Genetic Diversity In Grain Crops

Jim Holland

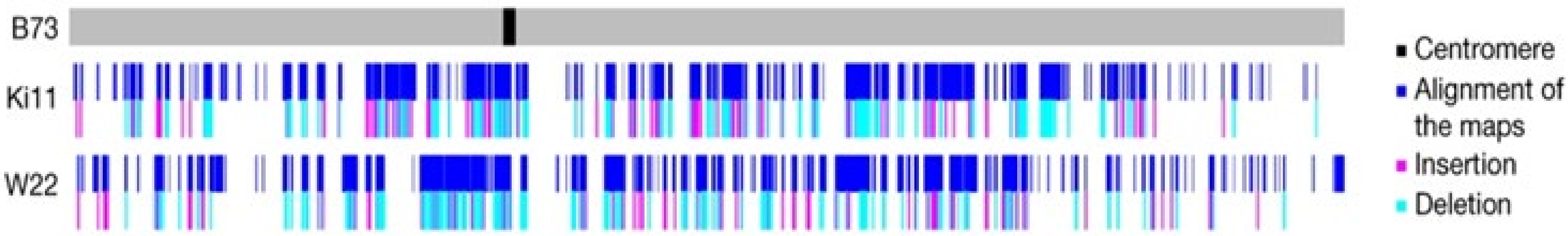
USDA-ARS

Maize: huge diversity, wide adaptational range, outcrossing

- 80% of maize genomes are smashed up repeated retroviral sequences
- 10s of Millions of Single Nucleotide Polymorphisms *after* removing repeated sequences
- Widespread structural variation (large chunks of DNA missing from one variety compared to another)
- A few traits (e.g, seed color) controlled by individual sequence variations of large effect
- Most traits controlled by 10s to 1000s of sequence variations with complex interactions with environment

Jesús Sánchez Gonzalez

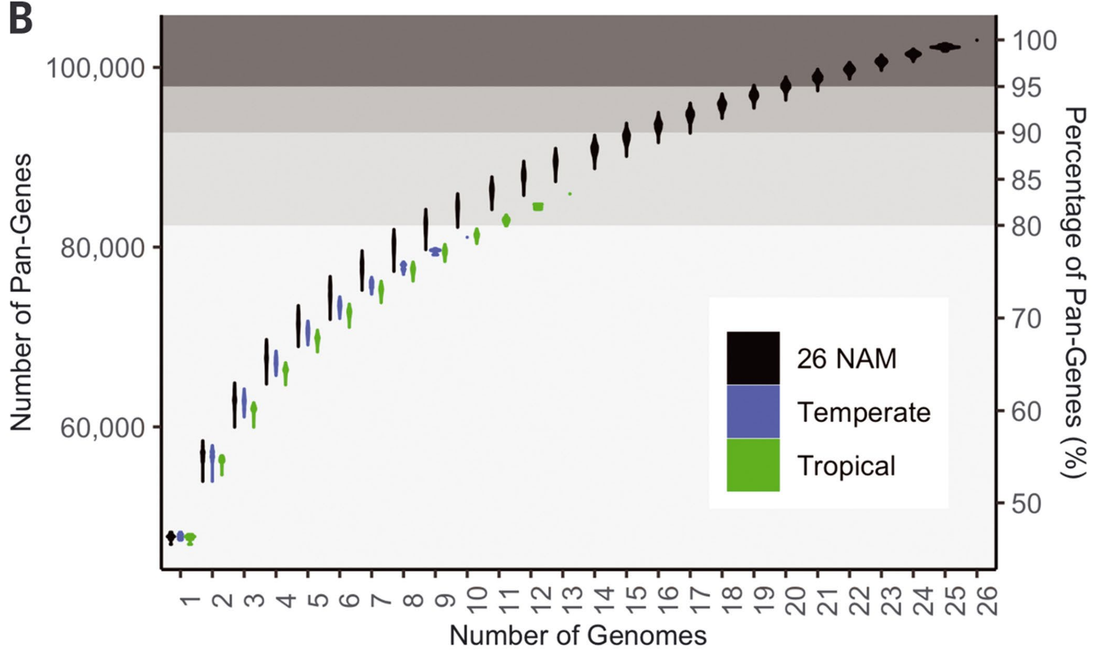
Structural sequence variation among maize genomes



