididae) and Natural enemies in Sorghum in Brazil**

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The *Melanaphis sorghi* (Thobald) (Hemiptera: Aphididae) causes damage in sorghum and became the primary insect pest in Brazil and South America. Thus, understanding the biotic and abiotic mortality factors and the reduction of pests in the field is a challenge in pest management. This study evaluated the occurrence of aphids and natural enemies in forage sorghum in the 2020/2021 and 2021/2022 crop seasons, on 60 hectares, with or without insecticide separately. The insects were collected weekly in Minas Gerais state -19.421310546397617, -4.48275145767204. Two aphid species were collected: *Ropalosiphum maidis* (Fitch) with the sporadic occurrence and *M. sorghi*, the dominant species. The first infestations occurred in January 2021 for the treatment without pesticides and in February for the treatment with the application. The highest percentages of *M. sorghi* infestation occurred in January 2020/2021 and were maintained until the harvest in both crop seasons. *Melanaphis sorghi* had the highest level of infestations in January 2020, reaching a peak of 88,904 insects per weekly sampling. Due to constant precipitation in 2021/2022, the aphid *R. maidis* was the most observed insect pest in December, at the beginning of the crop's season development. The natural enemies observed were the ladybug (Coleoptera: Coccinellidae), the earwig (Dermaptera: Forficulidae), and the syrphid (Diptera, Syrphidae). Ladybug was the most observed natural enemy in the treatment without insecticide application in the 2020/2021 season. We have not collected any parasitoid species in both seasons. The direct correlation in the first season was with the predators' insects (0.94) and precipitation (0.79). In the second season, the aphid infestation was poor, and we could not observe a correlation between biotic and abiotic factors. Then, the rain and predator presence was the principal mortality factors of *M. sorghi* in the field. When using insecticide spraying, the most critical factor was the syrphid presence.

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Performance of *Melanaphis sorghi* in sorghum supplemented with silicon fertilizer

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Currently, *Melanaphis sorghi* (Theobald, 1904) (Hemiptera: Aphididae) is a key pest in sorghum production in Americas. The silicon (Si) supplementation increases the resistance against aphid species in sorghum plants. It's due to formation of a Si layer on leaves surface, contributing to the reduction of aphid performance. Therefore, this study was carried out to characterize the effects of silicic acid supplementation in the hybrid BRS373, on *M. sorghi* performance. The hybrid BRS373 was grown in four doses of precipitated silicic acid (0, 2, 4 and 6 ton.ha⁻¹). Planting was done in pots, the Si source was divided into two applications in the soil, half at planting, and the remainder when the plant had six leaves completely developed. The evaluations were carried in laboratory conditions (24 ± 2 °C, 60±10% humidity and 12h photoperiod), using leaf discs, in 50 mL pots, using 50 replicates, each pot one replication. Starting from first instar nymphs until death, the pre-reproductive and reproductive period, fecundity, and survival rate of nymphs were evaluated. The data were submitted to analysis of variance individually, and when there were significant differences, identified by the F test (P < 0.05). The mean comparison was performed by the Tukey test (P < 0.05). When supplemented with a dose of 6 ton.ha⁻¹, the hybrid showed a lower survival rate (38%), fecundity (30.68 nymphs) and reproductive period (7 days), as well as a longer pre-reproductive period (4.68 days), when compared to the other silicon doses. These data suggest that, despite high, the dose of 6 ton.ha⁻¹ of silicic acid is the most efficient in reducing the reproduction of *M. sorghi*.

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Sorghum Anthracnose Intensity and Its Association with Bio-Physical Factors in Western and South-Western Regions of Ethiopia

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Sorghum is the fifth most cultivated cereal crop in the global after maize, wheat, rice and barley in terms of production and importance. Ethiopia is the second largest sorghum producer following Nigeria in Africa. Despite these potential, production and productivity of sorghum remained low. This is due to a lot of agricultural crops are being threatened by a wide diversity of factors that causes lowering grain quality and quantity leading to wipe out the entire harvests of sorghum yield. Among factors, sorghum anthracnose caused by *Colletotrichum sublineolum* is one of the main fungal diseases which substantially reduces sorghum grain yield. This study was undertaken in order to assess the intensity of anthracnose on sorghum fields, to determine the importance and associated factors of sorghum anthracnose. Potential sorghum growing regions, zones, and districts were selected by following purposive multi-stage sampling procedure. Sorghum fields were assessed from October to November in 2020 and 2021 during early milk to hard dough stages. The severity was determined by the modified Horsfall-Barrett scale. Infected sorghum leaves were sampled and associated factors were identified. Results of this study revealed that the overall prevalence of sorghum anthracnose on sorghum fields across western and southern-western Ethiopia was 93.88 %. Sorghum fields were shown varying levels of sorghum anthracnose incidences that ranged from 46.15–100 % in Assosa, 55.5–100 % in Jimma, and 75–84.62 % in East Wollega 78.5% in Bako, and 85.7 –100% in Gambella respectively with the mean incidence of 79.2 %, 80.45 %, 79.81 %, 67.7%, and 91.07%. Besides, the severity of anthracnose was high in Jimma, Assosa, Gambella, Bako, and East Wollega with mean field severity of 34.5%, 32.63%, 35%, 28.97%, 27.6% respectively. On the other hand, Assosa, Gambella, Jimma and Bako Zones were founded with higher mean field severity index of 61.22%, 55.6%, 48.45, and 43.6%, respectively.

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Small-scale agricultural mechanization as a mechanism for the dissemination of improved sorghum, maize and bean varieties

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Multi-level diagnosis of agrosystems in Haiti underlined major constraints negatively impacting labor productivity and production. These constraints concern particularly : unavailability of agricultural labor at critical times in the calendar of different cropping systems, unavailability of the tools for plowing (animal traction or engine powered) and the tools for weed management, poor management of planting densities, the misuse of fertilizers, and finally poor access to quality seeds with enhanced resistance to pests and diseases and well adapted to Haiti agro-climatic conditions. However, small integrated changes in production systems can overcome these constraints and lead to substantial production and labor productivity increases. In our latest studies, we are experimenting with the integration of small-scale mechanization as a mechanism for the dissemination of improved variety and quality seeds. The studies consist in some demonstrations of results allowing a comparison of effects of the integration of these technologies with the control which are the plots managed by the farmers with their technologies and the local seeds. We have demonstrated that small-scale mechanization services including no till planting, fertilizing and weeding potentially have lower cost for farmers than traditional ones with a cost reduction of up to 50%. We also hypothesized that mechanical no till planting services could also lower the time. We have obtained as a result a significant difference in the time consumed for the realization of the operations between the service and the traditional. Farmers expressed very high levels of appreciation for the service in general and for the integrated improved seed in particular. They have been also willing to pay for this type of service with an unconditional probability of 93%. This experiment is being duplicated on different crops for different seasons.

Keywords : Cereals - Protein crops - Mechanization - Mechanization services - Production - Yield - Cost - productivity - Demonstration of results - Willingness to pay.

Development of biological control measures for management of striga weed in sorghum and screening sorghum for resistance to striga

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Striga hermonthica is a major parasitic weed of sorghum and other cereals in western Kenya. The current striga management practices comprising mainly of striga resistant and striga tolerant sorghum varieties are not completely effective. Resistant varieties are not long lived as resistance breaks down due to presence of striga biotypes and climate change. Integrated management of striga comprising among others resistant and tolerant cultivars and biological control could be an effective means of managing striga in sorghum in face of climate change. Kichawi Kill™ is a striga bioherbicide recently registered in Kenya for management of striga weed in maize. The active ingredient is a native virulence enhanced *Fusarium oxysporium* sp. *strigae*, a specific pathogen of striga weed. The objective of this study was to evaluate Kichawi Kill for control of striga weed in striga resistant, striga tolerant and striga susceptible varieties, and screen forage, fodder and grain sorghum genotypes for resistance to striga. Field trials were conducted at Alupe in Western Kenya during long rains, 2022. Data on striga and agronomic maize parameters was taken at 6, 8, 10 and 12 week after planting. Results showed that Kichawi Kill significantly reduced emerged striga and enhanced grain yield in resistant, susceptible and tolerant varieties in treated plots compared to untreated plots. There were no significant differences in striga parameters in forage and fodder sorghum genotypes. Significant differences were noted in emerged striga plants, number of heads and grain yield in grain sorghum genotypes, with previously confirmed resistant, tolerant and susceptible varieties remaining resistant, tolerant and susceptible respectively. Future studies should focus on studies on compatibility of Kichawi Kill with cultivated sorghum varieties, and screening of more sorghum genotypes for resistance to striga in order to continuously develop up to date integrated striga weed management technologies which keep up with climate change.

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Participatory variety selection of improved sorghum varieties in Homabay County, Kenya

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Although advances in crop breeding have led to the development of highly adapted sorghum varieties, many smallholder farmers in Kenya still grow local varieties. The low adoption rates of improved varieties result from minimal farmer involvement in the variety development process. The objective of this study was to determine sorghum varieties preferred by farmers in Homabay County and the basis of preference through participatory variety selection. Three sets of 12 sorghum varieties were randomly given to 240 farmers for testing through PVS. TRICOT methodology was used to conduct the trial. Data was jointly collected by farmers and researchers using observation cards and ODK and analyzed using plackett-Luce models with the R statistical package. Results showed differential ranking of the varieties based on different traits. MUK 27 was ranked best overall in all the sites based on variety taste, value in Market and seed color while the local variety was the worst ranked followed closely by RUE 117B based on similar parameters. Majority of farmers (79.4%) considered value in market as most important in variety preference, followed by taste and seed color (78.3%), plant height (70.3%) and grain yield (57.8%) while early vigor was lowly rated (2.2 %). These findings imply that farmers in Homabay county consider sorghum as a strategic cash crop for income. The emphasis on taste reflects the fact that many people in this county consume sorghum as part of daily diet and hence consider eating quality as a key attribute. Issues such as resistance to pests and diseases, early maturity, bird damage were not emphasized because there was low damage emanating from these factors. The study identified some of the most farmer preferred sorghum varieties for Homabay county and the factors that determined their preference. These varieties will be made available to farmers to enhance sorghum production.

Optimizing genotype x agronomic management interaction to enhance *rabi* sorghum productivity using APSIM

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Sorghum is a multi-purpose cereal crop important for the subsistence farmers in India. During post-rainy season (*rabi*), the crop is typically raised on residual soil moisture with negligible possibility of irrigation. Therefore, its productivity has remained stagnant for the past few years. The existence of large attainable yield gap shows potentiality to increase the *rabi* sorghum yields. However, high rainfall variability presents a big risk for the farmers to invest in best practices. Optimizing genotype selection, adjusting sowing window, and crop demand-based water management have the potential to alleviate the risk associated with rainfall variability. Thus, an insilico study was conducted to explore the best combination of genotype and management practices to enhance the productivity of *rabi* sorghum in India. APSIM sorghum was used to simulate the yields of *rabisorghum* in four homogenous system units (HSU - geographical units with reduced GxM interactions) using the set-ups from Ronanki *et al.*, 2022. The results showed that application of supplemental irrigation increased the yields by 2 to 5% for early duration varieties and 38 to 90% for medium and late duration varieties. The extent of yield increase varied with HSUs. The yield increment with supplemental irrigation was 42, 31, 25 and 1% for HSU 1, 2, 3 and 4 respectively. The response of genotype on grain yield varied with sowing time and water availability. Early sowing with early duration varieties gave higher yields in rainfed conditions. However early sowing with medium to late duration varieties coupled with supplemental irrigation increased the *rabi* sorghum yields across all HSU's. This modelling exercise shows that selection of appropriate genotype, adjusting the sowing dates and application of crop demand-based supplemental irrigation help to enhance the productivity of *rabi* sorghum.

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Environmental Characterization in dryland agrosystems

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To evaluate their varieties, breeders test them in different environments. The choice of these environments is often based on the availability of sites and especially their apparent environmental differences (temperature, rainfall, soil) between sites. By this approach, breeders overlook the importance of the Genotype x Environment interaction. All varieties do not necessarily respond in the same way to a water deficit or high temperature. Thus, this approach may work but it may also give a false representation of the TPE (Target Environment Population).

For example, to assess the behavior of varieties in the face of water stress, we compare the behavior of varieties when they are subject to water stress and their behavior when they are not subject to water stress. However, water stress coupled with heat stress does not necessarily have the same impact on varieties as water stress coupled with low temperatures.

In this work, we propose an approach that uses crop modelling to determine the behavior of a variety under different climatic conditions, different cropping practices and different soil types.

This approach makes it possible to establish the main production constraints and a classification of target environments by best integrating climatic uncertainty coupled with the crop's responses to stresses.

This will allow the breeder to consider whether there are separate breeding targets within the TPE.

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Selectivity and weed control of Imidazolinone herbicides over igrowth sorghum in Brazil

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Efficiency of weed control methods is critical to successful diversification of cultures and ease of production by growers. *Sorghum bicolor* L., has been planted in Brazil for many years with low options for growers to control narrow leaf weed species, using mainly atrazine in the production system. This has been one of the biggest challenges for area expansion and higher yields in the country. With new technologies been launched in the market such as igrowth, that confers sorghum tolerance to imidazolinone family herbicides, new questions arise. The integrated weed management in sorghum should be used to rationalize the use of production resources, avoid as much damage to the environment and allow the culture to obtain its maximum production. The objective of this study was to check the selectivity of four igrowth sorghum hybrids and the weed control efficiency by different commercial imidazolinones (Commercial product names: Zelone, Contain and Zaphir) with and without atrazine at 1x and 2x label dosis. Weed control results were: *Digitaria insularis* presented excellent control by all herbicides; *Digitaria horizontalis* wasn't controlled by atrazine; for *Eleusine indica* an excellent control (92-100%) was provided by imazapyr (530 and 1070 gai/ha) and imazapic & imazethapyr (60+180 gai/ha), (83-86%) was observed for imazethapyr (254 gai/ha), imazapic & imazethapyr (30+90 gai/ha); imazapic & imazethapyr (60+180 gai/ha)+ atrazine (1000 gai/ha); *Urochloa decumbens* control was provided by imazapyr (530 and 1070 gai/ha). The blend of strides+imazapic+imazethapyr+atrazine increased the phytotoxicity for all sorghum hybrids compared to imzopic+imazethapyr+atrazine without adjuvants at 7, 14 and 21 daa; the treatments provided higher phytotoxicity around 20-40% (ADV1133IG, ADV1151IG, ADV2450IG, ADV2650IG) and 70-85% (ADV1221) at 7 and 14 daa respectively; At 35 daa, the plants recovered from the stress and the phytotoxicity was around 2-8% (very slight to slight) for all hybrids (ADV1133IG, ADV1151IG, ADV2450IG, ADV2650IG).

