Alleviating wheat constraints through pre-breeding with wild relatives, landraces etc

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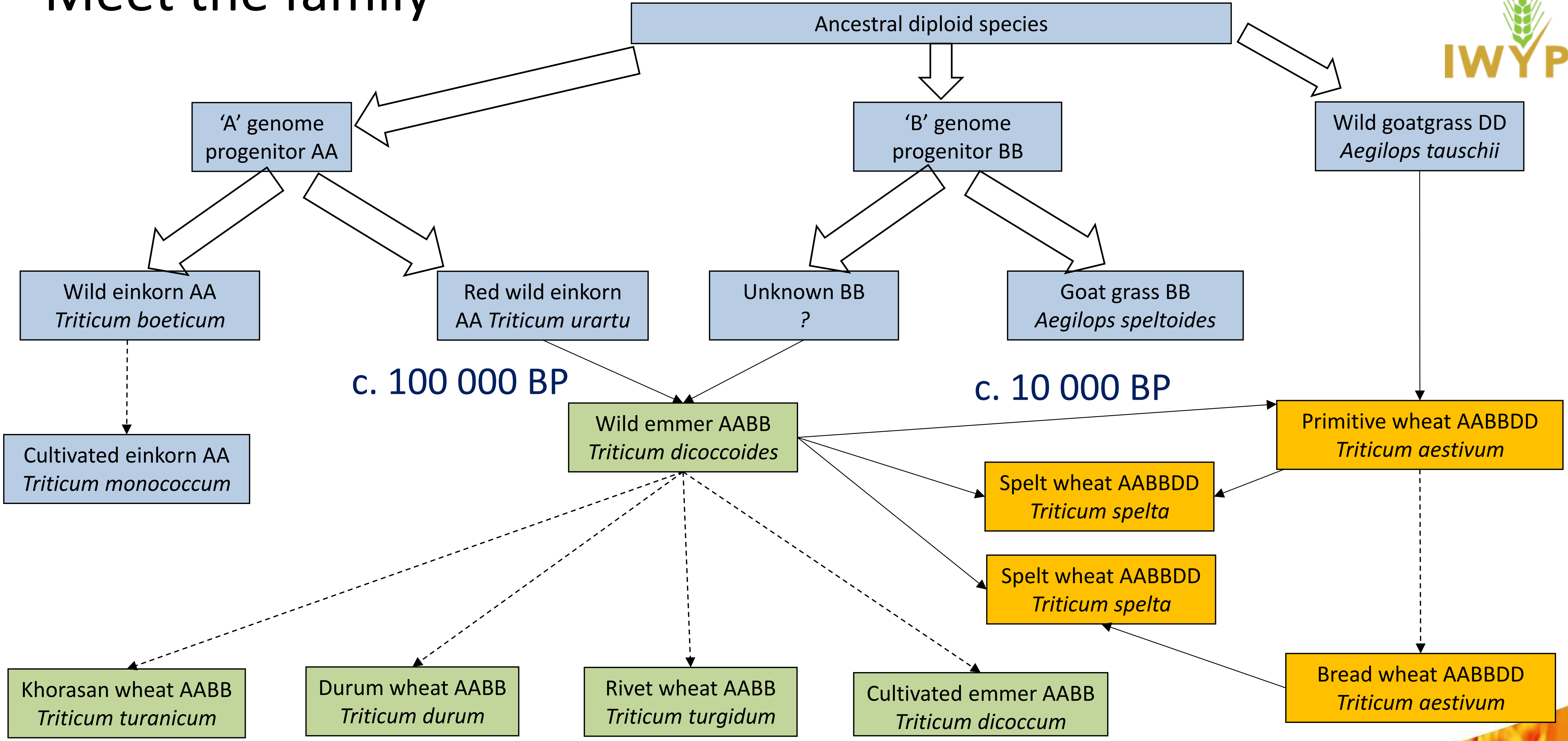
International Wheat Yield Partnership

