

Expanding sorghum into temperate Europe: Accelerating breeding progress with genomic data



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**Understanding of complex traits
Enhancing stress adaptation Accelerating breeding
progress Genomics / Phenomics**



Quantitative genetics



JLU Giessen sorghum team



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Fine
Luisa's dog

Sorghum as an alternative to maize

Benefits: Agri-diversification

Diversity = versatility



Dual-use hybrids (silage/energy or grain)



Grain hybrids (food/feed)

Sorghum as an alternative to maize

Benefits: More insect-friendly than maize

A rare late-summer food for bees on central European fields



Bees like sorghum...



...and sorghum likes bees

Sorghum pollen

- ...is a valuable protein source for bees
- ...is actively collected and consumed
- ...maintains health of colonies

Honeybee pollination

- ...maintains sorghum seed set and yield when pollen production is reduced by unfavourable weather conditions

Sorghum as an alternative to maize

Benefits: Drought tolerance

An increasingly important asset in Europe



Direct comparisons of sorghum vs. maize in central Germany
during severe droughts of 2018 & 2019

Sorghum as an alternative to maize

Climatic challenges

Cool temperature emergence



Juvenile survival (13°C day, 10°C night)



Field emergence
(compared to maize sown ~4w earlier)

Sorghum as an alternative to maize

Climatic challenges

Reproductive-stage cold susceptibility



Cold-tolerant genotype:
Successful grain filling

Cold-susceptible genotype:
Pollination & grain filling unsuccessful

Sorghum as an alternative to maize

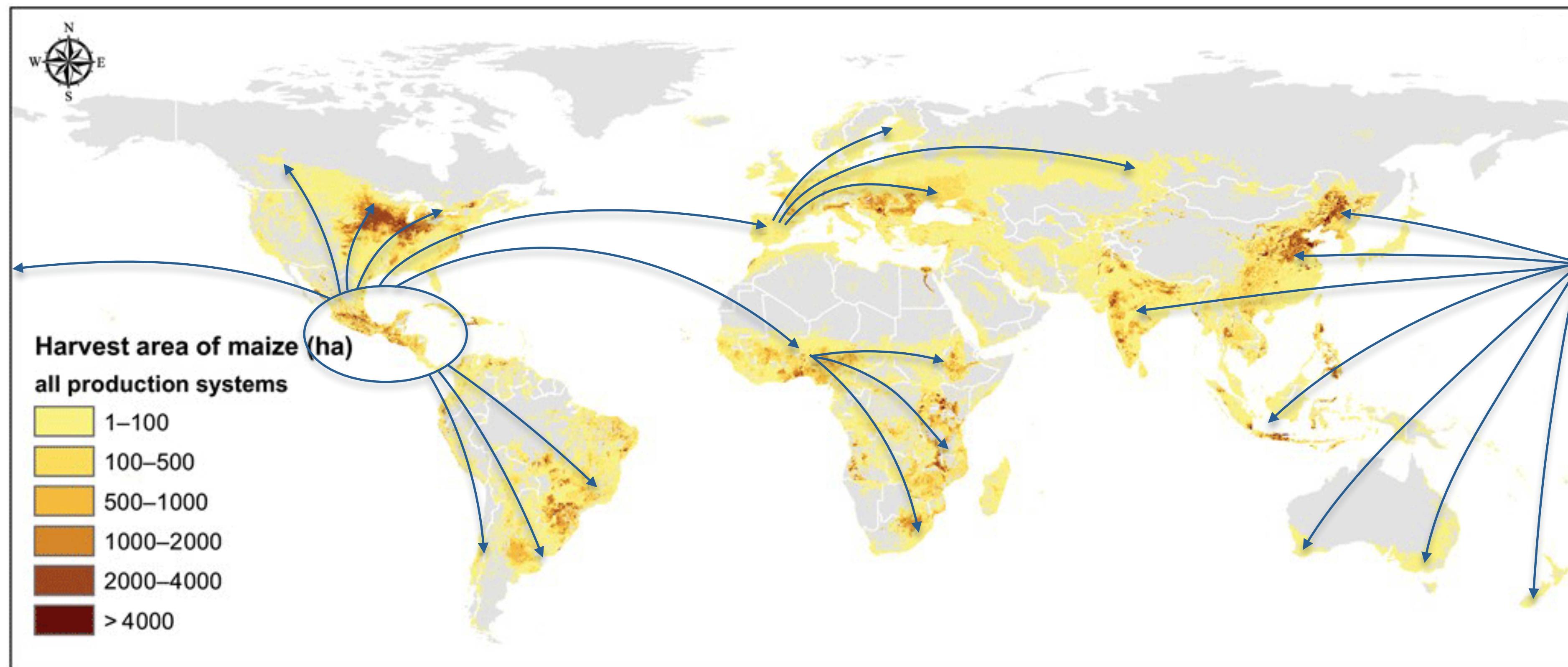
Challenging but possible

Good yield performance is already achievable with early hybrids in moderately temperate regions of central/southern Germany



However further north ($>50^{\circ}\text{N}$) the climate is marginal for grain setting

The benchmark for sorghum: Global maize production

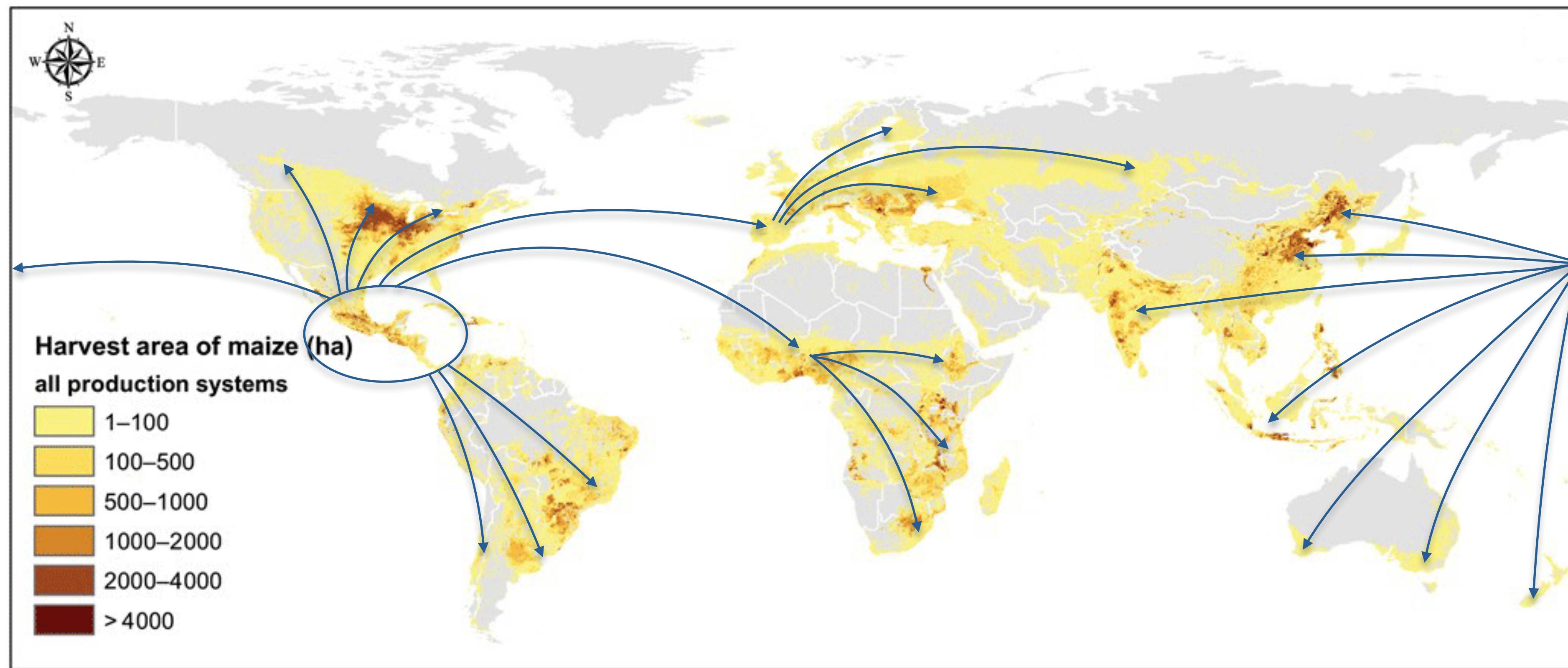


Keys to success:

- Early long-day flowering
- Cool temperature adaptation in juvenile & flowering stages
- Locally adapted heterotic groups for maximum hybrid yield

Yu et al. (2020) Earth Syst Sci Data 12: 3545–3572
<https://doi.org/10.5194/essd-12-3545-2020>

The benchmark for sorghum: Global maize production



But this took 50-100 years in maize!

- *The big challenge for sorghum breeding:*
Accelerate adaptive breeding and hybrid potential in less favourable production environments using genomic tools and data

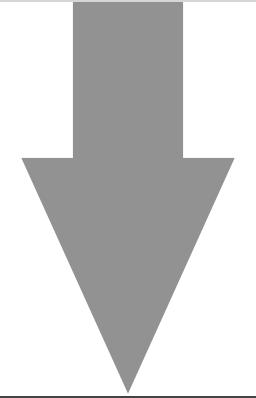
Yu et al. (2020) Earth Syst Sci Data 12: 3545–3572
<https://doi.org/10.5194/essd-12-3545-2020>

The basics of breeding (I)

Identification or generation of relevant
genetically determined variation

Recombination of desirable traits by
crosses among selected parents

Selection of the best offspring



Fixation of the best combinations in
new, improved **cultivars**

The basics of breeding (2)

Genetic gain \approx rate of response to selection

$$\Delta G = \frac{i * r * \delta_G}{L_g}$$

i = Selection intensity

r = Selection accuracy

δ_G = Genetic variance

L_g = Cycle time

Accelerating breeding progress

Genetic gain \approx rate of response to selection

$$\Delta G = \frac{i * r * \delta_G}{L_g}$$

i = Selection intensity

r = Selection accuracy

δ_G = Genetic variance

L_g = Cycle time

So how to increase ΔG ?

