Biotechnology and
Biological Sciences
Research Council

Breeding: why we need to start all over again

International Wheat Genome Sequencing Consortium Webinar

Thursday 15 May 2025, 11:00am EDT

Simon Griffiths

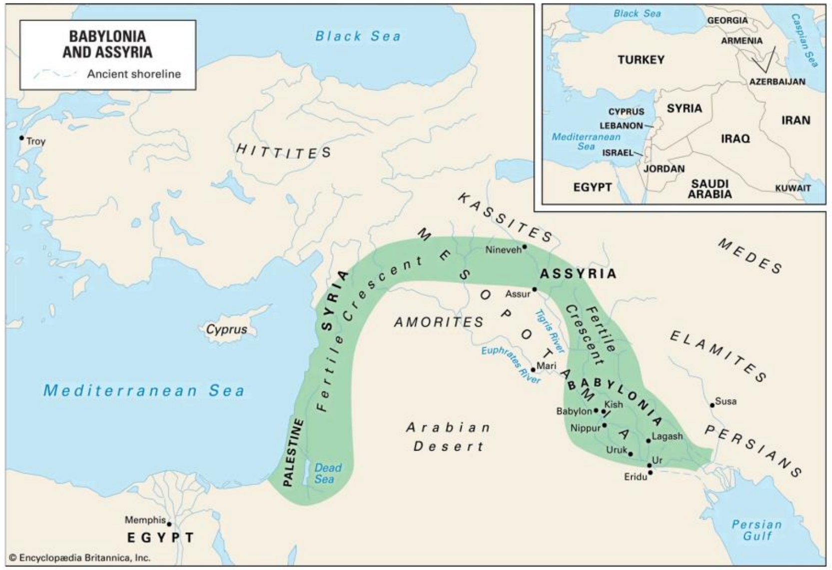
John Innes Centre UK

Department
for Environment
Food & Rural Affairs

DSW
DELIVERING
SUSTAINABLE
WHEAT

The evolution of wheat enabled the establishment of the first cities

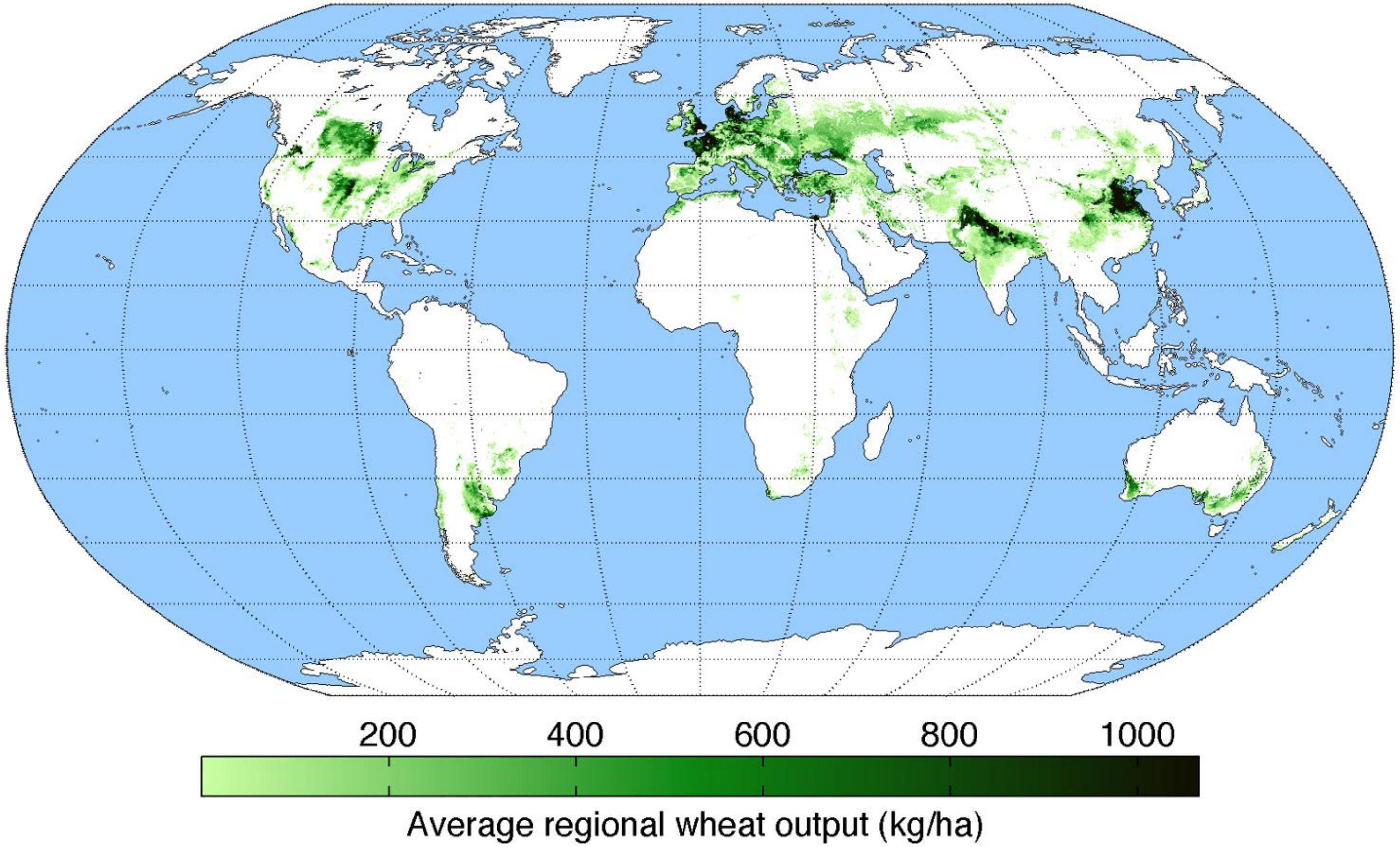
The Fertile Crescent



Grain storage at Çatalhöyük

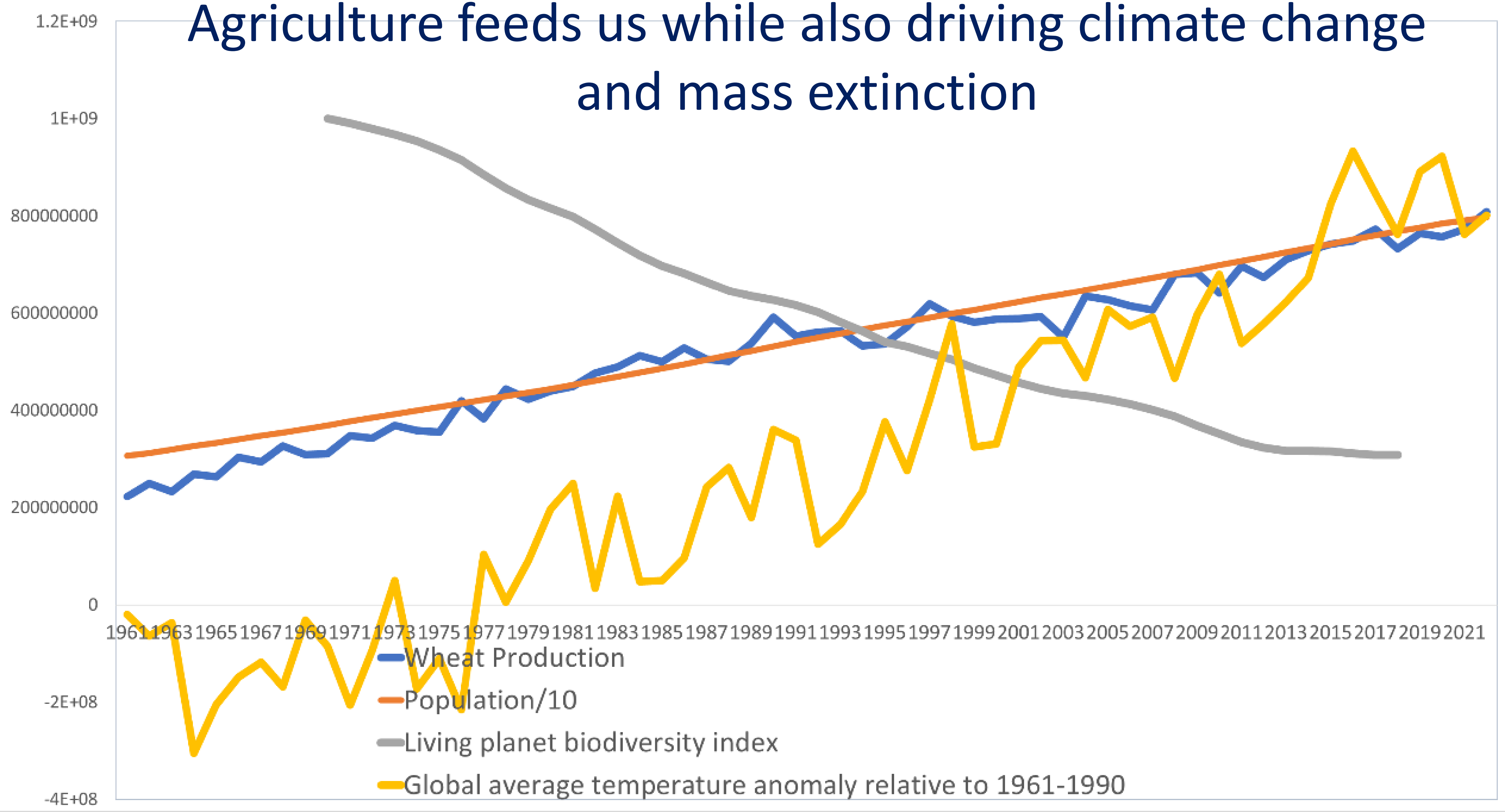
- The Neolithic Revolution saw the first cites 10,000 years ago
- Hunter gatherers became farmers
- These new civilisations were dependent on bread and pasta wheat
- Bread wheat does not exist as a wild species- it arose from polyploidisation events on farms in the fertile crescent
- These new systems caused a 10x increase global population to ~10 million

The cities of the 21st century still rely on wheat!



- Global population almost 8 billion
- Major wheat cultivation on every inhabited continent
- 780 million tonnes produced each year
- Most traded crop
- 20% of our calorific intake
- Increased production required for a population of 10 billion in 2050

Agriculture feeds us while also driving climate change and mass extinction



Where do modern wheat varieties come from?

OCTOBER 28, 1921.

WHEAT WIZARD.

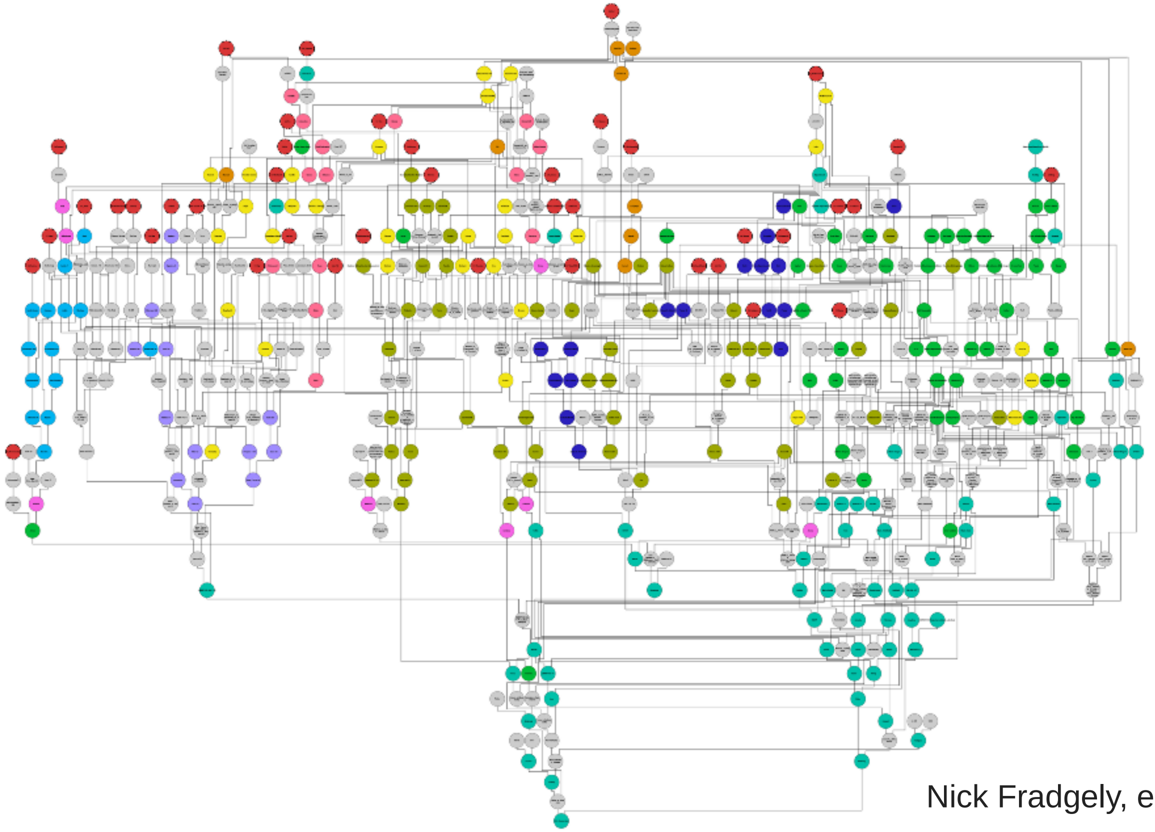
CURING CRIMINAL PLANTS.

What is probably the finest wheat in the world has been created at Cambridge, and this season it has been yet further improved. The maker is Professor Biffen and his staff, who have quite surpassed all the "plant wizards" of the age in this or any other country. Perhaps the strangest part of the improved "Yeoman" wheat, as it is called, is its parentage. Professor Biffen has performed the miracle of getting good offspring from a bad parent. For example, he found in America a most cantankerous and repulsive wheat. It had a little head and a stiff beard, but through these deficiencies a heart of gold was detected. By help of that astonishing law of heredity known as the law of Mendel the bearded wheat of criminal type was enabled to hand on to his grandchildren his strength and hardihood and golden heart without the beard and the small head. "Improved Yeoman," his lustiest descendant, has a huge ear of 80 grains or more and a "strong" transparent kernel.