Pollen-mediated gene flow from grain sorghum (*Sorghum bicolor*) to johnsongrass (*S. halepense*)

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Pollen-mediated gene flow (PMGF) from cultivated sorghum to its weedy relative johnsongrass may have ecological and environmental significance, but the frequency of outcrossing between the two species with johnsongrass as the female parent is not well understood. During the summers of 2021 and 2022, natural crosses under field conditions were made between johnsongrass and eight (2021) or ten (2022) different sorghum genotypes conferring resistance to the acetyl-CoA carboxylase (ACCase)-inhibitor herbicides quizalofop or fluazifop. The experiments were arranged in a randomized complete block design and replicated four times, with each plot surrounded by corn (2021) or tall biomass sorghum (2022) to prevent cross-contamination of pollen. Seeds harvested from johnsongrass plants growing in mix with the ACCase-inhibitor resistant sorghum were planted in trays in a greenhouse to screen for the presence of the resistance trait acquired through PMGF. The seedlings were sprayed with quizalofop or fluazifop (depending on the specific crop trait) at three- to four-leaf seedling stage. Survivors from the herbicide spray were then transplanted into pots and tested for ploidy status. Preliminary results confirmed the occurrence of gene flow from sorghum to johnsongrass, but the frequencies greatly varied across the genotype. All the tested survivors (i.e. hybrid progeny) were found to be tetraploids. Polymerase chain reaction assays are being carried out to positively confirm the hybrids based on the presence of the specific mutation and verify the frequencies of PMGF. The knowledge generated from this study will be helpful in developing gene flow mitigation strategies and sustainable management of johnsongrass in agricultural landscapes.

Multidisciplinary approach on the introduction of *Sorghum spp.* into Swiss forage production systems

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Rising temperatures and the associated increased frequency of droughts as well as presence of new pests require forage production systems to adapt also in Switzerland. Tropical and subtropical forage crops can indeed increasingly be grown under temperate conditions, to ensure fodder availability, providing biomass and nutrients during critical drought periods. In 2021, land cropped with *Sorghum spp.* was about 300 ha in Switzerland (Federal Office of Statistics, 2022) and is expected to increase based on the tons of seeds sold in 2022 (UFA Samen, personal communication). Although sorghum species are already integrated into rotations as partial substitutes for maize or mixed with legumes as cover crops and are used as pasture or silage for ruminants by innovative farmers, common and large practical knowledge about sorghum as forage resource are lacking. In the last few years, agronomic trials were performed with pure mono- and multicut sorghum varieties and mixtures of multicut sorghum with drought resistant clovers and grasses. The effect of variety and interrow spacing on crop height, biomass, and nutrients' yields were investigated. Small scale ensiling trials were also conducted with mono- and multi-cut types, to assess ensilability and evaluate silage quality. Further, first *in vivo* digestibility experiments with male castrated sheep and *in vitro* digestibility trials were conducted to determine the *in vivo* digestibility of the organic matter (dOM) of selected varieties, delivering preliminary data to predict dOM based on nutrient contents and near-infrared spectroscopy applications. Further, hydrocyanic acid concentrations in fresh and conserved sorghum were analyzed to assess the risk related to intake of cyanogenic compounds in ruminants. In conclusion, multidisciplinary research was initiated to improve knowledge on sorghum production under Swiss conditions, to develop recommendations (agronomic practices, forage harvest and conservation methods, forage nutritive value) for farmers intending to use sorghum in their forage production system.

Testing sorghum varieties with different cutting regimes and seeding densities in Switzerland

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Sorghum is a crop that is still relatively unknown in Switzerland. However, due to changing climatic conditions, its characteristics could be part of the solution to future challenges. In recent years, Swiss sorghum producers' turnover has been high, often dependent on summer fodder shortages. One issue that has discouraged farmers from growing sorghum has been a lack of knowledge about its cultivation and its perceived low fodder quality. However, sorghum can be an interesting choice, especially if maize production becomes more difficult: among other advantages, sorghum is more drought tolerant than maize, and is not attacked by the corn rootworm (*Diabrotica virgifera*).

To address this lack of knowledge, sorghum variety trials with a single cut (2018-2021) and a multicut strategy (2019-2020) were conducted in Zurich (Switzerland). The variety panel included different sorghum types, such as biomass-, BMR-, and sweet sorghum. Agronomic traits such as early vigor, height, maturity, lodging and yield of seven up to 13 commercial single-cut sorghum varieties were compared with two maize varieties and a sorghum-maize-mixture, as well as nine varieties that were evaluated for use in a multi-cut strategy. Moreover, two different seeding densities (20 and 35 seeds/m²) were tested between 2018 and 2020. In addition to the agronomic traits, much emphasis was placed on forage quality. A calibration to estimate various quality traits has been developed for near-infrared spectroscopy applications (NIRS). This research has shown the importance of variety choice for sorghum yield and quality, but also the limitations of sorghum as a maize replacement for certain purposes. Further information on factors influencing forage quality should be gathered in order to develop improved recommendations for farmers. It is concluded that, with the use of appropriate varieties and good agricultural management practices, sorghum can be considered a valuable crop for forage production under Swiss environmental conditions.

Lines selection for striga tolerance using Nigerien sorghum land race : Mota Maradi (MM), Matche Da Koumgna (MDK) and SRN39

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Striga hermonthica is one of the major constraint affecting sorghum cultivation in Niger. Thus with the increase of striga impact around the world coupled to drought and rain fall scarcity, there are some genotypes that can better performed under high striga infestation through low strigolactone production and other resistant mechanism. The best and easiest way to fight the weed is to develop resistant varieties through resistant gene (Lgs1) introgression. So for a better result there is a need to develop new striga resistant population based on farmers preferred varieties and preferences in Niger. The main objective of this study was to assess and select sorghum genotypes for their resistance to striga through a field day at Konni (Niger). As a result, among the 44 F8 evaluated at Bazaga under natural striga infestation 19 lines were selected by farmers based on their preferences criterions.

Gendered trait preferences for new striga tolerant sorghum genotypes in Konni region, Niger

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Sorghum crop is an important staple food cultivated by men and women for household consumption in Sub-Saharan African country (SSA). In Niger, the crop is mainly produced by men, but women are also growing sorghum as a cash crop. In Niger, a rural areas where poverty is very high, there are significant disparities in terms of land ownership, field management and resources access. Women h. Nonetheless, they are playing a crucial role in crop cultivation, transformation and the processing, but they are rarely consulted on the type of crop to be grown in the different fields. and also the quantity to sell. Farmer's preferences studies may put in light their needs and their preferences for technology adoption. Women largely prioritize food security traits based on the earliness and the multiple harvesting capability. Indeed, in addition to variety and trait preference prioritization, rural farmers are faced with yield decreases which challenge them in feeding their families. One of the most damaging constraints is striga hermonthica which causes impediments to sorghum cultivation. The main objective of this study is to examine the gendered trait preferences for new striga resistant sorghum genotypes development that will be easily adopted by the farming community (both men and women) in Konni region.

SoBinEn: Insect friendly energy cropping systems: combination of sorghum with flowering undersown crops

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Many reasons are discussed for the current depletion of insects. The intensification of agricultural production, leading to a lack of flowering plants in agricultural landscapes, is one of them. Therefore, our interdisciplinary research project SoBinEn aims at developing suitable combinations of Sorghum bicolor dual-purpose type hybrids with insect-friendly seed mixtures and undersown crops. With this intercropping approach it is possible to extend the flowering period markedly, so that valuable nectar from the undersown species can be provided for bees and other pollinators, while the sorghum pollen itself serves as a valuable protein source sustaining bee brood raising. Further, these crop mixtures will improve the ecological significance of bioenergy crop rotations in terms of diversity, erosion protection, reduction of nitrate leakage during winter (in case of continuation of the undersown crops) and humus balance.

Five different institutions are involved in this joint research project, covering all aspects of agronomy, insect research and both academic and private (commercial) plant breeding. Principal work packages include:

- testing of a high number of different undersown species in mixed-cropping with sorghum for both insect attractivity and agronomical performance in multi-location field trials;
 - agronomical optimization (e. g. sowing density and –techniques) of selected combinations;
 - detailed evaluations of insect attractivity for the selected combinations, using both tent trials and free flying bee colonies;
 - selection of undersown varieties with superior shade tolerance;
- development of novel erectophile (i. e. vertical roots and erect leaves) sorghum ideotypes, aiming at the reduction of light- and water use competition.

Altogether, this project will contribute to an enhanced sustainability of bioenergy cropping systems, and, in consequence, improve the acceptance of bioenergy crop cultivation for both farmers and the whole society.

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Optimizing the GREET Model to Predict Carbon Intensity for US Grain Sorghum

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Accurately predicting carbon emissions from agriculture is increasingly important when seeking to achieve net zero emissions. The Greenhouse gases, Regulated Emissions, and Energy use in Technologies (GREET) model developed by Argonne National Laboratory attempts to do just that. GREET examines carbon intensity (CI) variations of different farming inputs and then calculates the feedstock-specific, farm-level CI of biofuel feedstocks. In this study, values obtained by the Feedstock Carbon Intensity Calculator (FD-CIC) were compared to values found in the field using eddy covariance and trace gas analysis to test the accuracy of the model and provide for its future refinement.

To estimate the CI of grain sorghum grown in the Southern Great Plains region of Kansas, Oklahoma, and Texas, county level data from NASS was used to plot yield, then the fertilizer application rate was derived from the relationship determined by Kansas State. For yields of 50 to 150 bu/ac, yield increased by 1 bu/ac for every 1.12 lb/ac additional N applied. These values were entered into the FD-CIC to produce county-level CI/ac values.

Eddy covariance measurements yielded different results than those predicted by the GREET model. While seasonal N₂O emissions observed in the field were proportional to the GREET output (57 kg CO₂/ac), the field was a net carbon sink due to CO₂ sequestration and buildup of biomass resulting from the reduced-tillage cropping practice implemented. The GREET model does not include these practices in its calculation, and therefore produced only positive emission values. To correct this, soil carbon loss trends from tillage were studied to create an operator that would accurately predict the carbon impact of reduced-tillage or no-till systems so that the model may better represent these increasingly common farming practices.

Resistance of Sorghum Genotypes to *Meloidogyne* spp. And *Pratylenchus* spp. Nematodes

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Nematodes are among the numerous factors that contribute to the low performance of crops since they can develop during almost the whole year in tropical and sub-tropical regions that and can damage several different crops. Several crop management strategies can be used to control the nematodes in infested area such as seed treatment, crop rotation, use of tolerant cultivars. This study was conducted to evaluate soybeans, crotalaria, sorghum and corn hybrids reproduction factor (RF) for *Meloidogyne incognita*, *Meloidogyne javanica* and *Pratylenchus brachyurus* under greenhouse conditions with artificial infestation in Brazil, and to *Meloidogyne javanica* and *Pratylenchus zae* in Argentina. Brazilian trials evaluated the number of eggs + J2 per gram of root for *Meloidogyne* species and number of specimens per gram of root for *Pratylenchus* species at 35 and 61 days after the infestation (DAI) to calculate the RF. In Argentina the evaluation of number of eggs + J2 per 50 grams of substrate (*M. javanica*), and number of larvae per 50 grams of substrate/5 grams of root (*P. zae*) was made 90 DAI. In Brazilian studies sorghum ADV Jumbo low RF<1, demonstrating to be a hybrid immune to *M. incognita* and *M. javanica* equal to Crotalaria, the other tested products presented a RF between 1.2 and 2.0 being moderately and not resistant to these nematodes; all sorghum hybrids showed resistance to *P. brachyurus*, with RF<1; as a conclusion all sorghum hybrids studied can be used as option in rotation of crops in areas infested with *M. incognita*, *M. javanica* and *P. brachyurus*, since they were immune, resistant or moderately resistant to nematodes in Brazil. In Argentina all sorghum hybrids tested decreased the inoculated populations of *M. javanica* and *Pratylenchus zae*, but only ADV Jumbo had a significant reduction according to statistics.