Select more intensely

Select more accurately

Increase genetic variance

Do all those things faster

Prerequisite #1 – Sorghum has enormous genetic variation (just like tropical maize)

Example: Uganda National Genebank sorghum collection, n=3333

(DFG project PEGASUS)

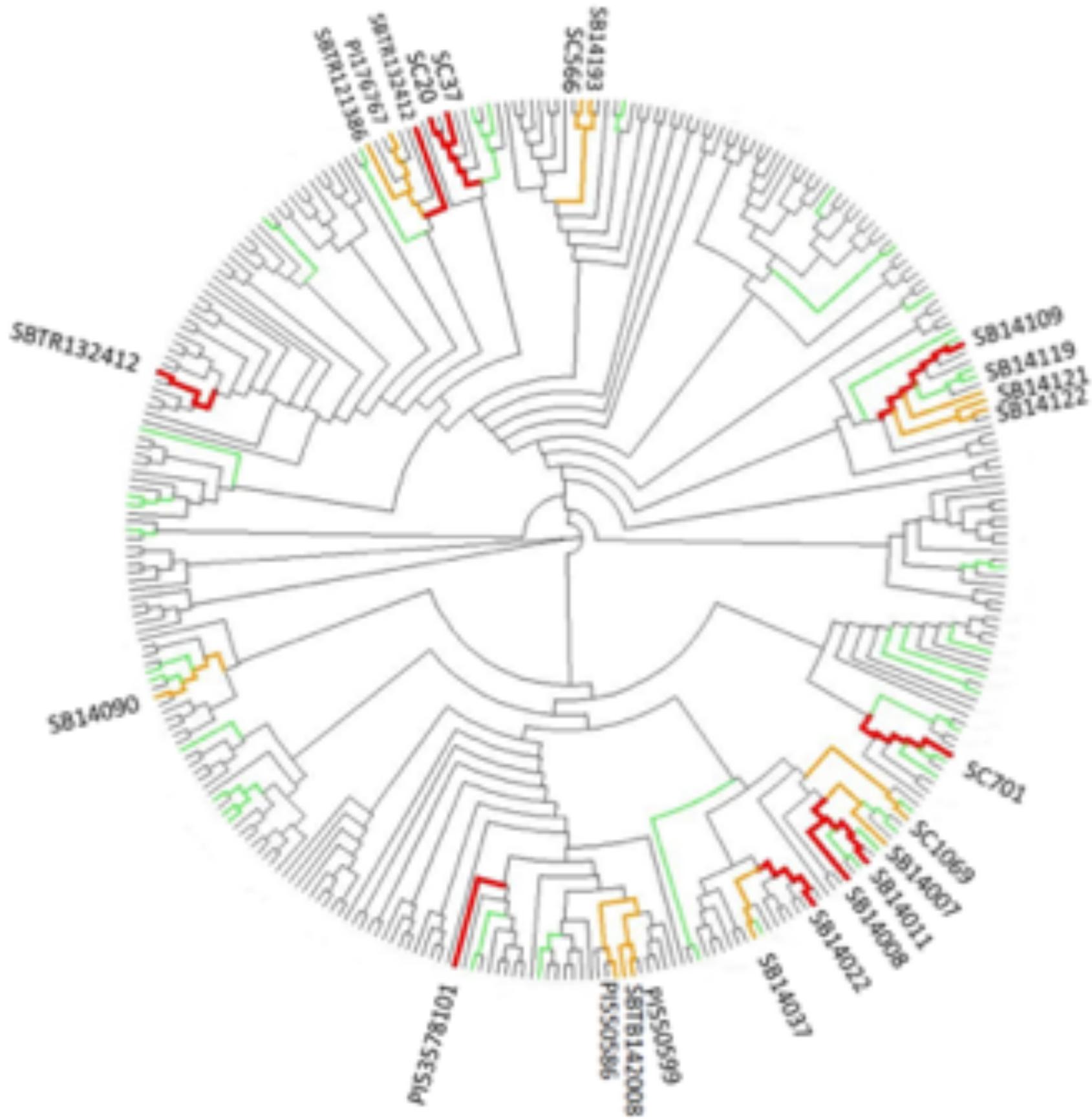


- Extreme diversity for all agronomic traits of interest including cold tolerance from highlands
- Genomic prediction of juvenile & reproductive cold tolerance (~20,000 DArTseq SNPs)

Identifying and utilising useful, adaptive genetic variation

Diverse materials of highland origin carry very useful juvenile & reproductive cold tolerance

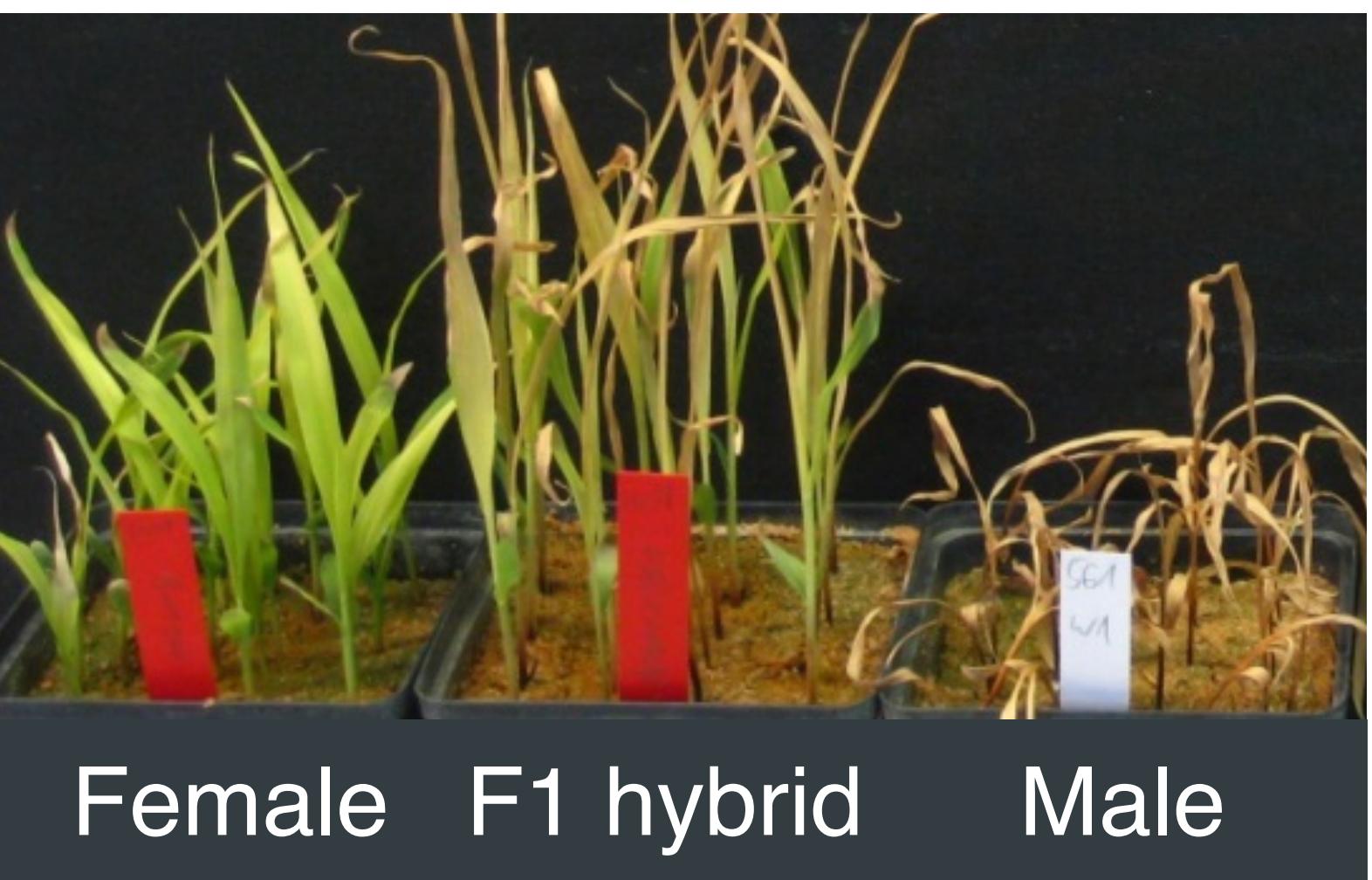
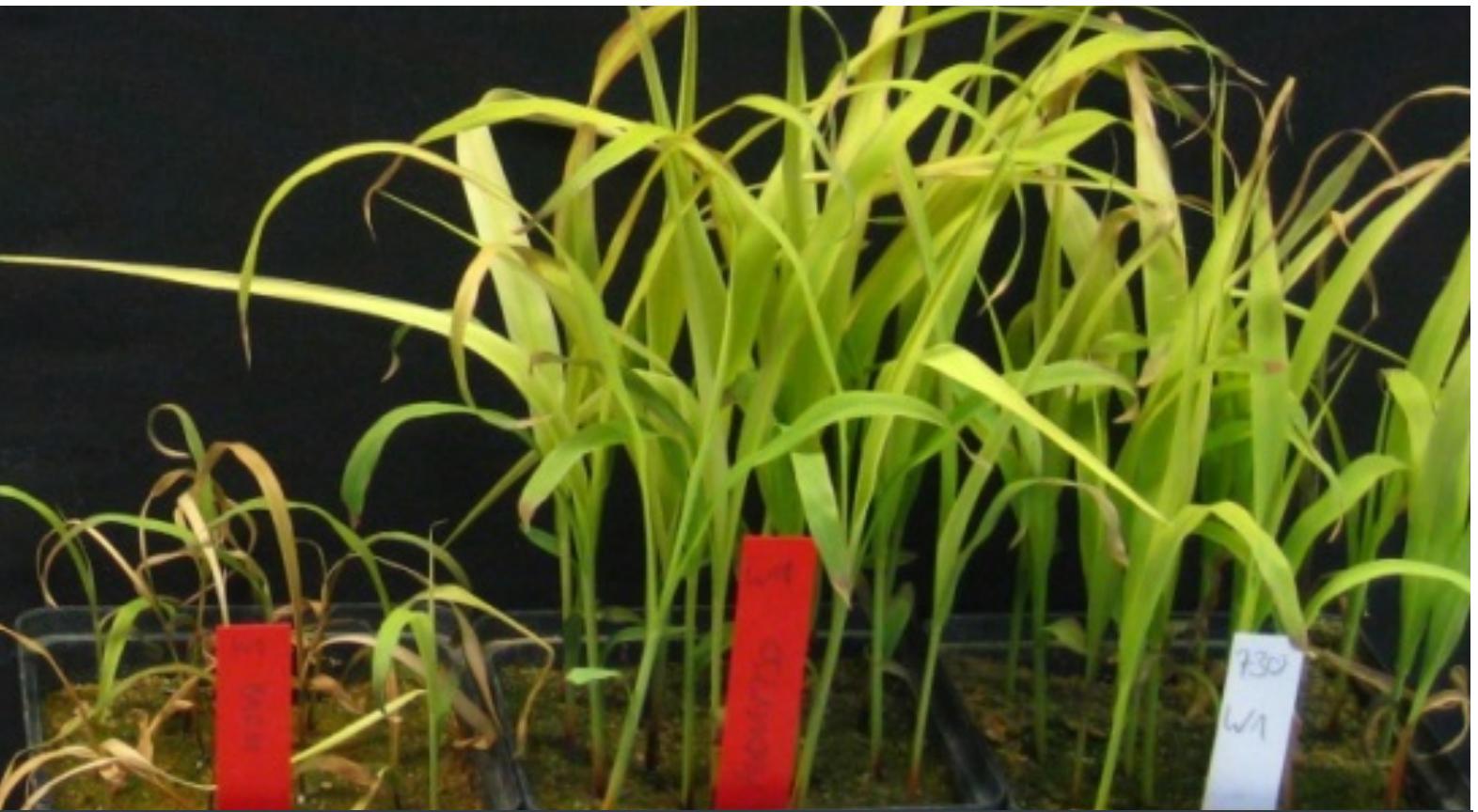
Example 2: SoNaBi diversity panel, JLU Giessen (conversion lines, n~330)