CUP FOR ORIGINATOR OF "LITTLE JOSS" WHEAT.—The Hon. E. G. Strutt (left) presenting at the Shire Hall, Chelmsford, yesterday, an 84-oz. cup to Professor Biffen, of Cambridge, as an acknowledgment by Essex farmers of his signal services to agriculture in producing "Little Joss" wheat. [*Daily Mail.*

Sarah Bailey et al 2024

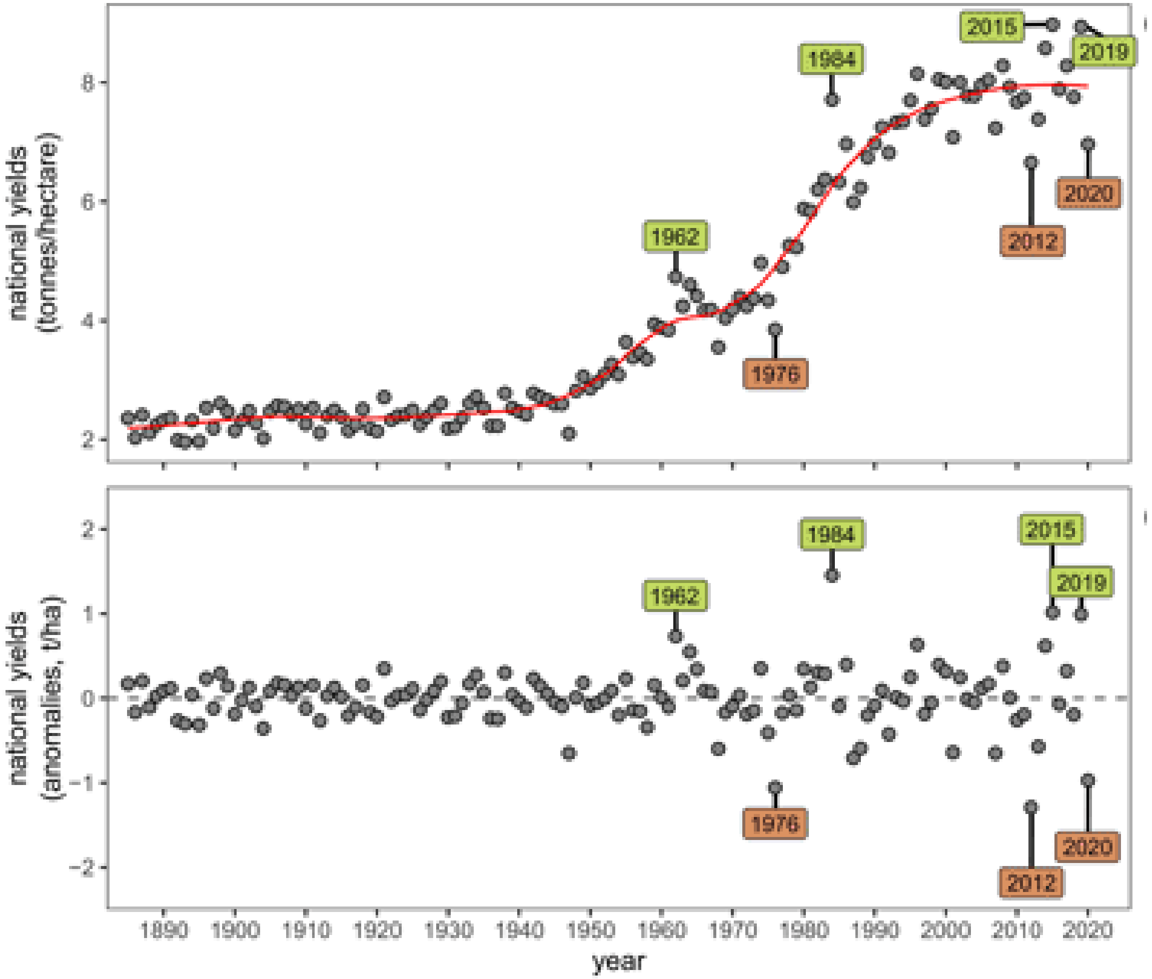
The founders of European wheat breeding introduced a potential bottleneck



Nick Fradgely, et al.

As breeding programmes mature the diversity of pedigrees is reduced

Genetic gains achieved by conventional breeding have declined



Slater et al 2022 10.5194/esd-13-1377-2022

- Is it possible that increased genetic progress can be achieved by increasing genetic diversity in modern wheat?
- Where would this diversity come from?

Genetics Society Magazine, August 2023, issue 89

Arthur Ernest Watkins: Geneticist and Collector

By Robert Koebner

Robert spent 20 years as a wheat cytogeneticist, initially at the Plant Breeding Institute in Cambridge and later at the John Innes Centre in Norwich, with a particular focus on the potential of the crop's secondary genepool as a source of novel genetic variation.

The GENETICAL SOCIETY

The collection of crop germplasm from every corner of the globe promoted by the Russian geneticist Nikolai Vavilov during the years preceding World War II was highly influential in establishing the importance of plant conservation. In the UK, one of the two most prominent scientists involved in this activity was Arthur Ernest Watkins at the University of Cambridge (the other being John Percival at the University of Reading).

Watkins was born in London on April 23rd 1898, the only child of Arthur Charles and Edith Isabel Watkins. His father worked for the company John Lyons & Co., a firm which had begun its operations in 1894 as a teashop in Piccadilly, London, but which later expanded into the popular chain of "Lyons' Corner House" teashops. By the time of Arthur Charles' retirement as a manager in the 1930s, the company had diversified into the London top end restaurant and hotel business, and was marketing a range of teas, biscuits and cakes sold in grocery stores across the world. Arthur Ernest was educated at the fee-paying Latymer Upper School, founded in 1624 and still very much in existence today. He won a scholarship to study Mathematics and Natural Sciences at St. John's College, Cambridge, but was unable to take up his place until 1919, as – at the age of just 19 – he was inducted into the army as a second lieutenant and saw action in the trenches in France from Christmas 1917 until the end of World War I. Having been brought up in London, Watkins was unlikely to have had much exposure to rural life, but his war service would have changed this. He served with the Royal Field Artillery, a unit which employed many horses for draft purposes; an entry in his battalion's war diary from March 31st 1918 reads "*During the last 10 days we have had some 50 casualties, and have inflicted enormous losses on the enemy ... men and horses have been exceedingly tired most of the time*". Then, between the Armistice in November 1918 and his demobilization in England at the end of January 1919, the army assigned him as an "Assistant Agricultural Officer", tasked with liaising with the local French farmers to secure food for the many troops who remained in France for some months after the end of the war.

Watkins finally arrived in Cambridge sometime during 1919, graduated at the end of 1920 and was awarded a Diploma in Agriculture in 1922. In 1923 he married Amy Marjorie Blanch, with whom he had one son (John Halse); sadly, Amy Marjorie died in 1941 and John Halse was killed during the D-Day landings in 1944, aged just 19. Watkins' professional career was spent entirely in Cambridge. In 1924, he joined the then relatively new Plant Breeding Institute, and in 1931 was appointed as a lecturer in Cytology at the University of Cambridge's Faculty of Agriculture. He served as a member of the committee of the Genetical Society (the current day Genetics Society) during the 1930s and later as its secretary, where he interacted with many of the greats of British genetics of the time, such as K Mather, CD Darlington, JBS Haldane and RA Fisher. He retired in 1948 at the rather early age of 50, and died on January 3rd 1967.

Triticum: The importance of the grass genus *Triticum* is that its members include bread, emmer and einkorn wheat. Triticum, the Latin word for wheat, is derived from the perfect passive participle of the verb terere, meaning to grind.

Watkins' research for the most part focused on gaining an understanding of the genetics of key anatomical traits in *Triticum*, such as awnedness and glume shape. Recognizing that variation in these traits had some taxonomic significance, he embarked on assembling a collection of landrace wheats from around the world.

Coincidentally, perhaps, a similar effort was being mounted at around the same time by John Percival. While Watkins and Percival clearly knew one another, it is unclear whether they regarded each other as either rivals or as colleagues; Percival would doubtless have considered himself the more senior, given that he had been appointed as the Professor of Agricultural Botany at Reading in 1907 and had published his seminal book *The Wheat Plant* already in 1921. Watkins explained that "*... the object is to collect as many wheat varieties as possible from all over the world. Primarily the reasons were (a) partly purely scientific and (b) partly in connection with breeding improved varieties of wheat for English conditions. A third reason came (c) when it occurred to me that if a more or less complete collection of existing varieties were made, we might as well take advantage of the opportunity and distribute suitable varieties for trial in the colonies and dependences (sic)*".

A. E. Watkins, 1920s- 1930s, Cambridge

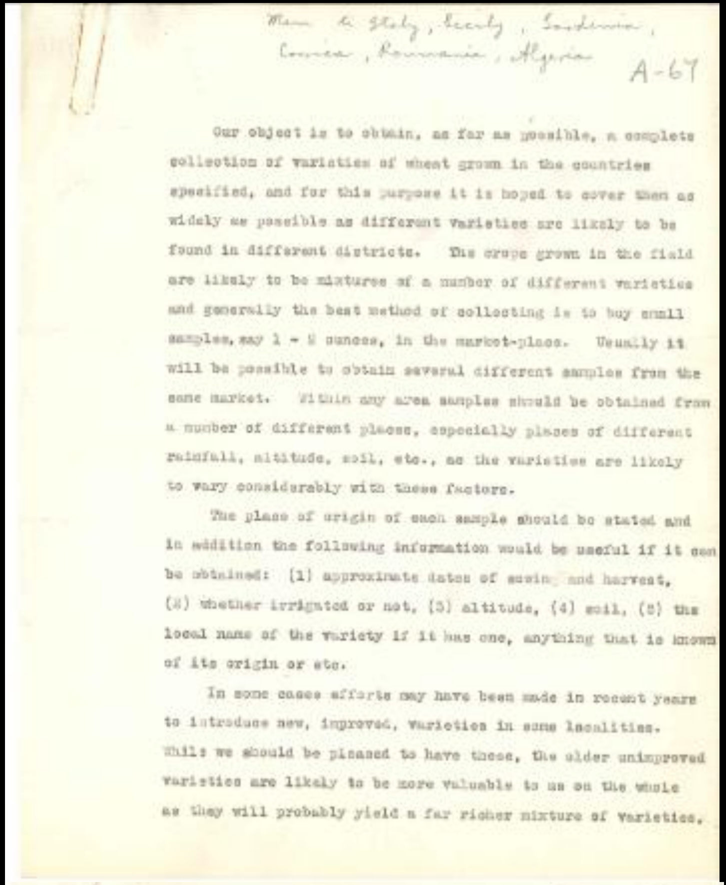
Images:
Above: Watkins (circled in red) has placed himself apart from the students - perhaps indicative of his shy nature.
Left: Cover of the Genetical Society 1937 Annual Report. Below: Sample of Watkins' correspondence

While some of Watkins' materials were obtained from collections assembled by colleagues such as Nikolai Vavilov in Russia, Shen Zonghan (沈宗瀚) in China and Otto Frankel in New Zealand, most were collected by persuading the authorities in London to task their far-flung network of consuls and agents with the job of visiting local farms and/or grain markets on his behalf, and dispatching the grain to Cambridge. The result was a steady flow of samples throughout the 1930s. Watkins recognized that grain acquired either directly from farmers or purchased from local markets would inevitably be genetically heterogeneous: in a covering letter to one of the co-operating government officials, he writes "*the wheats grown by the cultivators is nearly always a mixture of many distinct types so that a sample of wheat bought in a market will, if sown, yield a great many types in most cases. But important for collecting is that fact that the types vary from one locality to another, while some types may be peculiar to a definite region (e.g. Tibet perhaps). It is therefore of the first importance to collect from as wide an area as possible and a single collector should collect from a number of different places in that area, principally places with different altitudes, different rainfalls or etc.*". Because few of the consular staff tasked with collecting the material had any knowledge of what a wheat grain looked like, some of the samples did not even consist of wheat. Watkins worked on purifying his materials largely by selecting on the basis of the anatomical traits which he understood so well. At its height in the late 1930s, his collection numbered several thousand accessions, including diploid, tetraploid and hexaploid forms of *Triticum*.

Due to the exigencies of war, both the Watkins and the Percival collections were neglected during the 1940s, suffering extensive damage as a result of poor storage conditions and insect infestation. The bulk of the Percival collection (which numbered over 2,500 entries) is still stored in its original boxes and its associated collection of herbarium sheets survives intact. Apart from a small number of accessions rescued by NIAB in Cambridge in the 1950s, the Percival collection as it exists in the UK is no longer viable. However, in 1932, some 1,700 accessions were imported into China, where they have contributed significantly to efforts to genetically improve the national wheat crop. The Watkins collection, which numbers 827 distinct accessions, is curated by the John Innes Centre in Norwich. Over the past few years, a substantial effort has been invested both in characterizing the phenotypic diversity captured within the collection and exploring it as a resource for gene discovery. In order to extend the characterization to the genotypic level, a manuscript (currently under peer review) has been prepared to describe the re-sequencing of the entire collection.

Over 50 years since Watkins' death and about 100 years since his collection was assembled, the memory of this ostensibly quiet, shy scientist and his life's work lives on in the form of a resource of relevance to both the genetics and improvement of the UK's most important crop species.

How and why the Watkins landrace collection was assembled



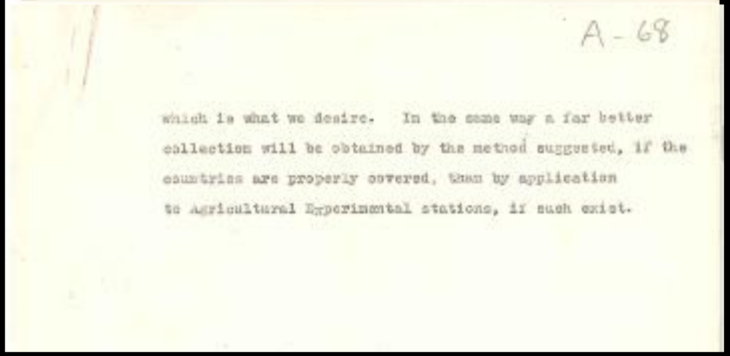
Mem to Italy, Sicily, Sardinia, Corsica, Roumania, Algeria

A-67

Our 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 field are likely to be mixtures of a number of different varieties and generally the best method of collecting is to buy small samples, say 1 - 2 ounces, in the market-place. 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.

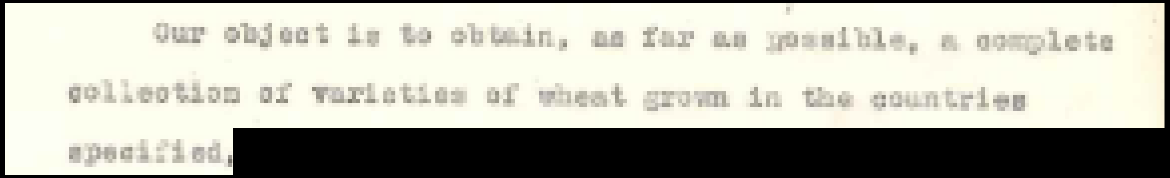
In some cases efforts may have been made in recent years to introduce new, improved, varieties in some localities. While we should be pleased to have these, the older unimproved varieties are likely to be more valuable to us on the whole as they will probably yield a far richer mixture of varieties,



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.