Micro-dosing organic and inorganic fertilizer application for improved Sorghum-Bambara groundnut intercrop performance

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Soils in western Kenya are deficient in phosphorous and nitrogen. This contributes to low crop yields, especially in low input smallholder production systems. There is need to deploy eco-friendly and inexpensive innovative technologies to address the prevalent nutrient deficiencies for high crop productivity. Field experiment was conducted in 2022 in western Kenya, to evaluate the response of sorghum-bambara groundnut intercrops to fertilizer application in terms of yield. Six fertilizer treatments were applied as full dose, 50% or 25%NP rate as sole or combined application of inorganic NP and sugarcane pressmud (PM). Full rate consisted of inorganic NP application at 75kg N and 30 Kg P ha⁻¹ while the lowest (25%NP) supplied 18.75 Kg N and 7.5 Kg P ha⁻¹. The treatments comprised of T1: Full rate inorganic NP, T2: 4 ton/ha PM, T3: full-rate NP (inorganic NP+2 ton/ha PM), T4: 50%NP (inorganic NP+1 PM ton/ha), T5: 50%NP (inorganic NP+1.5 ton/ha PM), T6: 25%NP (inorganic NP+0.5 ton/ha PM). A randomized complete block design with three replicates was used. Sorghum variety RUT30b recorded higher grain yield than RUE1 in all treatments and sites. RUT30b yield ranged from 2.0-3.5 ton/ha while RUE1 produced 1.6-2.4 t/ha. Bambara groundnut yield ranged from 121.4 - 214.1 kg/ha when intercropped with RUT30b while with RUE1 it varied from 59.4 – 170.2 kg/ha in different fertilizer combinations. Fertilizer treatments T2 and T3, gave similar sorghum yield as inorganic NP full rate application. Further, performance of both sorghum and Bambara under T4 (50%NP) was comparable to T3, indicating that reduction of fertilizer rate to half-dose could be adopted for sorghum-bambara nutrient management under the test conditions. These findings demonstrate that choice of sorghum variety to intercrop with Bambara and fertilizer micro-dosing integrating use of pressmud and inorganic sources presents a feasible option for resource-limited sorghum farmers.

Improving protein solubility and digestibility in tannin and tannin-free sorghum grain with germination

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Sorghum storage proteins (kafirins) form large protein aggregates, a propensity further exacerbated by complexation with tannins. In consequence, compared to other cereals, their digestibility is lowered and even more after cooking. In this context, seed germination has been proposed as a promising bio-process to improve protein digestibility. Thus, the objective of this contribution is to assess the impact of germination on biochemical (solubility) and nutritional (digestibility) protein properties.

The study was carried out on germinated seeds from two sorghum genotypes, with (T⁺) and without (T) tannins, the former showing a lower *in vitro* digestibility. Seeds were examined at 2 different germinating stages ($G_{50\%}$, $G_{100\%}$) with G_{max} coincide to 100% of seeds achieving radicle emergence (~3mm). The amino acid composition analysis revealed modest modifications upon germination with the exception of cysteine which increased significantly. Consistently, we found a significant increase in free thiols for germinated seeds. Sequential extraction of the kafirin and their subsequent size distribution analysis by size-exclusion chromatography revealed a slight but significant decrease in kafirin cross-linking. The feature happened at the time of the radicle emergence without notable change of the kafirin overall solubility. Microcopy analysis of ungerminated and germinated seeds showed alterations in the protein matrix cohesiveness, in protein bodies and starch granules during germination. These structural modifications were accountable for by newly synthesized proteases and amylases. Finally, we showed that germination improved significantly the *in vitro* digestibility of proteins for both genotypes and that even after cooking. The results indicate that germination would be a valuable mean to improve the nutritional value of this cereal and to counteract in part the detrimental effect of tannins.

An integrated approach for enhancing improved sorghum seed demand and supply in Ethiopia: a promising path

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Sorghum is a food security crop for more than thirty million population largely residing in drought-prone areas in Ethiopia. More than 60 improved sorghum varieties were released in 50 years primarily targeting areas vulnerable to biotic and abiotic stresses. Irrespective of the concerted efforts by research and extension institutions over the past the availability of seeds of improved varieties was scanty. This paper assesses a promising approach to enhance improved sorghum varieties seed demand and supply in Ethiopia. Sorghum shared only 0.19% of certified seeds of major cereals while it occupied 18.39% of the area in 2021. Sorghum is unable to adequately contribute to transforming production due to limited availability of early-generation seed; lack of demand-based seed production; limited capacity for seed producers and low level of commercialization resulting in a low adoption of improved varieties. Targeted community-based seed production by trained farmers, parastatal and private seed companies were the approaches used to enhance the availability of quality seed. Awareness and demand were created about the seed of new varieties using mass media from result demonstration fora. Farmers, government, and non-government organizations were instrumental in seed dissemination. A case in point is a local concept and practice of “*sanyiin korma*” a social obligation of sharing quality seeds with those in need played a significant role in Hararge zones. More than 2.24-ton certified seed was produced over the recent decade which can plant more than a million hectares given the local seed dissemination scenario. Community-based seed production was also vital from large-scale demonstrations resulting in 80% adoption at the targets. Sorghum remains vital due to changing climate, fast-growing population, and demand for feed. Collaboration among stakeholders in seed systems is vital in availing information and early generation seeds, quality seeds production, and distribution for developing resilient and profitable sorghum seed systems.

Sorghum technology dissemination and adoption in moisture stress areas in Ethiopia: challenges and opportunities

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In Ethiopia, sorghum (*Sorghum bicolor*) supports about 30% of the people in the second populous country in Africa in various agroecologies as food and feed. The shift of production from landraces to improved varieties and associated packages of technologies has been low compared to other major cereal crops. This study aimed to investigate the factors that drive or hinder the adoption of improved sorghum production technologies. A survey was conducted involving six hundred sixty representative sorghum grower households. The result showed that sorghum is consumed mainly in the form of injera, porridge, local drinks, and bread. The predominant source of new information for the farmers is government extension services while farmers-to-farmers, media, research, and non-government organizations fill the remaining gap. Regarding the seed source, more than 75% of the farmers use their own saved seeds while local markets, gifts, farmer-to-farmer exchanges, local seed producers, and from demonstration plots make the remaining balance. Our result also showed that the adoption rate of improved sorghum technologies in moisture stress areas was 35% with varying results across locations. The adoption of improved sorghum was high when farmers need the crop mainly for food and early maturity and have alternative feed sources. Inaccessibility to quality seed, lack of technical support, poor palatability of the variety, and shortage of fertilizer were identified as the major production challenges. With the ongoing changing climate and its multi-purpose use the crop, sorghum will remain vital food and feed crop in moisture-stress areas where other crops do not perform well. Boosting the production and productivity of sorghum in risk-prone agroecology tends to depend on the use of sorghum technology packages which calls for concerted efforts of the stakeholders along the value chain.

Research Problems and Achievement of Solutions to Scale from SMIL Project Phase I and II Projects (2014 -2023) for Ethiopian Industrial Food Applications

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1 Commercial underutilization of sorghum resources in Ethiopia

- Gaps in Science & Technology for commercial food application of sorghum

Sorghum value chain and food processing technology to scale for commercial application.

2 Export ban of teff, while it has huge healthy food market gain

- The need to partially substitute with sorghum & liberate teff export

Partial substitution of teff with sorghum ingredients in injera production are made possible.

3 Import of huge barely malt (about 60%) for brewery industry

- the need of partial malt & adjunct substitution to barley & sugar

Partial substitution of barley malt and adjunct with sorghum are possible to scale in brewery

4 The then import of wheat for bakery & low nutrition of its white flour

- Wheat import substitution using whole sorghum flour as partial ingredient of bread, cookies, snacks, etc. with enhanced nutrients

Partial substitution of wheat with gluten free whole sorghum flour for nutritious cookies, snacks, and bread are possible to scale in bakery, cookies and snack factories. Snacks were in school feeding program.

5 Qualified manpower capacity building for commercialization of sorghum

- Limited qualified human capacity

Qualified and vibrant young scientists are working on utilization of sorghum in Ethiopian foods for commercial application.

Human and Institutional Capacity Development (HICD) within the Sorghum and Millet Innovation Lab Global Network

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The Sorghum and Millet Innovation Lab (SMIL) with management entity based at Kansas State University has implemented a 10-year research for development program. At inception, country led prioritization meetings informed a wide call for research proposals. The SMIL programmatic pillars include global network development, Human and Institutional Capacity Development (HICD) and technology development and deployment. A total of 97 (PhD / Masters) level students (32% female) received long-term trainings, 13,500+ persons benefitted from short-term skills courses (45% female) within the overall program.

Ethiopia is a center of origin for sorghum and a collection of over 10,000 sorghum lines curated at the Ethiopian Biodiversity Institute were the basis for a core working collection that was phenotyped and genotyped by the Ethiopian national sorghum program with SMIL support. Multiple students engaging this core collection have been successful in unique gene discovery, translation of genes into farmer appreciated local materials and national seed registration. Gene discovery in the areas of disease resistance, water use efficiency, striga resistance, high protein availability / digestibility traits are some of the key research outputs now being commercialized as improved seed.

A synergistic process amplified the HICD experience through demand driven research projects led by principle investigators who planned activities on “equal footing” with their national counterparts. This provided strategic research, learning and mentoring opportunities for students to integrate their research proposals and findings into much larger research for development goals. These students upon completion of their research quickly transitioned into next generation scientists back in their countries of origin. The active inclusion and participation of actors as “research team members” along the entire value chain from farmer associations, small scale women processors / entrepreneurs, private seed companies, large food companies, public institutions and global research teams also lead to more relevant and effective learning and technology delivery.

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Delivering improved sorghum and pearl millet seeds in Senegal using a community-based approach

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In Senegal, as in many other developing countries, about 80 to 90% of the seeds used by farmers are sourced from informal seed systems, especially for essential subsistence crops like sorghum and pearl millet which are key cereal crops for food security.

Meanwhile, there are accredited seed multipliers within farmers organizations who can supply their fellow members with certified seeds of improved varieties if they have access to early generation seeds.

With the support of the Feed the Future Innovation Lab for collaborative research on sorghum and millet (SMIL), led by Kansas State University management entity, the Regional Center of Excellence for dry cereals and associated crops, led by ISRA/CERAAS, is using an approach that localizes formal seed production and distribution at the community level.

In each community location, the accredited seed multipliers entrusted by their organization are empowered to produce certified seeds locally and to distribute them to their fellow farmers with potential to support other farmer networks in their region.

Scaling and Commercialization of Sorghum and Pearl Millet Nationally Registered Seed (Phase 1 - 4)

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East and West Africa are key centers of genetic origin for sorghum and pearl millet where hundreds of millions of people in agro-ecologically challenging production environments depend on these two cereal crops for food security. The National Agricultural Research Systems (NARS) in West and East Africa collaborated to develop genomics assisted (GA) plant breeding platforms within a global network supported by the Kansas State University led Sorghum and Millet Innovation Lab (SMIL).

A “pipeline” for improved seed delivery was developed. Teams moved materials from Phase 1 research level of gene discovery, which was based on documented product profiles with key adaptation traits. This included gene discovery in areas such as heat/drought resistance, striga resistance, protein digestibility, stay green, anthracnose resistance, etc..

Teams then managed a process to move materials along the pipeline to Phase 2 field testing, on to Phase 3 national seed registration / available for uptake with final goals of Phase 4 actual scaling and commercialization of improved seed. The NARS teams linked to these GA breeding platforms leveraged cutting edge scientific networks and moved improved materials consistently from a Phase I gene discovery, to Phase 2 field level trials in close collaboration with smallholder farmers and end users, on to actual delivery of improved seed represented by Phase 3 and Phase 4.

An array of seed products are now nationally registered and available represented by Phase 3 and 4 level seed products. Active scaling and commercialization of these improved seed products are taking place in collaboration with public, private and community based seed system actors.

Different monocut sorghum used as forage: some guides to advise farmers

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There is a high genetic diversity within fodder sorghum and multiple ways of valorization depending on their type: production of fodder for animal feed or biomass for industrial use, grain production, plant cover, etc. This diversity is a real opportunity for ruminant nutrition but also a brake due to the complexity of choosing its variety according to its use. The objective of this poster is to clarify typologies of mono-cut sorghum for fodder use in relation to their major characteristics (morphology, chemical composition, and feed value).

Sorghums are distinguished first of all by their harvesting's method: they are called «mono-cut» if they are harvested once or «multi-cut» if they are intended to be harvested in several times. Mono-cut fodder sorghums are generally harvested in silage to produce fodder for ruminant feed or biomass for industrial use (methanisation). There are also “grain” mono-cut sorghums which are harvested as grain for food or feed but can also be ensiled for forage production. In France, mono-cut sorghums are classified into three categories (silage, dual-use and mainly industrial use) according to their level of net energy value calculated via an equation specific to fresh mono-cut sorghum (Férard et al., 2014).

Genetic type impacts the energy profile of monocut-cut sorghum. Their main features affect the proportion of grains and fibres, the content of soluble sugars and the fibre digestibility. A database gathering the chemical composition and net energy value characteristics of sorghum varieties was created from 3730 samples from French experimental networks collected between 2008 and 2018. The sorghum classes were determined according to the characteristics of the varieties (sweet or grain, other characteristics: brown mid rib, sensitive photoperiod, male sterile). Qualitative recommendations for the use of sorghums according to the type of animal are also proposed in this poster.

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Development of rapid and inexpensive phenotyping tests for the prediction and characterization of aphid resistance

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Melanaphis sacchari proliferation in *Sorghum Bicolor* has started in 2015 in Haiti and has spread all over the country. One of the scientifically interesting solutions is the development of resistant varieties. Phenotyping prediction and resistance of sugarcane aphid is becoming very urgent. Our research (and that of our partners) has shown resistance to sugarcane aphid to be oligo or polygenic. Two major genes have already been characterized (RMES1 and RMES2). Identifying the mechanism underlying this resistance is essential for breeding ever more resistant varieties (under polygenic scenario). However, phenotyping can be very expensive and time-consuming because of the usual phenotyping via chemical characterization of several hypotheses such as concentration of trans-aconitic acid, jasmonic acid, salicylic acid, dhurrin and HCNp in the leaves and stems. The development of methods to phenotype, quantify molecules, characterize mechanisms involved in Sorghum aphid resistance will be reported in this paper. New high throughput and low-cost phenotyping methods for sorghum aphid resistance characterization/prediction will be tested for this purpose.

Keywords: Sorghum - Aphid resistance - High throughput phenotyping - Phenomics

Contribution of multispectral autofluorescence imaging to histochemistry in understanding sorghum internode hydrolysis pattern ?

