



Genomics-informed sorghum improvement

Ian Godwin



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*2nd European Sorghum
Congress 2018*

GENOMICS INFORMED SORGHUM IMPROVEMENT

Better yield, better quality, better resilience

- Genomics and key breeding traits
- New breeding technologies
 - CRISPR/Cas9 genome editing
- Focus on end-use quality
- Yield and yield components
- Future crop design



It's a major staple for >500 million



And through an animal intermediary

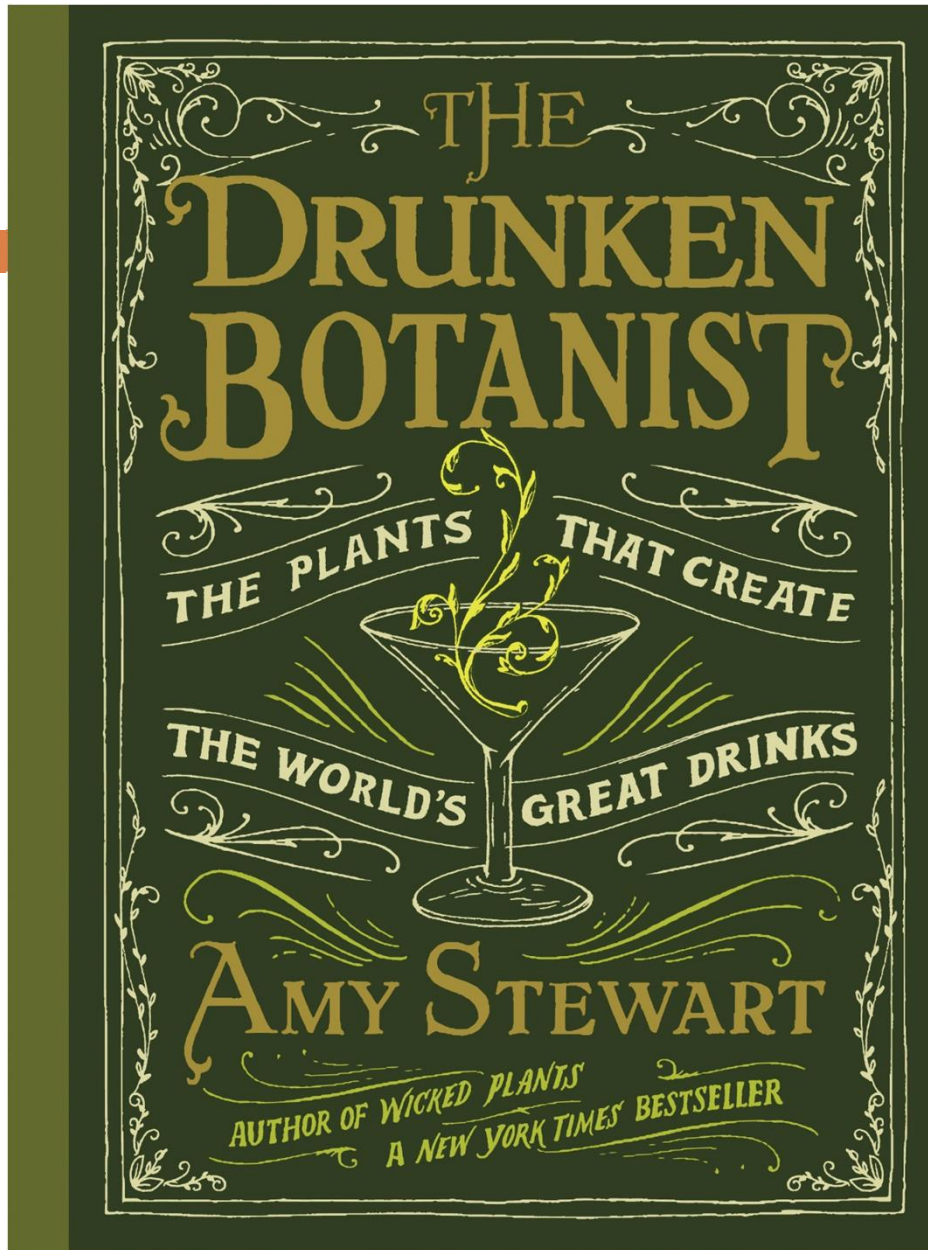
You can make these



And you can make
bio-ethanol and beer
from sorghum

So what's not to like?