“Cold tolerance in sorghum is a heterotic trait”

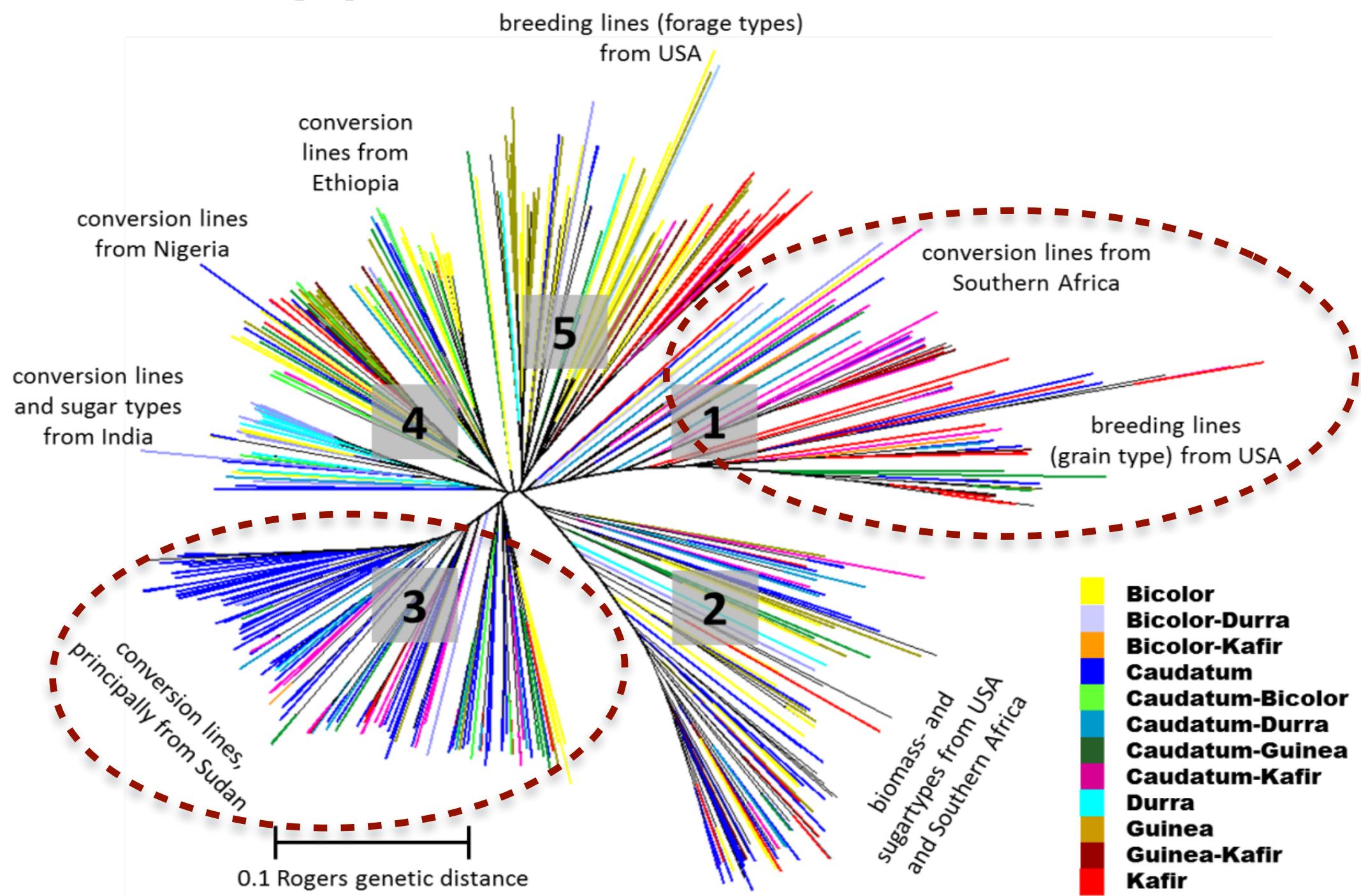
Schaffasz et al. (2019) Agronomy 9: 535
<https://doi.org/10.3390/agronomy9090535>