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Digestibility of plant feedstock is one of the key properties and is largely dependent on the overall lignification of the plant which is monitored at the tissue scale by the relative amounts and composition of plant organ. To obtain details on anatomy and spatial distribution of main components high-throughput histochemical methods have been developed on maize and sorghum internodes [1,2]. FASGA staining procedure is based on the competition between 2 dyes and reveals regions with differentiated in terms of tissue lignification [3]. In addition to staining procedures, the specific spectral properties of phenolic compounds could also be exploited to map their distributions using spectral imaging technics. Multispectral autofluorescence imaging was successfully applied to maize stem internode to reveal differences in cell wall phenolic compounds distribution (lignin and hydroxycinnamic acids) [4]. The objective of this work was to evaluate the relevance of multispectral autofluorescence imaging to better understand contrasted hydrolysis patterns observed inside the sorghum stem internode.

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Strengthening farmer-managed seed systems for improved seed quality and access to preferred varieties of finger millet in Malawi

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Small holder farmers across Malawi grow crops that are especially valued for unique uses and tastes. However, these crops have been either neglected or underutilized (NUS) by research and extension. Consequently, seed of most of these NUS crops is only available when saved by farmers from their previous harvest. Our project is working with farmer research networks and farmer field schools to strengthen their capacity to produce high quality seed and make it available for local use. The project started the work in five Extension Planning Areas (EPAs) with varied agro-ecological environments in four districts of the country, with focus on finger millet varieties that were prioritised by farmers and released varieties. The team together with farmers identified best of the preferred varieties to increase seed for local production. Challenges that farmers pointed out in the production of finger millet seed included the scarcity of quality seed, lack of markets and low profit margins. High diversity of finger millet exist and farmers have over the year preserved their preferred cultivars that prove to be well adapted to the local environments. Agronomic and seed yield performance vary across and within sites. Some farmer cultivars performed better than released varieties. Farmer variety preferences varied within farmer groups and across sites. Promoting seed multiplication of finger millet varieties in environments where they are best adapted will ensure production of quality seed.

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Phenotypic correlation between protein digestibility and agro-morphological characteristics of sorghum BC3F7 lines in the groundnut basin of Senegal

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Sorghum (*Sorghum bicolor* (L.) Moench) is a widely cultivated cereal crop in Senegal and has great potential as food and feed. However, its proteins are poorly digested after wet cooking. High lysine-high digestible alleles from P721Q have previously been introgressed into the background of Faourou, a Senegalese elite sorghum variety. A total of 18 backcross lines with improved protein digestibility resulting from that study were evaluated in Bambey in 2019. The objectives of this study were to evaluate the 18 lines to establish the relationships between protein digestibility and agro-morphological traits and to identify sorghum lines that combined increased protein digestibility with yield potential comparable to the local variety, Faourou. The field experiment was conducted in Bambey (CNRA), and the *in vitro* pepsin digestion performed in the biochemistry laboratory of CERAAS using a 8x12 row by column design in a 96-well plate. Absorbance values read at 562 nm using an EL x 800 UV spectrophotometer were used to calculate the percent protein digestibility. A positive phenotypic correlation was detected between protein digestibility and yield. Nine among the 18 tested lines combined high protein digestibility (>60%) and high yield (up to 2161,5 kg/ha) with up to 20% increase in protein digestibility compared to Faourou. This study provides genetic material that can be used in breeding to improve the nutritional quality of sorghum grain to contribute to fight malnutrition especially in developing countries.

Keywords: Sorghum - Protein digestibility - Lines, phenotype - Grain yield - Senegal.

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Diversification and advancing whole sorghum-based foods in Ethiopia

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Sorghum is an important food security crop for about 1 billion people in developing countries in the tropical arid and semi-arid regions. Ethiopia is one of the significant producers of sorghum as a food security crop. However, the crop is limited to household level food use and is not popular ingredient for the food industries, which presents limitations in the sustainability of its value chains. A research project was designed to develop varieties of whole grain sorghum-based commercial foods in Ethiopia. The research project had two wings where, on one hand, different local and novel varieties were evaluated for their suitability for snack and breakfast type products and on the other hand, an annealing technique was used to modify sorghum endosperm to check its suitability for injera making. The results from the first wing of the trials showed that some of the local varieties of sorghum are suitable for the production of popped sorghum snack (up to 55-70% yield), grits (kinche) and couscous (up to 82% total yield). The second wing of the research with the annealing treatment resulted in better functionality of sorghum in injera, making samples comparable to that of tef. It is therefore apparent that existing varieties of sorghum in Ethiopia could be recommended for different industrial applications to enhance its value chain in the country for enhanced food security and livelihoods of the farmers.

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Sorghum Grain Storage and Aflatoxins Occurrence in Zambia

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Sorghum ranks second as an important staple cereal in Zambia after maize. Production is concentrated in Northern, Western, North-western and Southern Provinces. National average yield is very low at 0.65 t/ha and compares poorly to Nigeria (1.3 t/ha), Ethiopia (3 t/ha), Brazil (3.1 t/ha), USA (4.8 t/ha) and China (5.2 t/ha). Sorghum utilisation has gone up due to its increasing importance in the food industry. Companies utilising sorghum include; (i) Zambia Breweries in malt-based beverages; (ii) Shais Foods milling white and red grain sorghum; (iii) Sydney Bakery, in bread making and (vi) Yanza Amansa for poultry stockfeed. Sorghum, has previously been regarded less susceptible to aflatoxins than other cereals. However, in recent years, poorly stored sorghum grain has been reported to contain high aflatoxin levels and thus negatively affecting public health, food security and safety, and economic stability. Large volumes of grain sorghum in storage pose a high-risk potential of aflatoxin contamination. Considerable amounts of aflatoxin content makes foods and feeds unsafe, chronic dietary exposure to aflatoxins causes morbidity, and acute dietary exposure can result in mortality. Quantification of aflatoxins contamination in maize and groundnuts has been done in Zambia. However, such information is lacking for sorghum. The following interventions are being undertaken; (i) Screening for reduced susceptibility to aflatoxin contamination; (ii) developing and evaluating sorghum varieties tolerant to aflatoxins; (iii) Procurement of equipment for quantification of aflatoxins in sorghum; (iv) Capacity building for determination and quantification of aflatoxins in sorghum; (v) assessment of aflatoxin knowledge and awareness levels among sorghum farmers and examining aflatoxin management practices and methods applied from production to storage; and (vi) understanding the relationship between storage pests and aflatoxin contamination. These initiatives are expected to provide the basis for creating awareness about aflatoxins and providing strategies to prevent aflatoxin contamination in grain sorghum storage.

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Hundred farmers' stories: the importance of culture as a driver for sorghum cultivation

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The construction of strong market value chains and the implementation of incentive mechanisms such as subsidies, are often seen as the most important drivers of change in agronomic systems. In many cases however, traditional crops have been successfully maintained by farmer communities in the absence of market- and political incitation. A good example is the story of quinoa. This crop was suddenly booming in the 2000s after being neglected for a long time. This kind of example illustrates the importance of other mechanisms related to culture and tradition in the preservation of valuable agro-biodiversity resources. In this study, we have investigated the cultural reasons that motivated tribal farmer communities in Adilabad District, India, to maintain the cultivation of sorghum, despite an overall declining trend in the region. For that purpose we performed an ethnographic study with 89 farmers, composed of interviews and photographic documentation. The farmers' narrative emphasized the strong attachment to a crop that for them represents the best option in terms of nutritious- and energy-rich food. The nutritive- and conservation advantages of the sorghum stover for animal feed is also an important reason for these populations to cultivate this crop. However, the strongest motivation for the farmers to maintain sorghum cultivation seems to take its roots in rituals and cultural practices. Seen by many farmers as a crop of divine nature, sorghum plays a central role in almost every ceremony and celebration, forming a rich palette of cultural activities that gives its rhythm to the lives of the Adilabad tribes. Even though the constraints of modern life form a concrete reality, such as problems with access to water, quality seeds or space to cultivate a subsistence crop with a relatively poor market value; it does not prevent the tribes from being confident in the future of sorghum.

Study of effectiveness of *Eucalyptus camaldulensis* Dehnh powder on *Sitophilus zeamais* (Motschulsky) and *Tribolium castaneum* (Herbst) pests of stored sorghum in SenegalFatou Welle¹ (welle.fatou@yahoo.fr), Karamoko Diarra², Ibrahima Sarr³, Momar Talla Gueye⁴¹ ITA/ISRA, Diourbel, Senegal ; ² UCAD, Dakar, Senegal ; ³ ISRA/CNRA Bambey, Diourbel, Senegal ; ⁴ ITA, Dakar, Senegal

Sorghum is one of the most important cereals for people subsistence in sub-Saharan Africa. Despite its importance, the storage remains a problem due to insects such as *Sitophilus zeamais* and *Tribolium castaneum*. Synthetic pesticides are one of the most effective means of controlling these pests, but require alternatives due to negative environmental and humanitarian impacts. The dried *E.camaldulensis* powder was tested in the laboratory against *S. zeamais* and *T. castaneum* for the storage of sorghum. This powder, a 0.3 mm particle size, was applied against these two insects at increasing doses of 1, 2, 3 and 4 g/100g. All doses and controls

were repeated 3 times. For each insect, 12 adults were used with a ratio of 5 males for 7 females. Untreated batches and others with actellic respectively served as control and experimental groups. Monitoring of insect mortality was carried out over a period of 14 days after application of the product. Emergence, damage, and losses were monitored after one to three months. The results revealed efficacy of the doses particularly 3 g and 4 g. Greater than 50% mortality were noted with 4 g of *S. zeamais*, and greater than 20% with 3 g of *T. castaneum*, against 100% for the actellic and 0% for the untreated control. Emergences evolved inversely to mortality. At 4 g, great efficacy was observed in controlling *S. zeamais*, which was significantly more sensitive.

A 20% damage was recorded in the untreated control after infestation by *S. zeamais*, but only 3% damage and losses once the dose reached 3 g. For *T. castaneum*, the damage was 13% with 8% losses in the untreated control and 2% losses with the 4 g dose. The *E. camaldulensis* powder showed effectiveness against *S. zeamais* and *T. castaneum* for the storage of sorghum.

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Development of sorghum and teff sourdoughs for gluten-free bread

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Production of gluten-free bread with good quality and of sourdoughs from gluten-free cereals requires specific technological approaches. Various food additives are mostly used to compensate the lack of gluten and to improve the viscoelastic properties of the dough and increase the development of loaf volume. Sourdough use is the oldest approach to leaven bakery goods, which results in products with richer flavour and improved rheological and storage characteristics over products obtained by using baker's yeast. These effects vary depending on the flour matrix and the sourdough strains, therefore it is essential to select appropriate matrix-strain combinations in order to obtain gluten-free breads with good quality characteristics.

Our study aimed to obtain non-gluten sourdoughs from sorghum and teff flours with applying single cultures of *Pediococcus acidilactici* 02P108, *Pediococcus pentosaceus* 12R2187 and *Enterococcus durans* 09B374. The flours had protein content of 12.49% (sorghum), and 10.20% (teff), and fiber content of 12.39% and 9.56%, respectively, which indicate teff and sorghum as excellent sources of protein and dietary fiber. Analyses also showed high antioxidant activities of the flours. Active acidity, total titratable acidity, total cell counts and rheological properties of the obtained sourdoughs were analyzed after 24-h fermentation at 37°C. The viscometric studies of the sourdoughs were modeled according to the following power law: $\eta = K\dot{\gamma}^n$, where K - consistency index, n - power law index. The data from the performed analyses show a significant influence of the raw materials and the starter cultures on the parameters of the model. The addition of starter cultures increased the power law index. It was less than 1 for all tested samples, which identified the fluids as pseudoplastic. The data obtained in the study are useful to describe the differences in the behavior of different sourdoughs and the selection of the most appropriate flour matrices and sourdough starter cultures.

Role of malting and fermentation in enhancing bioaccessibility of phenolic compounds and phytochemical-related health-promoting properties of sorghum

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Background: Sorghum [*Sorghum bicolor* (L.) Moench] is well-known as a significant source of bioactive phenolic compounds with health-promoting properties to offer protection against non-communicable diseases. The major phenolic compounds in sorghum are phenolic acids and flavonoids. Both are mostly found in the form of soluble conjugates covalently linked to sugar moieties (glycosides), or insoluble bound forms. The latter are esterified to cell wall components like cellulose and hemicellulose (arabinoxylans) or cross-linked to cell wall polysaccharides within the endosperm. Sorghum phenolics can exert their health-promoting properties if they are rendered bioaccessible by their release from the food matrix for subsequent absorption. Traditional food processes such as malting, and fermentation have the potential to release phenolic compounds in sorghum and make them more bioaccessible.

Objective: The objective of our study is to determine the effect of malting and fermentation on the extractability, bioaccessibility, and radical scavenging properties of phenolic compounds from sorghum porridge, with the aim of achieving improved health-promoting properties.

Method: Malted and fermented sorghum flours from whole grains sorghum type I (non-tannin red and white sorghum) were prepared. Simulated in vitro gastrointestinal digestion and liquid chromatography-mass spectrometry will be used to determine the extractability and bioaccessibility of phenolic compounds followed by their uptake in a Caco-2 cell model. Radical scavenging and cellular antioxidant activity will be used to determine health-promoting properties.

Expected outcome: Malting and lactic acid fermentation will enhance the bioaccessibility and hence, the health-promoting properties of sorghum phenolics.

Keywords: Malting - Fermentation - Bioaccessibility - Health-promoting properties - Phenolic compounds - Non-tannin sorghum.