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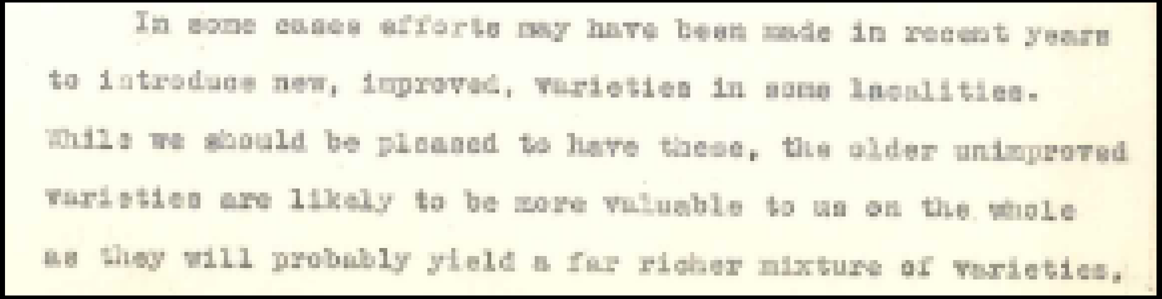

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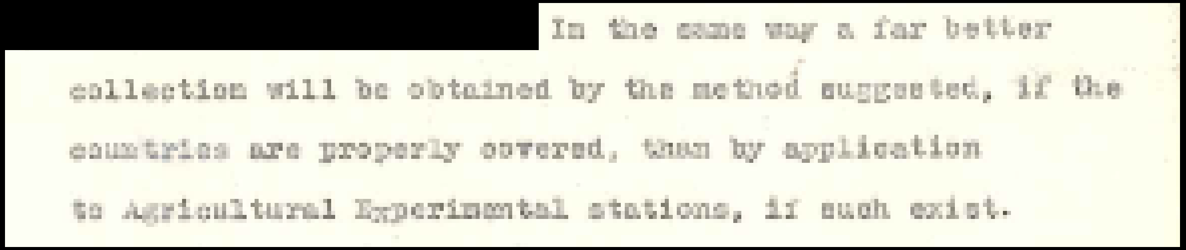

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A. E. Watkins organised collection of wheat cultivars in 1920s and 30s

John Innes Centre

The BBSRC Wheat Improvement Strategic Programme (WISP)

The A. E. Watkins Landrace Collection Platform 'Recovering Lost Genes'

BBSRC 20 Years of Pioneering Great British Bioscience

Utilising the Global Landraces in WISP

1. Arthur E. Watkins had the foresight to collect landraces from around the world in the 1930s using his connections with the London Board of Trade. The collection totals over 800 lines and is stored at the John Innes Centre Norwich UK. Sources are represented on this map.

2. WISP has used SSR molecular markers and geographical origins to create a core subset of landraces from this collection that represents maximum diversity possible in a more manageable 85 lines.

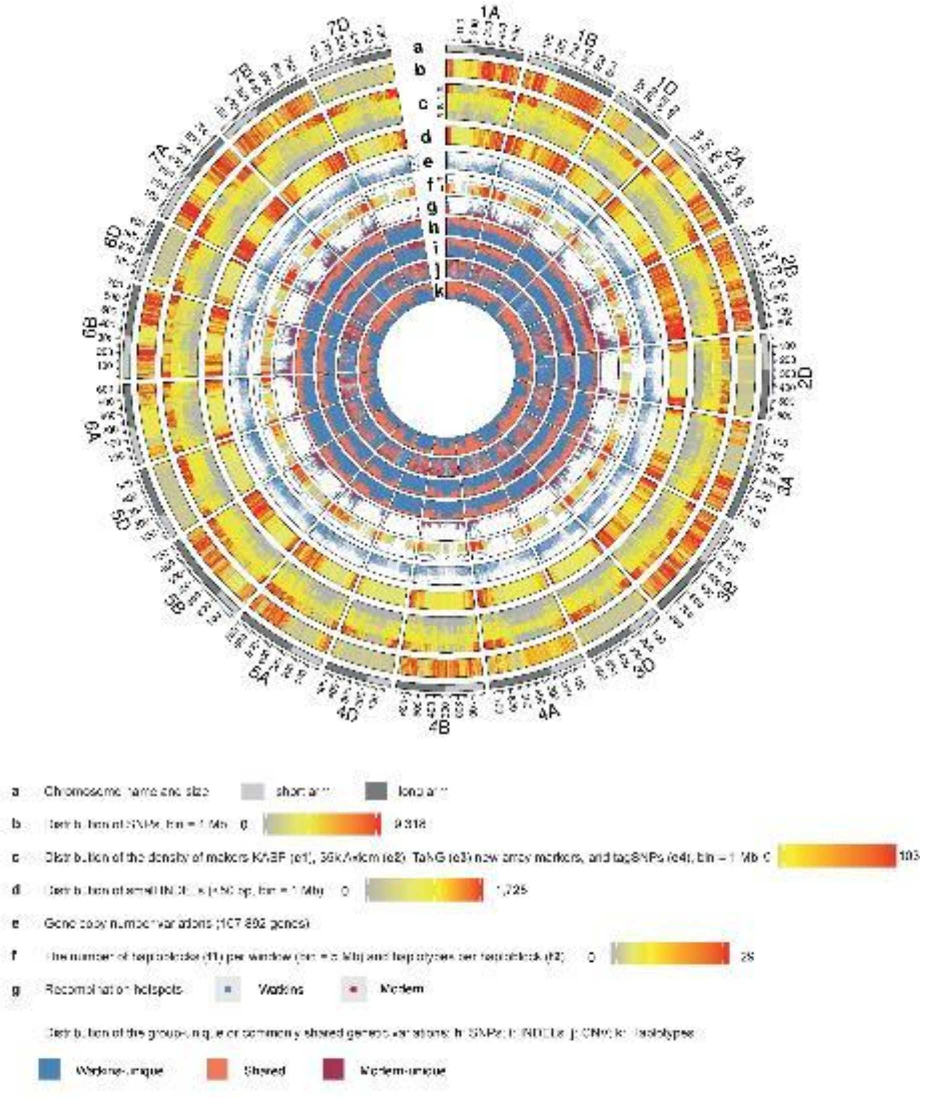
3. The landraces in this core set have been crossed into the UK spring bread wheat Paragon and mapping populations developed through inbreeding the offspring.

4. These Populations are then genetically mapped using high throughput KASPar molecular marker technology platform to assign traits to regions of chromosomes

5. Genes for traits discovered important for wheat improvement and global food security are then bred back into non host parental material in a precise manner called Near Isogenic Line (NIL) production to prove concept of theory and allow a resource tool to be made available to the wheat industry.

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

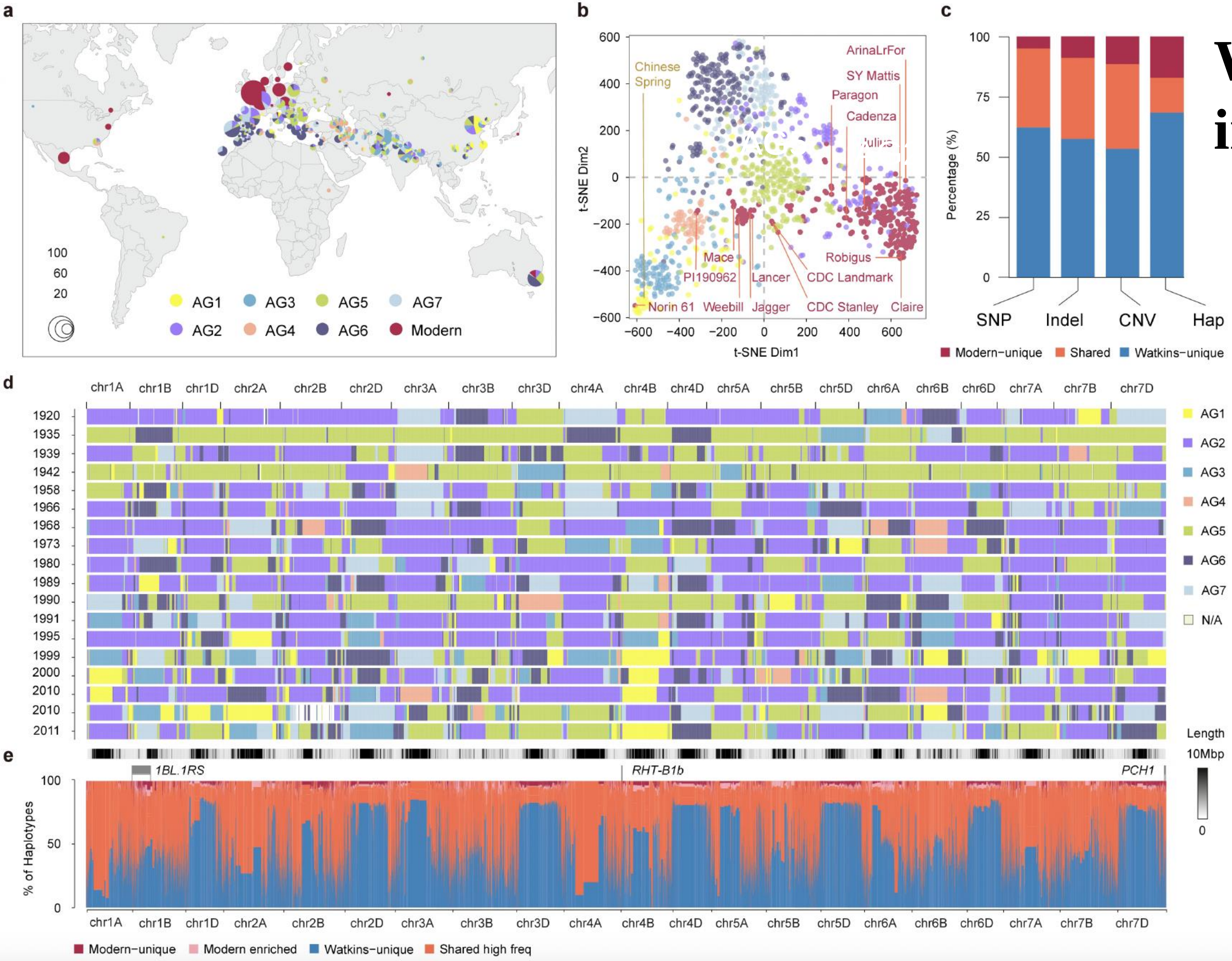
Whole genome sequencing of AE Watkins Collection and a modern wheat sample



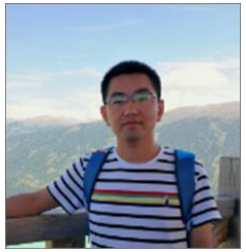
- >5 years (2018-):
- 1047 wheat genotypes
  (827 landraces x 220 elites)
- 220Tb raw data, >1Pb data for analysis