Research to Deliver Wheat for the Future

Unlocking the Genetic Yield Potential of Wheat

Meet the family



Ancestral diploid species

'A' genome progenitor AA

'B' genome progenitor BB

Wild goatgrass DD *Aegilops tauschii*

Wild einkorn AA *Triticum boeticum*

Red wild einkorn AA *Triticum urartu*

Unknown BB *?*

Goat grass BB *Aegilops speltoides*

c. 100 000 BP

c. 10 000 BP

Cultivated einkorn AA *Triticum monococcum*

Wild emmer AABB *Triticum dicoccoides*

Primitive wheat AABBDD *Triticum aestivum*

Spelt wheat AABBDD *Triticum spelta*

Spelt wheat AABBDD *Triticum spelta*

Bread wheat AABBDD *Triticum aestivum*

Khorasan wheat AABB *Triticum turanicum*

Durum wheat AABB *Triticum durum*

Rivet wheat AABB *Triticum turgidum*

Cultivated emmer AABB *Triticum dicoccum*

Simplified wheat family tree. Diploids are shown in blue, tetraploids in green and hexaploids in orange. Block arrows show species divergence through natural selection, dashed arrows show divergence through domestication, and solid arrows indicate species formed through hybridisation.

Overcoming bottlenecks

- Working backwards:
- ‘Cross the best with the best and select the best” – nearly all breeder crosses are within narrow pool of elite material
- Domestication itself was a bottleneck – early selection at the dawn of cultivation will have constrained the diversity passed down
- And most powerfully there are the ancient bottlenecks of hybridisation itself: relatively few D genome donors contributed to the first hexaploid wheats

- Genomics tells us that since domestication, gene flow has been much greater between AB /ABD than between D / ABD

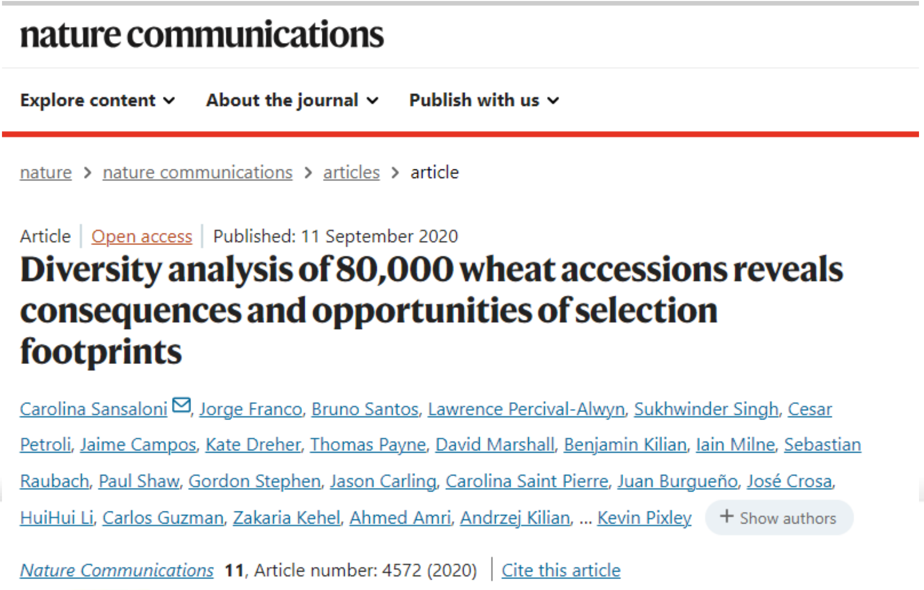
The need for diversity

- Diversity is the raw material for crop improvement
    - Sources of disease resistance to protect against “new variants”
    - Resistance and tolerance to insects and other pests
    - Tolerance to abiotic stresses – waterlogging, drought, heat
- Diversity can/should be introduced into our existing crops
- Pre-breeding – “cross the worst with the best and hope for the best”