- “If we had a way to accurately tally the world’s vast and complex drinking practices, **sorghum is clearly one of the world’s most imbibed plants.**”

(Stewart, 2013)

Sorghum: least digestible cereal for monogastrics (humans, pigs etc)



- ❖ low starch and protein digestibility
- ❖ high starch gelatinization temperature (important for processing and digestibility)
- ❖ protein:starch matrix is protease resistant
 - ❖ Cysteine-rich leads to S-S bonding
- ❖ Small/variable grain size

Whatever the quality – birds love it!

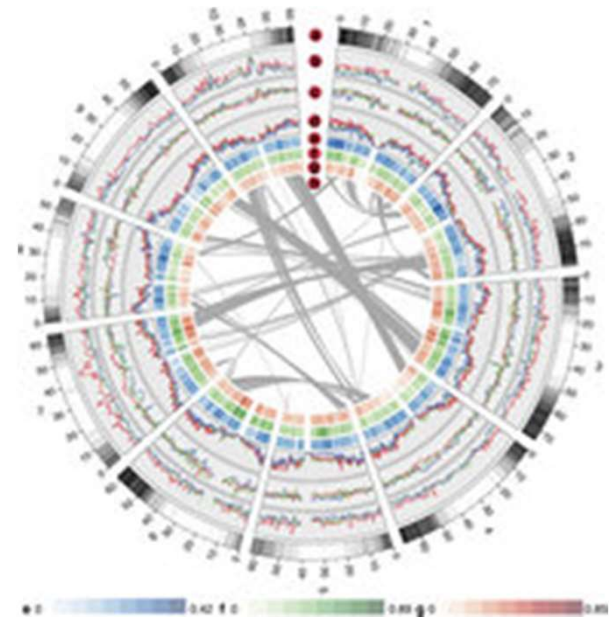


Exploiting genetic diversity

- Association genetics for improving a trait of importance
- GWAS in 400 diverse sorghums
- Sorghum starch digestibility

Association with digestibility

- Across the panel, 1 genomic region appeared to confer improved digestibility
- Near the distal end of the short arm of chromosome 6
- A candidate gene was located here – **pullulanase** – a starch debranching enzyme