Characterization and Functionality of Fermented Sorghum and Enset Flours

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Sorghum is the fifth most produced cereal crop in the world. It has the highest phenolic content among cereals. However, the poor starch digestibility limited its utilization. Merera is a newly released Sorghum variety in Ethiopia. It has shown a unique and interesting aroma attribute in preliminary testing of a co-fermentation with Enset (*Ensete ventricosum*), which is a staple food crop for over 20 million Ethiopians. Thus, the aim of this study was to characterize the composition and functionality of Sorghum-kocho flour as gluten-free food products. To this end, Merera flour was co-fermented with fresh enset pulp (kocho) with a predetermined ratio of 40% Merera and 60% kocho. The mixed mass was allowed to ferment in a Sauerkraut jar for fifteen days. Physicochemical, microbial and nutritional profiles of the fermented mixture were investigated on days 0, 5, 10 and 15. Also, the pasting profile of the flours were determined using Mixolab. Sorghum-kocho flour showed a significant ($p < 0.05$) pH reduction from day 0 (6.09) to day 15 (3.48), indicated a fast fermentation process. The total aerobic count attained a maximum of 8.94 log cfu/g at day 0 and the lowest at day 15, which is 7.66 log cfu/g. Sorghum-kocho co-fermentation increased lactic acid bacteria counts indicating a desirable microbial dynamic. Furthermore, the protein content of the fermented Sorghum-kocho flour (4.58%) was higher as compared with kocho flour alone (2.08%), while increased Ca, K and Mg contents were observed for the Sorghum-kocho flour as compared with the Sorghum flour alone. However, kocho flour has a much higher starch gelatinization and retrogradation peak than Sorghum flour, indicating a better functionality. In conclusion, Merera sorghum-kocho flour has a great market potential as shown by its improved functionality and nutritional profile.

The Role of Sorghum and Millets in Reshaping Global Food and Agriculture Paradigms

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Recently published peer-reviewed research from academic institutions around the world concur in regard to previously unrecognized health and nutritional benefits of sorghum and millets in human and animal diets. Further scientific papers have also been published which detail environmentally sustainable attributes of sorghum and millets as they pertain to water, wildlife, and soil health, as well as being an optimal tool for carbon sequestration. This research, coupled with increasing consumer demand and awareness through the 2023 International Year of Millets, has created the conditions by which existing food and agricultural paradigms might be challenged to better address food security, climate change, and access to value-added markets for small-holder and conventional farmers around the world.

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New exploration of kafirin biochemical and physical chemical properties by the mean of size-exclusion chromatography

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Kafirins are the main storage proteins of sorghum grain. Compared to other cereals, kafirins are highly hydrophobic and are less digestible by gastrointestinal proteases. Our working hypothesis is that the low digestibility is related to kafirin biochemical and physicochemical properties. Our study aimed to examine the impact of decortication, solvent type, extraction time, sample to liquid ratio and temperature on kafirin extraction yield, according to an experimental design approach. The study was based on the chromatographic assessment of the kafirin extracts composition by size exclusion chromatography (SE-HPLC). To obtain quantitative estimates of the extraction yields we determined the kafirin extinction coefficient at 210 nm, in reference to the Kjeldahl method. Kafirin composition was also evaluated by polyacrylamide gel electrophoresis in the presence of SDS. We showed that preliminary grain husking, use of tert-butanol-water 60% (v/v) solvent, temperature of 60°C, sample to solvent ratio of 1:10 and 3 extractions provided maximum extraction yield. In conclusion, the effect of the parameters on the extraction of kafirins were disclosed allowing the set-up of a robust protocol.

Keywords: Sorghum - Kafirin - Experimental design - Digestibility - Extraction - SE HPLC

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Evaluation of the effect of processing processes on nutrient levels of fortified sorghum varieties and derived products in Mali

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Sorghum is one of the most widely consumed cereals crops in Mali, but poor in nutritional value. The fortification of sorghum is done in order to improve its nutritional qualities. The aim of this study is to evaluate the nutritional, physicochemical and sensory characteristics of two fortified sorghum varieties (Saba nafantè and Dougouyiriwa) and their parent (Séguifa) as well as their derived processed products (Tô and Couscous). The protein contents were determined by the Kjeldahl method. The lysine and threonine contents were determined by the ACC-Fluor Reagent Kit method. The iron and zinc contents were determined by the atomic absorption spectrophotometry assay method. Ash was determined by AOAC (1993). Humidity was determined by the ISO 712:2009 method. The moisture content of fortified sorghum varieties ranged from 8.20% to 8.76%. The fortified varieties of sorghum studied varied in protein (9.68% to 12.05%), Threonine (0.32% to 1.71%), Lysine (0.93% to 2.64%), Iron (5.37mg/100g to 8.05mg/100g) and Zinc (1.46mg/100g to 1.67mg/100g). The results show that fortified sorghum varieties are richer in nutritional value. The nutrient content of the whole grains is higher than in decorticated grains and processed foods (tô). This shows that processing processes negatively influence the nutrient content of fortified sorghum varieties. In addition, the results show that fortified sorghum varieties are richer in nutrients than its parent. Complementary flours based on these varieties have been formulated and characterized to help in the fight against malnutrition. The tô and couscous of fortified sorghum varieties were the most appreciated (Very good by more than 73% of tasters).

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Improving Nutritional Value of Sorghum Budena Complementing with OFSP in Hararghe, Eastern Ethiopia

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In Hararghe zones of eastern Ethiopia, daily diets are heavily based on sorghum products where the most common dish are budena for both adults and children almost every day. However, sorghum budena is very poor and contains low level of vitamins and health promoting compounds. Vitamin A deficiency is widespread among young children in the area and the problem is severe in children. Therefore, this study was carried out to improve the nutritional profile of commonly consumed sorghum budena complementing with orange-fleshed sweetpotato (OFSP). Two sorghum varieties (Melkam and local variety) with OFSP puree ratio of 90:10, 80:20 and 70:30 respectively were formulated for budena making. Budena making quality and physico-chemical analysis were performed using standards methods. The protein, fat, ash, fiber, moisture and carbohydrate contents of the treatments ranged from 9.5 to 12.14, 1.96 to 3.56, 1.6 to 2.6, 2.11 to 3.49, 60.70 to 68.15, 79.61 to 82.7%, respectively. Although significant differences were found among the products for fat, protein and fiber contents, the parameters tended to decrease with the increase in OFSP proportion whereas the carbohydrate content rose as the proportion of OFSP puree was increased. On the contrary, a significant ($p \leq 0.05$) increase in beta-carotene content (from 0.3 to 43.14 $\mu\text{g}/\text{gm}$) was found in the budena as the OFSP puree proportion increased from 0% to 30%. Sensory acceptability of budena made from composite consisting of 80:20 sorghum and OFSP puree was more preferred by panelists than other proportions for both sorghum varieties. Therefore, consuming such product could increase access to and intake of vitamin A rich food among the most vulnerable groups, pre-school children, to alleviate malnutrition and related health problems prevalent in the area.

Keywords: Budena - Nutritional composition - OFSP puree - Quality and sensory value - Vitamin A.

Grain Sorghum as a Sustainable Ingredient in Aquatic Feed - Grinding and Processing Energy Studies

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In aquatic feed manufacturing, requirements for sustainable ingredients and processing methods are emerging. This research focused on grain sorghum as a sustainable carbohydrate ingredient in aquafeed and studied process sustainability through grinding efficiency and energy inputs. Grain sorghum was ground through 3 hammermill screens (1.27, 1.02 and 0.61 mm). Ground sorghum was incorporated into nutritionally balanced diets formulated for shrimp and tilapia and processed through a pilot-scale single-screw extrusion system to produce sinking and floating feed, respectively. As particle size of diets decreased, tilapia feed expansion increased and bulk density decreased (433 to 354 b/L), while energy requirement of the process increased (273 to 335 kJ/kg) leading to impacts on pellet aspects such as pellet size. Water absorption capability increased as particle size decreased (202% to 377.8%) and was impacted by grain source, with sorghum-based diets having lower water absorption than wheat-based diets at the same particle size. Grain source also impacted various pellet quality aspects, with sorghum-based diets having a higher PDI on average. Increase of thermal energy input into shrimp feed in the preconditioner led to decrease in expansion ratio of pellet, very little change in bulk density and no noticeable improvement in quality in wheat-based diets. However, as steam input decreased, water stability of sorghum-based feeds also decreased (77% to 59%). Higher grinding intensity for grain sorghum impacted floating tilapia feed properties at the expense of higher energy requirements and greater steam loss. Thermal energy input during extrusion had a noticeable impact on sinking shrimp feed quality, particularly in sorghum-based diets and water stability. In optimization of aquatic feed processing, quality improvements should be weighed against process criteria such as energy inputs. This data will be useful for feed processors to meet sustainability goals within their organization and future regulations in the aquafeed industry.

Brown midrib 6 and 12 genes may provide new forage opportunities in West Africa

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In Niger, cereals stover are a significant source of feed for livestock during the long and dry season which coincides with shortage of feed for small scale farmers particularly in the context of limited availability of natural pasture. In addition, stover market is currently a growing business in Niger. Improving the dry matter yield and the nutritional values of local sorghum elites lines may contribute to mitigate the stover shortage in the country. Through conventional breeding method, *bmr6* and *bmr12* genes were introgressed in two Nigerien elites sorghum varieties to improve their stover value. The derived progenies and parental lines were phenotyped for agronomic performances specially for the grain, fresh stover and dry matter yields and their nutritional contents: dry matter, P, Ca, CP, NDF, ADF, ADL were estimated. The results showed very highly significant statistical differences between the entries for grain yield, stover fresh and dry matter yields and nutrients content. Promising lines were identified. We conclude that the introgression of *brown midrib* genes enhanced the nutritional values of sorghum lines and constitute a sustainable way to improve sorghum lines for dual purpose uses for local farmers.

Keywords: Sorghum - Dual purpose - Feed - Brown midrib - Nutritional potential.

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Formulation and acceptability of an instant powder mix using sorghum and pigeon pea as alternative to traditional 'ji kole' beverage in Haiti

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'Ji kole' is a cold, thick beverage made from boiled vegetables such as breadfruit, potatoes, yuca, carrot mixed with milk, sugar and spices (cinnamon, vanilla). It is mostly consumed in the evening as a meal replacement. Due to its composition, the beverage has a short shelf-life. Extrusion has been used in order to produce instant foods that are cooked, shaped and partially dried during the extrusion process. This study focused on the extrusion of sorghum and the addition of extruded pigeon pea as a local alternative to imported milk in the formulation of the instant beverage powder mix. Extrusion is hypothesized to improve the functional properties of the starch in sorghum and the protein in pigeon pea. We determined several parameters that affect the extrusion process such as extruder screw speed, ratio of sorghum to pigeon pea, granulometry and moisture content of the ingredients. The effects of these parameters on the powder mix are currently being studied in order to determine optimal parameters. Additionally, physical and chemical characteristics of the ready-to-use drink powder and the subsequent beverage will be analyzed. Such characteristics include viscosity, moisture content and nutritional value. Lastly, organoleptic characteristics of the instant beverage will be determined and consumers acceptability evaluated. The results of the study will help identify optimal parameters for extrusion and instant beverage formulation as well creating new markets for sorghum and pigeon pea.

Physicochemical and functional properties of starches from Dutch sorghum varieties

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Sorghum is a nutrient-dense, resilient, and multifunctional crop suitable for circular economy and advancing food security goals. Whereas breeding strategies demonstrate the potential in enhancing functionalities for Nordic regions, starch qualities of new accessions have not yet been characterized. This study seeks to assess the nutritional, physicochemical and functional properties of starch from five new Dutch Dusormil sorghum accessions (HD7, HD19, HD100, HD101, and HD102), cultivated at 51° Northern Latitude 3° Eastern Latitude, in cool growing conditions, to validate their food prospects. Wet milling of sorghum was carried out to obtain starch for further analyses. Standardized analytical methods were employed, and results were statistically analyzed. Preliminary scanning electron microscopy analysis showed particle sizes between 1µm and 20µm with diverse granule morphology. HD7 starch was lightest, recording L* a* b* values of 90.35±0.04, 2.85±0.03, and 3.06±0.03 while the bright HD102 had values of 82.63±0.01, 4.23±0.01, and 5.09±0.02, determined using AN-1005b colorimeter. The water absorption capacity of the samples ranged from 94±15-126±16.5% with HD7 and HD100 recording the lowest and highest values, respectively. All samples depicted type-A starch with X-ray diffraction pattern peaks at angle 2θ values of 15° and 23° and double peaks at 17° and 18° similar to wheat starch. The thermal properties obtained using a differential scanning calorimeter depicted peak temperatures from 65.98±0.42-69.50±0.12 °C, with HD7 and HD100 having the lowest and highest values. HD19 had the lowest onset temperature (60.43±0.87°C) and HD100 had highest temperatures for; onset (64.73±0.11) peak (69.50±0.12°C), conclusion (80.14±1.13°C), and enthalpy of gelatinization (12.23±1.05 J/g). From the RVA analysis, HD7 had the highest peak viscosity (3842.33±49.34 cP), HD19 had the lowest peak time (4.47±0.07 min), and HD100 had the least breakdown and setback viscosities. Our findings validate the prospects as substitutes for gluten-containing starches for industrial application and consumption of these new Dutch sorghum accessions.

Sorghum in Spain (2012-22)

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Sorghum in Spain is still a testimonial crop. Although it had better moments, in recent years there have been no more than 5,000 hectares of grain sorghum, which are those recorded by the Ministry of Agriculture (MAPA), almost all irrigated. In Spain there is a much longer tradition of growing corn (350,000 hectares in 2021), mainly in the regions of Castilla y León, Aragón and Catalonia (all in the northern half) and, despite the benefits of sorghum, if there is water to irrigation, the Spanish farmer prefers to grow corn. We will see with climate change.