Landrace + Crop Wild Relative diversity

- Seeds of Discovery - CIMMYT and ICARDA combined wheat collections
  - > 79 000 wheat accessions in combined collection
    - 56.3k domesticated hexaploids, 18.9k domesticated tetraploids, 3.9k Crop Wild Relatives
  - Diversity analysis using DArTseq
  - Large proportion of landrace variation not present in modern elites
  - Evidence of QTLs avoiding ‘trade-off’ paradigms eg yield and grain protein

https://doi.org/10.1038/s41467-020-18404-w

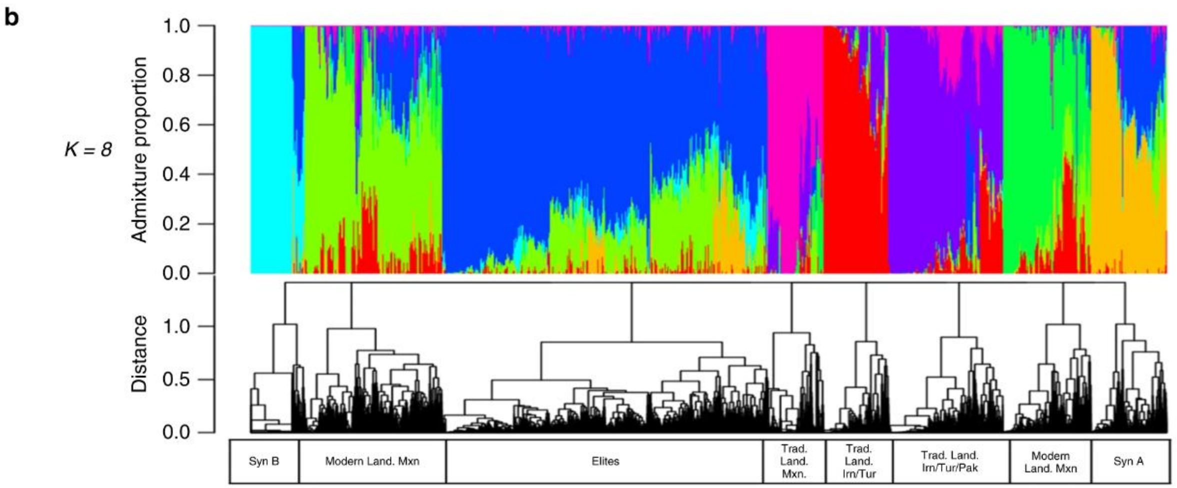


Article | Open access | Published: 11 September 2020

Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints

Carolina Sansaloni, Jorge Franco, Bruno Santos, Lawrence Percival-Alwyn, Sukhwinder Singh, Cesar Petroli, Jaime Campos, Kate Dreher, Thomas Payne, David Marshall, Benjamin Kilian, Iain Milne, Sebastian Raubach, Paul Shaw, Gordon Stephen, Jason Carling, Carolina Saint Pierre, Juan Burgueño, José Crosa, HuiHui Li, Carlos Guzman, Zakaria Kehel, Ahmed Amri, Andrzej Kilian, ... Kevin Pixley

Nature Communications **11**, Article number: 4572 (2020) | Cite this article



Landrace diversity – Watkins collection

- AE Watkins collection, held at GRU (John Innes Centre)
  - > 1000 bread wheat landraces collected from 32 countries during 1920s-30s via Watkins' contacts through the London Board of Trade
  - Some mistakes, some losses but 827 landraces still actively conserved representing Europe, Asia and N Africa
  - Significant effort led by Simon Griffiths to establish these as a key genetic resource
  - Association panels, core collections, NAM and biparental RIL populations, QTL NILs
  - With AGIS/CAAS, collection sequenced and curated via portal https://wwwg2b.com/
  - Key publication in Nature 2024
  - https://doi.org/10.1038/s41586-024-07682-9