Shifeng Cheng AGIS

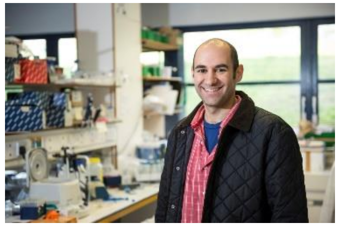
Watkins genomics in a nutshell



Luzie
Wingen



Xiaoming
Wang



Cristobal
Uauy

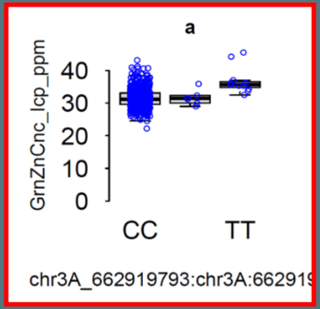
Feng
Cong

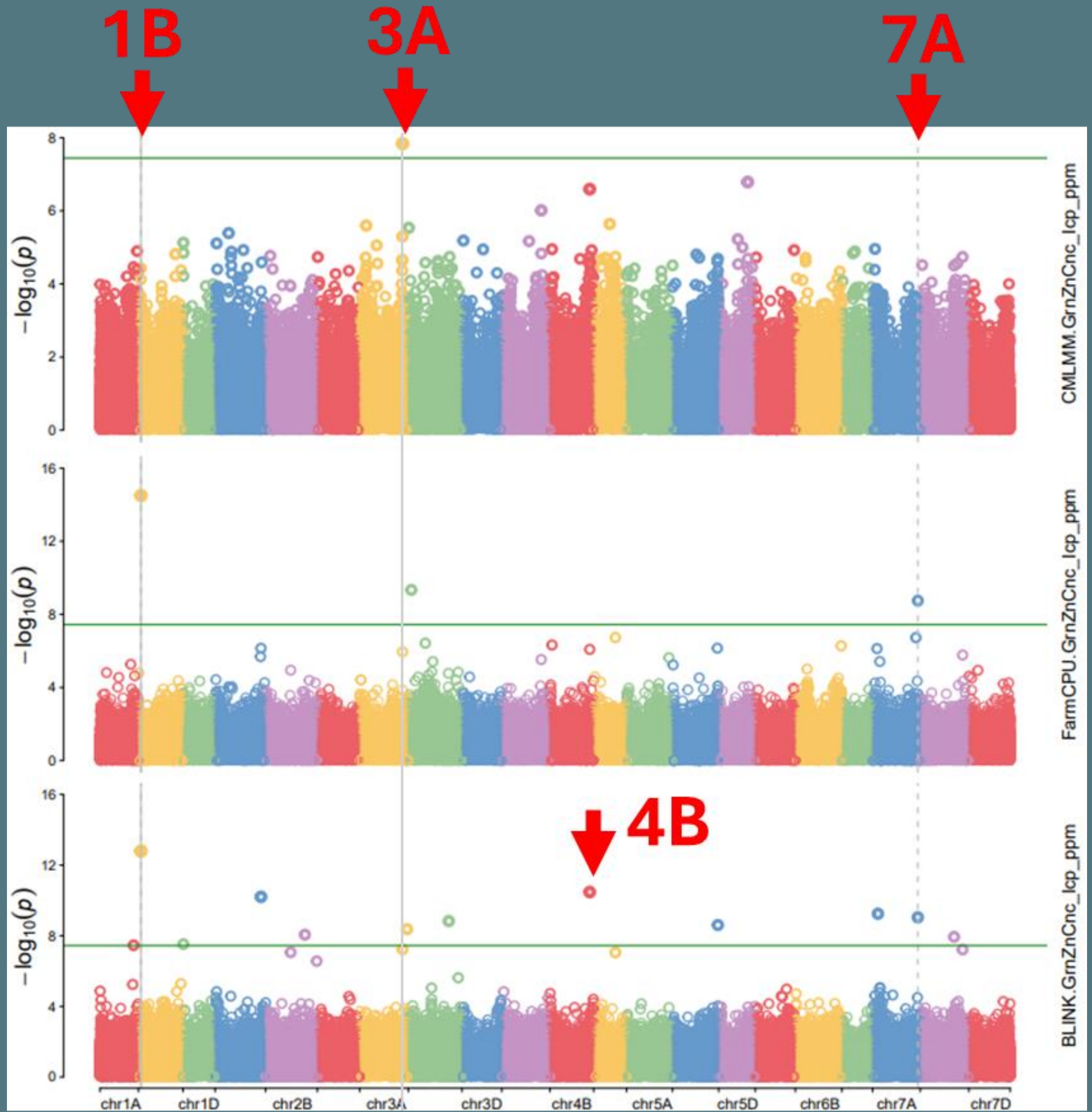
Zn example of Watkins whole genome GWAS

Andrew
Riche

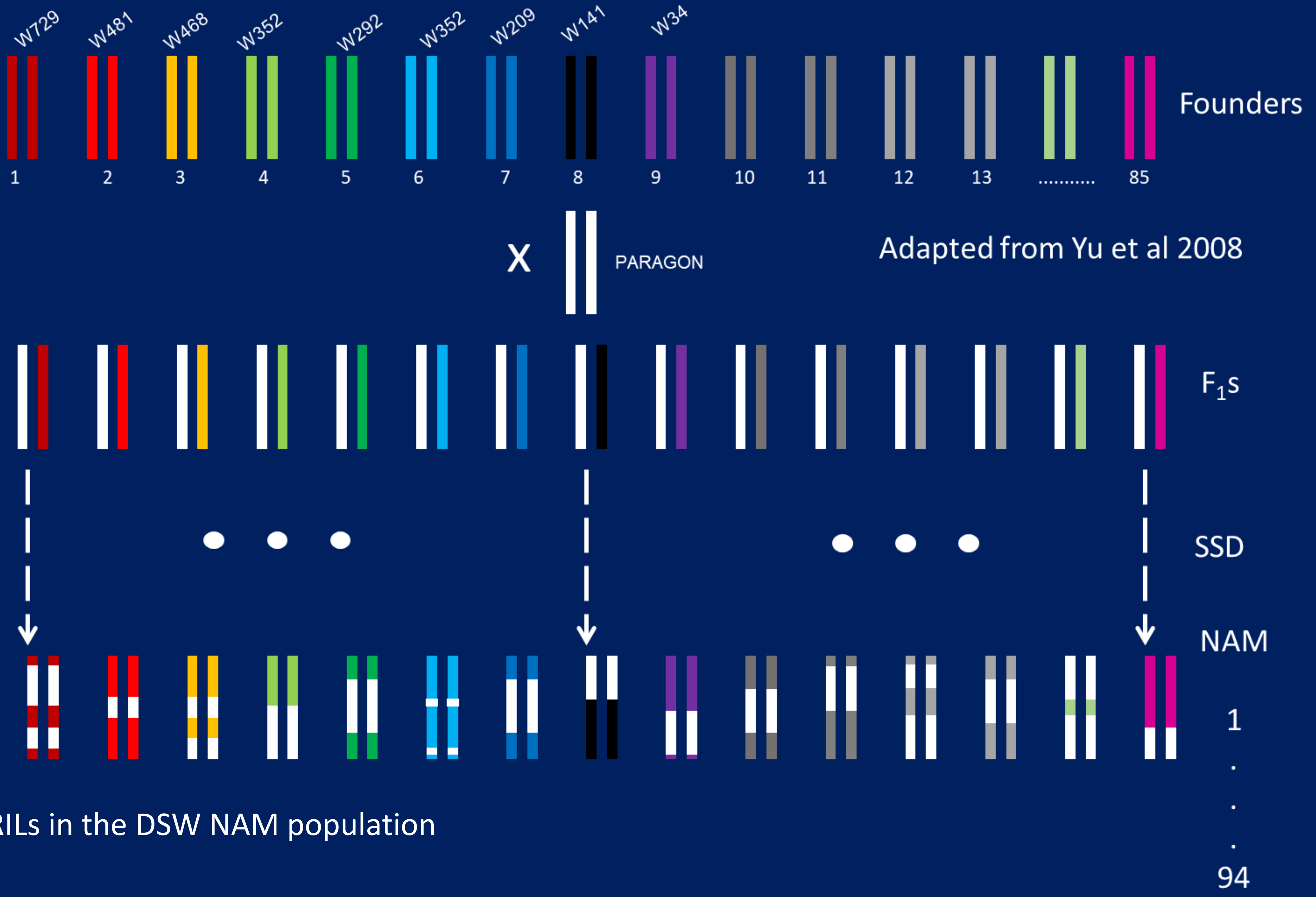
Abdul Kader
Alabdullah

- GWAS peaks: 1B, 3A, 4B and 7A
- Rare alleles increasing Zn found on 3A and 4B
- Not associated with yield





Development of Nested Association Mapping Panel from the Watkins Collection



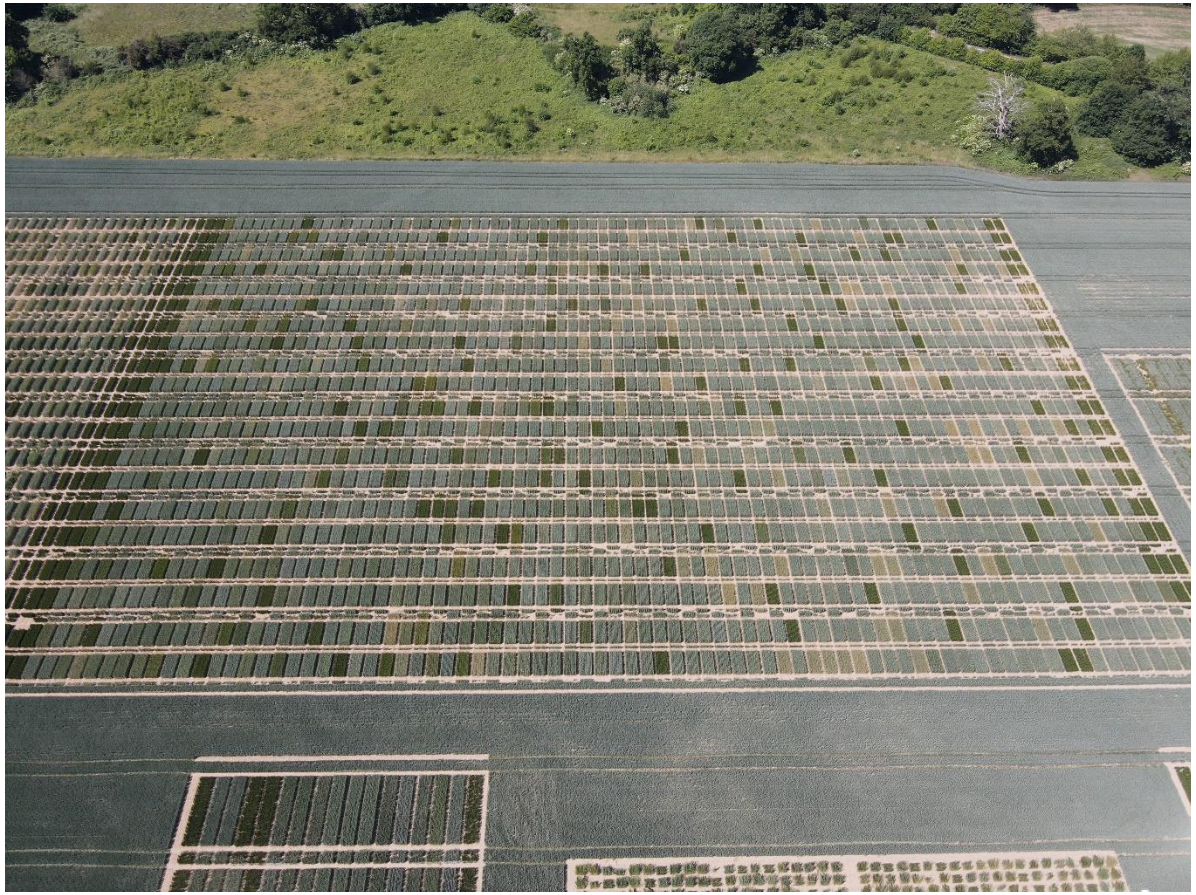
Adapted from Yu et al 2008

Simon Orford

Rajani Awal

Over 12000 RILs in the DSW NAM population

Is the “left behind” landrace variation useful? NAM populations in the field.



JICs Field Experimentation Team

ROTHAMSTED RESEARCH

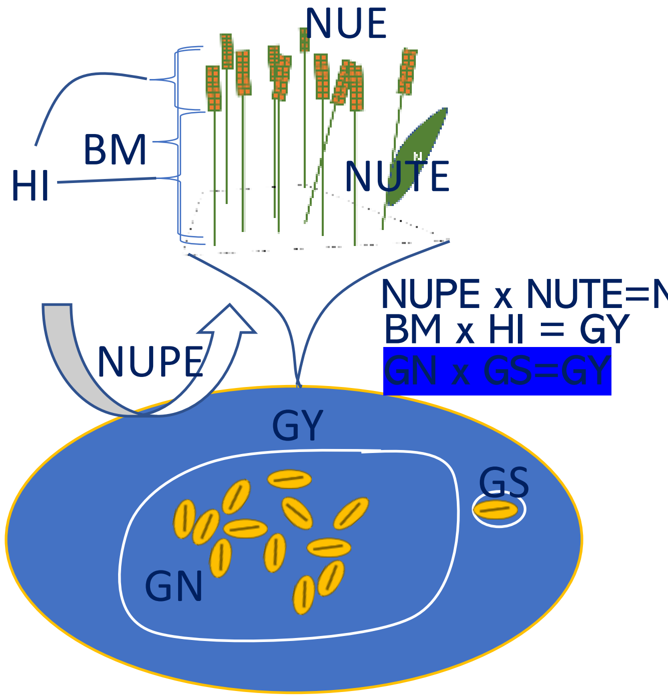
- Ten years of field experimentation at JIC and Rothamsted