Coloured bars = high reproductive cold tolerance

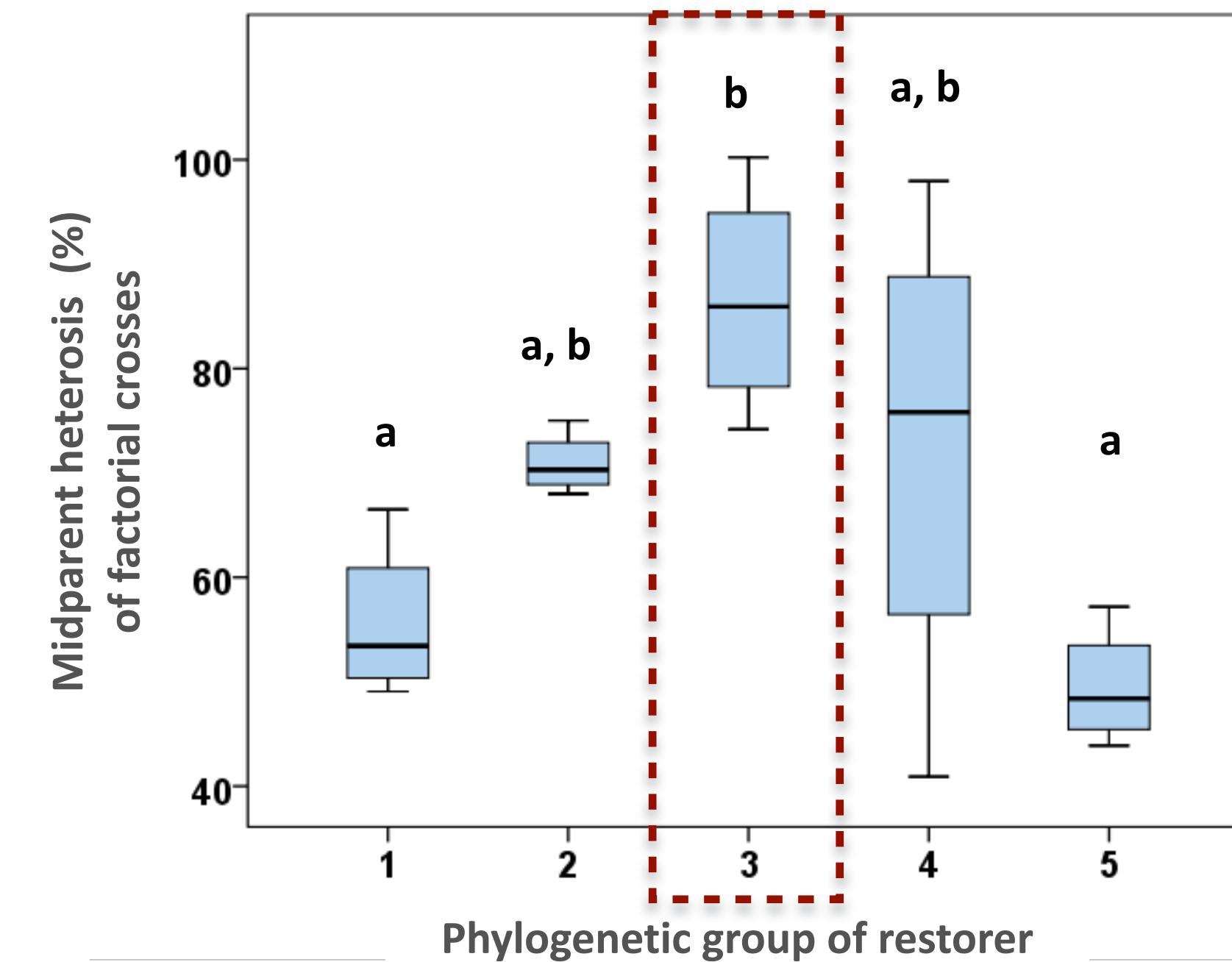


Recombining diverse founders to establish heterotic groups

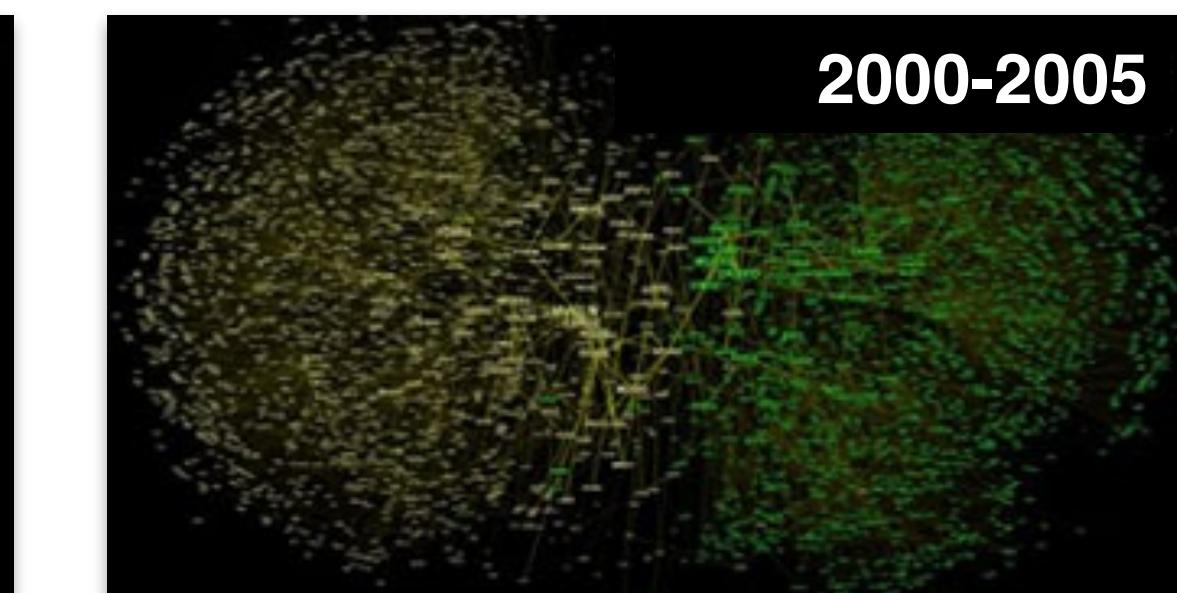
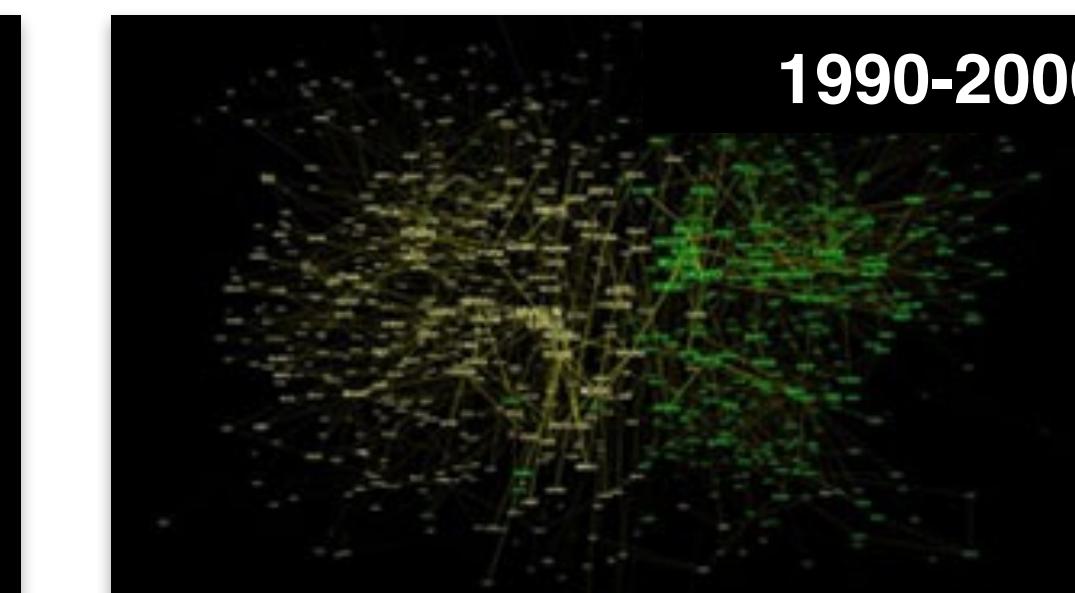
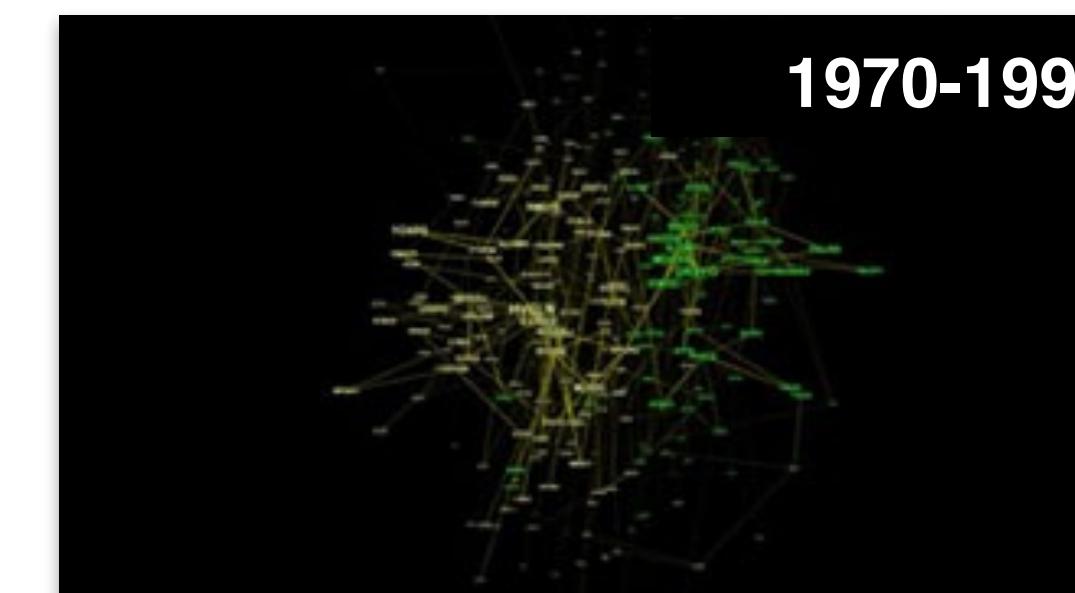
SoNaBi diversity panel, JLU Giessen



Schaffasz, Windpassinger et al. (2019) Agronomy 9: 535
<https://doi.org/10.3390/agronomy9090535>



Benchmark: US maize heterotic group development, Du Pont-Pioneer

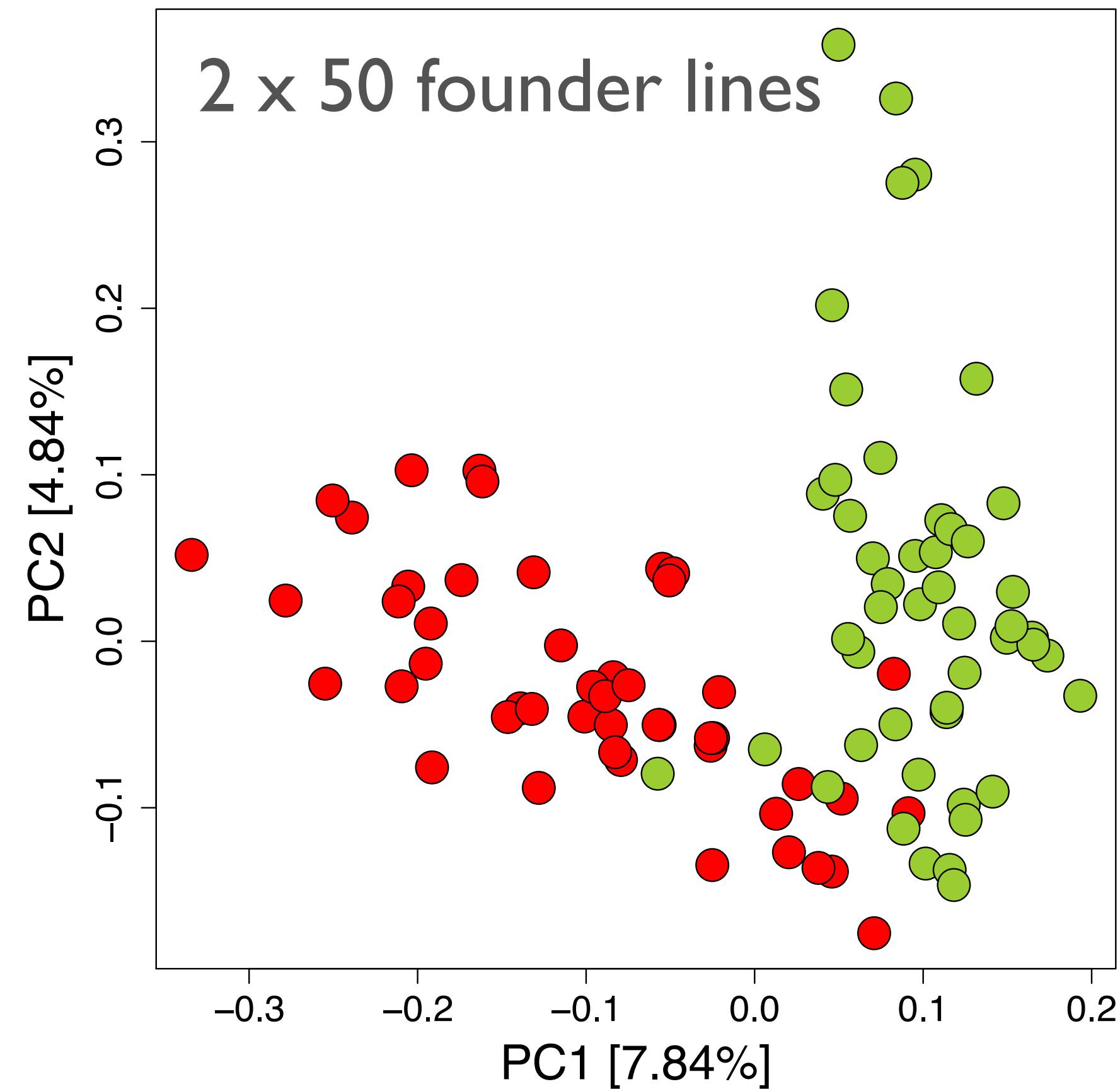


Source: A. Rafalski 2007

Genomics-guided breeding accelerates pool development

Fast-tracking pool development using genome-wide SNP data,
computer-simulated crossing designs and genomic selection