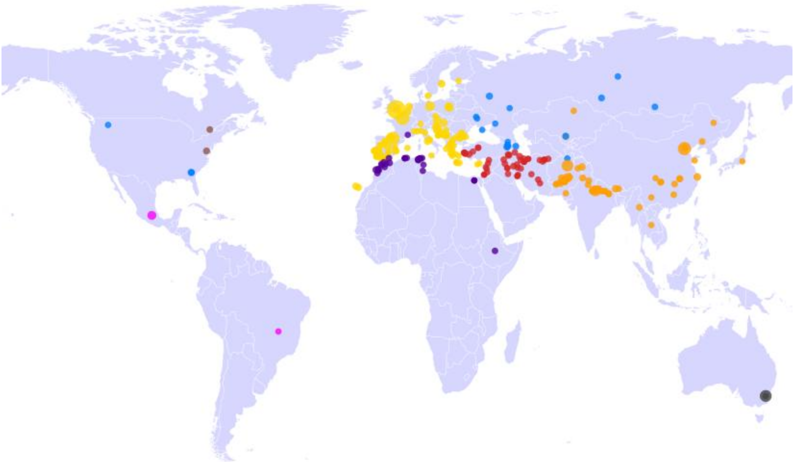
Article | Open access | Published: 17 June 2024

Harnessing landrace diversity empowers wheat breeding

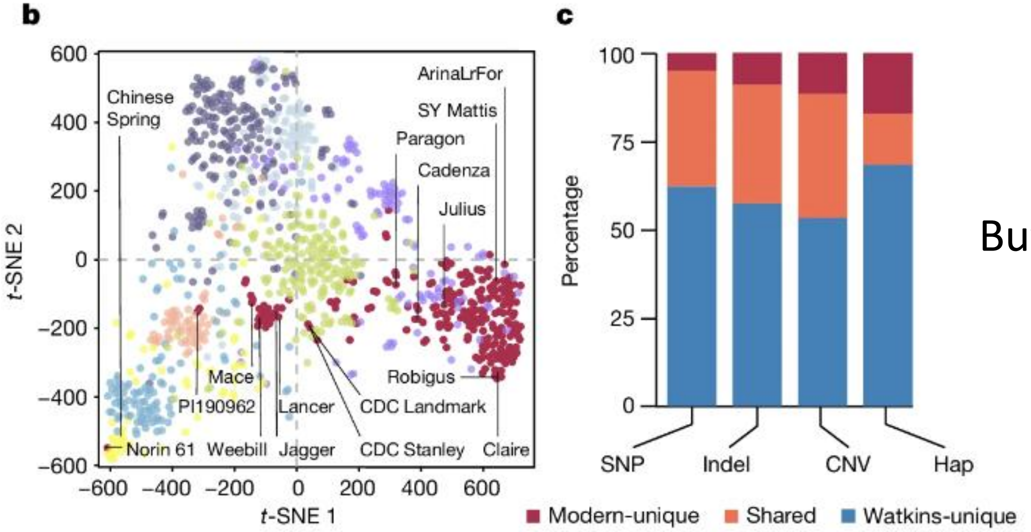
Shifeng Cheng, Cong Feng, Luzie U. Wingen, Hong Cheng, Andrew B. Riche, Mei Jiang, Michelle Leverington-Waite, Zejian Huang, Sarah Collier, Simon Orford, Xiaoming Wang, Rajani Awal, Gary Barker, Tom O'Hara, Clare Lister, Ajay Siluveru, Jesús Quiroz-Chávez, Ricardo H. Ramírez-González, Ruth Bryant, Simon Berry, Urmil Bansal, Harbans S. Bariana, Malcolm J. Bennett, Breno Bicego, ... Simon Griffiths

Nature **632**, 823–831 (2024) | Cite this article

“Reservoir of untapped diversity”