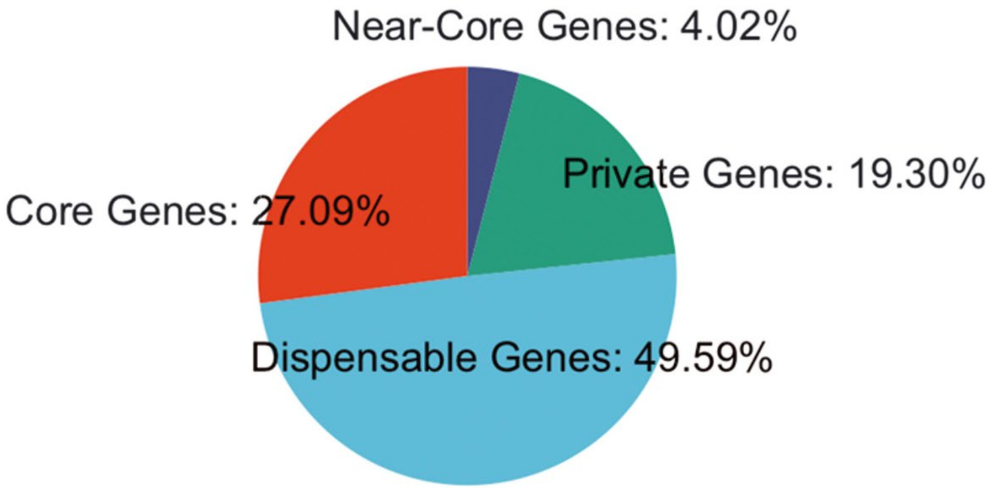
Jiao et al (2017)

20,470,711 SNPs among 26 maize inbreds
71,196 Structural variants > 100 bp in size
Many entire genes vary between lines

Hufford et al. (2021)



The maize “Pan-Genome”



Historical classification of diversity in maize

Geographic and “racial” complexes

Cónico

Caribbean Dents

Southern popcorns

Northern S. Am. pops

…

Cravos

F_{ST} measures the proportion of total variation due to differences among groups

Landraces

F_{ST} ~ 0.10 – 0.23

Pepitilla

Palomero Toluqueño

Arrocillo Amarillo

Chalqueño

Cónico

NSL 2837

JAL 167

NSL 2844

JAL 153

JAL 154

…

CHIH 7

Accessions

F_{ST} ~ 0.15

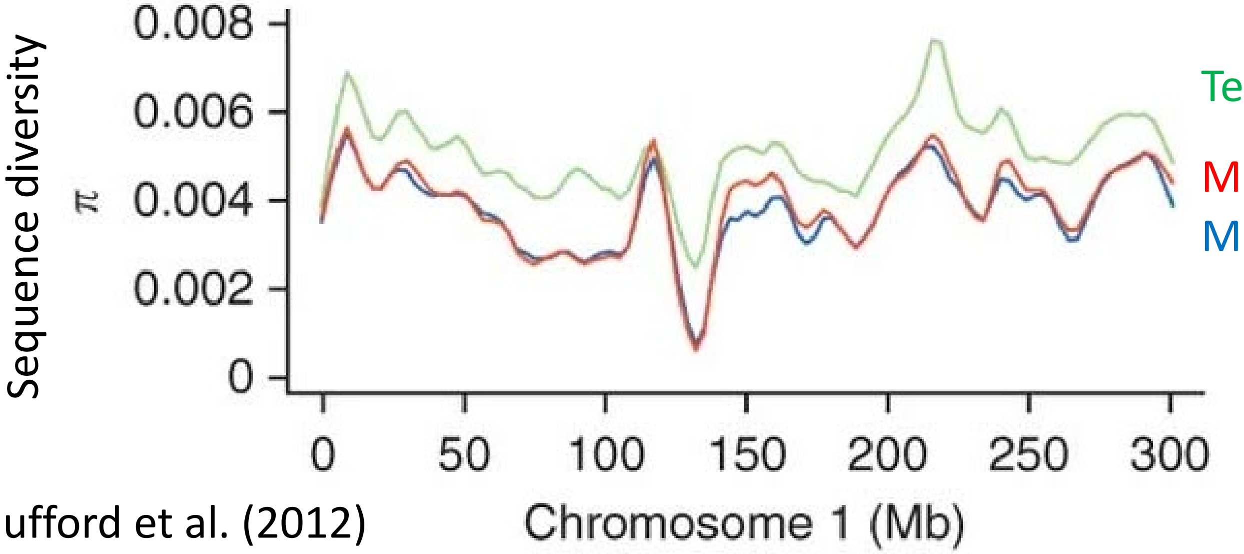
USDA PI collection has ~ 20,000 maize accessions

Individual plants

Eliud Castaño Suárez, CONABIO

F_{ST} estimates from Goodman, Sanchez, Doebley papers

Reduced genetic diversity due to domestication and modern breeding



Hufford et al. (2012)

Teosinte

Maize landraces (83% of diversity in teosinte)