Production and Uses: The sorghum harvest in Spain is very limited, with a maximum production of 8,961 tons in 2016 and 14,400 tons in 2022 according to MAPA data). The average production of sorghum in Spain in the last 5 years has been 21,000 tons. If Sorghum ID reports that Spain imports an average of 325,000 Tm/year, it means that it does not cover more than 6.5% of its needs. It is mainly used for feed for pigs, cattle and poultry.

Spain annually imports more than 93% of its sorghum needs. The Catalan cooperative Bonarea (with more than 120,000 tons/year) is the entity that imports the most sorghum, mainly from the south of France. Feed factories in the interior of Spain state that sorghum could enter the rations of pigs and cattle, but they do not buy more due to the lack of nearby cultivation and the high cost of transport from the port.

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Refining sorghum-teff injera formulations and technology for commercial food applications in Ethiopia

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Drought will be one of the major impacts of climate change and alternative cereals like sorghums that are well adapted to harsh climatic conditions will be appropriate. Preparing injera from sorghum also has considerable economic benefits over teff, as sorghum commands a much lower price and preparation of teff is very much time consuming and expensive. Sorghum injera is inferior in quality as a result of staling and poor keeping quality. Formulations (sorghum-teff flour mix) that do not affect consumer choices of injera are required to take advantage of the economic benefit. In this study sorghum-teff injera formulations and technology were refined with trained panelists for commercial food applications. Three types of sorghum that showed better injera making quality were used in higher proportions (50 & 35% sorghum) and lower limits (30% regular sorghum and 50% waxy sorghum). The sorghum-teff injera formulated at 30:70 produced same injera quality as of 100% teff injera. Waxy sorghum added more than regular sorghum (50%) resulted injera of better quality. Whenever more sorghum mix is required waxy sorghum could be an option. The formulations are promising for commercially viable productions, industrial applications and marketing of injera products (including the mix flours and injeras).

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Sorghum adjunct brewing with barley malt and potentials for alternative commercial beer making

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Beer is made of barley malt, water, yeast & hops. The malt is fermented to yield CO₂ and alcohol with a characteristic flavor, aroma & color. Barley malt is preferred grain for beer making due to its higher capacity of extract development, enzymatic activity and yeast growth during fermentation. Other grains (rice, maize and sorghum) has been introduced to brewing in African countries. Ethiopia has been significantly deficient in meeting the ever-increasing malt barley demand of the breweries from domestic production. Sorghum adjunct used in brewing should not negatively affect important beer quality and should not be highly compromised sensory characteristics. Evaluation of the effect of partly adding sorghum adjuncts (malted and unmalted) on quality of beer in terms of physicochemical and sensory properties was studied. Sorghum adjunct to barley malt formulations (15, 25, 35 and 45% sorghum as malted and unmalted) were considered. The results showed that these formulations resulted similar hot water extract to Barley malt reference. Trained sensory panel identified 22 quality descriptors to screen beers of different formulations. Characteristics of color, bitterness, haziness, alcoholic, fermented taste and foam were attributes that change when adding more sorghum into barley malt beer formulations.

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Malted sorghum and adjunct brewing potentials of local and improved sorghum genotypes

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Alternative cereals to barley for malting and brewing are essential because of climate change, non-viable cultivation of barley in tropical and sub-tropical regions. Sorghum malt is used in many African beers and porridges, in modern lagers, stouts, and beverages. The use of sorghum malts in modern beers and non-alcoholic beverages is limited due to incomplete degradation of its starch into fermentable sugars, low β -amylase activity and limited proteolysis. Sorghum lines that express waxy-HD traits have been developed by Texas A&M University and showed potentials for brewing. However, optimization and pre-scale-up of these lines has not been studied. Thus, the aim of this study was to optimize malted adjunct sorghums for brewing potentials of the local and improved sorghum genotypes. Debir, Macia, ESH4 and ESH-1 had excellent brewing quality in terms unmalted adjunct attributed to their higher hot water extract (HWE). Melkam (45.53%) and ESH-1 (47.37%) produced higher HWE when malted and had better malted adjunct quality. The results showed that the malting and adjunct quality characteristics checked seemed to exhibit comparable results. The sorghums (malted or unmalted) have a potential to be used for brewing process – partly replacing barley malt in case of limited production in waxy sorghum lines.

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Effect of cowpea seed flour pigmentation on the nutritional and sensory properties of a gluten-free sorghum bread

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The purpose of this study was to evaluate the nutritional and sensory properties of gluten-free bread containing *Vigna unguiculata* (L) Walp (white and red cowpea) seed flours pigmentation in the *Sorghum bicolor* bread formulation. Gluten-free bread recipes were formulated by mixing sorghum flour, xanthan gum, sugar, salt, and yeast. The control was 100% sorghum bread flour. The ratio white and red cowpea to sorghum bread flour were 90:10; 80:20 and 70:30. The physicochemical properties and nutritional profile of the novel flour were determined. The compositions of innovative gluten-free bread were determined such as crude fibre, protein, and carbohydrates. Physical properties such as bread-specific volume, crumb, crust, hardness, chewiness, and colour attributes as well as amino acids were conducted. A sensory quantitative descriptive analysis of the breads was conducted using nine (9) trained panellists as well as consumer acceptance testing for 112 panellists. Principal component analysis showed trained panel intensely perceived the sorghum 90% and white cowpea 10% and sorghum 100% which is the control to be dense, hard crumb and have grainy mouthfeel as compared to other composite breads with red cowpea flour. Trained sensory panel described the gluten-free composite breads as having a yeasty and nutty aroma. Consumers accepted sorghum 90% and white cowpea 10% more with a 9-point hedonic rating scale of 6.56 compared to other composite bread. High rating of 7.93 was for whole wheat bread. Gluten-free bread showed significantly higher ($p < 0.05$) content of crude fibre and protein than the control bread. Addition of flour from white and red pigmented cowpea showed improved crumb hardness and a higher crumb chewiness. Gluten-free bread had higher protein and crude fibre levels. Finally, a gluten-free sorghum bread incorporated with each white and red cowpea improved the nutritional and physicochemical properties and a clear sensorial profile was described.

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Novel instant millet *fura* (popular thin porridge) process for West African consumers

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Fura is a popular thin porridge millet beverage commonly consumed in West Africa. The traditional process of making millet *fura* porridge is laborious and time-consuming and produces a limited quantity of product. In this study, processing conditions using a low-cost single screw mini extruder were developed and optimized to produce an instant millet *fura* porridge flour. The product has the advantage of short processing time with daily throughput of 10-fold higher yield than that made by the traditional manual *fura* process. The instant millet *fura* porridge flour is reconstituted by just adding hot or cool tap water. Physicochemical characteristics between the instant and traditional millet *fura* porridges, and consumers acceptability and sales potential in Niamey, Niger were assessed. Rheological results indicated instant millet *fura* porridge has higher viscosity and gel strength and better elasticity and shear thinning property compared to the traditionally-prepared *fura*. Instant millet *fura* had better textural attributes (creamy, elastic, gelling) than the traditional porridge. Color was also slightly, but significantly, better for the instant millet *fura* product. Overall, consumers' acceptability of instant millet *fura* porridge was good and comparable to the traditional *fura*. A market test in Niamey over 20 weeks showed repeat purchases with good frequency of sale for the new instant millet *fura* porridge. Moreover, the instant millet *fura* porridge flour sold well in the Niamey market compared to 35 traditional cereal foods. Supported by the Sorghum and Millet Innovation Lab (SMIL).

Analysis of the malting qualities of pre-released and released varieties of sorghum in Zambia for industrial food production

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Sorghum (*Sorghum bicolor* (L.) Moench) is traditionally a cereal of choice for malting in Zambia. Malt is used for alcoholic and non-alcoholic beverages, food products such as instant porridge and as a galactagogue. Malting involves steeping, germinating and drying sorghum grain to convert it to maltodextrines, maltotriose and maltose (Malt). The demand for sorghum malt has drastically increased as it is cheaper compared to industrial enzymes. However, limited information is available on the best varieties for malting in Zambia. Literature suggests that varieties with good malting qualities germinate rapidly after steeping but retard embryo development. As roots are often removed during malting, a variety that minimizes embryo growth during malting is considered to have good malting properties. Additionally, it should have higher levels of α -Amylase and β -Amylase enzymes, diastatic power of over 36 units and must have free amino nitrogen (FAN).

Screening will be done for 30 carefully selected sorghum germplasm for good malting properties using a Randomized Complete Block Design (RCBD) in three locations; Chibombo, Lusitu and Zimba districts. Laboratory tests will investigate the thousand-grain weight, moisture content, germinative capacity, germinative energy, and tannins, as well as malting quality parameters such as diastatic power and amylase activity using standard methods.

The materials that will show high malting quality will be recommended for utilisation in the malting industry and be used as a basis for developing varieties with good malting properties.

Keywords: Sorghum - Malting - Diastatic Power - β -Amylase - α -Amylase

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Effect of hydrocolloids (gum Arabic and maltodextrin) on the production of fast-cooking millet and sorghum-based “arraw”

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Rolled flour or «arraw» from millet or sorghum is a Senegalese traditional porridge-like product that takes about 35 min to cook, which lessens its appeal as a convenient food. The objective of this study was to examine the use of extruded flours to make a fast-cooking arraw, and the effects of hydrocolloids to improve its quality. Extruded millet flour-based arraw had total granule yields of 65% with gum Arabic and 67% with maltodextrin, respectively, compared to 76% for the traditional arraw. The cooking time for the extruded millet flour arraw was 9 to 10 min with gum Arabic and 11 min with maltodextrin (using a 4 mm sieve) compared to 33 min for the traditional arraw. Water absorption index varied from 3.6 to 4.6 g/g with gum Arabic and 3.6 g/g using maltodextrin. Water solubility index of related granules were from 13.2 to 15.2% with maltodextrin addition, while for gum Arabic values ranged from 13.2 to 15.2% with non-significant difference ($P < 0.05$). The final viscosities of porridges made from fast-cooking Arraw were lower (164 to 193 RVU) than traditional (1738 RVU). Similar trends were obtained for extruded sorghum-based fast-cooking arraw though with somewhat higher yield (77%) with maltodextrin and lower yield with gum Arabic (60%) compared to the traditional arraw (85%). This fast-cooking arraw has potential as a new convenient food form of the traditional arraw.

Effect of local edible oils on the sensory acceptability of sorghum cookies

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In strategies for formulating new food products and improving their qualities, it is important to use local raw materials whose tastes are already well appreciated and accepted by local populations. In this study, red palm oil, refined palm oil and refined cottonseed oil were used at three levels of incorporation (16 %, 20 % and 24 %) for the production of sorghum cookies. In comparison with control cookies, produced with 20 % of margarine. The sensory acceptability and ranking tests were carried out by 48 tasters using standard analysis methods. Cookies presented an average acceptability (about 60 %) for all the descriptors studied. Cookies produced with 16 % of red palm oil, 20 % of refined cottonseed oil and palm oil were the most liked with overall acceptability of 60 %, 80 % and 80 % respectively. Those produced with 20 % of refined cottonseed oil were more preferred than the control cookies and were therefore ranked first. Cookies produced with red palm oil were ranked fourth, therefore less appreciated. The results of this study showed that refined palm and cottonseed oil could be used in the production of sorghum cookies with similar acceptability to cookies produced with margarine.

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Effect of fermentation, roasting and malting on the nutritional and sensory quality of sorghum cookies

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Cereals contain anti-nutritional factors that prevent the absorption of nutrients by the human body. Several technological treatments make it possible to reduce or eliminate these anti-nutritional factors in food. This work focused on the study of the effect of fermentation, roasting and malting on the quality of sorghum cookies. Sorghum grains have been fermented, roasted or malted and made into flour for the production of cookies. The physico-chemical and nutritional parameters (humidity, fatty acidity, pH, ash content, proteins, lipids, phenols, total phenols) and the sensory quality of the cookies (acceptability and ranking test) were determined using standard methods. Organic digestibility and lignin levels of cookies were determined by near infrared spectrometry. Cookies produced with malted sorghum grain flours showed the lowest lignin levels (3.63 %) and the highest organic digestibility (68.20 %). Roasted sorghum grain cookies showed the highest protein levels (6.35 %). Cookies produced with fermented sorghum grains (84.6 %) were the most appreciated compared to cookies produced with roasted (72.6 %) and malted (69.4 %) sorghum grains. Fermentation significantly improved the nutritional quality of sorghum cookies and keep good sensory quality.

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Sweet sorghum-based biscuits manufactured in a one health approach

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Sorghum is a gluten free cereal that meets societal expectations corresponding to a sustainable food system. Development of a sector for human nutrition is however required. To do so, one way of valorization of sorghum can be biscuits manufactured with naturality and healthy objectives. We characterized whole grain flours from sorghum (WSF), chickpea (WCP) and wheat (WWF, control) and the biscuits prepared from these flours alone or mixed (100 % WSF, 75 % WSF +25 % WCP, 50 % WSF +50 % WCP and 100 % WWF). Biochemical (Aw, water content, protein content, fat acidity), functional (water and oil absorption capacity) and physical (color, density, spreading ratio, granulometry) analyses were performed in order to determine the impact of the flour characteristics and its functional properties on various qualities of the biscuits. In our storage conditions of sorghum flour, fat acidity increased, which can promote the development of rancid taste. Sorghum flour had a higher water absorption capacity than chickpea flour. Size of the flour particles, protein and fibers contents can influence this characteristic. Sweet sorghum - based biscuits were prepared using only four ingredients (flour, sugar, oil and water). The dough containing only sorghum flour was crumbly and fatty. Chickpea addition influenced some properties of doughs and biscuits : it resulted for example in a more malleable and cohesive dough and the biscuits obtained were less hard with a lighter color. However, the biscuits were generally drier and harder than those made with wheat. Biscuits made with the three different formulations using sorghum and / or chickpea refined flours were evaluated by consumers during a meeting (SIA 2023). Public acceptance and assessments show the interest to develop sorghum-based biscuits with nutritional interest (gluten-free products, source of proteins, dietary fibers, bioactive compounds, vitamins and minerals).