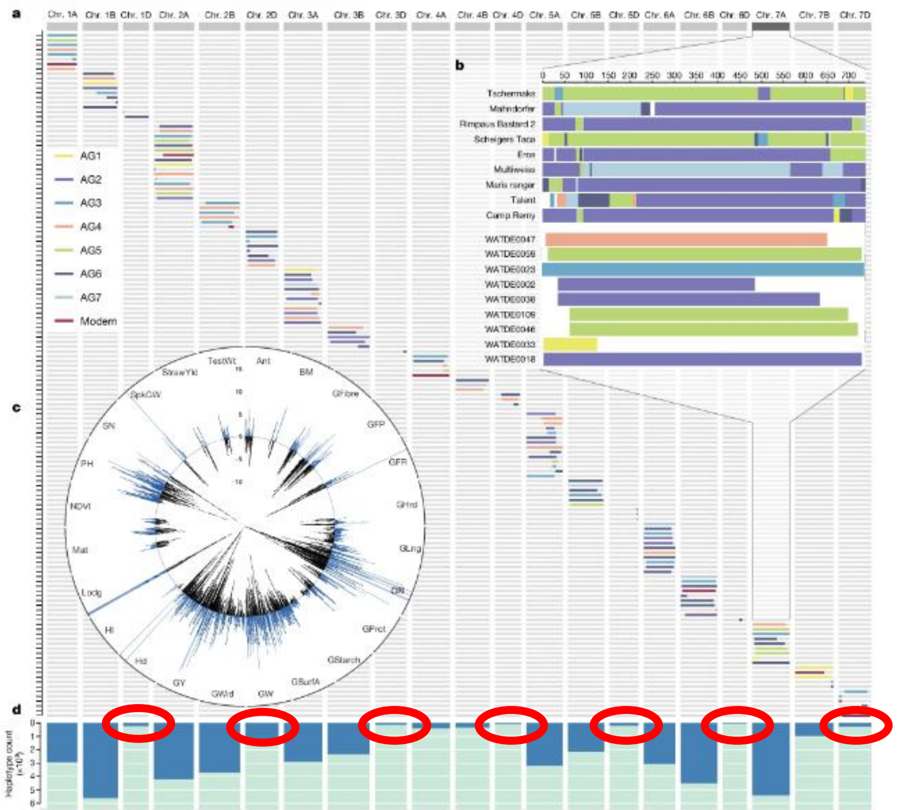
Full collection clusters into diversity groups AG1-AG7
Modern varieties nearly all trace back to AG2 & AG5
Some variation unique to modern – largely from wild relatives
Most variation unique to Watkins, including Yr resistances
Other beneficial traits appear to avoid “trade-off” paradigms eg yield and protein



