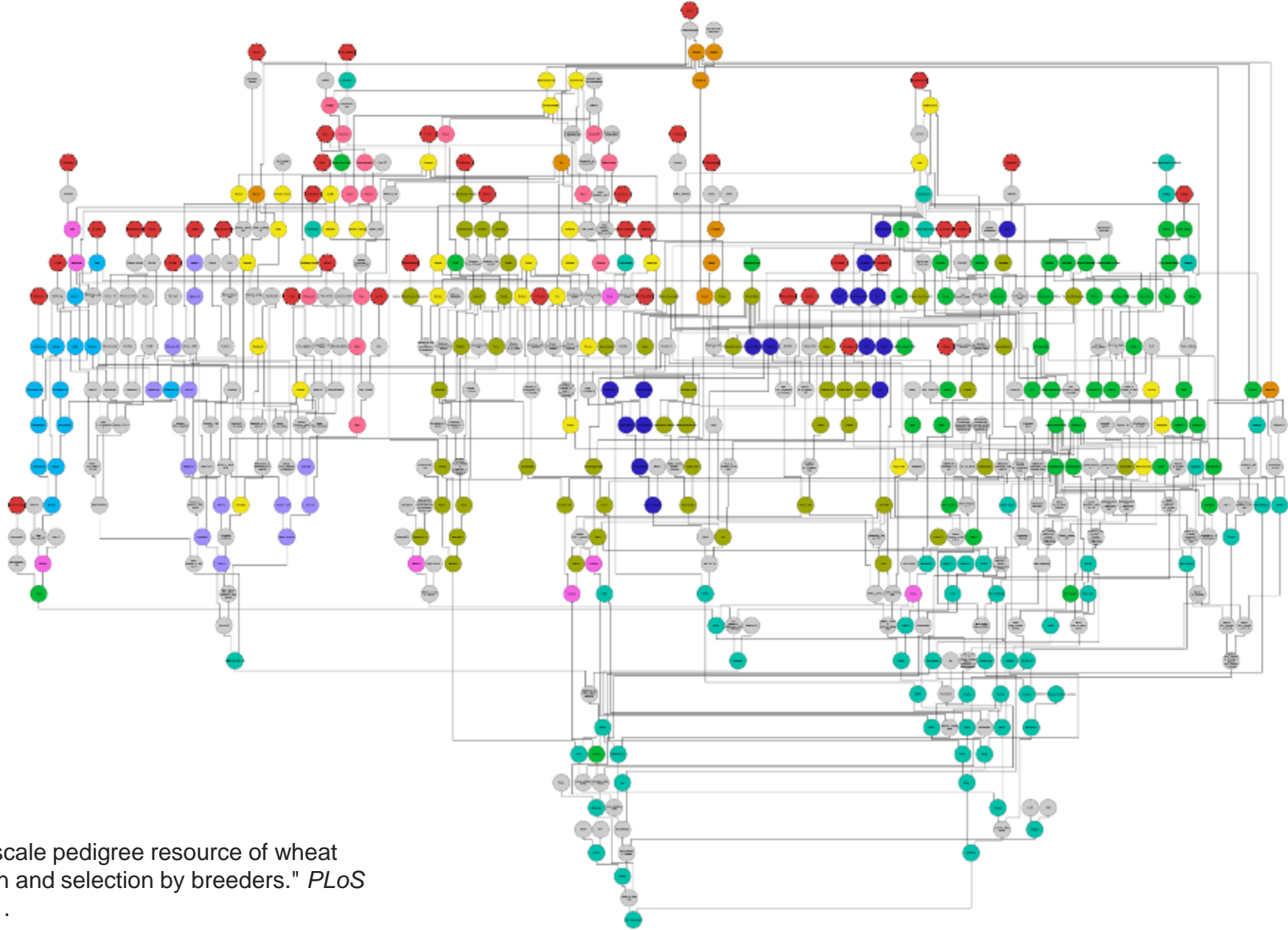


Genomics of the AE Watkins Wheat Landrace Collection

IWGSC workshop at PAG32
January 11th 2025

Simon Griffiths

As breeding programmes mature the diversity of pedigrees is reduced



Fradgley, Nick, et al. "A large-scale pedigree resource of wheat reveals evidence for adaptation and selection by breeders." *PLoS Biology* 17.2 (2019): e3000071.

How and Why the Watkins landrace collection was assembled

Man & Italy, Sicily, Corsica,
Rumania, Roumania, Algeria A-67

The object is to obtain, as far as possible, a complete collection of varieties of wheat grown in the countries specified, and for this purpose it is hoped to cover them as widely as possible as different varieties are likely to be found in different districts. The crops grown in the land are likely to be mixtures of a number of different varieties and generally the best method of acquisition is to buy small samples, say 1 - 2 ounces, in the market-places. Usually it will be possible to obtain several different samples from the same market. Within any area samples should be obtained from a number of different places, especially places of different rainfall, altitude, soil, etc., as the varieties are likely to vary considerably with these factors.