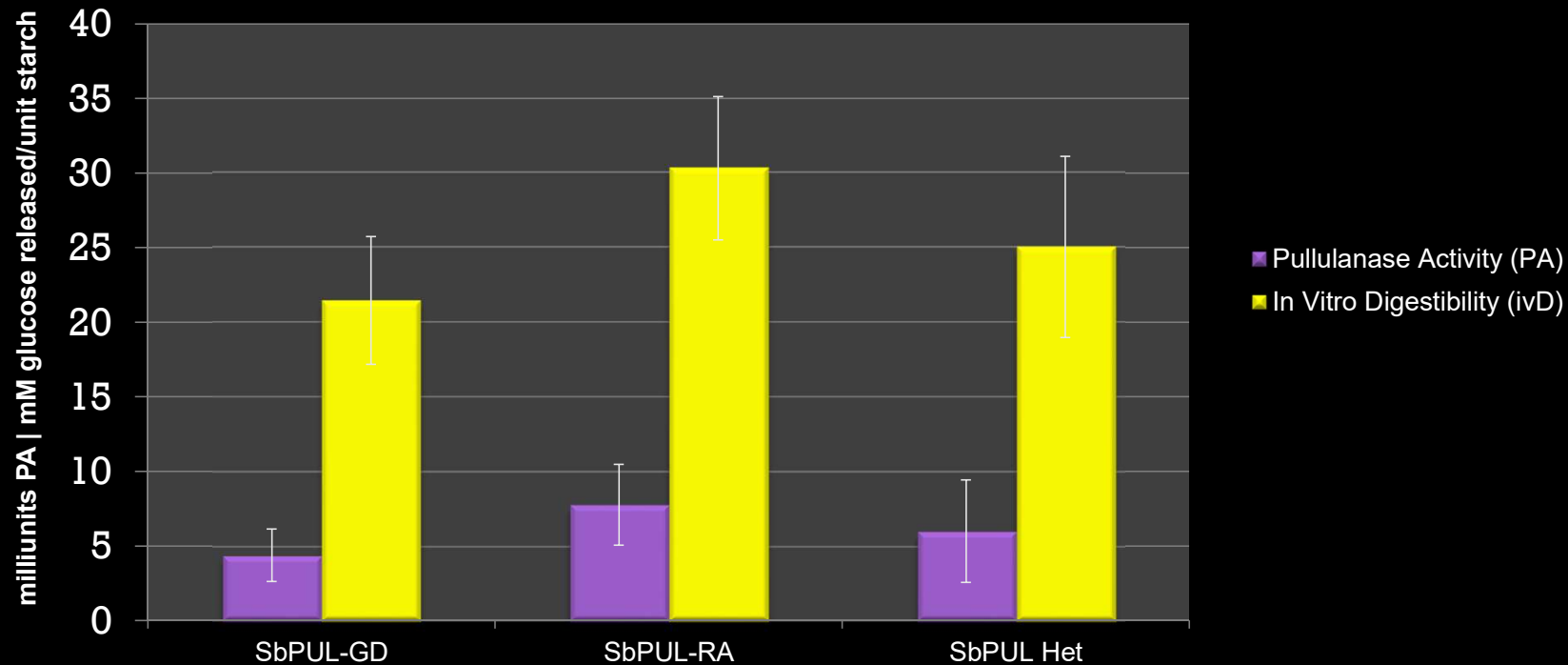


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↑ Pul activity → ↑ digestibility