Malcolm Hawkesford

Andrew Riche

137 Traits measured

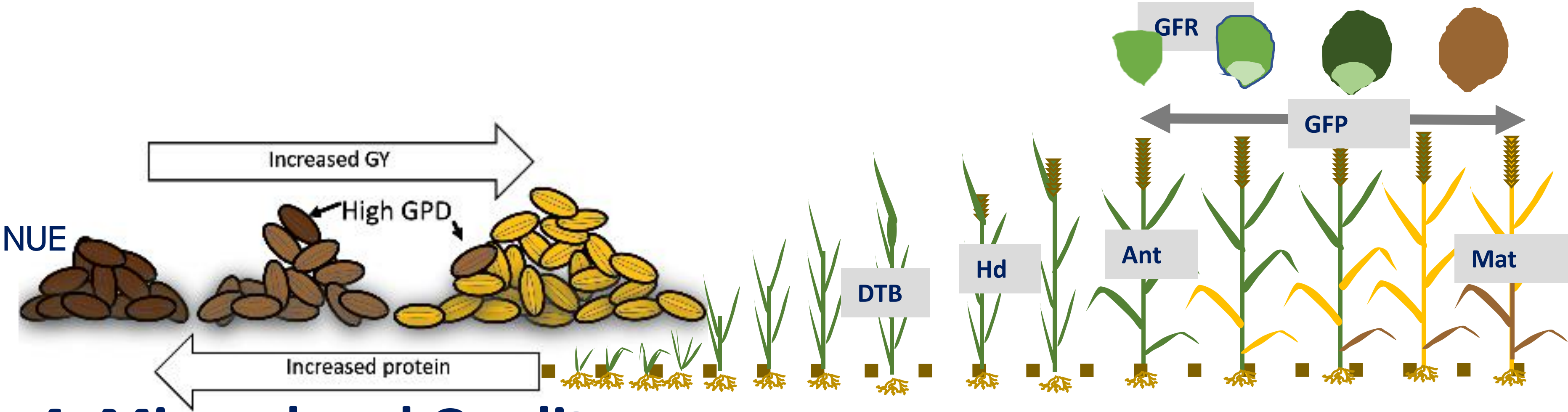
1. Biomass partitioning traits



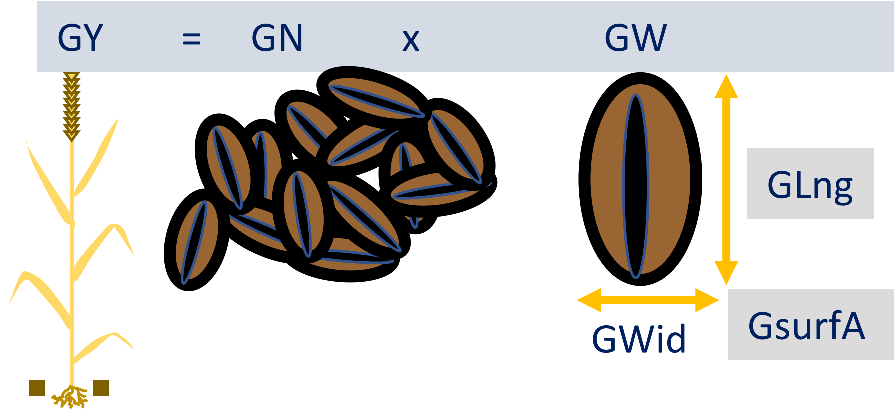
NUPE x NUTE=NUE
BM x HI = GY
GN x GS=GY

2. adaptation: Phenology components

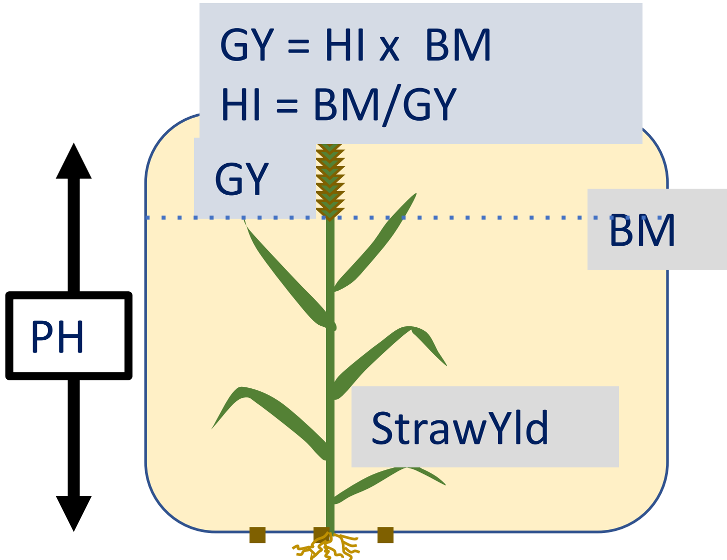
4. Mineral and Quality



3. Yield Numeric components

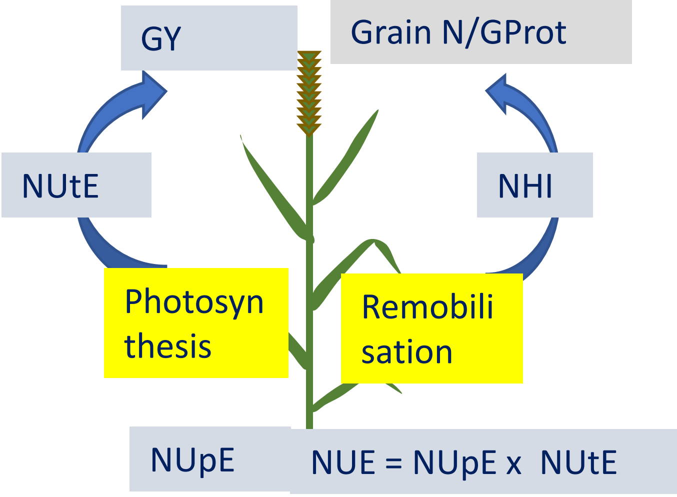


5. HI and BM



GY = HI x BM
HI = BM/GY

6. Nitrogen component traits

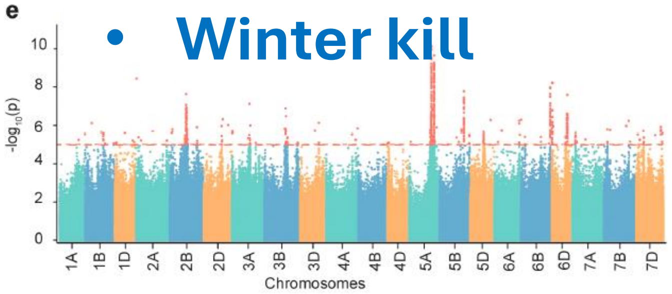


NUE = NUpE x NUtE

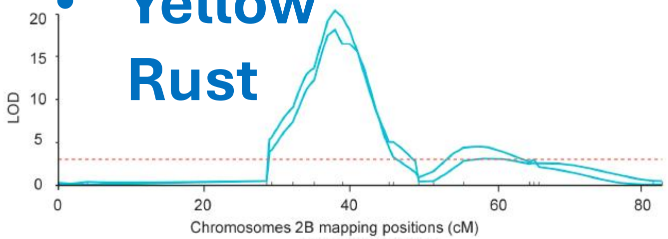
Thousands of genetic effects identified using complementary gene discovery methods

Trait examples:

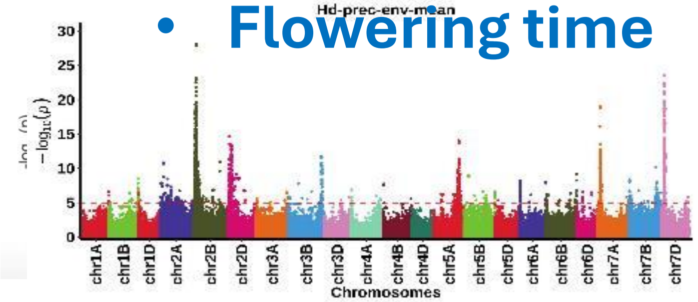
- **Winter kill**



- **Yellow Rust**



- **Flowering time**



Overall numbers:

GWAS (1428 MTAs)

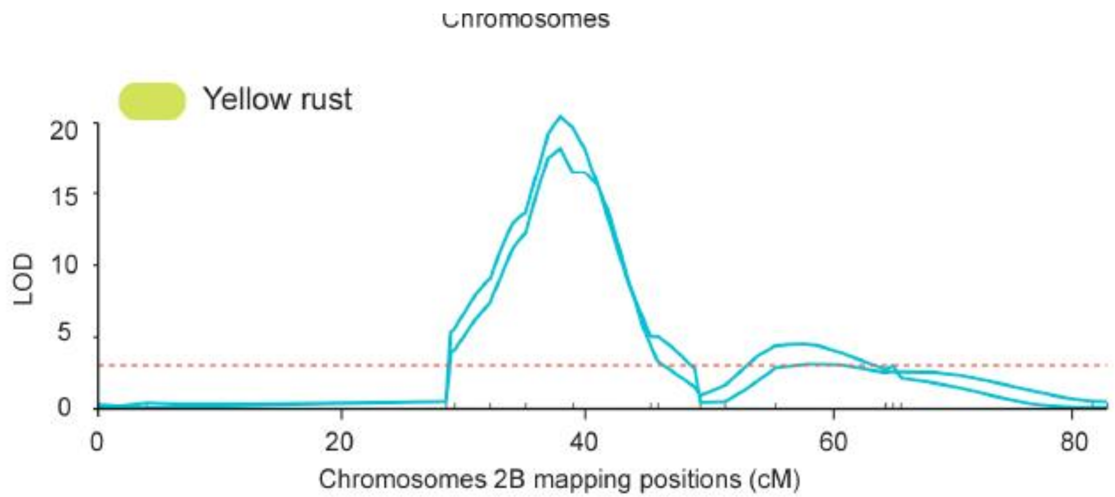
QTL Mapping (3280 QTLs)

NAM GWAS (3545 MTAs)

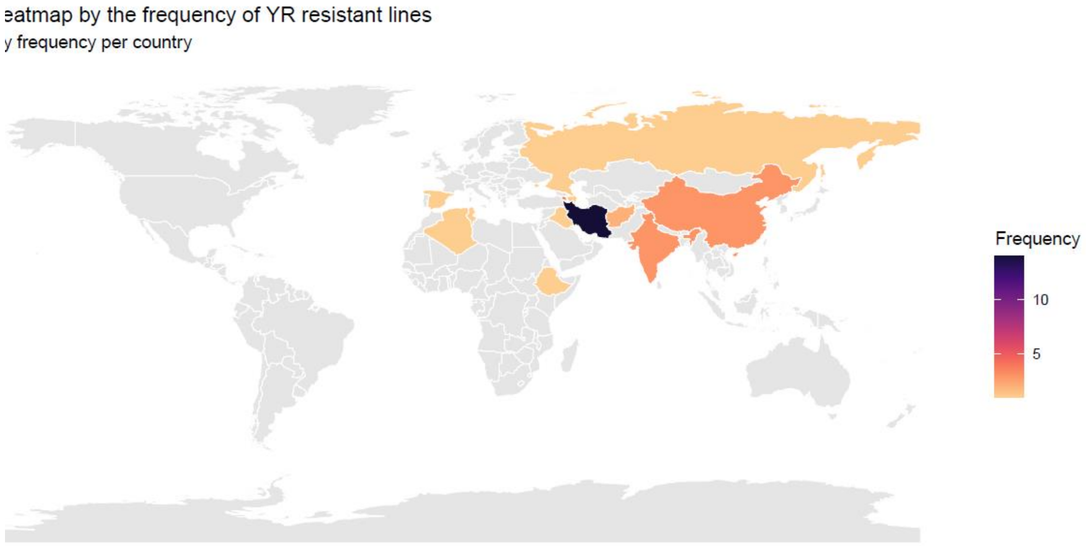
Thousands of genetic effects identified using complementary gene discovery methods

Trait examples:

- **Yellow Rust “Warrior” race**



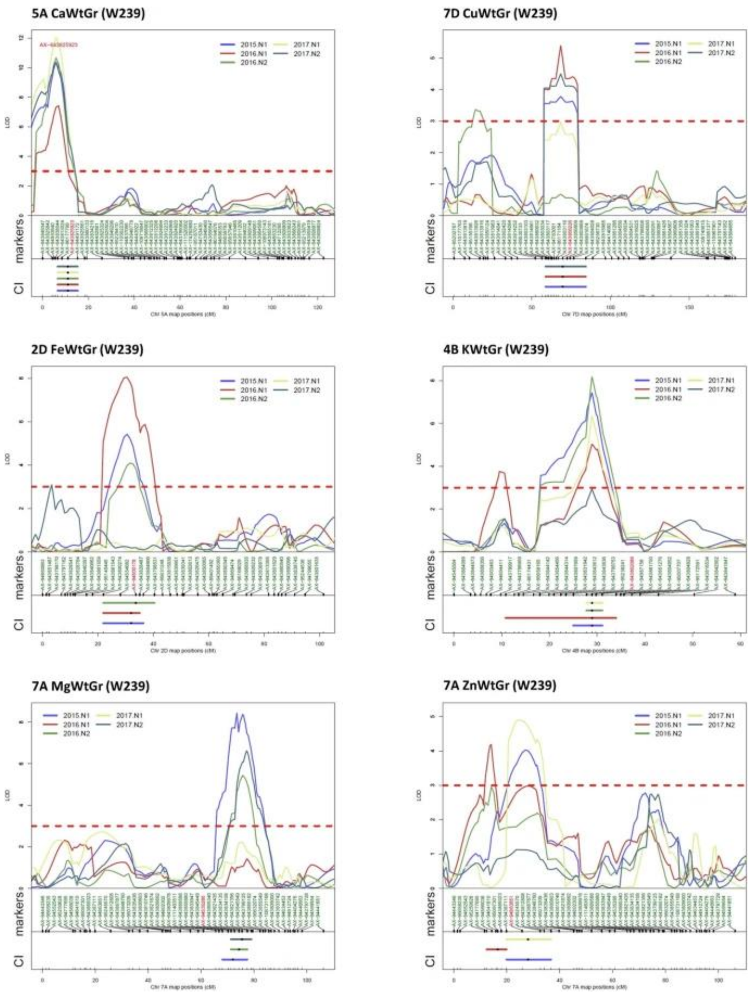
Yellow rust resistance sources centred on Iran



Data source: S. Griffiths

Novel alleles for grain mineral content

QTL for increased calcium, copper, iron, potassium, magnesium and zinc

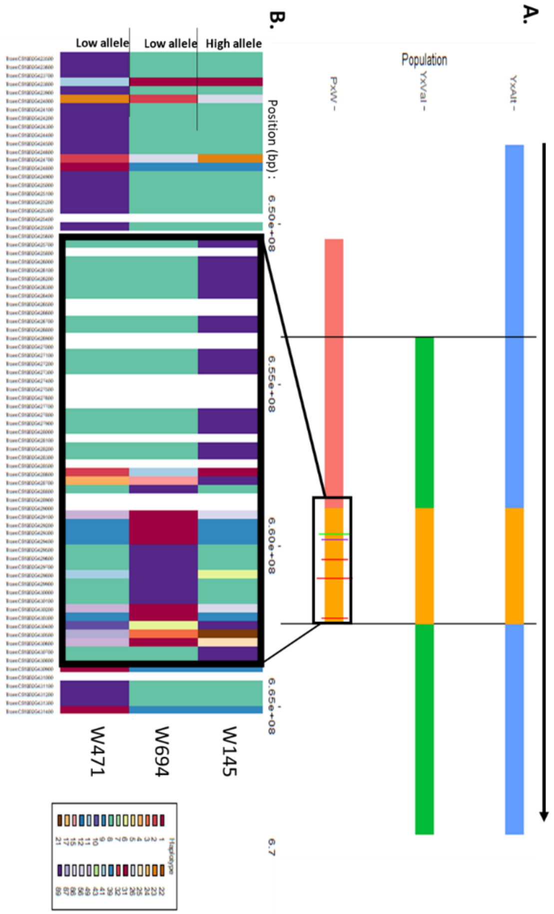


Petros Sigalas

Watkins alleles for increased dietary fibre

James Brett

High resolution mapping of known QTL



Allelic series with **extra high** Watkins alleles

Watkins accession	WATDE Code	allele	Allele R
1190045-1	WATDE0009	high	H1
1190079-1	WATDE0010	high	H2
1190145-1	WATDE0019	high	H3
1190273-1	WATDE0036	high	H4
1190397-1	WATDE0052	high	H5
1190398-1	WATDE0053	high	H6
1190474-1	WATDE0063	high	H7
1190546-1	WATDE0069	high	H8
1190238-1	WATDE0031	high	H9
1190300-1	WATDE0040	high	H10
1190750-1	WATDE0108	high	H11
1190811-1	WATDE0115	high	H12
1190103-1	WATDE0013	high-watkins	HW1
1190299-1	WATDE0039	high-watkins	HW2
1190308-1	WATDE0042	high-watkins	HW3
1190471-1	WATDE0062	low	L1
1190475-1	WATDE0064	low	L2
1190685-1	WATDE0091	low	L3
1190694-2	WATDE0093	low	L4
1190700-1	WATDE0095	low	L5
1190740-2	WATDE0103	low	L6
1190110-1	WATDE0014	low	L7
1190560-1	WATDE0071	low	L8
1190749-1	WATDE0107	low	L9

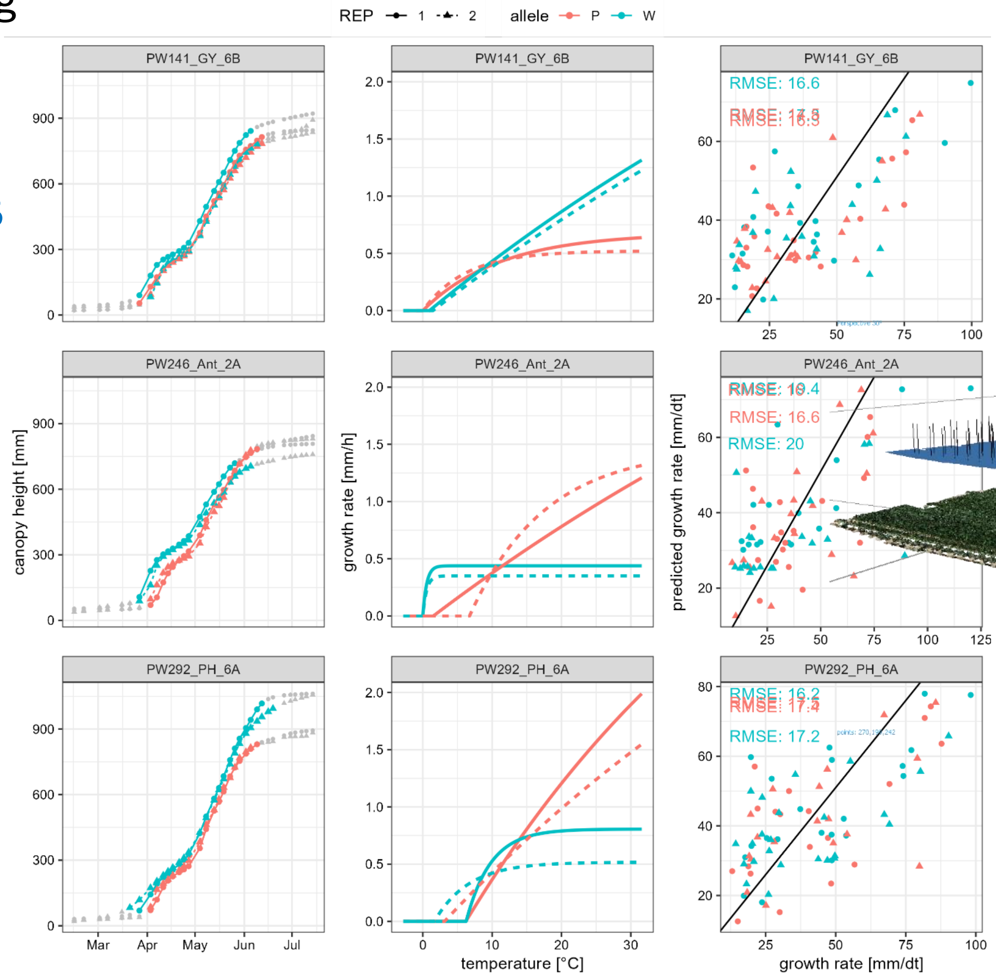
New alleles for adaptation through changes in temperature sensitivity