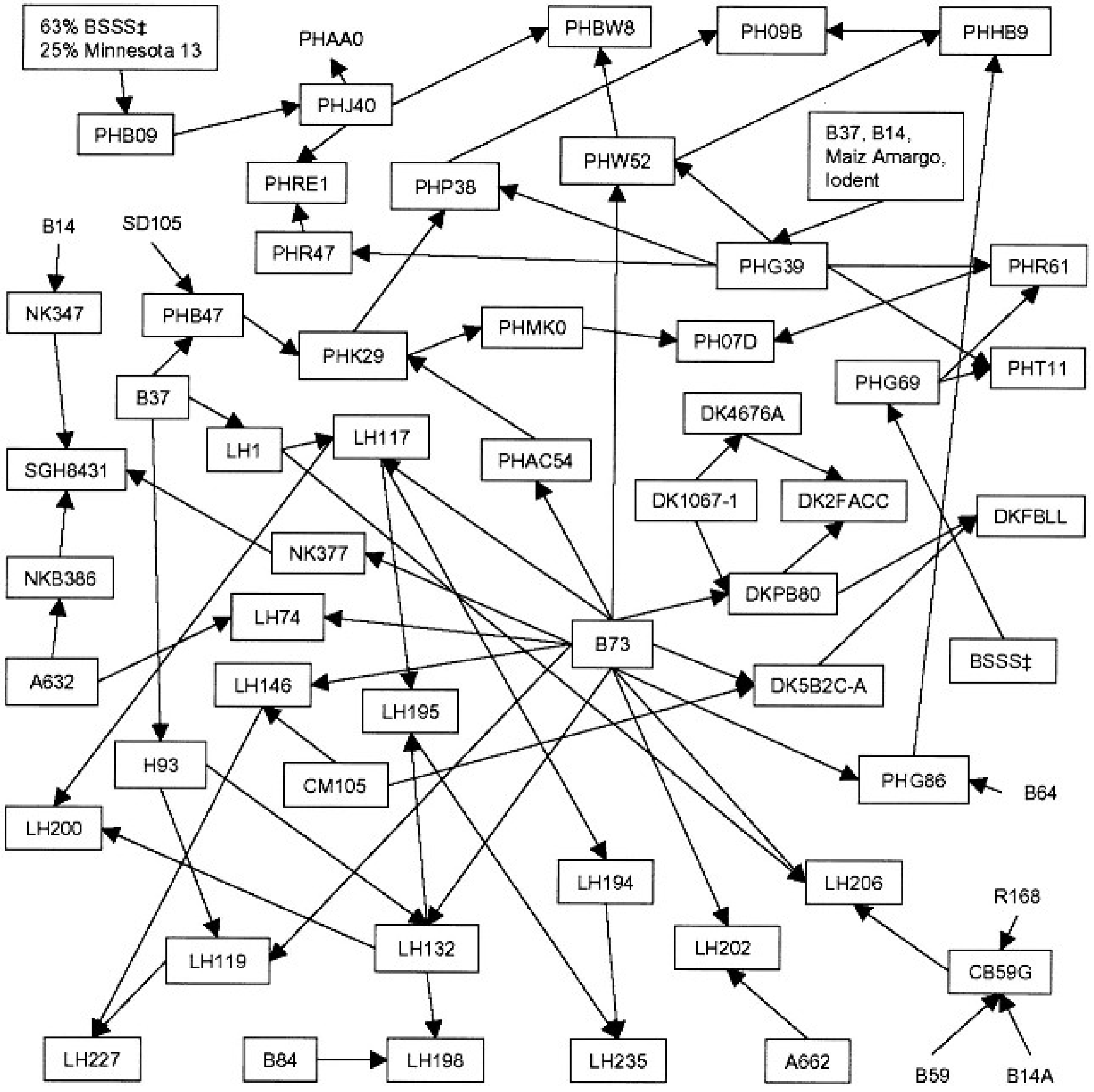
Maize global inbreds

Similar to landrace diversity in Hufford et al (2012)

but

USA inbreds have 23% reduction in diversity compared to landraces (Tenaillon et al. 2001)

Extensive recycling of elite lines in USA corn breeding.



Commercial Stiff Stalk Inbred Pedigrees (Mikel and Dudley 2006)

- Extensive use of a small number of key founder lines (e.g., B73).
- Recycling of elite lines results in closed pedigrees.
- ~3% of hybrid pedigrees represented by exotic germplasm (mostly temperate origin).
- Pioneer hybrids from 2000s have fewest # SSR alleles of any decade (survey starts in 1920s, Duvick et al., 2004)

Why Broaden the Genetic Base?