NILs illustrate PA~ivD relationship



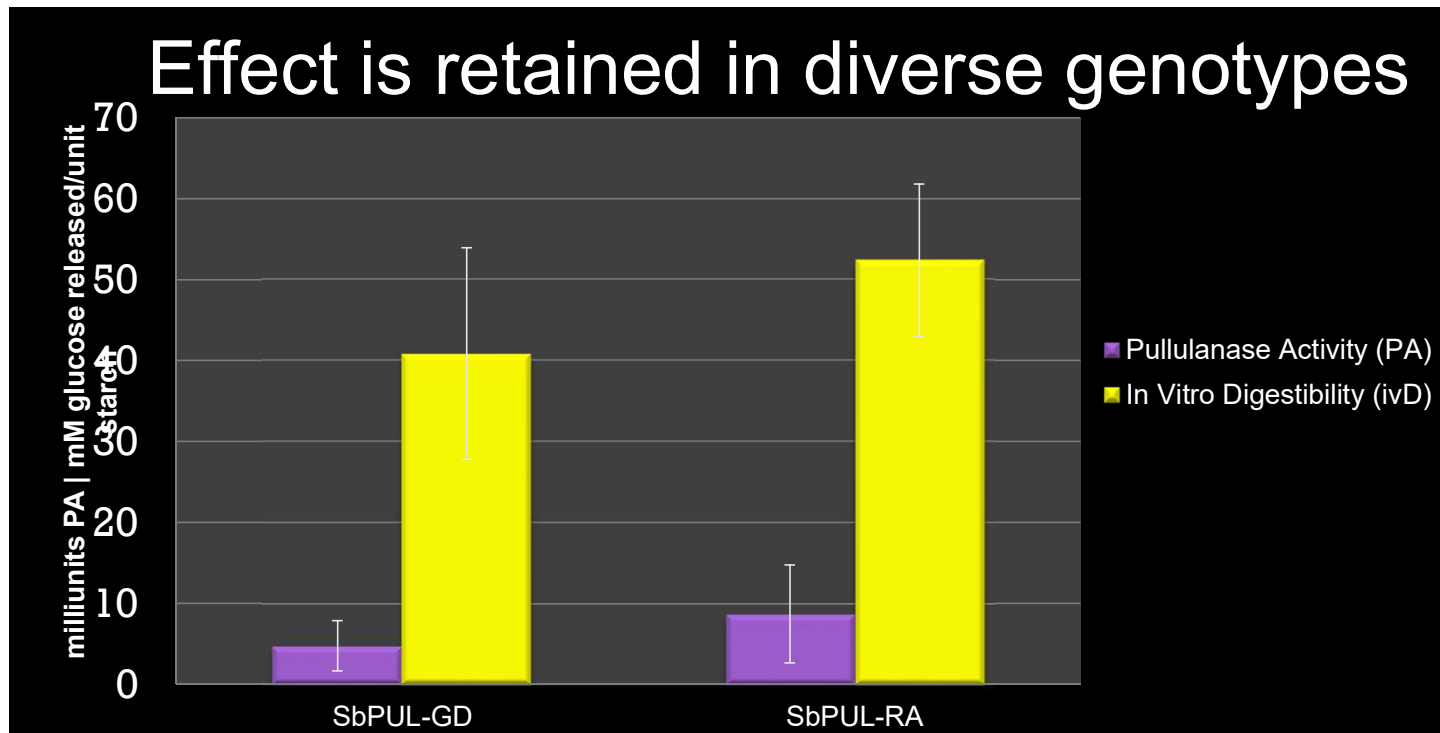
Gilding, Frere et al, 2013



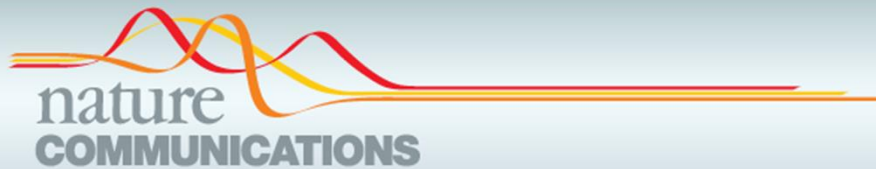
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Association holds up in another population



Starch debranching – changes starch structure



ARTICLE

Received 30 Aug 2012 | Accepted 4 Jan 2013 | Published 12 Feb 2013

DOI: 10.1038/ncomms2450

OPEN

Allelic variation at a single gene increases food value in a drought-tolerant staple cereal

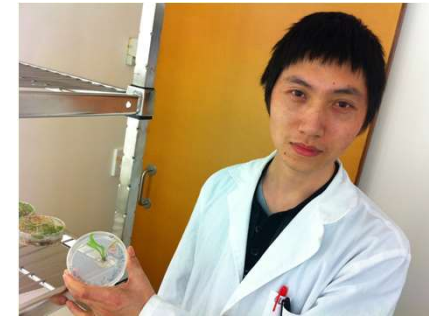
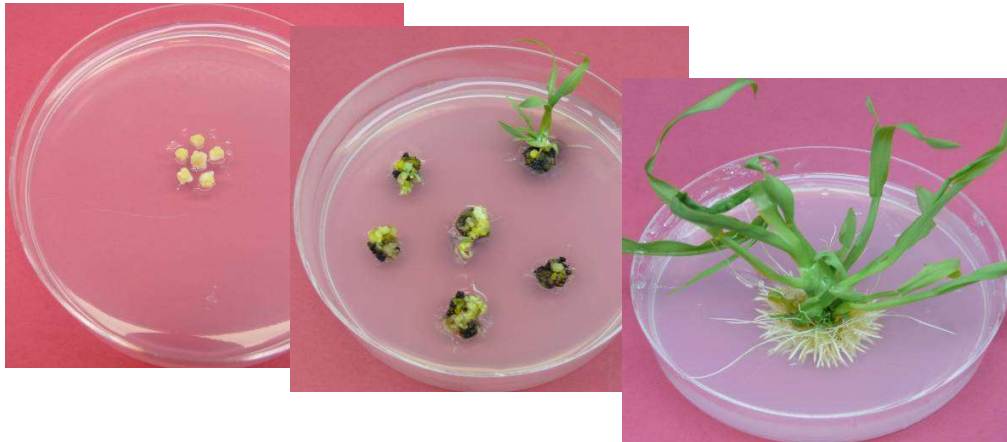
Edward K. Gilding^{1,*}, Celine H. Frère^{2,*}, Alan Cruickshank³, Anna K. Rada⁴, Peter J. Prentis⁵, Agnieszka M. Mudge¹, Emma S. Mace³, David R. Jordan⁶ & Ian D. Godwin¹

Pullulanase sorghum lines

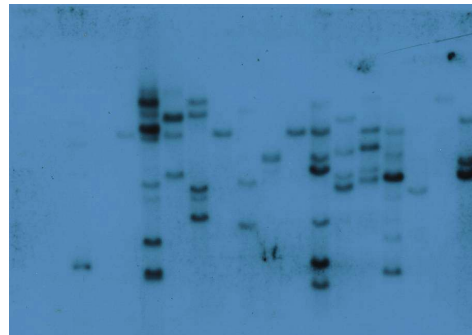


- NILs grown in field trials under bird-netting
- Replicated poultry feeding trials in progress at Sydney University

Genomics can inform Transgenic and Editing approaches



Guoquan Liu
20-25% efficiency
Liu and Godwin, 2012, Plant Cell Rep.



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Natural β -kafirin null mutants

Theor Appl Genet (2010) 121:1227–1237
DOI 10.1007/s00122-010-1383-9

ORIGINAL PAPER

β -kafirin is not essential

That makes it a target to play with!