Example: winter rapeseed, a crop with poor diversity & low heterotic performance



Approach: Iterative, genomics-assisted chain crossing

Crossing scheme: Designed using computer simulations

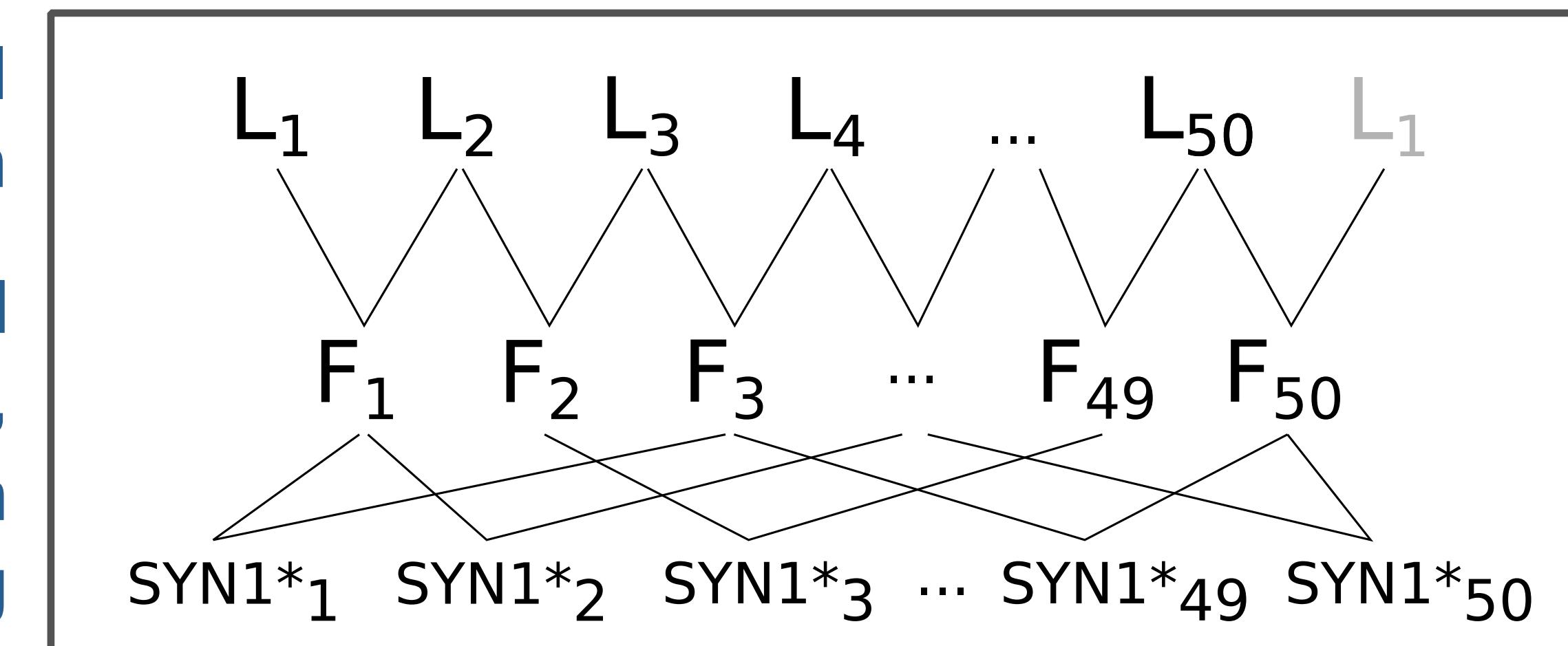
Aim: Retain, recombine & fix complementary diversity in each pool