- We could make better gains from selection if unique favorable alleles from exotic germplasm sources could be incorporated into U.S. elite germplasm base.
- Tropical germplasm contains unique grain characteristics.
- Enhanced diversity could provide buffering against shifting pathogen populations and stresses.

“Most genetic variation is not favorable” – Arnel Hallauer

- Favorable gene variants in tropical maize are linked to unfavorable variants for modern temperate production environments

Photoperiod-sensitivity of tropical corn – flowers too late in USA summer

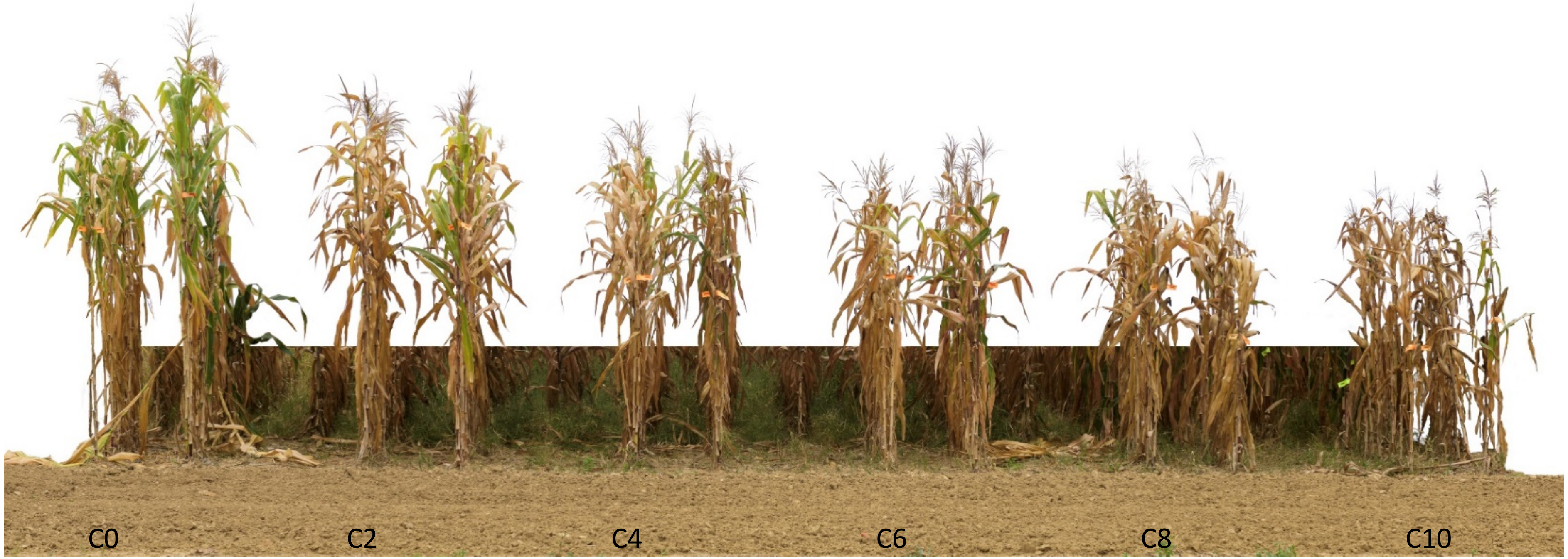
USA hybrid

Mexican Tuxpeño landrace

Smut susceptibility

Lodging

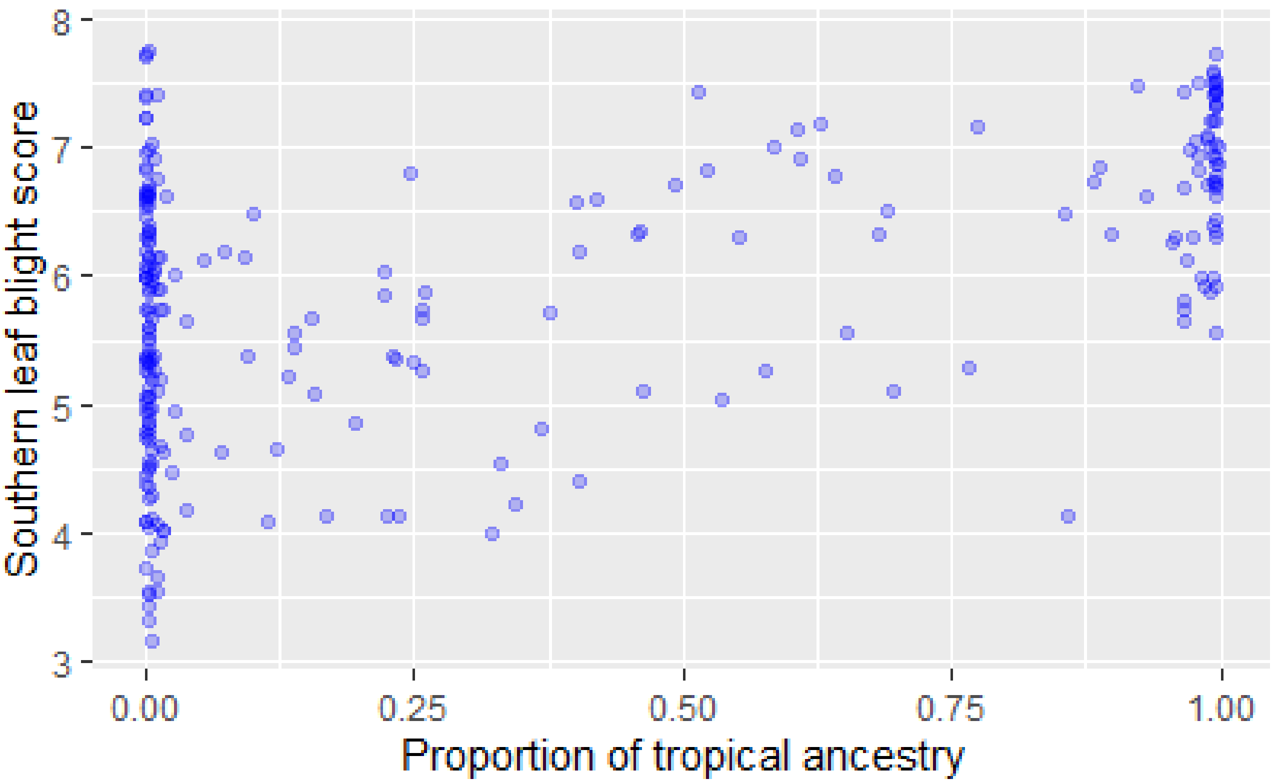
Selection for adaptation of tropical populations works



Ten cycles of phenotypic selection for early flowering in Tusón by Hallauer (Teixera et al. 2015): About 30 day decrease in mean silking date.

- A few major genes + thousands of very small effect genes involved in selection response. (Wisser et al. 2020)
- We are researching using genomic selection and gene editing approaches to speeding this up.
- But this is only the first step to getting tropical germplasm incorporated into elite adapted maize!

Tropical maize harbors disease resistance alleles