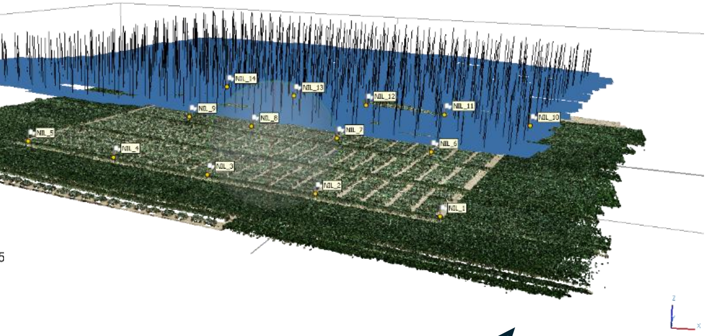
Lukas Kronenberg

Watkins 141_6B

Watkins 248_2A

Watkins 292_6A





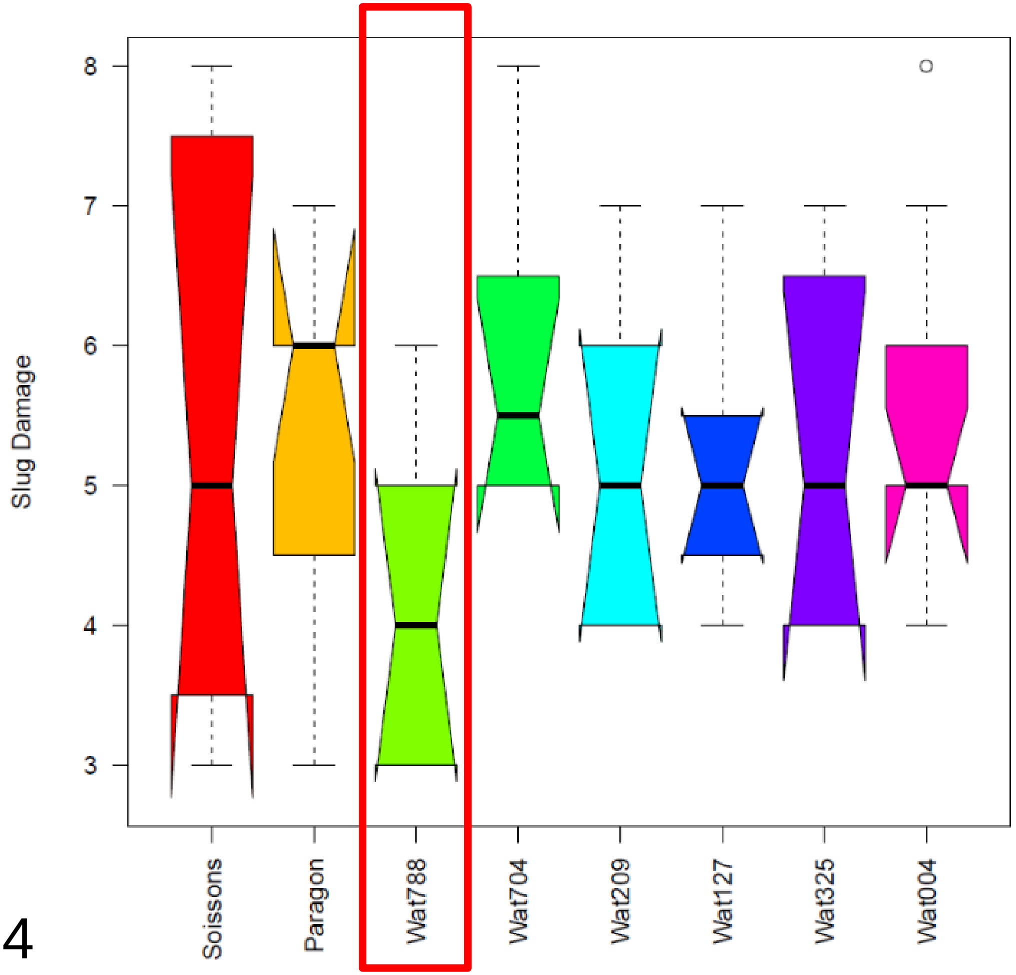
2015 choice assays & 2016 field trial

Jake Stone

Screening of Watkins Core Origins Collection

6 slugs, 3 varieties (1 control) per assay, 10 seeds each, 8 replicates

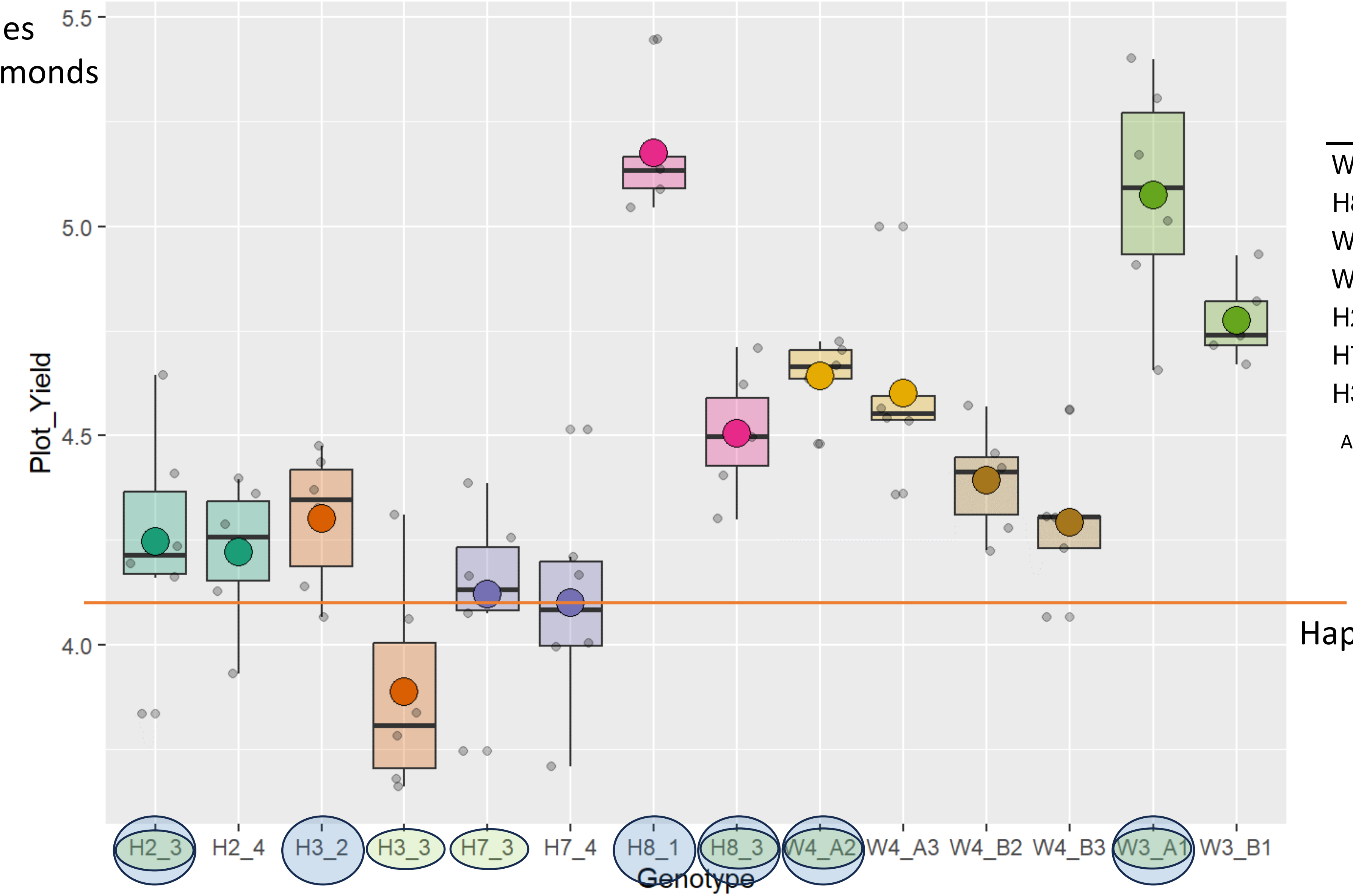
Slug feeding damage



3 lines experienced most damage: 704, 127, 004
3 lines experienced least damage: 788, 209, 325

Toolkit validation of novel Watkins alleles for yield

James Simmonds



Hap3 Mean

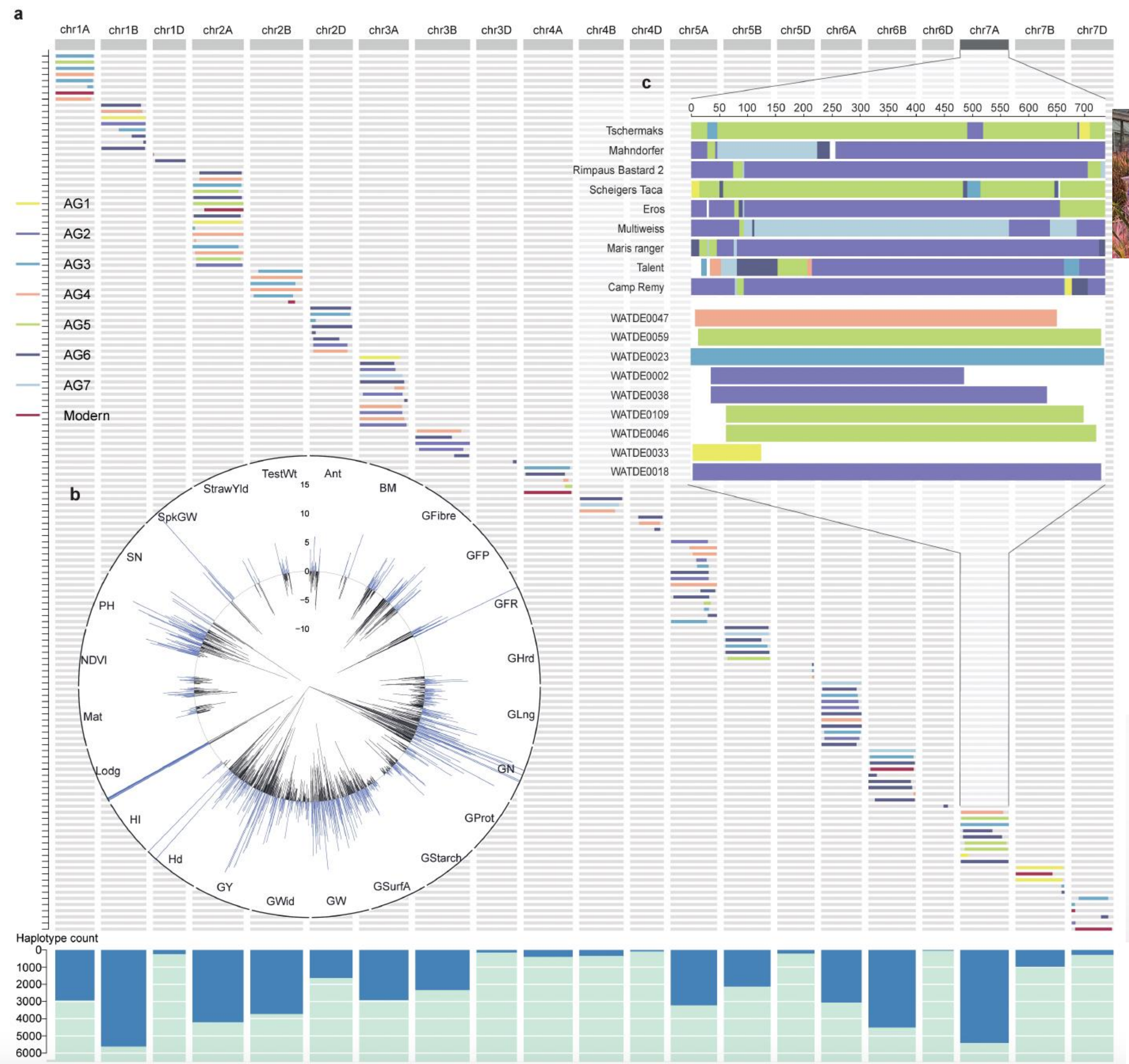
	Plot_Yield		% difference
W3	4.94	a	20.6%
H8	4.81	a	17.5%
W4_TK19	4.62	ab	12.8%
W4_TK23	4.35	bc	6.2%
H2	4.23	c	3.4%
H7	4.11	c	0.4%
H3	4.09	c	-