50 founders per pool
chain-crossed, twice each

50 F1s chain-crossed
twice each,
then
3 generations of inbreeding

10 plants chosen from
each $SYN1^*_e$ family

Repeat across
3 cycles

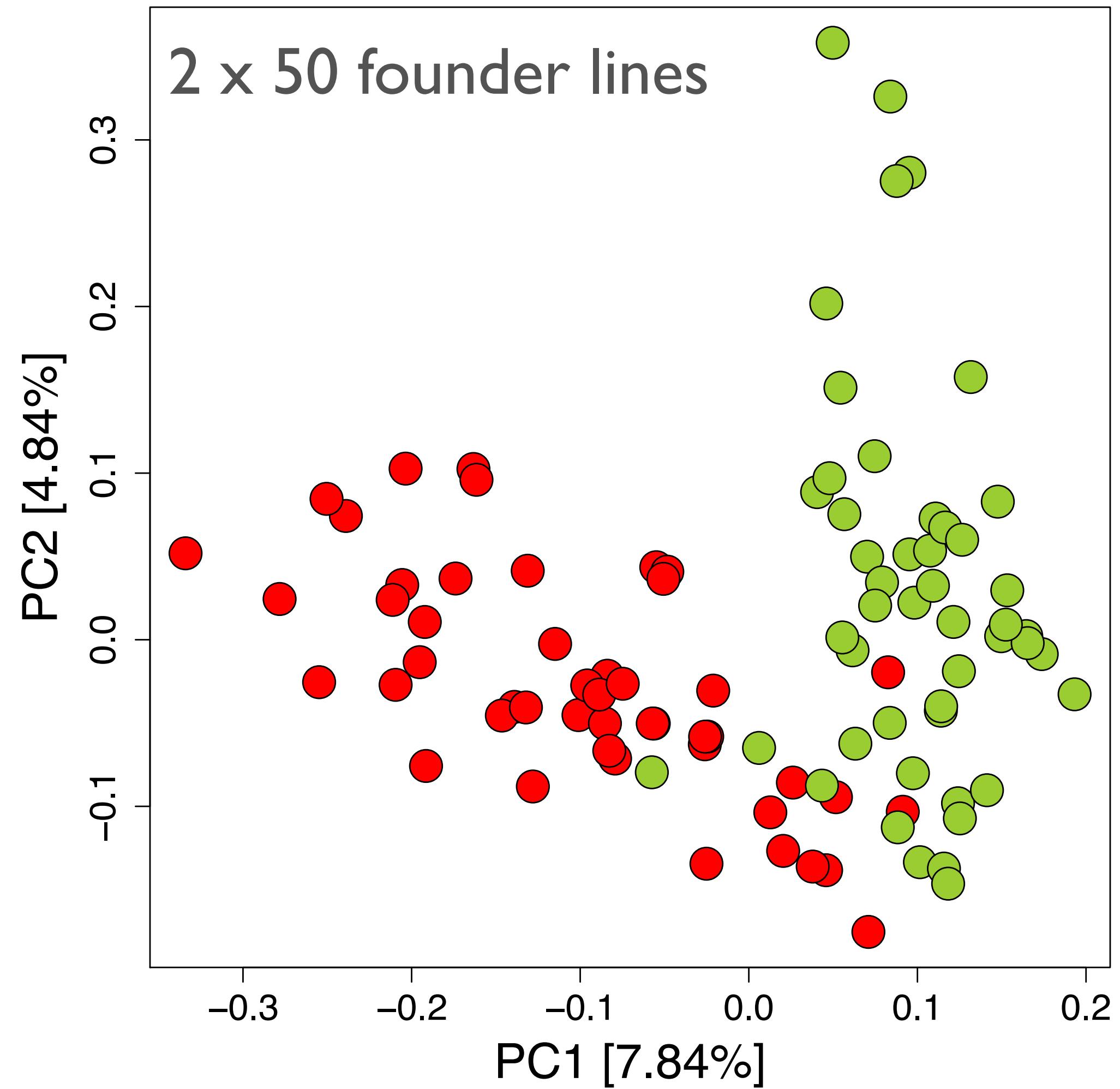


Target: Generate and genotype 500
“SYN” individuals per pool per cycle

Genomic recurrent selection to select
crossing parents for each generation

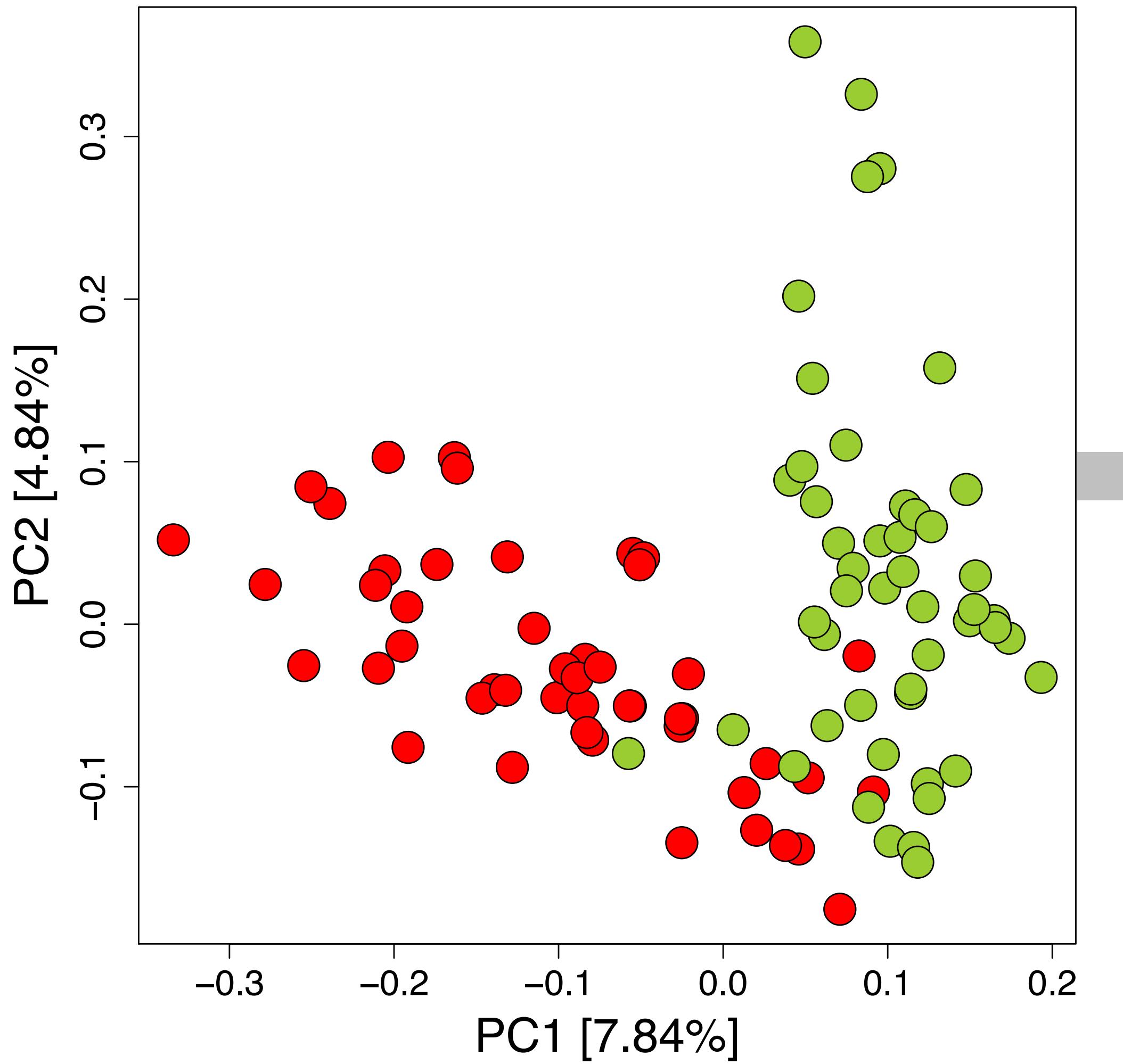
Nice idea, but does it work?

Two diverse founder pools pre-selected for *per se* performance and general combining ability (including multiple donors for all other “must-have” traits)

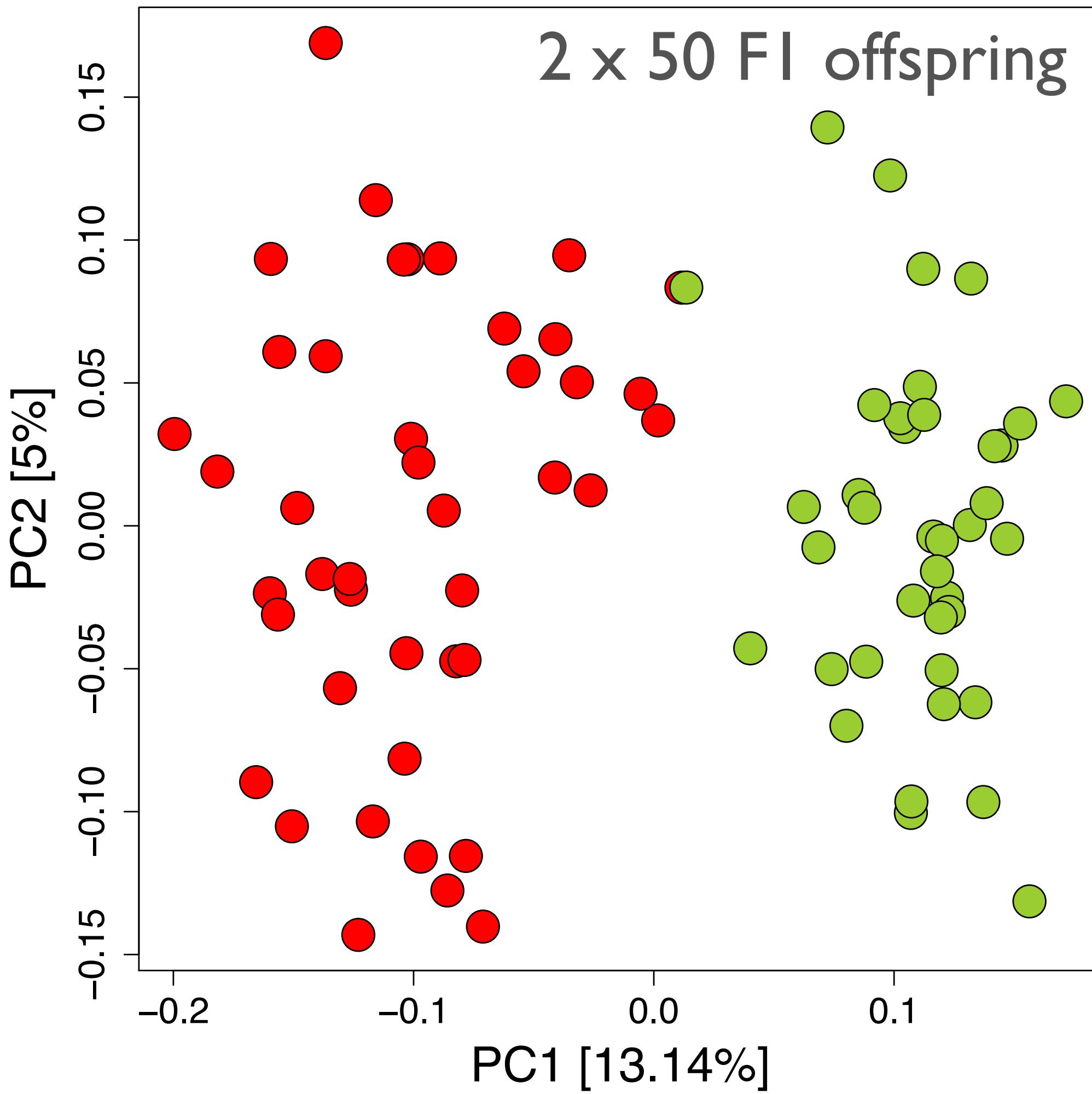


FI: Rapid separation of pools

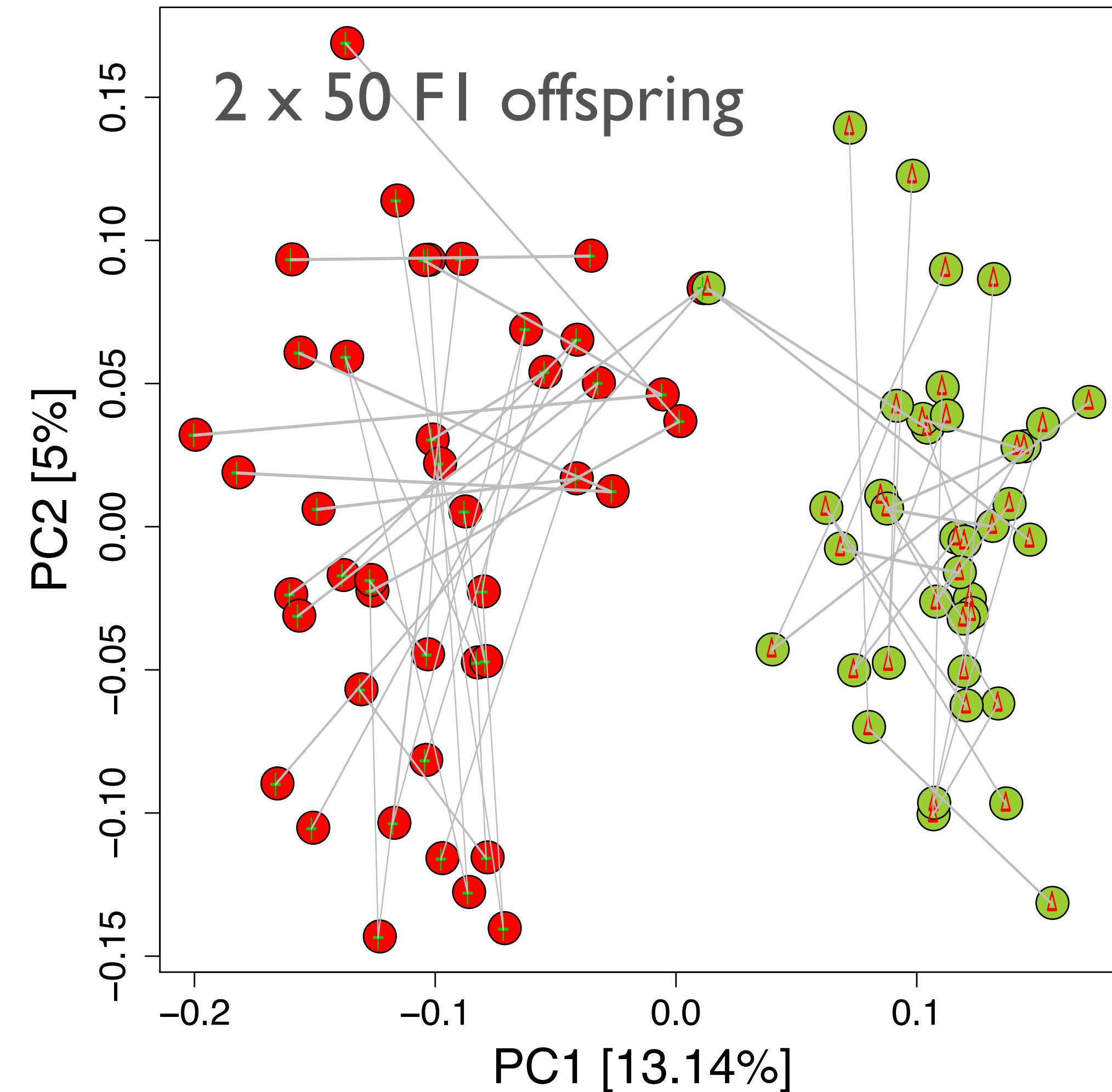
Founder pools pre-selected for *per se* performance & GCA including multiple donors for all “must-have” traits