Correlation between tropical ancestry and Southern leaf blight resistance in 282 diversity panel = 0.51

- Rcg1 anthracnose resistance gene (commercialized in Pioneer hybrids) is an insertion variant found only in older lines of tropical origin (Frey et al. 2011)

Tropical maize also has useful yield genes

- Long-term effort by Major Goodman (NCSU) has created a unique temperate-adapted all-tropical breeding pool.
- Selection within tropical by tropical line crosses can greatly improve their adaptation.
- High heterosis between tropical lines and temperate lines of any group suggests tropical lines have unique complementary alleles for yield.

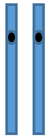
USDA Germplasm Enhancement of Maize Project

Candace Gardner, USDA

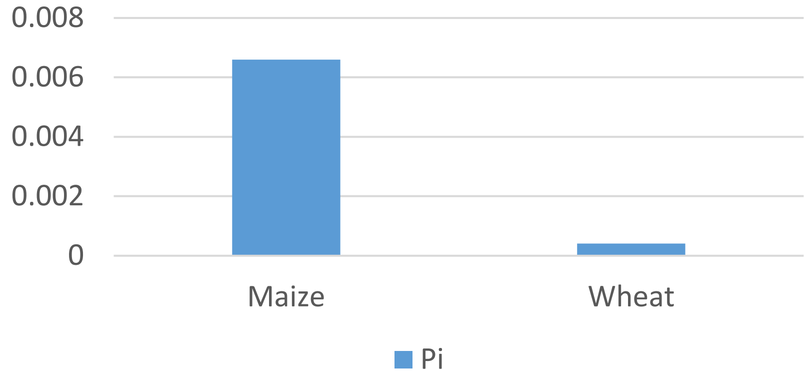
- Cooperative project between USDA, universities, and private industry
- Develop inbreds with 25% - 50% exotic parentage in combination with elite commercial lines
- Visual selection for adaptation, extensive yield trial evaluations
- Publicly released inbreds can be used by breeding companies

Maize

- Outcrossing
- Diploid (2 copies of each chromosome)



- High genetic diversity
- Domestication bottleneck
- Few good major effect genes for any traits
- Wild relative (teosinte) rarely used for breeding
- Global breeding lines and landraces are best genetic resource