Analysed as means of both lines

○ Lines already sent for BOP

○ Proposed Lines for BTK

wheat programme

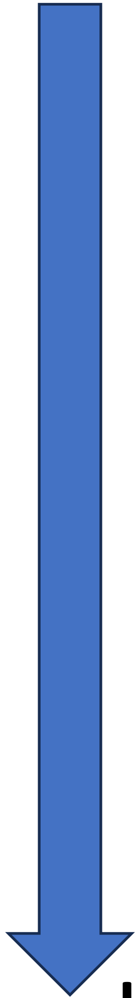


Sarah Collier

Rajani Awal

Michelle Leverington Waite

Charlie Philp



Genebank

Noam Chayut

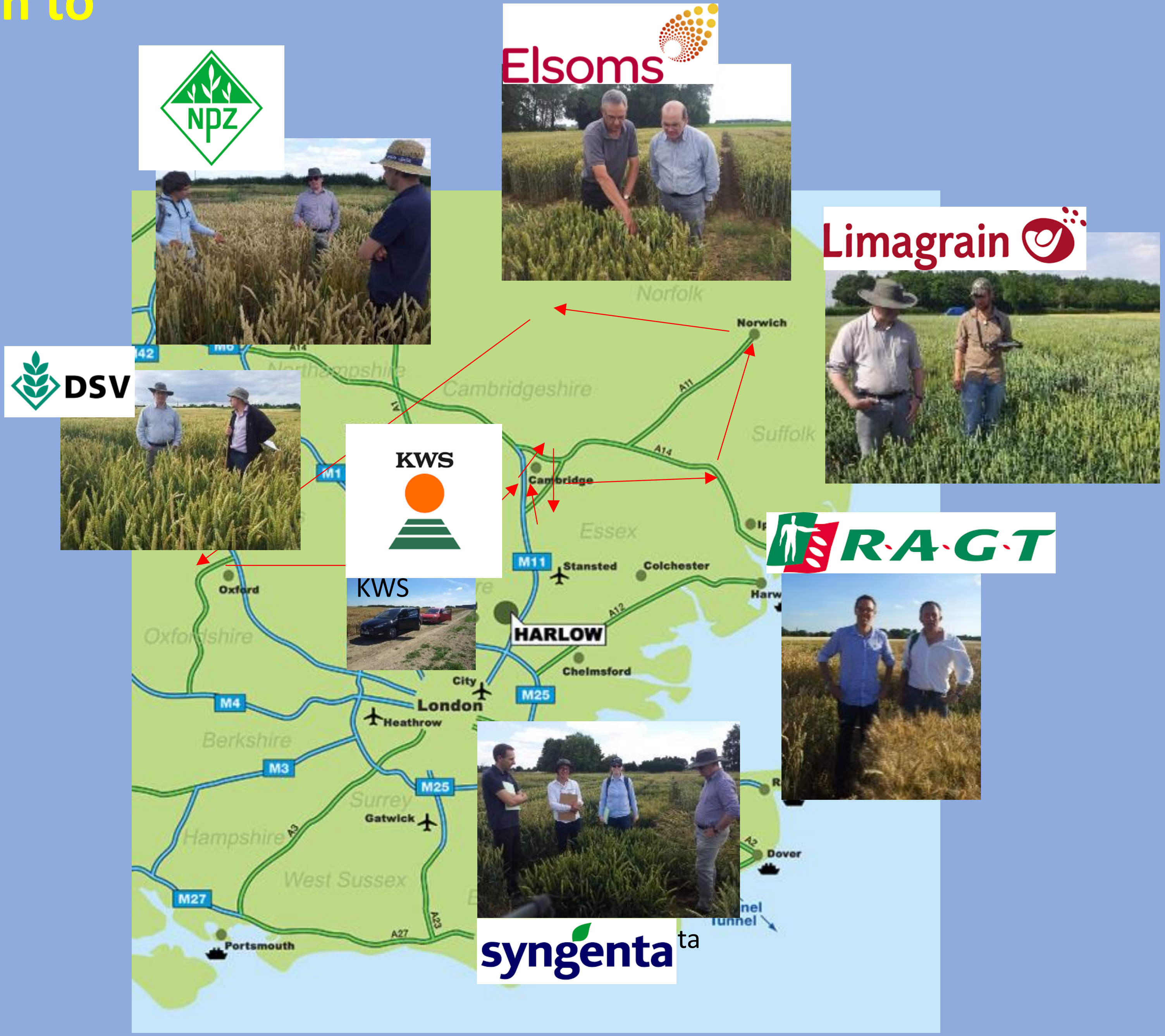
Simon Orford

Germplasm Resources Unit

.... a national capability supported by the BBSRC at the John Innes Centre

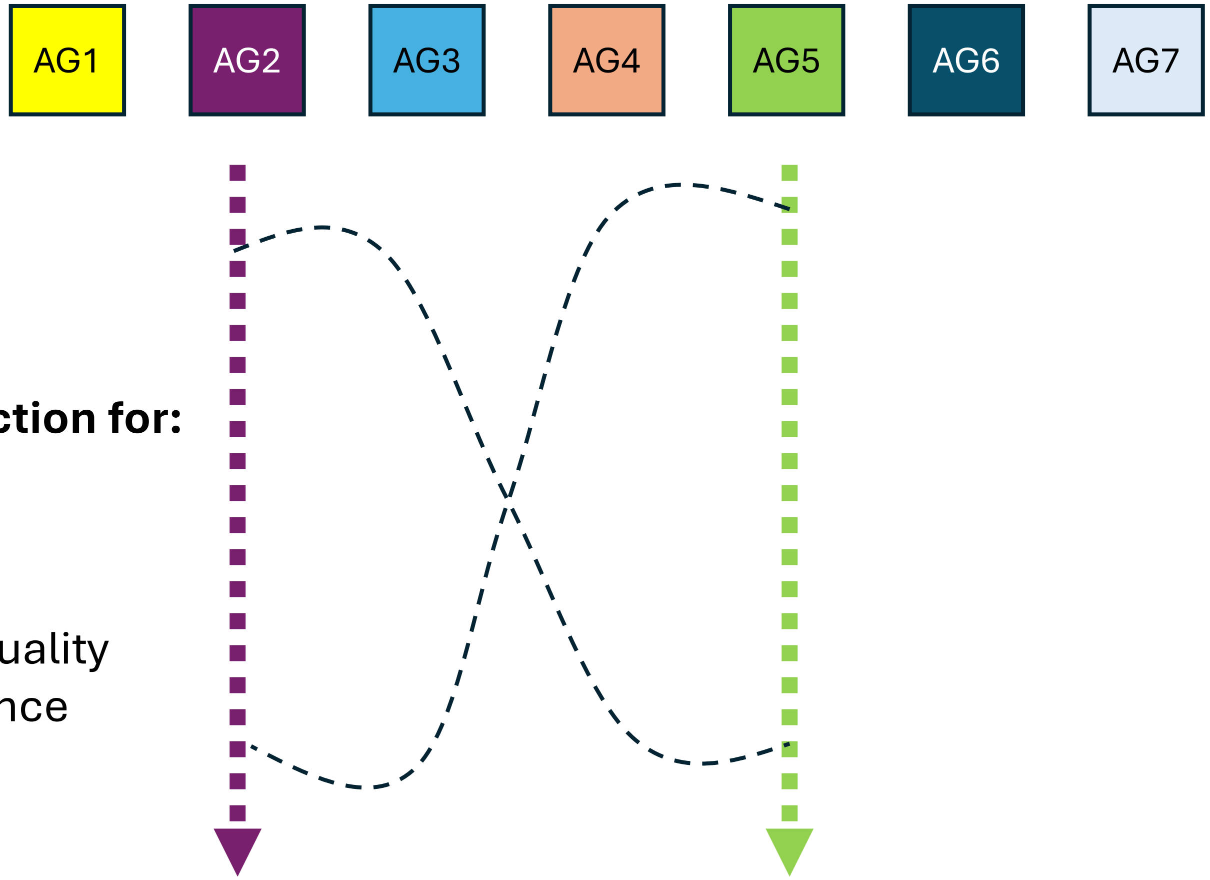
Breeders Toolkit winners move on to commercial trials network

- This is the DSW Breeders Toolkit
- Very successful but…..
- It was designed for 10s-100s of genes alleles not 1000s
- Extreme under deployment of landrace diversity was a shock
- Should we restart pedigree breeding programmes?



A landrace centric view of wheat breeding history

1880
1900
1920
1940
1960
1980
2000
2020



Empirical selection for:
Adaptation
Height
Yield
Bread making quality
Disease resistance

Technological step changes for breeding:
Line selection
Mendelian genetics
Haber-Bosch Process

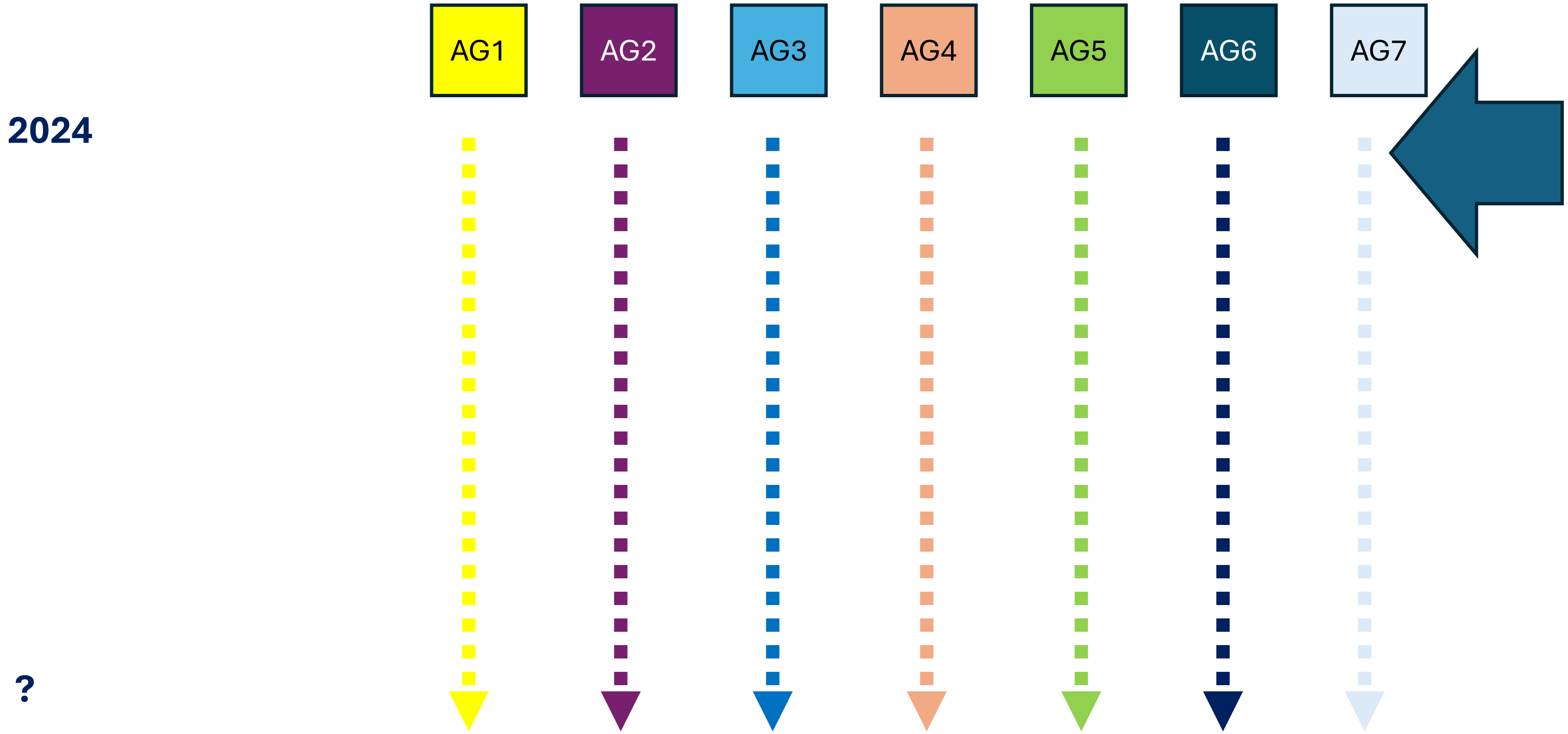
Statistical genetics

Mechanisation

Semi Dwarf varieties

Marker assisted selection
Genomic Selection
Wheat genomics
Gene editing

A proposition for systematically designed wheat pedigrees



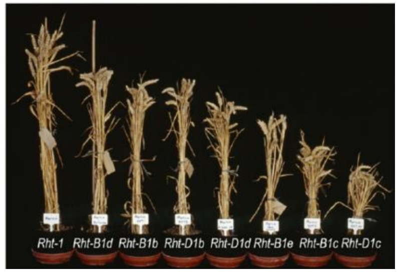
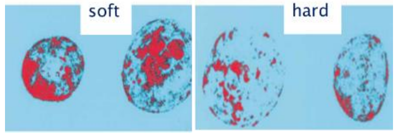
Technological step changes for breeding:

Marker assisted selection
Genomic Selection
Wheat genome/s
Gene editing

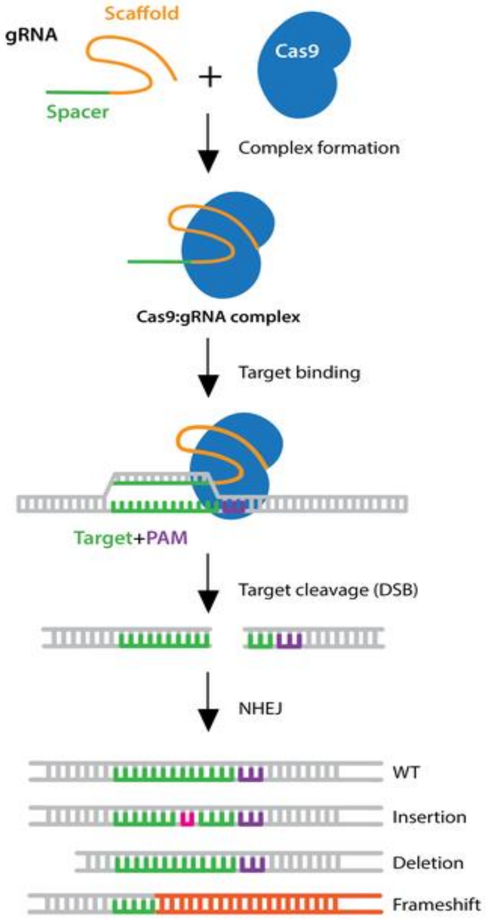
Semi dwarfing alleles are absent from the Watkins collection

- 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

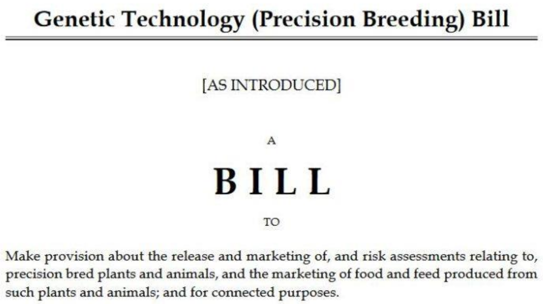
Examples of our chosen targets for fixation in our precision bred Watkins pedigree

	Trait	Gene	Why?	Required edit
	Height	*RHT-1*	Reduce lodging	Delete DELLA domain
	Flowering time	*PPD-1*	Adapt to UK season	Reduce PPD-B1 copy number
	Grain colour	*R*	Prevent sprouting	Restore reading frame
	Grain texture	*PIN*	Suitable for leavened bread	Remove whole gene/s

Gene editing allows us to fix the “must haves” from the very start



CRISPR Cas9 mechanism



Genetic Technology (Precision Breeding) Bill

[AS INTRODUCED]

A

BILL

TO

Make provision about the release and marketing of, and risk assessments relating to, precision bred plants and animals, and the marketing of food and feed produced from such plants and animals; and for connected purposes.