Year I: Initial FIs from crosses between complementary founder lines



Chain crossing combinations designed based on computer simulations

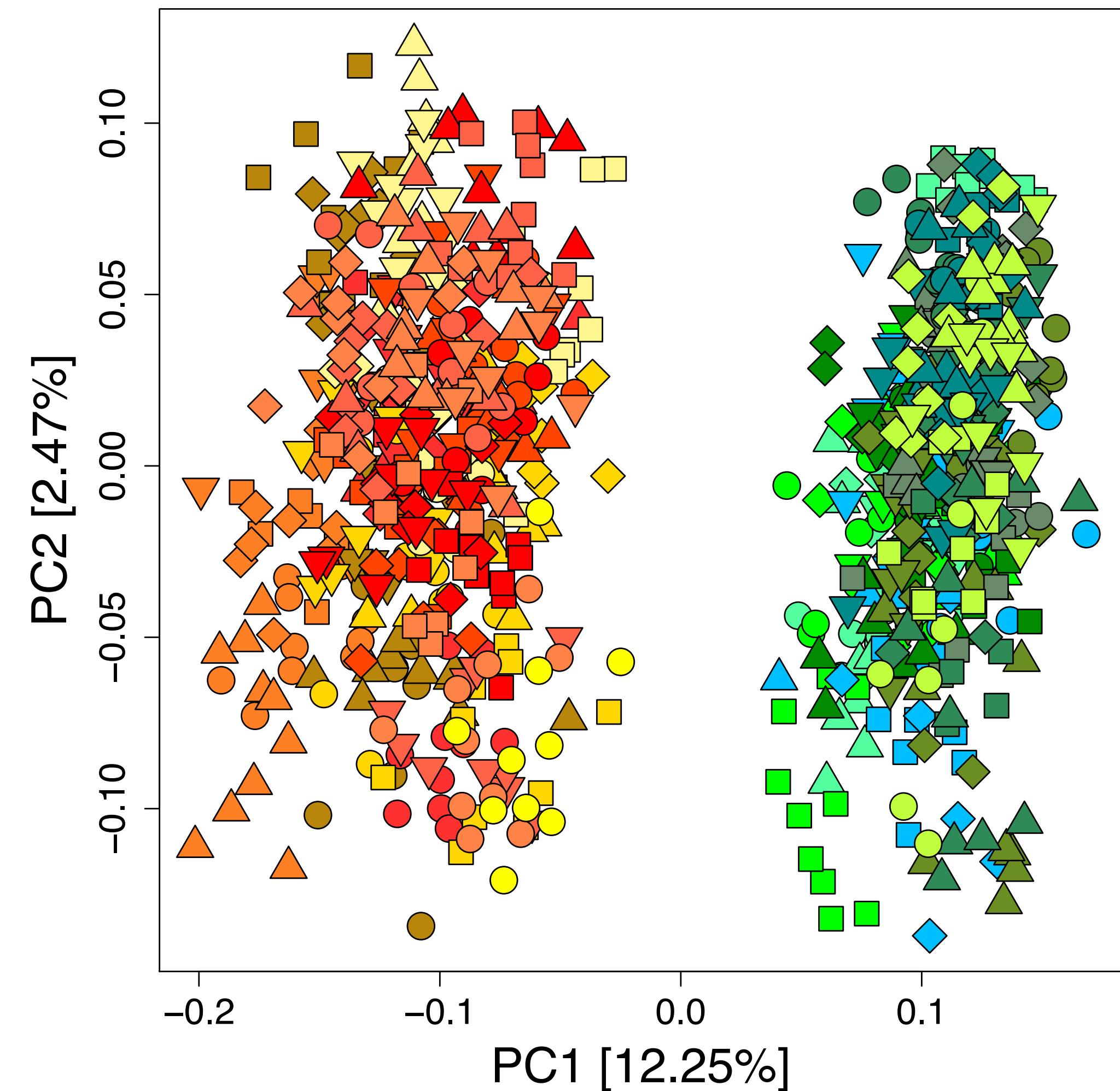


Criteria:

- Distance from opposite pool
- Distance from crossing partners
- Distance between the two cross partners
- Recombination patterns within pool
- Genome structure between pools

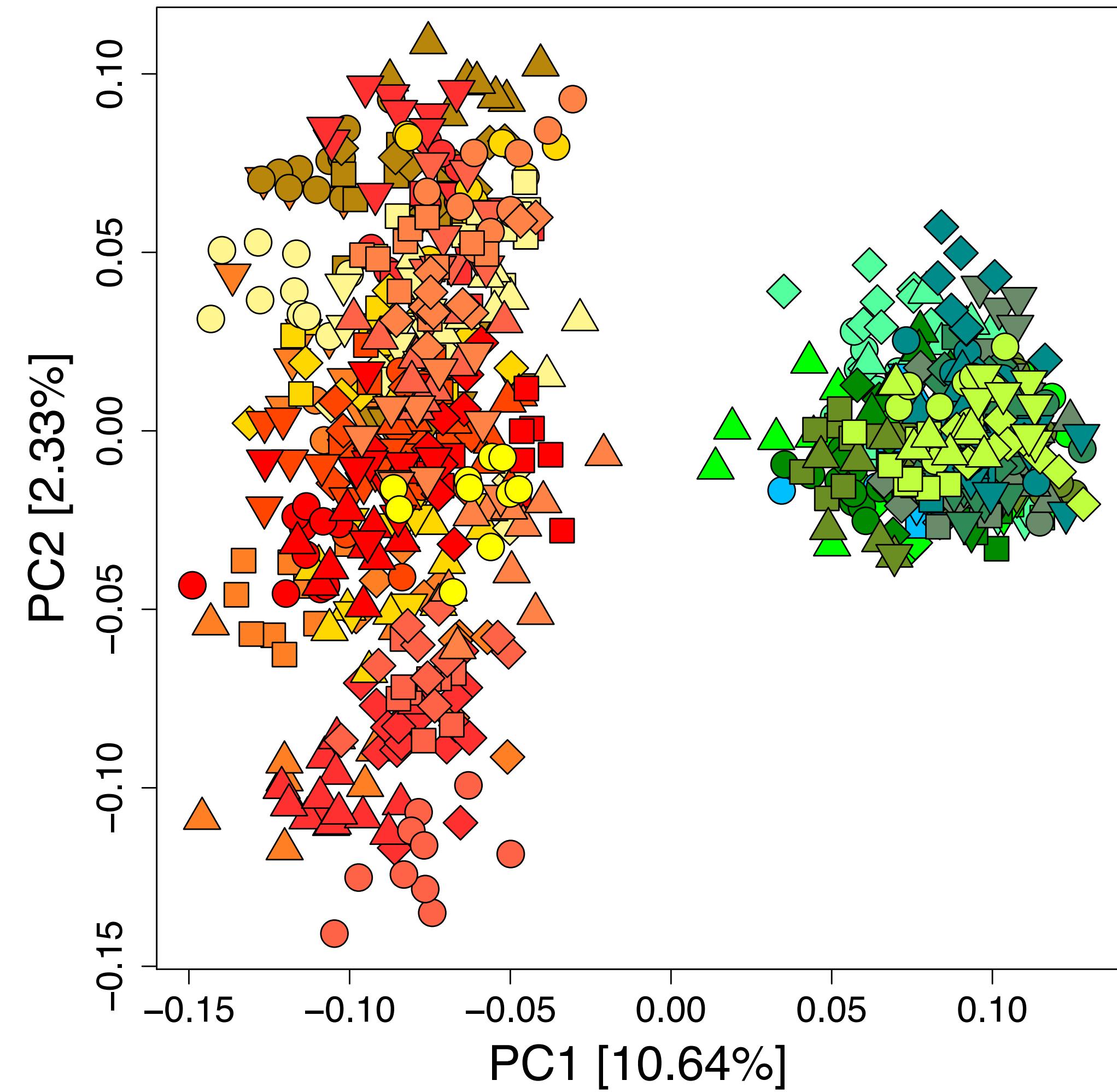
Crossing design: Testing by simulation

Year I: Simulated SYNL offspring from best simulated crossing scheme



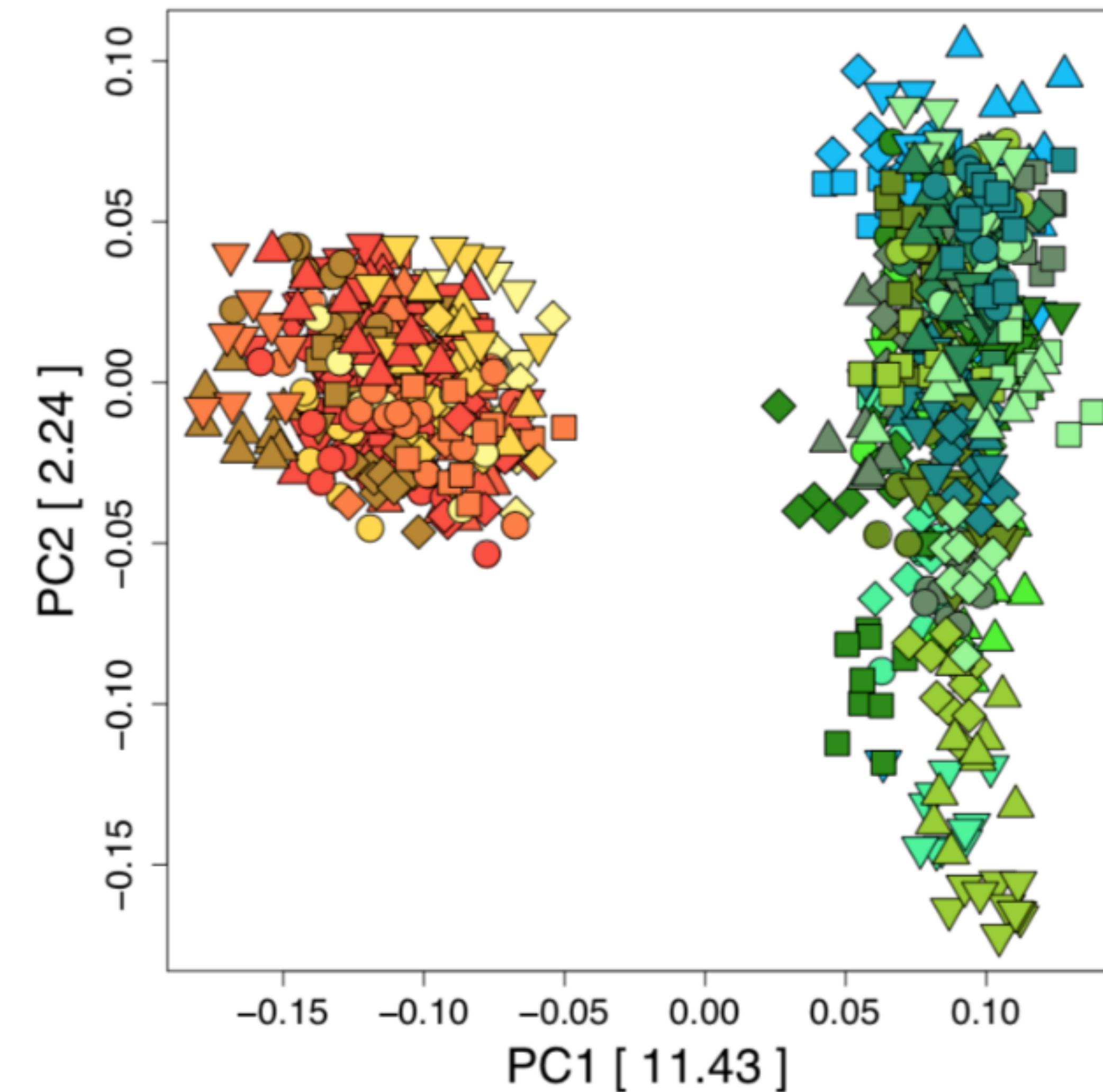
Result: Simulations worked pretty well!