- ❖ Higher protein
- ❖ Higher digestibility
- ❖ Ogi porridge in West Africa



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Transgenics and genome editing

Approaches to improve grain quality

BIGGER GRAIN and MORE DIGESTIBLE PROTEIN

1. Overexpress a synthetic β -kafirin (Liu et al JCS 2018)
2. Change the way proteins fold (RNAi-foldase)
3. Manipulate G-proteins associated with grain size

G protein gamma-subunits

1. Overexpression
2. RNAi silencing
3. Overexpression of truncated genes

- ❖ RNAi silencing (~50-70% downregulation) from independent transgenic events
 - ❖ GGC1 (GS3) – mean 7% increase in seed size
 - Same as the QTL in NAM
 - ❖ GGC2 – mean 7% increase in seed size
 - ❖ GGC3 (DEP1) – mean 9% increase in seed size



Grain size characteristics



Tx430

C1R-35



10 seeds

RNAi GGC1 (GS3)

No reduction in grain number

9-12% increase in TKW

“Foldase RNAi lines: larger grain, higher protein



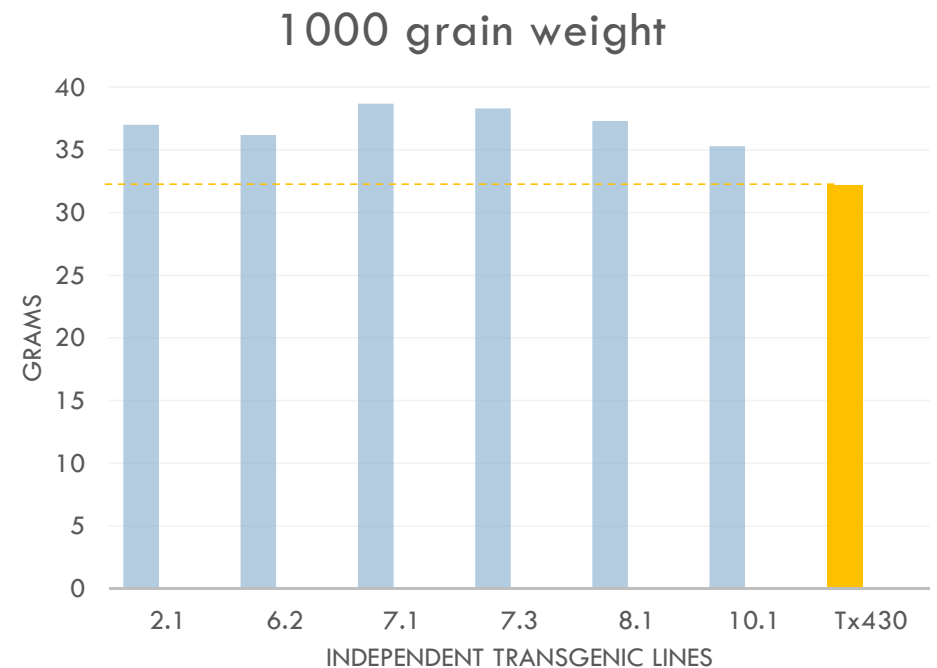
Tx430

Foldase RNAi 8.1

Field trials summer 2018

- Inbred lines

In grain fill in SE Queensland



Gene editing in sorghum – our progress

Brown Midrib sorghum – lignin biosynthesis (rice U6 promoter)



Sorghum albinism

(rice v sorghum U6/U3 promoters)

Latest: beta-kafirin knockouts – higher protein content



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Gatton campus and Research Farm 80 km from Brisbane

27 transgenic lines – 5 genes manipulated 2018



UQ + NuSeed + Qld Dept of Agriculture and Fisheries collaboration

Aims: Larger Grain or More Grain or Higher Protein?