The place of origin of each sample should be stated and in addition the following information would be useful if it can be obtained: (1) approximate dates of sowing and harvest, (2) whether irrigated or not, (3) altitude, (4) soil, (5) the local name of the variety if it has one, anything that is known of its origin or etc.

In some cases efforts may have been made in recent years to introduce new, improved, varieties in some localities. Still we should be pleased to have these, the older unimproved varieties are likely to be more valuable than on the whole as they will probably yield a far richer mixture of varieties.

- An attempt to produce a global wheat survey.
- Taking into account that landrace cultivars are mixtures.
- Market collection.
- Multiple collection points in each country taking into account regional adaptation.
- Capturing true landraces before they are displaced by improved landraces and varieties.

A-68

which is what we desire. In the same way a far better collection will be obtained by the method suggested, if the countries are properly covered, than by application to Agricultural Experimental stations, if such exist.



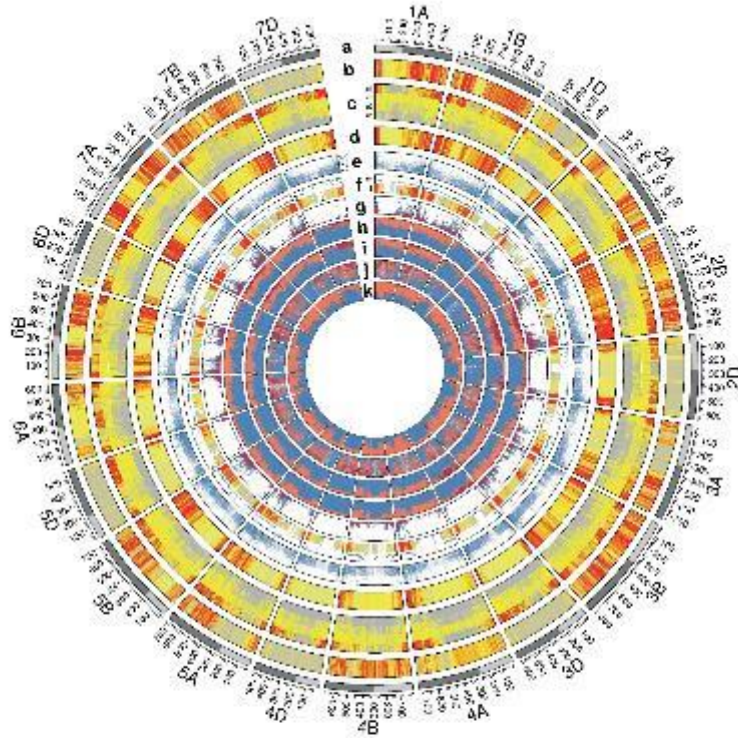
Draft for letter (~1929) from AE Watkins to collectors in Italy, Sicily, Corsica, Romania, and Algeria. Similar letters sent to India and Persia.

A. E. Watkins organised collection of wheat cultivars in 1920s and 30s

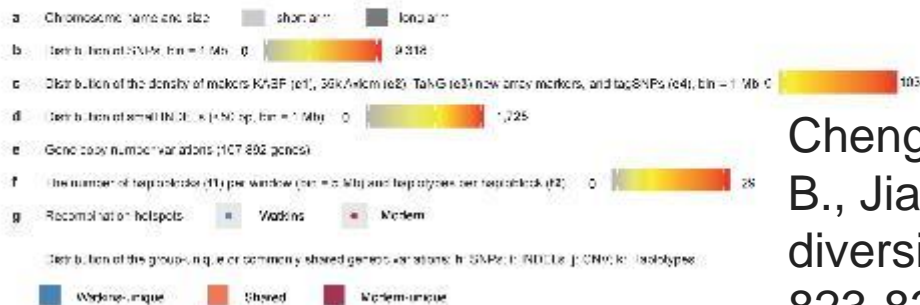


Over 827 accessions collected in the 1930s using London Board of Trade from 32 countries.

Whole genome sequencing of AE Watkins Collection



- >5 years (2018-):
- 1047 wheat genotypes (827 landraces + 220 elites)
- 220Tb raw data, >1Pb data for analysis