Bio-oil production from sorghum (*Sorghum bicolor* L. Moench) via pyrolytic process (zeolite, ZSM-5)

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Sorghum bicolor (L.) (Moench) stands out for dry matter yield per hectare and has been considered a potential raw material for biofuels and electricity generation. It has a production cycle of six months, the possibility of mechanization of cultivation and harvest, and good adaptation to most regions of Brazil. This study proposes a screen of variables that have an influence on the modification of the bio-oil chemical composition as a unique critical quality attribute (CQA) throughout the pyrolytic process (zeolite, ZSM-5) by using a 2⁴ full factorial design, followed by optimization through a response surface methodology (RSM) based on central composite design (CCD) involving samples of biomass sorghum BRS716 (*Sorghum bicolor* L. Moench). The pyrolysis of pure biomasses and the biomass impregnated with the catalyst (ZSM-5) was carried out in a vertical bench furnace at 500 °C. Screening design involved factor variation in two levels (-1 and +1) of four variables as critical process parameters (CPPs) such as furnace heating rate (°C min⁻¹), nitrogen flow (mL min⁻¹), amount of biomass (g), and catalyst (% m/m), leading to obtaining bio-oil. The bio-oil chemical composition was obtained by Gas chromatography coupled with mass spectrometry (GC/MS) and mid-infrared (MIR) spectroscopy. The pyrolysis of the raw sorghum resulted in a product consisting of three fractions, that resulted in one liquid (condensed phase) 35.0% m/m, one gas (non-condensable phase) 35.0% m/m, and one solid (residual) 30.0% m/m. The use of zeolite as a catalyst in the pyrolysis process shows a tendency to reduce the content of oxygenated compounds in the bio-oil. However, these are still predominant. The hydrocarbons are mostly naphthalenes belonging to the polyaromatic hydrocarbons (PAHs) class. The production of a bio-oil rich in hydrocarbon compounds is possible, but a large amount of catalyst was required.

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Denaturation of aflatoxin in processed millet products

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Introduction: In Africa, poor post-harvest management of cereals is problematic due to aflatoxin contamination associated with public health problems such as liver cancer. The aim of this present study is to significantly reduce the concentration of aflatoxin in millet at the level of processing units in Dakar and Touba, Senegal.

Methods: Raw material (millet) and processed product samples were taken at processing units in Touba and Dakar and their baseline aflatoxin content was determined using the 'Test AFLA-V AQUA (0- 100 ppb) protocol and high-performance liquid chromatography (HPLC). Then the raw material was treated with sodium bicarbonate (broadly used in food industry) , then extruded and processed into food products in the form of 'thiere' (couscous) and 'thiakry' (roughly rolled and pre-cooked millet flour}. Their aflatoxin contents were determined by the methods cited above.

Results: 57.14% of untreated 'thiere' and 42.85% of untreated 'thiakry' samples were contaminated with levels of aflatoxin varying between 11.70 ppb and 12.37 ppb, well above European standards (5 ppb) where these products are often exported. Chemical treatments of the raw material (soaking for 16 h) with 3% sodium bicarbonate and 3% citric acid solutions led to 63% and 57% aflatoxin reductions, respectively. More interestingly, sodium bicarbonate combined with extrusion causes higher aflatoxin reduction rates : 71%, 92% and 92%, with concentrations of 2%, 4% and 6% of sodium bicarbonate solutions, respectively.

Conclusion: We have shown for the first time that high concentrations of aflatoxin present in cereal products can be strongly reduced to accepted levels, using a combination of a chemical (sodium bicarbonate) and a mechanical (extrusion) treatments.. This is a major finding because aflatoxin is the biggest public health problem in African agricultural produce blocking their access to international markets. This innovative protocol could be extended to sorghum and other cereals.

Changes in the structural and functional dynamics of the microbiota of Huangjiu (Chinese-rice-wine) fermentation from different varieties of sorghum

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Although sorghum is widely grown all over the world for food and feed, its nutritional benefits are limited due to the presence of anti-nutritional factors. These compounds are known to interfere with protein and carbohydrate digestion and mineral bioavailability. Controlled fermentation can represent a suitable strategy to improve sorghum protein digestibility and increase functional properties. Fermented sorghum foods and drinks are widely used in other parts of the world, especially in Asia and Africa, but not yet in the United-States.

The objective of this study was to investigate the effects on fermentation dynamics and functional properties of Huangjiu (Chinese-rice-wine) from different varieties of sorghum.

Microbial succession, taxonomic diversity, associated physical-chemical changes during fermentation were monitored by culture dependent methods, metagenomic analysis and chemical analysis when three different sorghum whole grains varieties (White, Waxy, Sumac) were used as substrates.

Aerobic bacteria, yeasts and molds increased significantly after inoculating with starter culture ($P < 0.05$), and followed a steady decline by the end of the study: 8.06 to 5.34 log CFU/g for yeast and molds, and 1.28 to 2.11 log CFU/g for aerobic counts. The most prevalent and abundant taxa and bacterial genera were recorded. Sumac sorghum contained the highest polyphenolic and condensed tannin, while Waxy sorghum had the highest amylopectin. Sumac also showed the lowest yield after the 10-day fermentation process, as compared to White and Waxy. Fermented sorghum (spent grain) showed an increase in crude protein, total protein quality, crude lipids by up to 8.6%, 3.57%, and 5.3%, respectively. In-vitro protein digestibility analysis in spent Waxy and Sumac grains slightly decreased, while protein digestibility corrected amino acid score, and in-vitro protein digestibility increased.

This study demonstrated the possibility of using and improving nutritional value of sorghum in the production of Huangjiu.

Effect of pre-processed whole sorghum flours on technological properties of gluten-free cakes

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Sorghum is a gluten-free cereal with mild flavor and some genotypes are rich in health-promoting bioactive compounds. Due to these benefits, added to its agronomic advantages, its consumption has been encouraged around the world. Studies have shown a positive sensory acceptance of sorghum based foods. However, in some products, as cakes, technological characteristics, especially with regard to volume and texture, need improvement. Thus, the aim of this study was to evaluate five pre-processing conditions of BRS 305 whole sorghum flour to improve technological properties of gluten-free cakes. Cakes were formulated with whole sorghum flour (16%), sugar (21.5%), corn starch (13%), egg powder (3%), butter (9%), xanthan gum (0.5%), baking powder (1.5%) and water (35.5%). Whole sorghum flour was pre-processed as follows and used in the five formulations: (RSF) raw sorghum flour; (TSF) toasted sorghum flour; (RTSF) 50% T1 + 50% T2; (CSF) cooked and dried sorghum flour and (ESF) extruded sorghum flour. The firmness of the cakes was analyzed in a TA.XTplus texturometer, the mass in an electronic weighing scale and the volume by the method of displacement of millet seeds. The masses of all formulations did not differ from each other. TSF and RTSF cakes presented greater heights, differing from the others. Regarding firmness and volume, RSF, TSF and RTSF formulations showed better results and differed from CSF and ESF, which showed greater resistance and smaller volumes, undesirable characteristics for cake. Although RSF, TSF and RTSF did not show differences among them, there is a greater expenditure of energy and working time in TSF, therefore, it is suggested that RSF and RTSF are the most viable for reproduction, both commercially and domestically. Sensory tests is necessary to confirm these results and to help select the best formulation, mainly in relation to the feeling of grittiness in the products.

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Whole sorghum flour added to chicken meatballs reduced the percentage of lipids and increased the sensory acceptance

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In the last decades, the consumption of processed meat products such as meatballs, has increased considerably due to its attractive flavor and versatility in cooking. However, they have high saturated fat content, which has been associated to the increased risk of developing chronic non-communicable diseases (NCDs). As fat is responsible for flavor, tenderness, juiciness, appearance and texture, characteristics attractive to the consumer, reducing this ingredient in these foods has been a challenge for the meat processing industries. Thus, this study aimed to evaluate physical, chemical and sensory characteristics of chicken meatballs added of BRS332 whole sorghum flour (WSF) as a partial fat replacer. Three formulations were prepared: 1) Control (with 17% fat and 0% WSF); 2) WSF5% (with 12% fat and 5% WSF); and 3) WSF10% (with 7% fat and 10% WSF). There was no difference ($p < 0.05$) among formulations for protein content. As expected, the fat content differed significantly, with the highest value found for the control, followed by WSF5% and WSF10%. Compared to control, WSF10% followed by WSF5%, showed the best results for the technological characteristics: higher yield and moisture retention, lower cooking loss and diameter reduction. Hardness, adhesiveness, and chewiness did not differ among formulations ($p > 0.05$). Springiness and cohesiveness were lower in WSF10% ($p < 0.05$) than the control and did not differ to WSF5%. Regarding sensory analysis, all formulations were accepted with mean scores nearly 7 (1-9 points scale) for all attributes. WSF5% obtained higher means for flavor, color, texture, and overall acceptability than the others treatments. Most WSF10% scores were similar to the control, although it changed the color of the chicken meatballs. Thus, sorghum flour reduced the percentage of lipids and increased sensory acceptance of chicken meatballs, revealing great potential to be added to this type of product.

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Improving sorghum injera quality through grain de-hulling and injera making protocol development

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Even though injera can be prepared from different cereal grains mainly from teff, sorghum injera has poor quality and less preferred by consumers in the urban. This study was aimed to increase the quality and product acceptability of sorghum based injera through grain decortication and using mustard seed flour as texture improver. Sorghum variety called Melkam was subjected to abrasion using de-hulling machine to remove the bran. Sorghum injera was prepared using different proportions of sorghum and teff flours. The result showed that sorghum grain decortication increased L* and b* color values but decreased a* color value. Inclusion of sorghum flour up to 75% resulted in an acceptable injera quality. However, 50% inclusion of sorghum flour preferred best by the panelists and rated similar with that of control sample which was made from 100% teff flour. Sorghum had the lowest minerals (iron, calcium, zinc, sodium and potassium) content compared to the teff and combining equal proportions of the flours increased the iron, zinc, calcium, sodium and potassium contents respectively to 42.29, 34.44, 52.39, 15.55 and 330.5 mg per 100 g of flour. Increased proportion of sorghum also resulted in decrement of flour functional properties such as swelling power and solubility during preparation. In addition, sorghum grain decortication significantly reduced the tannin and phytate contents of the flour. Adding 1 g of mustard seed flour in the mid-time of fermentation improved the texture of sorghum injera and prolonged the storability to three days at room temperature. As a conclusion, the result indicated that preferable and affordable sorghum based value added injera could be prepared by de-hulling the grain and, recipe and process optimization, and the use of natural emulsifier as means of texture improver.

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Assessment of growth, survival and cost of feeding improved indigenous chicken by sorghum farmers in western Kenya

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Rearing improved indigenous chicken (IIC) fed on locally available low cost, sorghum-based diets in drylands of western Kenya could address the region's food insecurity emanating from low crop and livestock productivity. This study assessed growth, survival, performance, and cost of feeding chicken reared on sorghum-based diets. A sample of 50 poultry keeping cum sorghum growing households across 5 wards considered to be semi-arid regions of Siaya and Busia Counties, were purposively selected and each supplied with eight 4-week-old IIC growers and trained on best management practices. Data were collected bi-monthly on breed preference, rearing systems, feeding regimes and chicken survival and growth, available feed resources, their cost and inclusion levels in rations for 16 weeks. Most farmers (69.4%) used sorghum variety *Nyadundo* together with maize, soybeans and fishmeal (*omena*) and/or *omena* dust to make rations, because of availability on the farm (78%) and often, on the market (67%). *Nyadundo* was available throughout the year, both on farms and in market. Most farmers (55%) reared chicken under free range. Most birds (75%) fed on home-made rations (HMR) where protein source was above 25% gained weight of 1.5kg. Farmers (67%) who mixed maize to sorghum at 1:1 ratio incurred a marginally higher cost compared to those (33%) who included more sorghum at a ratio of 1:2 or 0:1. Majority of the birds (79%) survived. The nutrient quality of the HMRs was quite comparable to commercial feeds on the market. Adoption of IIC production using sorghum-based feeds can help diversify chicken feed and broaden household diets to reduce malnutrition, hidden hunger, and food insecurity and alleviate poverty in the semi-arid regions of Western Kenya.

Keywords: Homemade rations - Improved indigenous chicken - Semi-arid regions - Sorghum-based diets.

Protein calibration models for single sorghum kernel NIR sorting

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Grain sorghum is an under-utilized cereal crop for food. It is well known that the composition of cereal kernels varies among kernels from the same panicle, which not only affects their processing properties, but also their nutritional value and application quality. To study the possibility of better utilization of cereal crops and to increase their commercial value, we developed a single kernel NIR sorting device to sort grain kernels by their differences in chemical composition. Our first goal was to sort grain sorghum kernels by their protein content. To accurately measure the small amount of protein in single sorghum kernels (~20-50mg), we first built a reliable calibration curve for our nitrogen analyzer using low levels of ethylenediaminetetraacetic acid (EDTA) (5-100 mg EDTA with R² of 1.000, SD of 0.017 and RSD of 0.178%) to support the NIR work as a reference method. Sorghum samples (n=96) grown in 2021 in Kansas and Texas with a wide range of protein content were selected for building our calibration model. Five kernels from each sample and three NIR spectra were collected for each kernel before protein content of each kernel was measured. Protein calibration models (both PLS with SNV correction and 8 factors) were built from either single spectrum or average of three spectra from each kernel. Results indicated the model built from the average of three spectra (prediction R² of 0.872, RMSE of 1.02%, and RPD of 2.79) was better than that from single spectrum (prediction R² of 0.771, RMSE of 1.34%, and RPD of 2.09) for each kernel. The NIR single kernel sorting device could be useful for breeders, researchers, and application scientists.