Some transgenic lines RNAi-GGC1 and GGC3



GGC1



GGC3



Tx430 control

Transgenic Lines – RNAi-foldase



P2
Plant height 125 cm

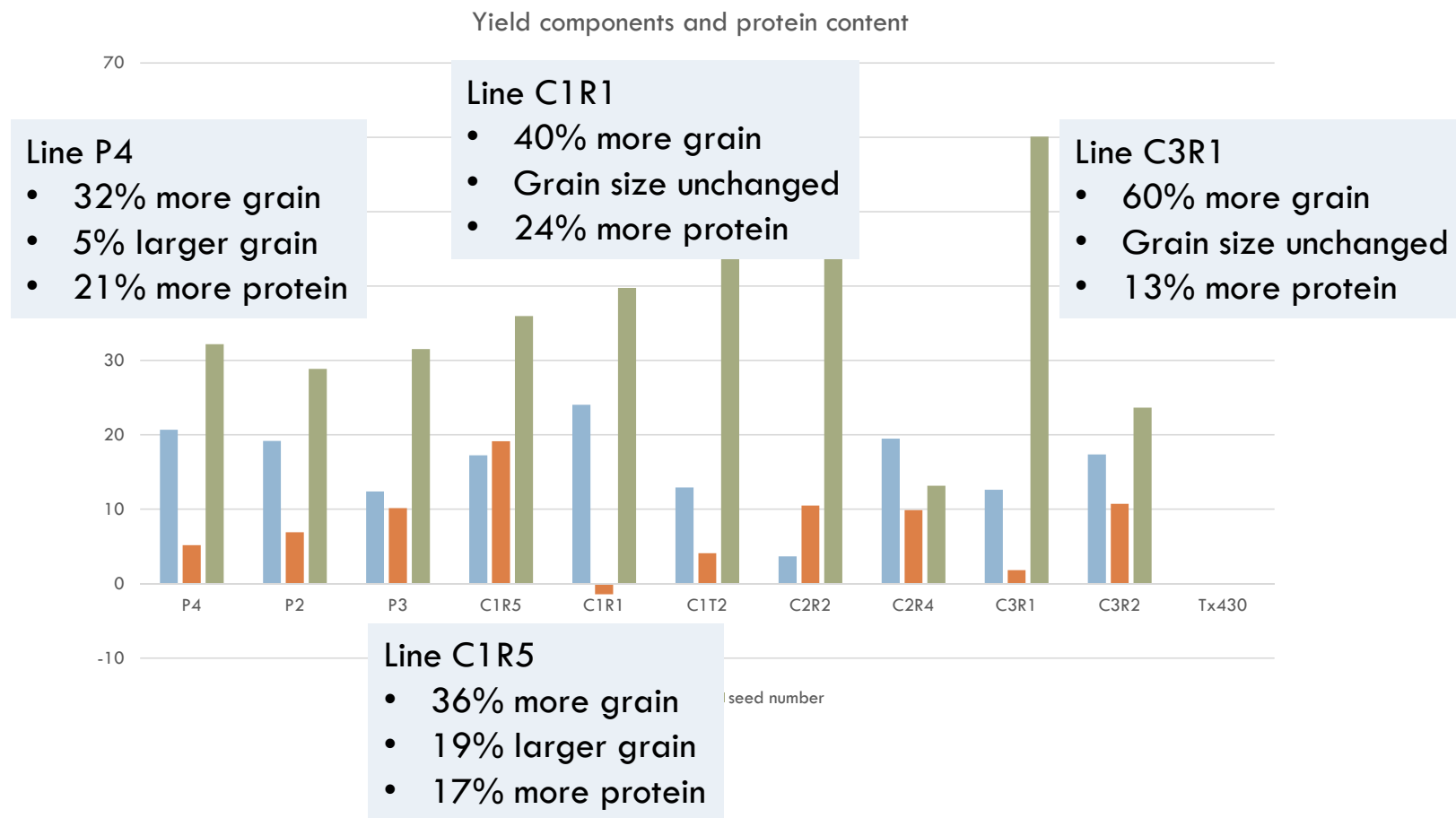


P4
146 cm

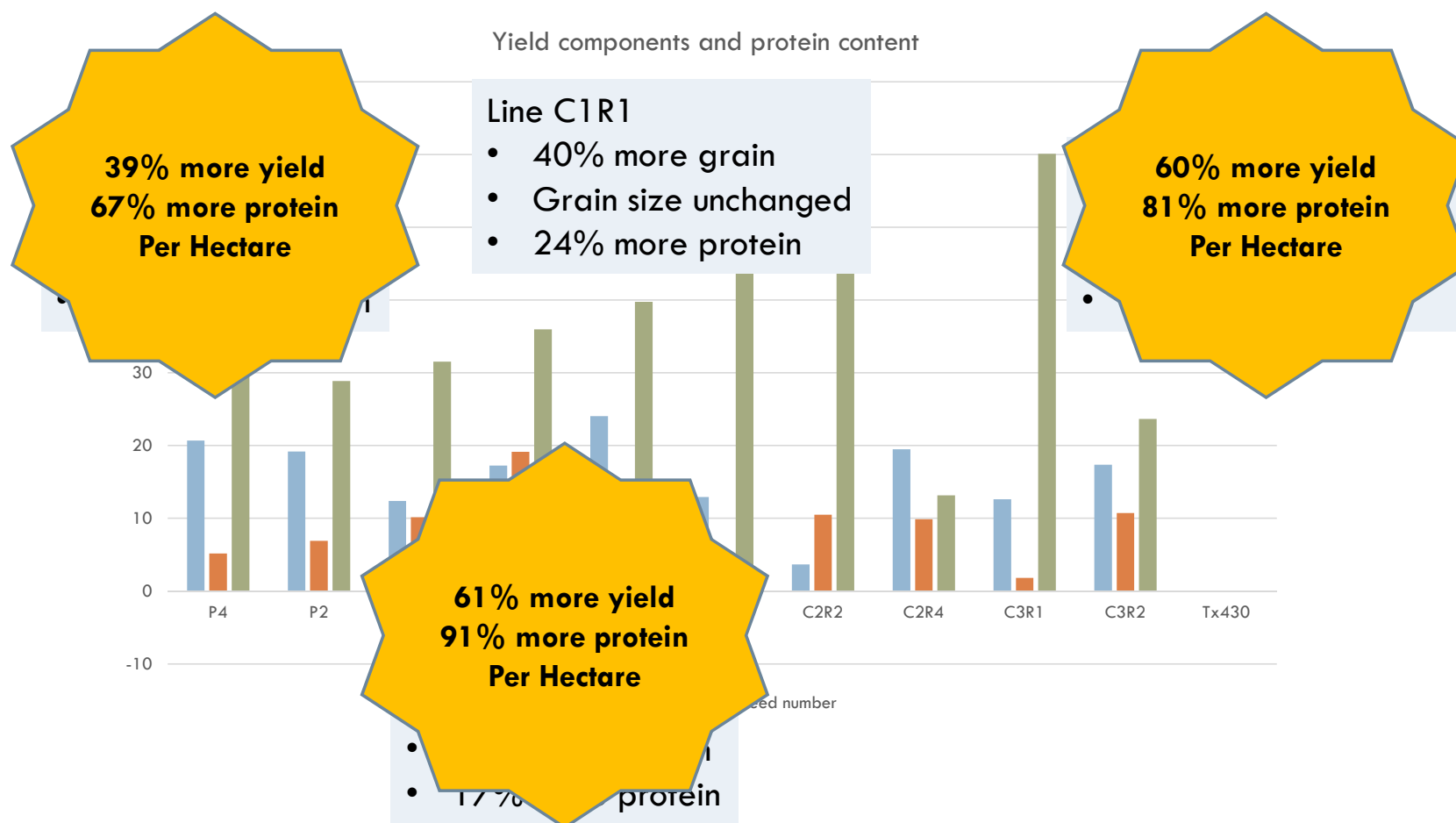


Tx430 control
119 cm

Higher Protein + all the good yield stuff!