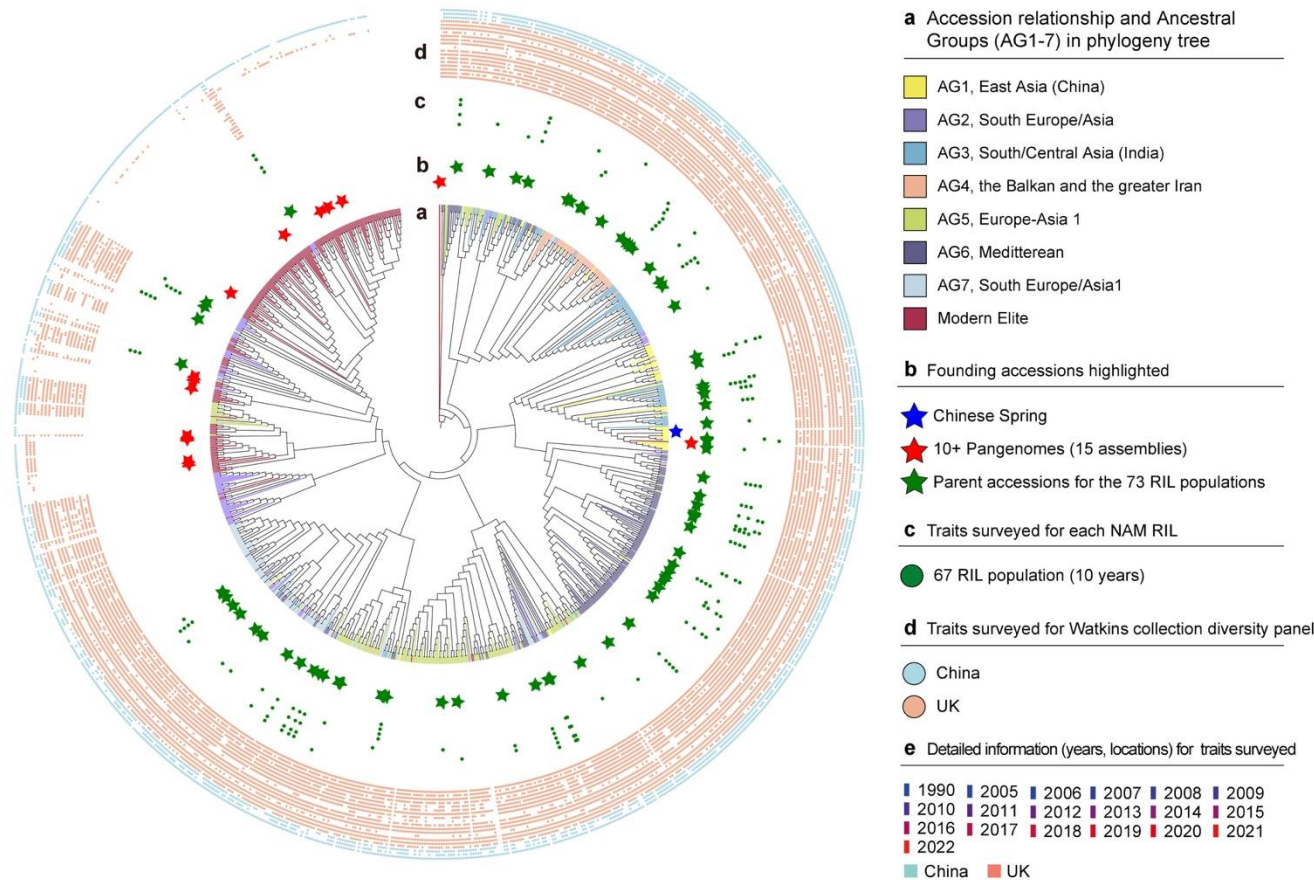


Cheng, S., Feng, C., Wingen, L. U., Cheng, H., Riche, A. B., Jiang, M., ... & Griffiths, S. (2024). Harnessing landrace diversity empowers wheat breeding. *Nature*, 632(8026), 823-831.