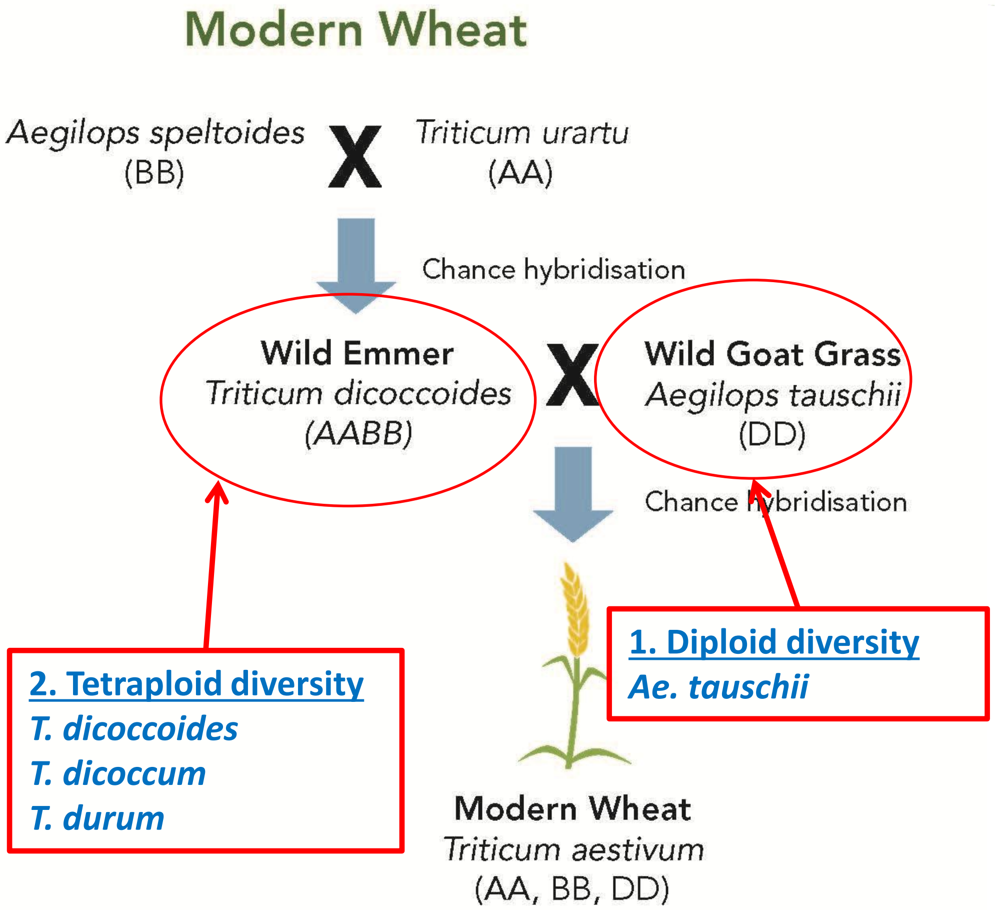
But little D-genome variation…

Fig. 4: Validation of the breeding value and delivery of target segments.

From: Harnessing landrace diversity empowers wheat breeding



Resynthesis and wide crossing: re-wilding wheat



Modern Wheat

Aegilops speltoides (BB) X *Triticum urartu* (AA)

Chance hybridisation

Wild Emmer *Triticum dicoccoides* *(AABB)* X Wild Goat Grass *Aegilops tauschii* (DD)

Chance hybridisation

Modern Wheat *Triticum aestivum* (AA, BB, DD)

1. Diploid diversity
Ae. tauschii

2. Tetraploid diversity
T. dicoccoides
T. dicoccum
T. durum

Major CIMMYT 1980s-90s resynthesis programme to broaden D-genome diversity

Mainly *T. durum* x *Ae. tauschii*

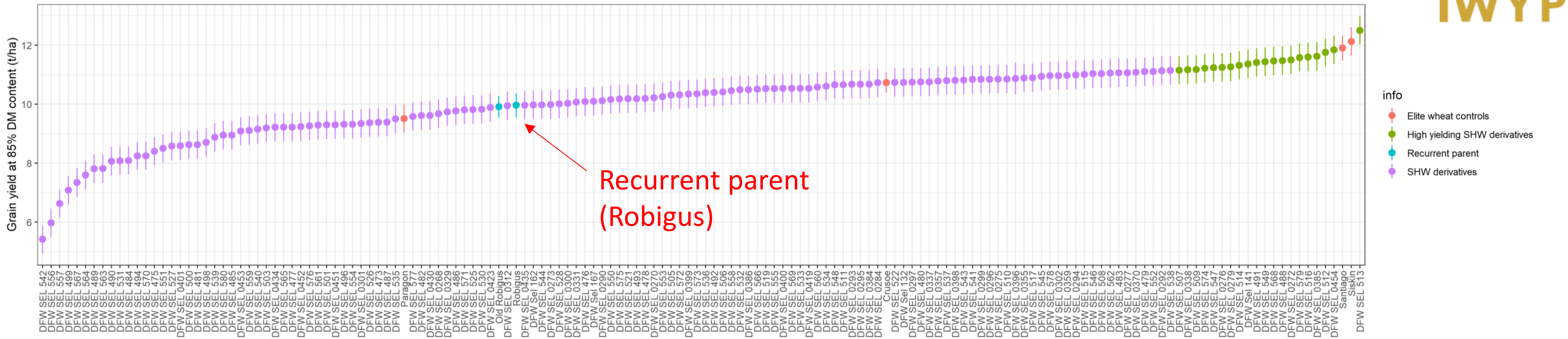
SHW-derivatives have had significant impact on global programmes, e.g. >30% of Chinese wheat area reported to be SHW-derived