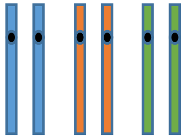


Average rate of SNP variation per base pair (Pi)

My ballpark estimates from sequencing maize (Gore et al, 2009) and wheat (Walkowiak et al, 2020) varieties

Wheat

- Selfing
- Hexaploid (2 copies each of A, B, and D genomes)



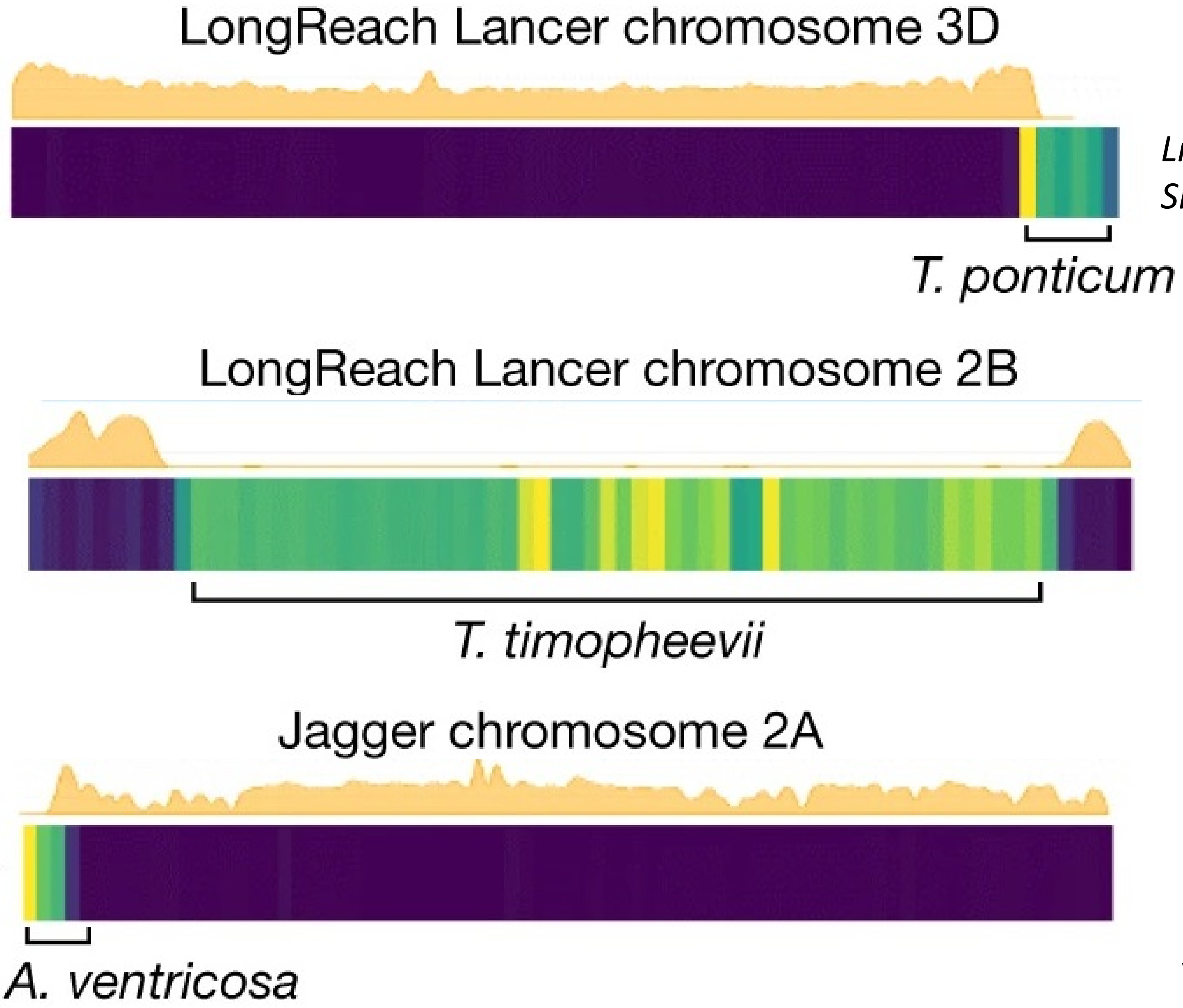
- Low genetic diversity
- Extreme domestication bottleneck associated with rare polyploidy event
- Numerous large-effect disease resistance genes introgressed from wild relatives
- Global wheat collections and wild relatives regularly used for introgression breeding

Feldman and Sears (1981)

Wild species introgressions in modern wheat variety genomes

% Identity to wheat

% Identity to wild



Lr24 (leaf rust) and
Sr24 (stem rust)