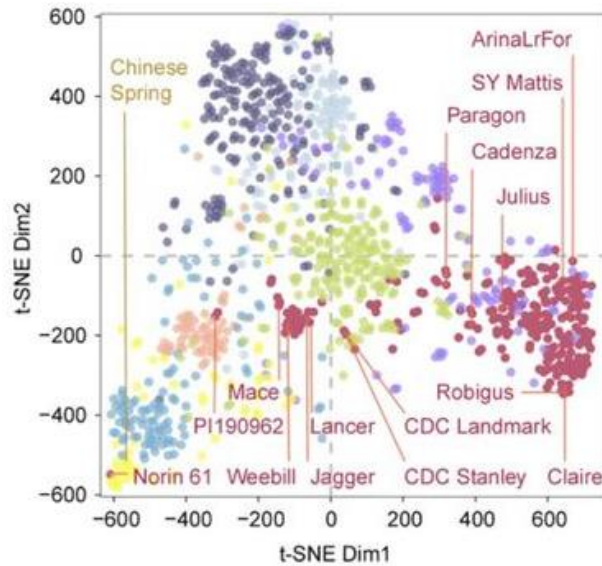
Shifeng Cheng AGIS

Watkins landraces form phylogenetic clades which are isolated from modern wheat

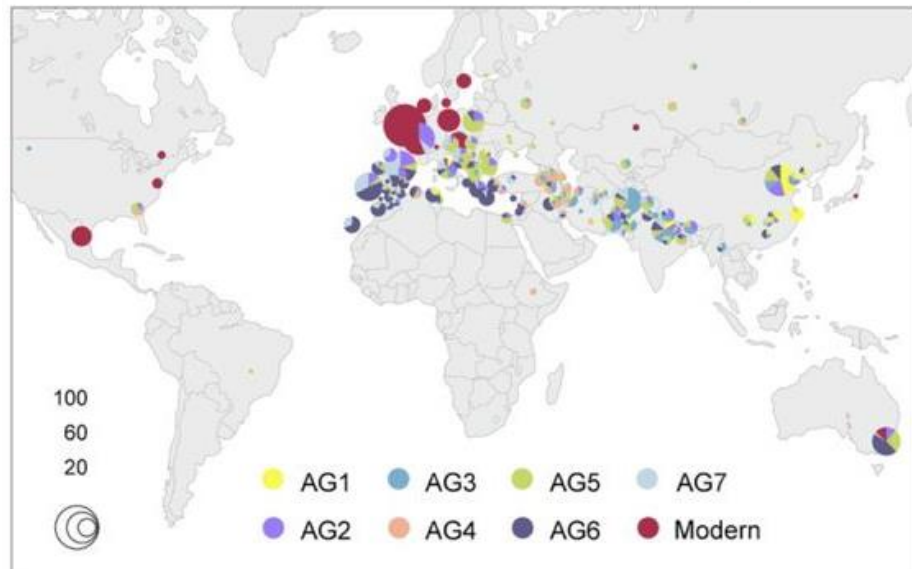


- Phylogenetic tree produced using 250 million single nucleotide polymorphisms (SNPs)
- 827 Watkins landraces
- 208 20th century wheat varieties
- 73 populations derived from Watkins for gene discovery

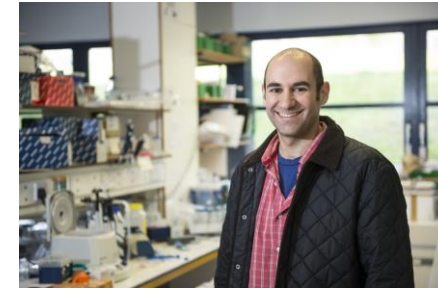
Modern wheat only captures a fraction of the genetic diversity available



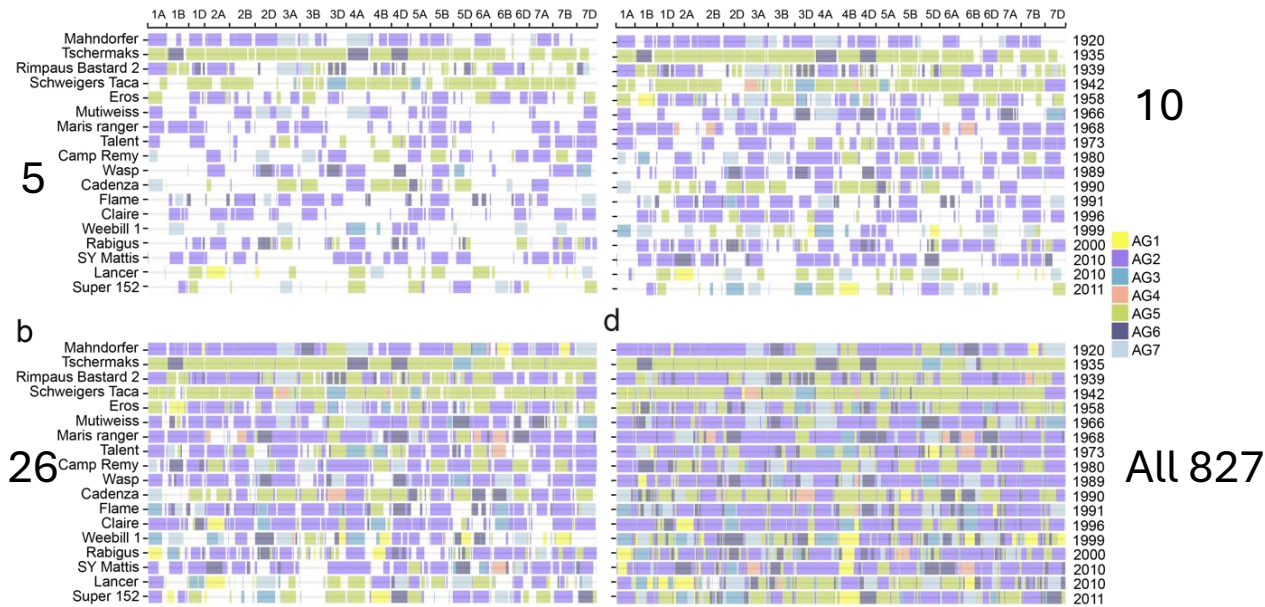
- Seven ancestral groups (AGs) emerge from analysis of the Watkins SNP data
- Modern wheat varieties overlap with AG 2 and AG5
- The genotypically defined AGs correspond with geographic clusters of Watkins collection sites
- 60% of the SNPs identified are completely absent from modern wheat



The footprint of AG2-AG5 founders are still very clear in modern wheat



Work of Xiaoming Wang and Cristobal Uauy



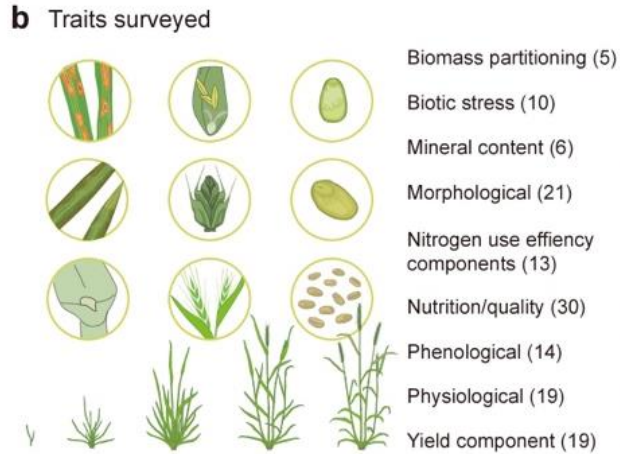
- More than 50% of modern varieties genomes can be reconstructed using 26 Watkins genomes
- On average landrace chromosomal segments remained intact along a length of 159.78 Mbp in modern wheat genomes

Is the “left behind” landrace variation useful?