Improving the functionality of health-beneficial components of sorghum

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Sorghum contains health-beneficial phytochemicals, which can be obtained and utilized in the form of oleosome structures in close association with lipids and polar lipids. The oleosome composition and structure is determined by the extraction conditions determining its functional properties in foods. In our study, we investigated the effect of wet-milling pretreatment on the extraction efficiency and physicochemical properties of oleosomes obtained from waxy burgundy sorghum. In addition, the use of novel and traditional extraction solvents (i.e., poly-ionic liquids and traditional solvents, such as ethanol and dichloromethane) was explored for controlling extraction yield, particle size distribution (dynamic light scattering), protein concentration (Dumas method), total phenolic content (Folin Ciocalteu essay), antioxidant capacity (DPPH method), fatty acid profile (FAME analysis) and macro molecular interactions (ATR-FTIR) of oleosomes. We showed that the use of ionic liquids and wet-milling pretreatment significantly ($P < 0.05$) and 100% increased the extraction yield. The major fatty acids of the highest yield sample was palmitic C16 (22.06 ± 0.007), oleic C18:1 ω 9-cis (23.66 ± 0.891) and linoleic acid (C18:2) (16.649 ± 1.336). The major flavonoids analyzed by HPLC included caffeic acid, p-coumaric acid, luteolinidin, apigenidin, 7-methoxyapigenidin, eriodictyol, luteolin, naringenin, apigenin, kaempferol. The FT-IR analysis showed that carbohydrate-protein complexes were weakened by pretreatment to improve extraction efficiency and antioxidant capacity. Oleosomes containing health-beneficial phytochemicals can be used in confectionery applications.

Understanding the phenotypic and genotypic variation among key Ethiopian core collections and introduced forage sorghum genotypes

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Sorghum is an important feed and fodder source for livestock in Ethiopia. While the importance of livestock in mixed farming systems is well recognized, much remains to be done to develop and promote forage sorghum technologies for sorghum farmers and beyond. The aim of this study was (1) to explore the diversity in key Ethiopian core collection for various forage purposes, (2) to develop dual-purpose sorghum (for both grain and feed) that can meet the needs of mixed-sorghum-livestock farmers with limited resources and (3) to develop and improve alternative uses of forage sorghum as hay and silage for dairy farming and fattening. A total of 520 genotypes (370 obtained from SMIL sub-core collection, and 150 introduced forage sorghum lines, including the Brown mid-rib lines) were evaluated in a row-column design with 2 replications trials. Preliminary results from the agronomic performance data showed that there is a significant variation ($P < 1\%$) in biomass yield ranging from 1.42 to 34.02 tonnes/ha in dry matter for Stover harvested at grain maturity from the SMIL sub-core collection, and 2.24 to 31.2 and 3.38 to 40.58 tonnes/ha in dry matter for fodder harvested from the introduced forage sorghum genotypes in booting (for hay) and early hard dough stages (for silage making), respectively. A detailed chemical analysis is being carried out and further QTL analysis will be performed to understand the underlying genetic mechanism for the observed variation. The development and promotion of such forage sorghum technologies add a new multidimensional approach to improving sorghum in Ethiopia and will create a great opportunity for the already existing framers cooperative (6,000 member farmers engaged in dairy farming and fattening) in the study areas and beyond.

The impact of drought on sorghum production, and farmer's varietal and trait preferences, in the north eastern Ethiopia: implications for breeding

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In Ethiopia the yield and quality of sorghum is affected by a wide array of production constraints, notably severe and recurrent drought stress. The aim of this study were to determine the impact of drought on sorghum production and productivity over time and space, and to identify farmers' trait preferences, production constraints and coping strategies when dealing with drought in north eastern Ethiopia.

Results and discussion: The present study found that productivity of sorghum was challenged by recurrent droughts, Striga infestation, insects, birds, diseases, a lack of varieties with farmers preferred traits and high yield potential, limited policy support, a lack of improved seed system, poor sorghum production practices and application of crop input and poor soil fertility, in a decreasing order of importance. Among the listed sorghum production constraints, severe drought in the post-flowering stage was identified by most interviewed farmers as the leading constraint across the three study zones. Focus group discussions and transect walk observations held in each Kebele revealed that farmers' had lost numerous valuable local landrace varieties due to extreme drought conditions over the years. A significant number of interviewed farmers preferred to grow high grain and biomass yielder medium-maturing sorghum varieties which can be sown at the normal planting time but which would escape post-flowering drought.

Conclusion: Overall, sorghum breeding programme should be directed at developing farmers' ideal sorghum varieties with high grain and biomass yield, adequate level of drought and Striga tolerance.

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Pilot-scale genome-wide association mapping in a diverse sorghum germplasms identified novel genetic loci linked to major agronomic, stomatal and root traits

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This study used a representative subset of 96 diverse sorghum accessions, constructed from a large collection of 219 accessions for mining novel genetic loci linked to major agronomic and physiological including root traits through genome-wide association studies (GWAS). Genotyping by sequencing (GBS) of the constructed subset yielded 43,452 high quality genome-wide single nucleotide polymorphic (SNP) markers that exhibited high allelic diversity. Population stratification of the subset showed distinct separation between caudatum and durra races. Linkage disequilibrium (LD) decay was rapidly declining with increasing physical distance across all chromosomes. The initial 50% LD decay was by ~5Kb and decay to the background level ($r^2 < 0.1$) was within or below ~80Kb. GWAS for plant height and grain color using FarmCPU and SUPER methods identified significant SNPs co-localized with dwarfing locus (*dw2*) and *chalcone synthase* respectively indicating the representativeness of the population and reliability of methods used. This study also identified a AP2-like ethylene-responsive transcription factor and a gibberellin receptor GID1L2 affecting single plant yield and biomass respectively. Overall, this pilot scale GWAS detected novel genetic loci linked to drought avoidance traits viz., a Leucine rich repeat family protein (root biomass and root system architecture), a AP2 domain containing protein (iWUE, intrinsic water use efficiency) and a serine/threonine protein kinase (abaxial stomatal complex total area (abaxial SCTA)). Thus this study justified the construction of a subset of diverse sorghum lines which can be used as a panel for mapping other agronomic, morphological, stress tolerance and grain quality traits to accelerate molecular breeding efforts.

Exploring Sorghum Forage Technologies in Ethiopia: a Comprehensive Package for Impact

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Sorghum is an important high biomass yielding food and feed crop for millions of farmers in Ethiopia. A multi-disciplinary research and demonstration work was carried out for five years with the objective of developing a comprehensive package for impact in sorghum forage production and utilization in Ethiopia. From 2010 core germplasm collection and that of varieties released for grain production, we identified two dual purposes food-feed cultivars/varieties and also released one forage type. Using these cultivars, we studied effects of varying seeding rates on forage yield and quality, and found that increasing seeding rates from 12 kg/ha (recommended for grain) to 100kg/ha resulted in a significant decrease in stalk thickness and up to 7% increase in Invitro Organic Matter Digestibility, and conversely decreased fiber (NDF, ADF and ADL) concentrations. An on-station and on farm feeding trails conducted also showed 1.7 and 1.6 kg/day increase in milk yield of dairy cows fed on dual purpose sorghum varieties grown at high population density when compared to feeding that grown at low seeding rates and local grass hay, respectively. Meanwhile, we developed a small forage chopping machine that can be powered by gasoline or electric power to assist farmers in chopping sorghum stover. We also evaluated suitability for use as green feeding, hay or silage with locally available low cost storage materials, and found that containers like Urea fertilizer bags can be used to make good quality silage. The technology packages were initially demonstrated to 200 farmers which have then grown to over 6000 farmers over the course of time in seven districts.

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Alta Seeds**Stand 42**

Alta Seeds is a premium brand of Advanta Seeds in Europe and North America. Advanta Seeds is a global seed company responding to growing food insecurity and climate change.

Mazaya Business Avenue - Tower AA1

11th Floor, First Al Khail Street

33421 DUBAI – UAE

+971 42782717

mariola.markiel@advantaseeds.com<https://www.advantaseeds.com>**CIMMYT****Stand 15**

International Maize and Wheat Improvement Center (CIMMYT) is an international non-profit agricultural research and training organization. It focuses on maize, wheat, sorghum, millet, pigeonpea and chickpea.

Carretera México-Veracruz, Km. 45

56237 EL BATAN - TEXCOCO – MEXICO

+254113318799

cimmyt@cgiar.org<https://www.cimmyt.org>**Cirad****Stands 14 - 18**

Cirad is the French agricultural research and international cooperation organization working for the sustainable development of tropical and Mediterranean regions.

FRANCE

+ 33 1 53 70 20 22

frederique.causse@cirad.fr<https://www.cirad.fr>**Corteva Agriscience****Stand 17**

Corteva Agriscience is the only major agriscience company completely dedicated to agriculture.

Johnston Global Business Center

PO BOX 1000

50131-0184 JOHNSTON, IA – USA

laura.mayor@corteva.com<https://www.corteva.fr>**Hiphen****Stand 19**

Hiphen is a company specialized in frictionless plant phenotyping for agricultural research. We transform images acquired with various sensors into valuable phenotypic information.

120 rue Jean Dausset

84140 AVIGNON CEDEX 9 – FRANCE

+33 7 84 14 31 63

contact@hiphen-plant.com<https://www.hiphen-plant.com>**Kansas State University College
of Agriculture****Stand 31**

The mission of the College of Agriculture is to advance agriculture; protect natural resources; increase economic activity; and improve the lives and livelihoods through education, research and outreach.

1603 Old Claflin Place

66506 MANHATTAN – USA

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kstateag@k-state.edu<https://www.ag.k-state.edu>**Lidea****Stand 41**

Lidea creates and provides customised, sustainable seed solutions generating added value for producers all along the year.

Avenue Gaston Phoebus

64231 LESCAR – FRANCE

frederic.guedj@lidea-seeds.com<https://www.lidea-seeds.com>**Seeds For Future - FNPSMS****Stand 16**

The Seeds For Future communication campaign, co-financed by the European Union, presents the advantages of European maize and sorghum seeds in 7 EU countries.

23/25 avenue de Neuilly

75116 PARIS – FRANCE

martin.gomez@fnpsms.fr<https://seedsforfuture.eu/>**Semences de Provence****Stand 13**

Semences de Provence is a French seed company, leader in France and Italy on sorghum market since 1975.

17 rue Gaspard Monge, ZI Sud

13200 ARLES – FRANCE

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US University conducting sorghum research.

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Global Collaboration for
Resilient Food Systems
Program - GCFRS****Stand 12**

The McKnight's CRFS program aims to cultivate resilient food systems globally by bridging farmer-centered agroecological research, action and influence.

710 S 2nd St Ste 400

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info@ccrp.org<https://www.ccrp.org/>**United Sorghum Checkoff Program****Stand 51**

A producer-funded organization dedicated to improving the sorghum industry through research, promotion and education.

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clint@sorghumgrowers.com<https://sorghumcheckoff.com>

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EXHIBITION PLAN - CORUM EVENT CENTER, MONTPELLIER

ANTIGONE 1, 2 & 3 AREAS - LEVEL 2

POSTER SESSION 1 - odd-numbered posters:
 MONDAY 5 JUNE - 5:30 pm to 6:30 pm
POSTER SESSION 2 - even-numbered posters:
 TUESDAY 6 JUNE - 5:30 pm to 6:30 pm



■ PASTEUR Auditorium - Level 1
■ SULLY 1 Room - Level 1
■ BARTHEZ Room - Level 2

PREVIEW ROOM (Submission and testing of presentation slides) = SULLY 3 BIS Room - Level 1

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CIMMYT	STAND 15	FNPSIMS	STAND 16
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CORTEVA AGRISCIENCE	STAND 17	TEXAS TECH UNIVERSITY	STAND 11
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190 rue d'Argencourt - 34000 Montpellier.
150 m from 'Le Corum' (direct access via footbridge, 2 minutes-walk). Private car park: € 15 / 24h.
- 2 Mercure Montpellier Centre Antigone *****
285 boulevard de l'Aéroport International - 34000 Montpellier.
20 minutes-walk (1.5 km) from 'Le Corum'.
Private car park: € 15 / 24h.
- 3 Hotel Océania Le Métropole *****
3 rue Clos René - 34000 Montpellier
10 minutes-walk (800 m) from 'Le Corum'.
Private car park: € 20 / 24h.
- 4 Ibis Style Montpellier Centre Comédie *****
6 rue Baudin - 34000 Montpellier.
8 minutes-walk (600 m) from 'Le Corum'.
Private car park: € 14 / 24h.
- 5 Campanile Montpellier Centre *****
11 rue Pagezy - 34000 Montpellier.
15 minutes-walk (1 km) from 'Le Corum'.
Parking: € 20 / 24h.

- 6 Ibis Montpellier Centre Polygone *****
95 place Vauban - 34000 Montpellier.
10 minutes-walk (800 m) from 'Le Corum'.
Private car park: € 16 / 24h.
- 7 Citadines Antigone Montpellier *****
588 boulevard d'Antigone - 34000 Montpellier.
16 minutes-walk (1.2 km) from 'Le Corum'.
Private car park: € 11 / 24h.
- 8 Hotel Eurociel Centre Comédie *****
1 avenue du Pont Juvenal - 34000 Montpellier.
13 minutes-walk (900 m) from 'Le Corum'.
Private car park: € 13 / 24h.
- 9 Kyriad Montpellier Centre Antigone *****
890 avenue Jean Mermoz - 34000 Montpellier.
17 minutes-walk (1.3 km) from 'Le Corum'.
Car park: € 12 / 24h.
- 10 Hotel Ulysse Montpellier Centre *****
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