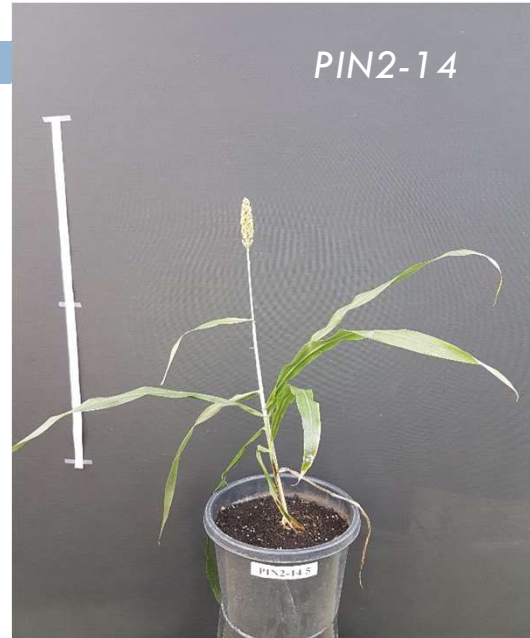


More protein per grain, more protein per hectare



PIN gene expression and plant architecture

- 1. *PIN* genes
- 2. Plasticity
- 3. Pleiotropy



Small canopy
expression

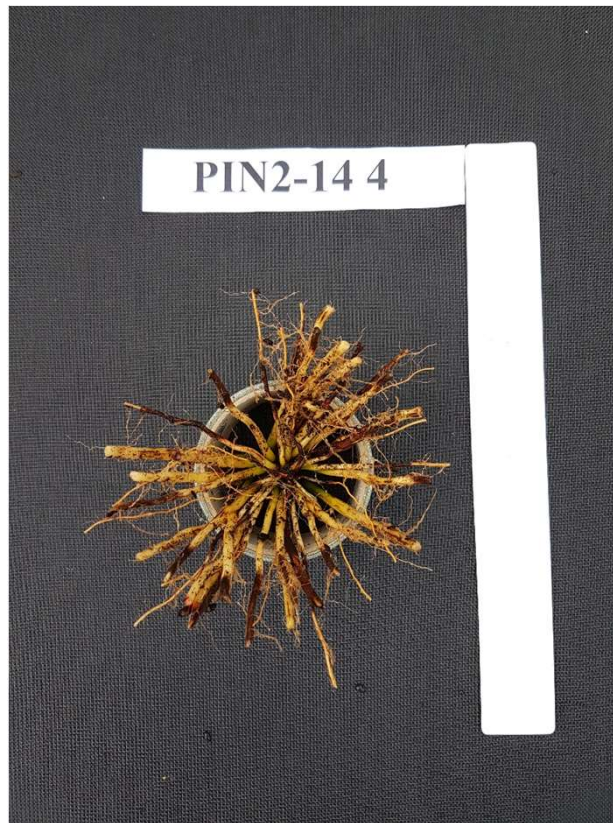


Large canopy
expression

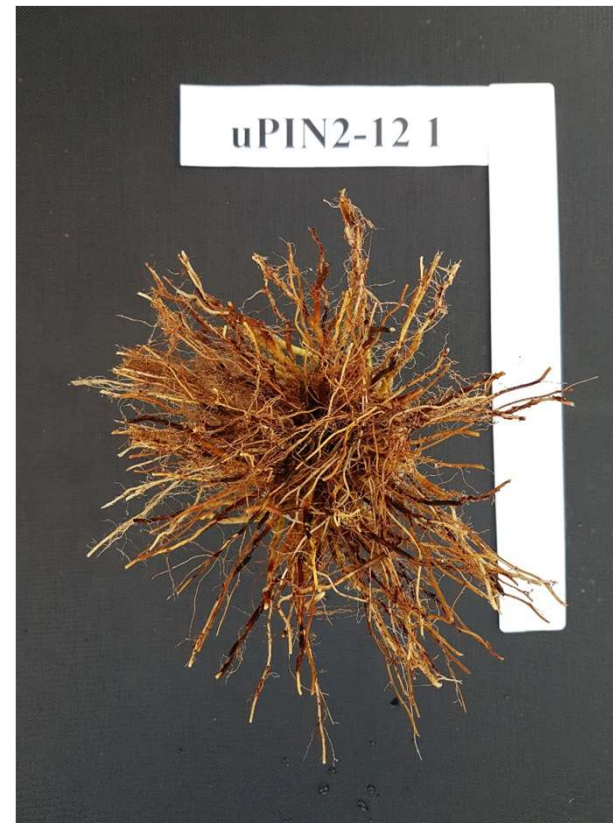


Andy Borrell, Guoquan Liu, Albert Wong

PIN genes confer 'nodal root number' plasticity in sorghum



Small root number



Large root number

Genomics + GM/editing + physiology → better sorghum





Special thanks to the **Sorghumheads:**

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Collaborators

Dave Jordan UQ QAAFI
Bob Gilbert UQ QAAFI
Glen Fox UQ QAAFI
Emma Mace UQ QAAFI
Andy Borrell UQ QAAFI
Alan Cruickshank DAF-Q
Erik van Oosterom UQ QAAFI
Jimmy Botella UQ
Susanne Schmidt UQ
Ed Gilding UQ IMB
Bruce Hamaker Purdue
Scott Bean USDA Kansas
Pete Prentis QUT
Shuaishai Tai BGI Shenzhen
Rod Snowdon JLU-Giessen
Evans Lagudah CSIRO
Janet Davies QUT
Luguang Wu UQ
Hai-Chun Jing CAS Beijing
Lu Xiaochen CAAS Shenyang
Clive Lo Hong Kong Univ
Chris Haire NuSeed
Nanna Bjarneholt Copenhagen
Jeiqin Li Anhui S&T Univ



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GRDC

Grains
Research &
Development
Corporation



DAAD

Deutscher Akademischer Austausch Dienst
German Academic Exchange Service



Queensland
Government



Australian Government
Australian Research Council



中国科学院
CHINESE ACADEMY OF SCIENCES



ADVANTA
SEED INTERNATIONAL