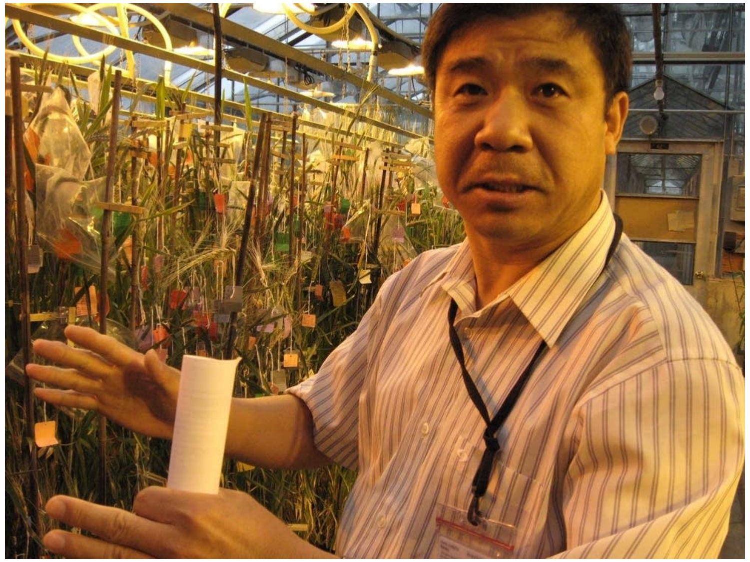
Sr36 (stem rust)

Lr37–Yr17–Sr38
multiple rust
resistance gene cluster
+ blast resistance

Walkowiak et al. (2020)

Introgression of new genes from wild relatives in wheat is ongoing

- Wild species introgression programs still active in:
- Kansas State
- USDA/North Dakota
- Canada
- UK
- Australia
- Require special techniques such as embryo rescue