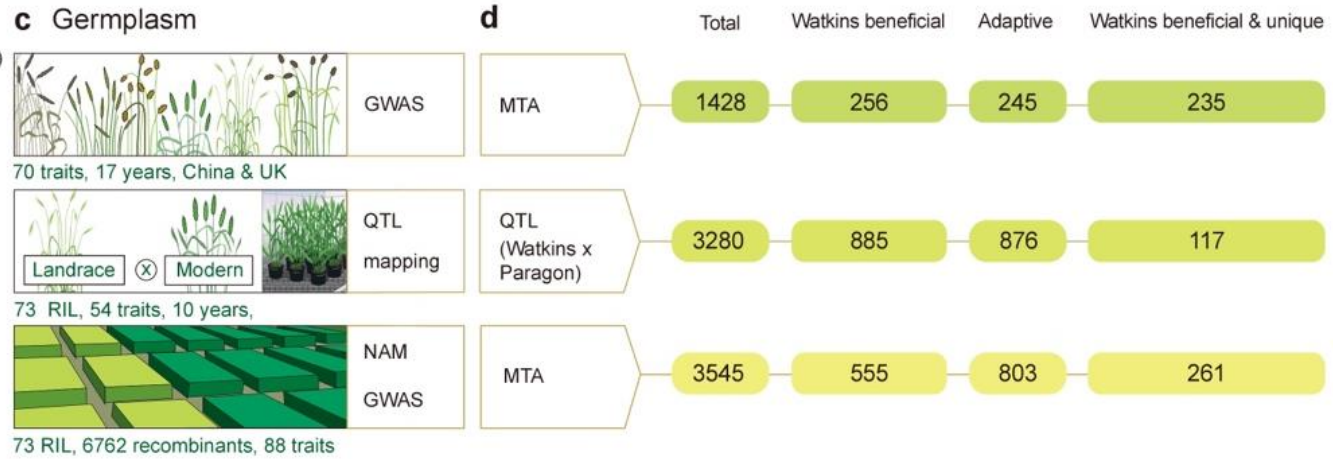


ROTHAMSTED
RESEARCH

- Key traits



- 1000s of QTL



- 100s are useful and novel



- Ten years of field experimentation

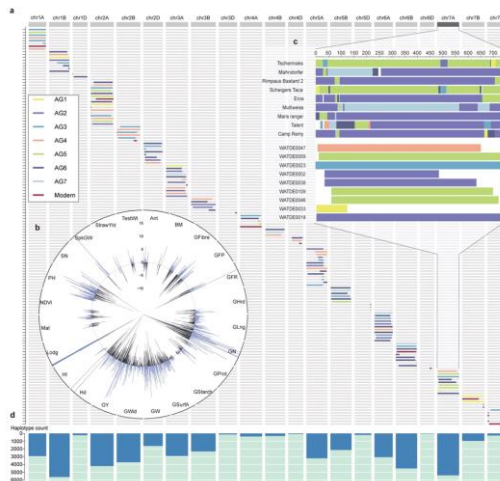
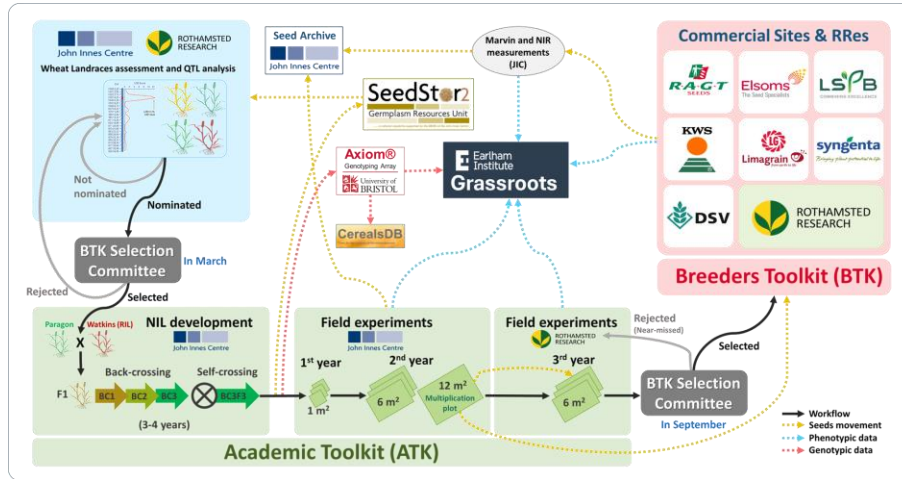