Other groups eg KSU have reported direct crossing with *Ae. tauschii*

Niab work with SHWs

- We have crossed with 50 of the CIMMYT SHWs, and also developed our own SHWs
- We typically work with BC1-derived material (approx. 25% SHW)
  https://www.niab.com/research/agricultural-crop-research/resources/niab-wheat-nested-association-mapping-nam-panels
- Increases in yield components
  - Biomass, spikelet number, spikelet fertility, grain size, TGW and overall yield itself
- Hints at improved resource use efficiency
  - Yield maintained under lower N, improved grain protein deviation
- Some novel disease resistances
  - Yellow rust, brown rust, septoria tritici blotch
- But also some naïve weaknesses
  - Disease susceptibilities, height, lodging risk, pre-harvest sprouting, sterility

Niab work with SHWs



Recurrent parent
(Robigus)

Data source: Rothamsted 2022 Academic Toolkit (NIAB material). Estimated means and standard errors (BLUEs).

Increased spikelet number from Niab SHW donor

Increased spikelet fertility from CIMMYT SHW donor

Increased grain size from NIAB SHW donor

Other wild relatives

- Many of the "unique to modern elites" variants from the Watkins study trace back to introgressions from crop wild relatives
- Increasingly these appear in pangenome studies and high-density linkage maps
- WRC Nottingham have combined classical (wide crosses, tissue culture and cytogenetics, *ph1* mutants) and modern approaches (doubled-haploids, genome assemblies, SNPs) to develop suites of introgression lines in several species including:
  - *Triticum urartu* (A^uA^u diploid)
  - *T. timopheevii* (A^tA^tGG tetraploid)
  - *Amblyopyrum muticum* (TT diploid)
  - *Aegilops speltoides* (SS diploid)
  - *Thinopyrum bessarabicum* (JJ diploid)
- Donors are reportedly rich sources of disease resistance and abiotic stress tolerance

University of Nottingham
BBSRC Wheat Research Centre

DFW

Linkage drag

- Anecdotally linkage drag can be a problem with wild relative introgressions
  - *ph1* required to enable initial introgession, but can cause infertility and genetic instability – so is only used in the first generation
  - In the absence of *ph1*, introgressed segments may not recombine further: linkage drag more likely in larger introgressions
- Classical approach is to intercross overlapping introgressions to promote further recombination; alternative designs like MAGIC might also work
- But some introgressions continue to recombine ok
  - 560 Mbp 3B.3G *T. timopheevii* segment, tagged with KASPs at either end
  - Recombinant progeny 7% (BC1), 16% (BC2), 22% (BC2F2)
- If we get down to a gene of interest, cisgenesis or genome editing would remove any linkage drag

Systematic interrogation needed

- Proper interrogation needed to fully extract the value from pre-breeding resources
- Bottom-up approaches can work for known targets – eg RenSeq of *Ae. tauschii* for novel NB-LRRs → identify derived SHW → segregating population → best BC1-derivative
- Top-down approaches may otherwise be needed, eg eyeballing of SHW x elite F2s identified the SHW donors most likely to give high yielding BC1-derivatives
- Also need to know the weaknesses as well as the strengths
  - Disease, lodging, height, pre-harvest sprouting, sterility, hybrid necrosis
- Test, test and test again for multiple traits – preferably in multiple contrasting environments
- Trait dissection, pre-breeding and validation

Takeaways

- No shortage of novel variation available (but always need to check it ***is*** novel)
- Key is to interrogate it through systematic screening to identify the ***useful*** novel variation
- Be open to stacking – landrace PLUS introgressions PLUS elites
- Genuinely novel variation will require recalibration to fit into genomic selection models used to elite haplotypes

Disruption

Elite varieties represent years of incremental improvements assembled over iterative cycles of selective breeding

Wide crossing threatens to disrupt this, hence the need for pre-breeding

Can we be bolder and redesign the wheat crop from scratch as a mosaic of high-performing haplotypes, without being constrained by interfering with the “elite” ideotype?

And who is brave enough to fund this?