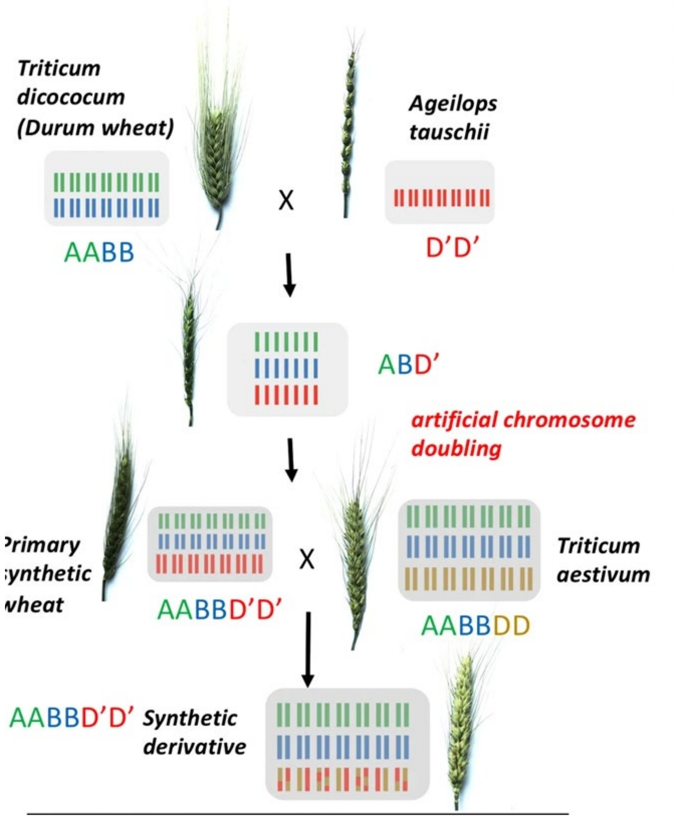
Steven Xu. Photo: Dan Gunderson

Stem rust. Photo: Yue Jin

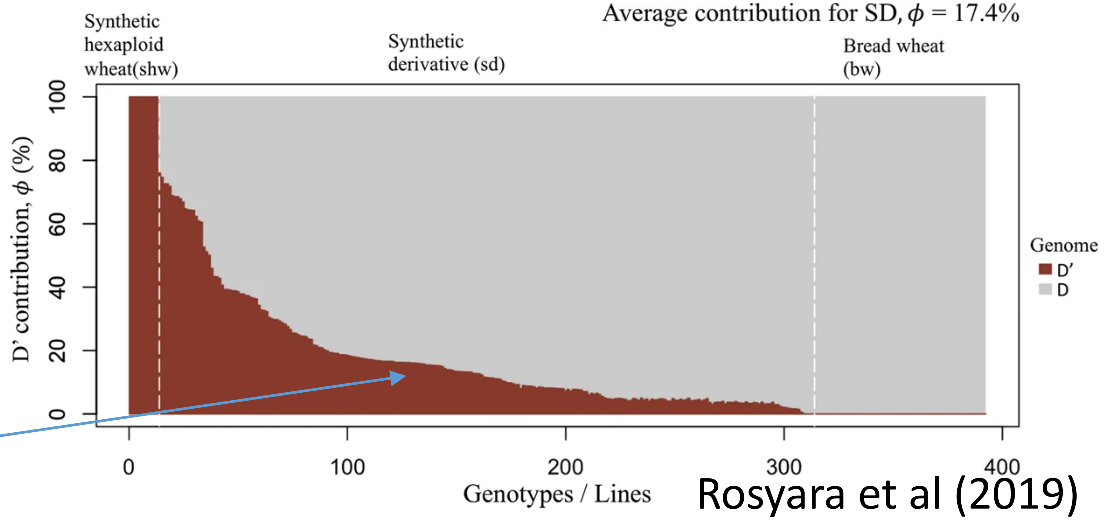
Synthetic hexaploid wheat

CIMMYT program to increase diversity of bread wheat using new genes from wild *A. tauschii*

- Increased climate resilience through drought tolerance
- Numerous disease resistances



Average of 17% of D-genome derived from *A. tauschii* among advanced lines in CIMMYT breeding program

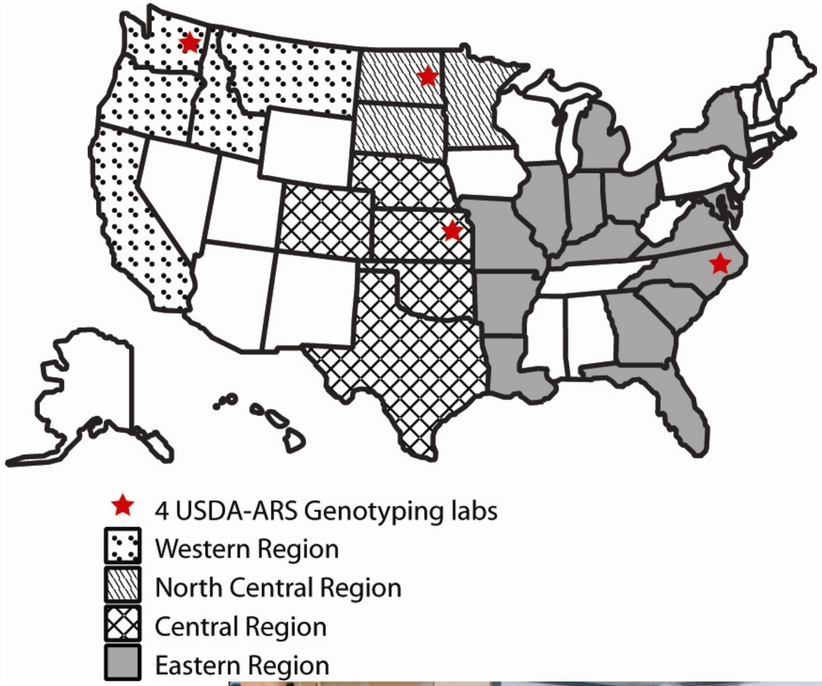


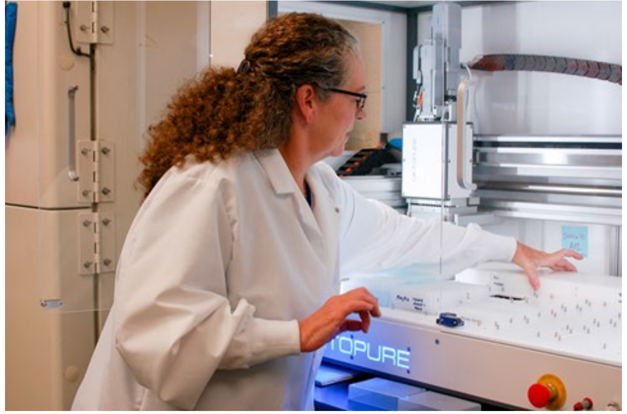
Rosyara et al (2019)

Wild species and global wheat diversity mined for disease resistance and stress tolerance

USDA Regional Small Grains Genotyping Labs

- Provide rapid genotyping evaluations targeted for major genes affecting:
    - Food quality
    - Disease resistances
    - Insect resistances
- Most of the targeted desired genes are derived from wild relatives or exotic domesticated germplasm
- Selection for yield and agronomics performed by breeders in field.
- Now being augmented by genomic selection as well





Gina Brown-Guedira