Malcolm
Hawkesford

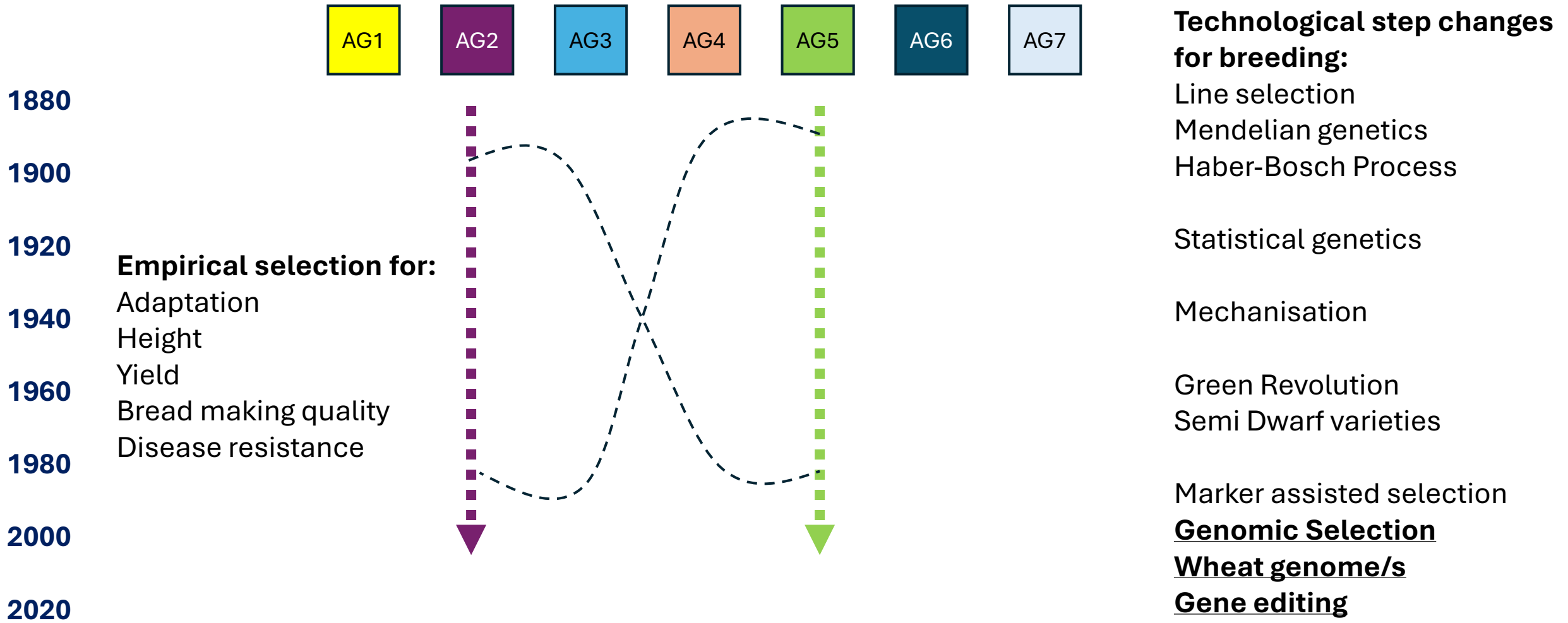
Andrew
Riche

Hundreds of new Watkins genes and alleles contributing towards the sustainable yield challenge

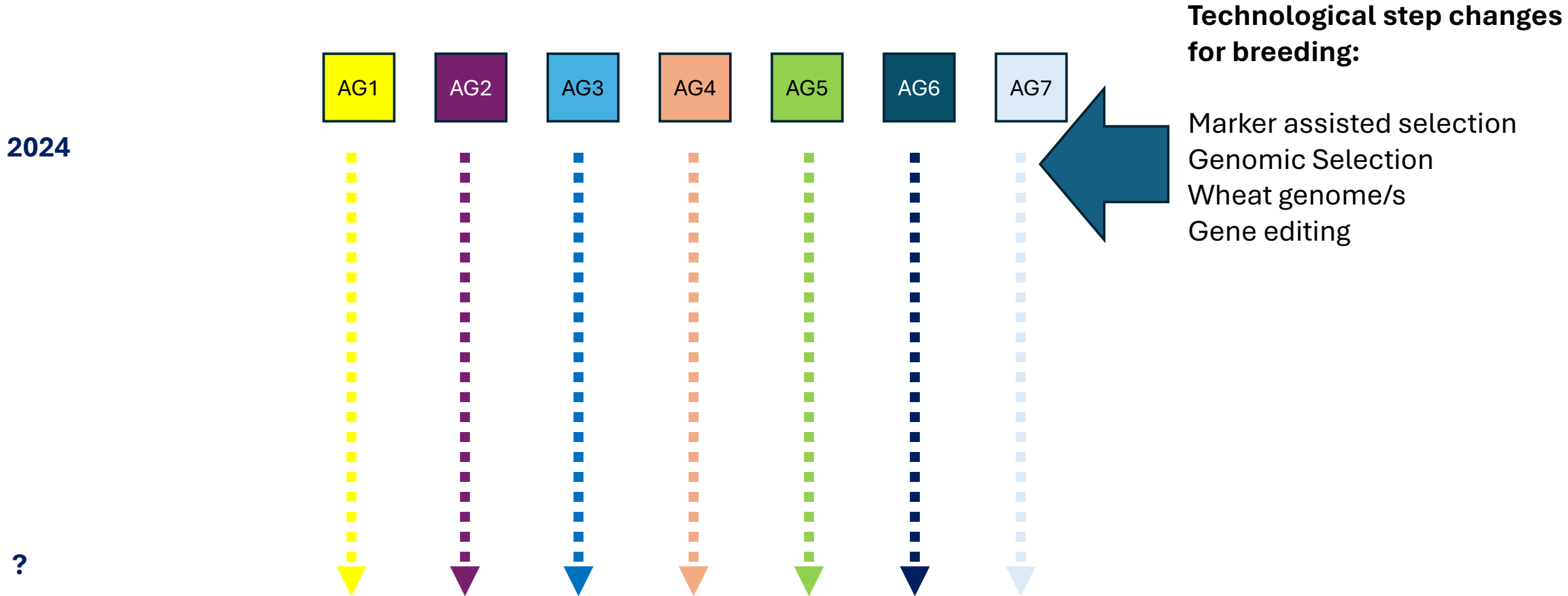
- The new and potentially useful Watkins alleles are backcrossed into elite UK varieties
- They are tested on commercial sites and then introduced into company pedigrees
- There now an influx of non AG2-5 diversity
- BUT- backcrossing only scratched the surface
- How to mobilise the 60% untapped variation???