| 8 months: Real SYNI offspring

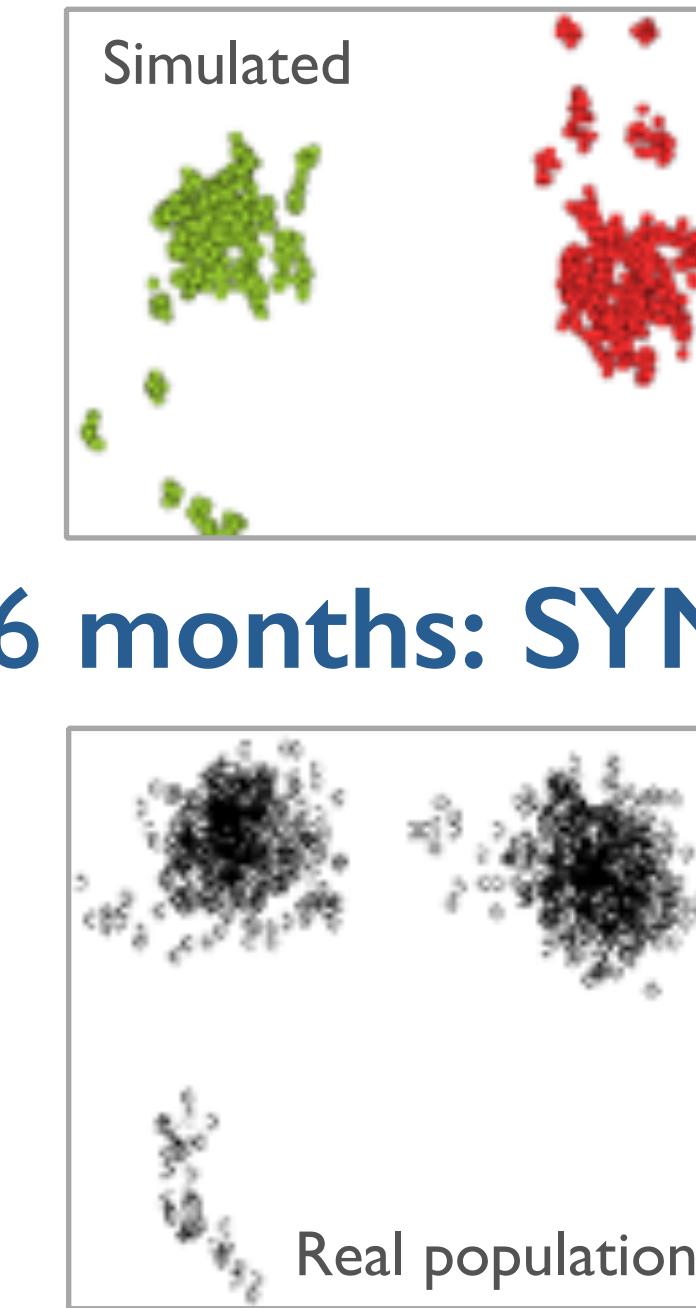


Overall: Emulated ~80 years of successful maize breeding in just 3 years!

28 months: Real SYN2 offspring



36 months: SYN3



Fast-tracking cold-adapted, heterotic pools for temperate Europe?

A lot of effort, but highly feasible in sorghum

- Extremely broad diversity, strong heterosis in clear heterotic groups
- Small, simple diploid genome

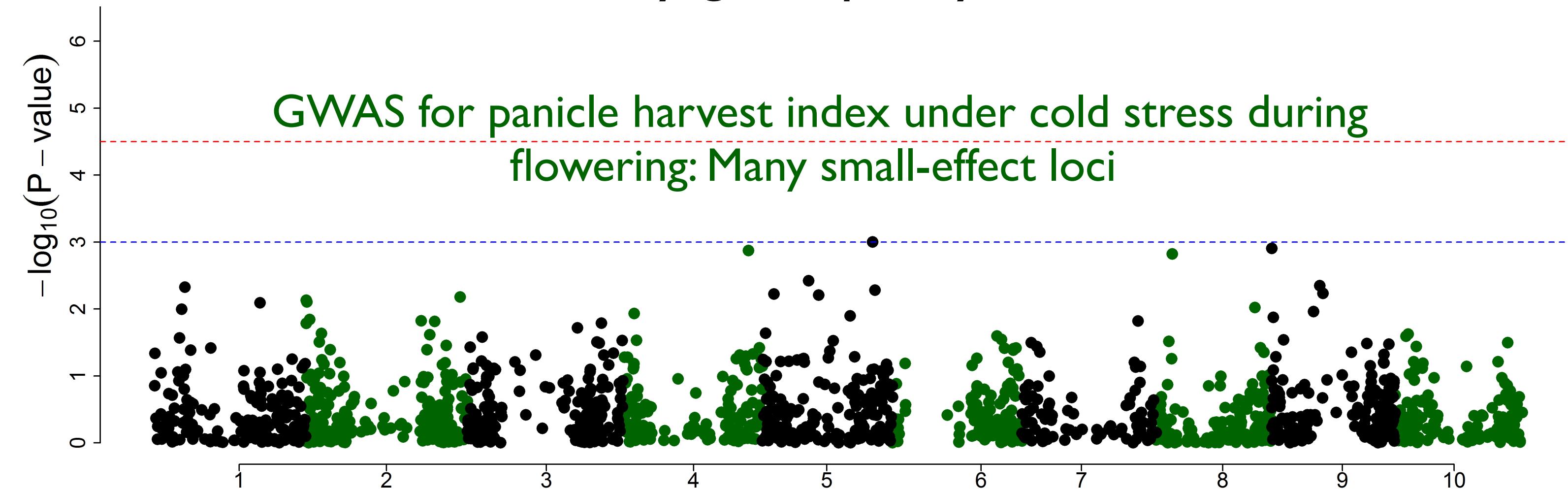
Prerequisites

- Well-characterised founders from two pools with good diversity for “must-have” traits (e.g. juvenile and reproductive cold tolerance), maturity, CMS, restorer genes
- A few years of intense effort for crossing, population development and genomic selection
- Robust and cheap platform for genome-wide SNP genotyping (GBS or array)

Identifying and utilising useful genetic variation

2) Reproductive cold tolerance (RCT) is complex but heritable

- If phenotyped in stable cold-stress environments (tropical high altitude), panicle harvest index is a very good proxy for RCT



Ideal prerequisites for the use of genomic selection strategies:

- Genome-wide SNP-based predictions of potential cold-tolerance sources
- SNP-based pre-selection of backcross offspring with high *per se* tolerance
- SNP-based selection for GCA, prediction of superior hybrid combinations

First results are very promising

- Good prediction accuracy within breeding pools
- Data collection for testing/application

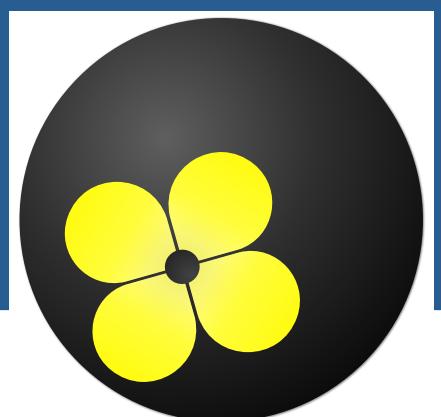
Prerequisites

- Robust and cheap platform for genome-wide SNP genotyping (GBS or array)
- High-quality phenotype data from large training populations (for adaptation traits: phenotype data from stable stress environments)

Take-hope messages

- Maize is the best example to show the potential to expand a versatile, highly diverse tropical crop into temperate crop production systems
- Use of genomics-based breeding techniques for identification, recombination and selection of useful diversity for sorghum hybrid breeding can theoretically help to achieve similar adaptive breeding success as maize in a fraction of the time
- However, enabling genomics-based breeding approaches in different steps of breeding programmes require a strong initial efforts to establish cheap, robust, standardised community genotyping tools

Sorghum cooperation partners, funding



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Plant Breeding
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University of Queensland, Brisbane –
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Makarere University, Kampala – Thomas Odong

Uganda National Genebank – Raphael Mufumbo

ICRISAT, Nairobi – Erick Mikwa, Damaris Odeny

Hessian State Bee Institute – Reinhold Siede



Deutsche
Forschungsgemeinschaft
DFG



Dual-purpose hybrid "Justus" (2020)
Bred by JLU Giessen, marketed by DSV Saaten