What Watkins tells us about wheat breeding history



A proposition for precision bred wheat pedigree

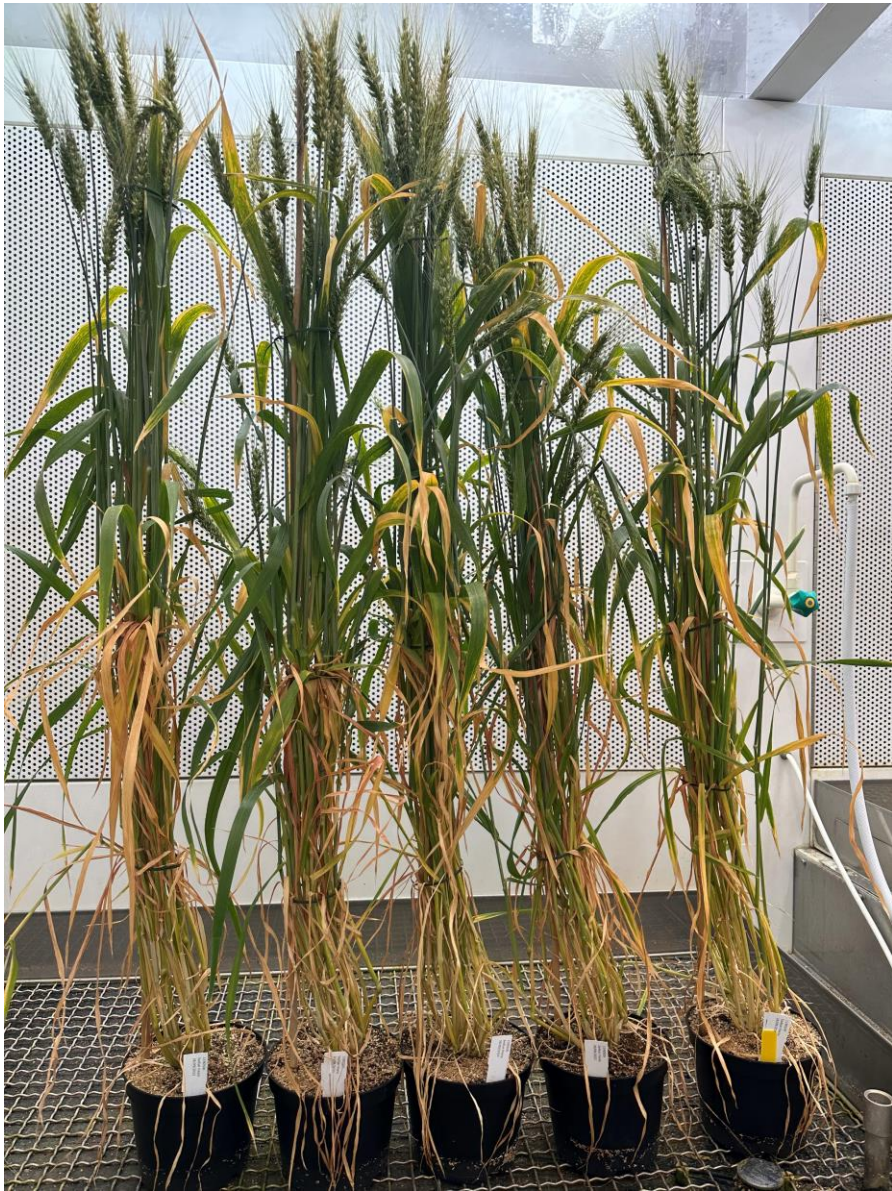


Semi dwarfing alleles are absent from the Watkins collection



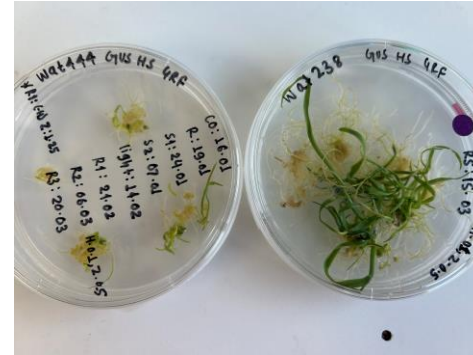
- In modern agriculture the semi dwarf trait is essential.
- Almost all Watkins accessions are very tall.
- To begin new landrace pedigrees we need to introduce semi dwarfing alleles
- Gene editing has the potential to achieve this efficiently

Transformations of Watkins Landraces



Starting landraces

Callus



8 Watkins landraces
now transformable

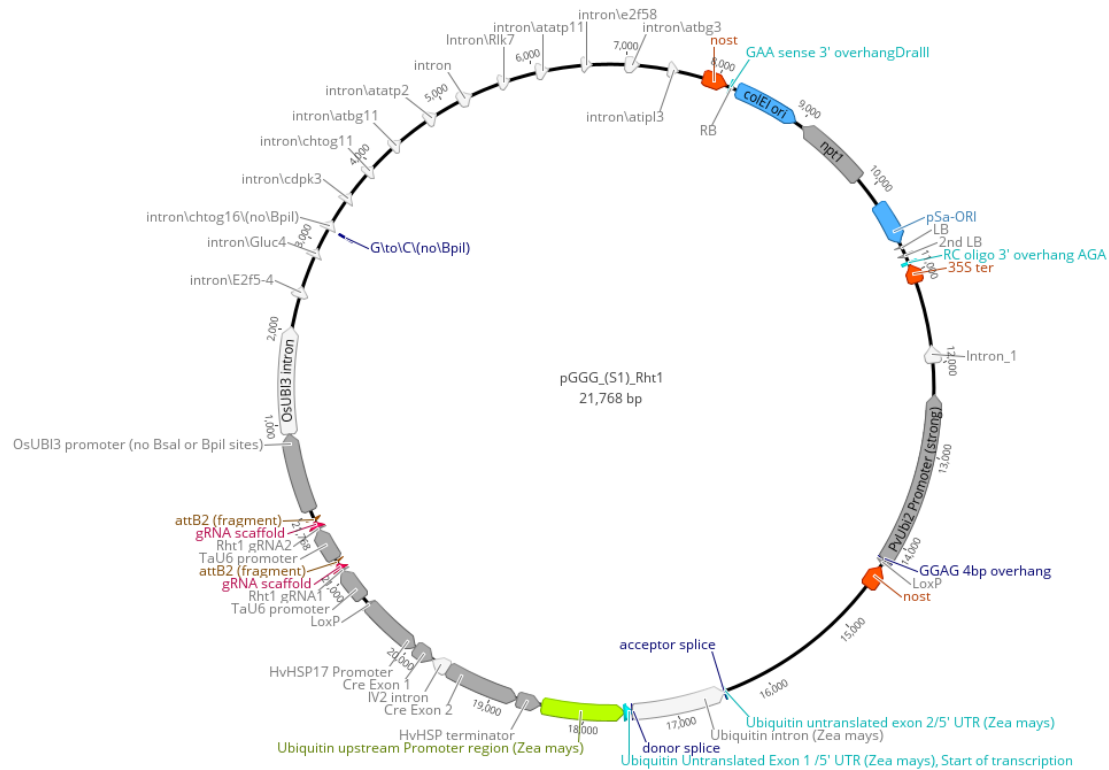
Plantlets



Wheat transformation and
editing team: Sadiya Hayta,
Mark Smedley, Rajani Awal



Construct for the removal of DELLA domain from RHT1



- Aim is to delete RHT1 DELLA domain.
- pGoldenGreenGate (S1) containing two guide RNAs targeting RHT1 both driven by the TaU6 promoter.
- Cre-LoxP heat-shock excisable GRF4-GIF1,
- Intron enhanced Cas9 driven by the rice ubiquitin promoter.

Successful development of semi dwarf Watkins landraces

DELLA domain
deleted



DELLA domain intact

- New results
- T0 plants are successfully converted to semi dwarves
- Now transforming as many accessions as possible
- Transgene free semi dwarves will be crossed and subjected to pedigree selection



Thanks

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Malcolm Hawkesford
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GRU

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Nottingham Uni

John Faulkes

DFW/DSW

Graham Moore

Griffiths' Group

Simon Griffiths
Michelle Leverington-Waite
Sarah Collier
Rajani Awal
Charlie Philp
Richard Goram

JIC Transformation Team

Sadiye Hayta
Mark Smedley

Wheat Breeders Toolkit Companies

RAGT
Elsoms
DSV
Limagrain
Syngenta
KWS
NPZ