More freedom to innovate in experimental breeding programmes

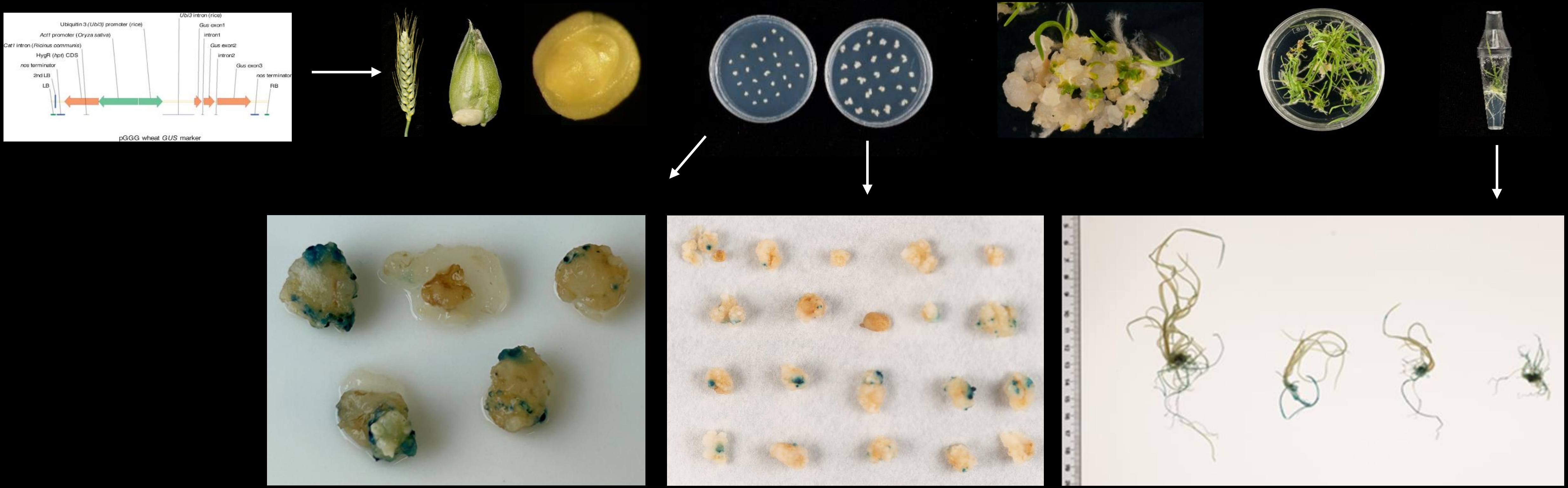
defra

Wheat Genetic Improvement Network

New funding began July 24

Department
for Environment
Food & Rural Affairs

Transformation optimisation of selected Watkins lines using a construct containing a reporter gene (GUS)

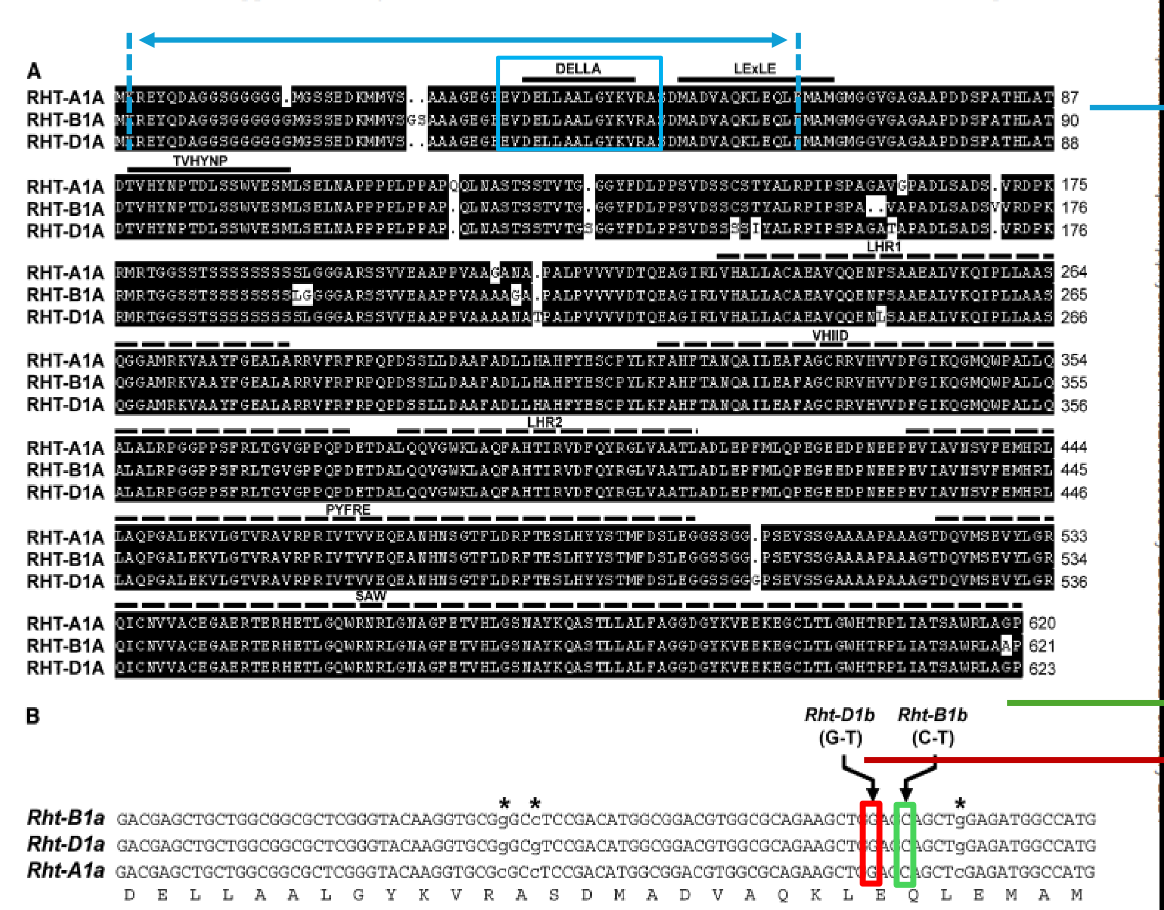


- 6 Watkins lines were transformed with GUS construct
- Transformation efficiencies (4-33%)

Rajani Awal

Rht-1-Gain of function

Reduced height (Rht)-B1b and Rht-D1b semi dwarfing genes



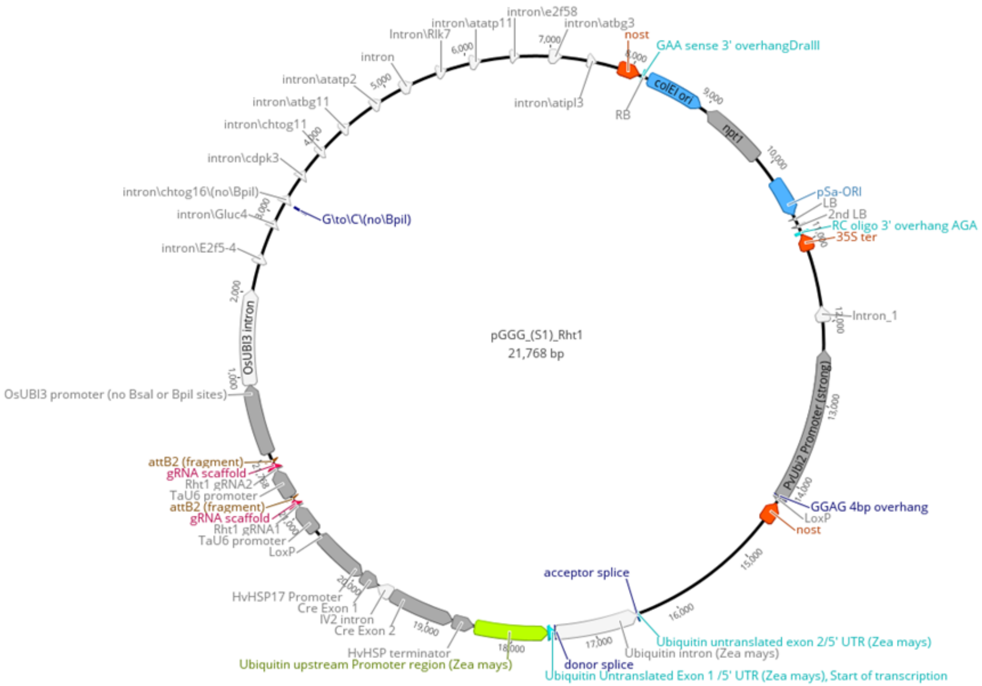
CRISPR /Cas9

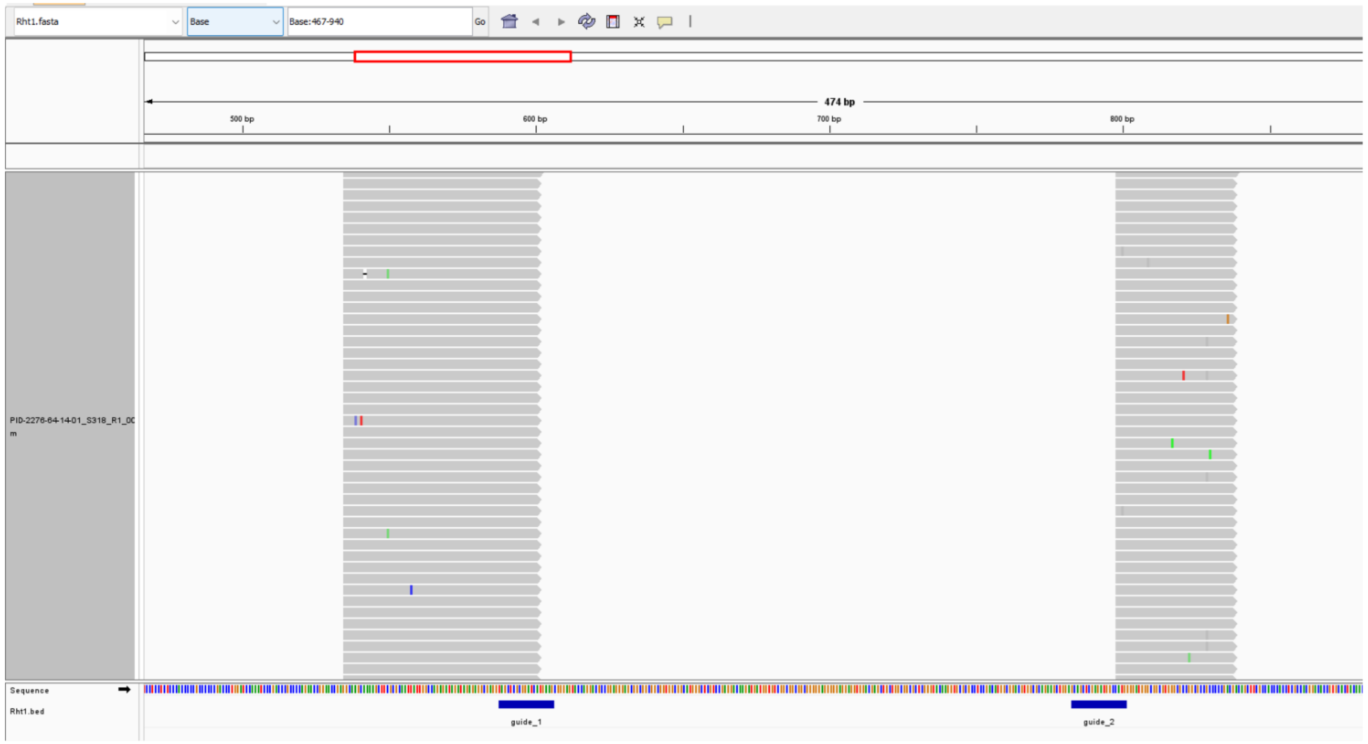
Base Editing

Prime Editing

Adapted from Pearce et al., 2011

pGGG-(S1) Rht 1

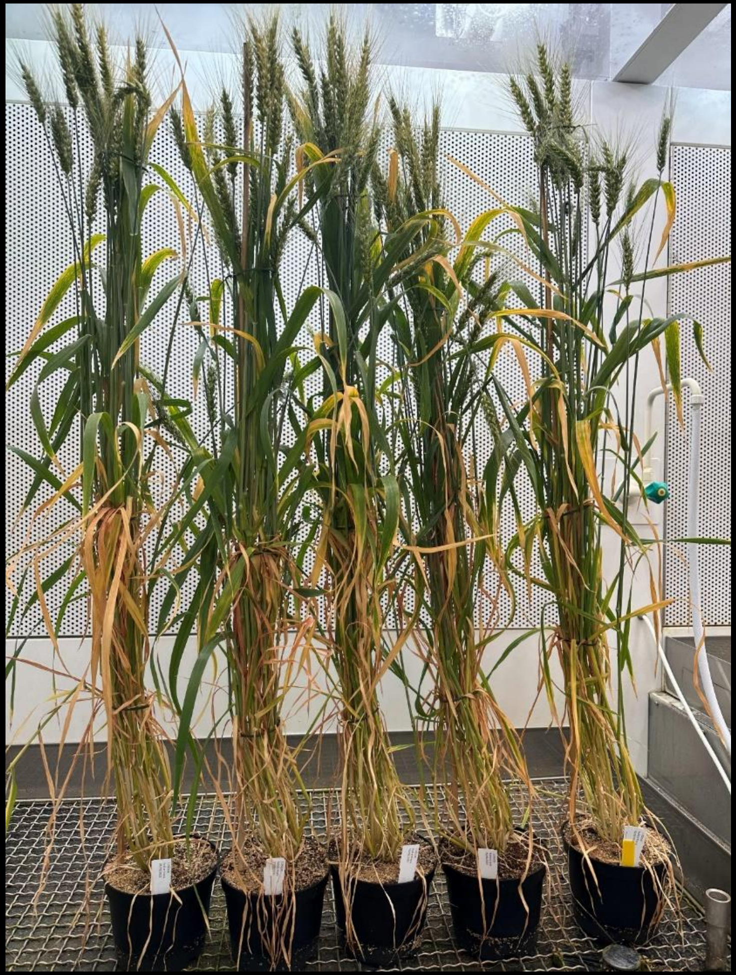




- The pGoldenGreenGate (S1) containing two guide RNAs targeting the Rht1 both driven by the TaU6 promoter, hygromycin selectable marker, Cre-LoxP heat-shock excisable GRF4-GIF1, and the intron enhanced Cas9 driven by the rice ubiquitin promoter.

- RHT1 CRISPR mutant WATDE0585 NGS confirms perfect 195 bp deletions.

Rht1 gene-edited Watkins line



Watkins lines

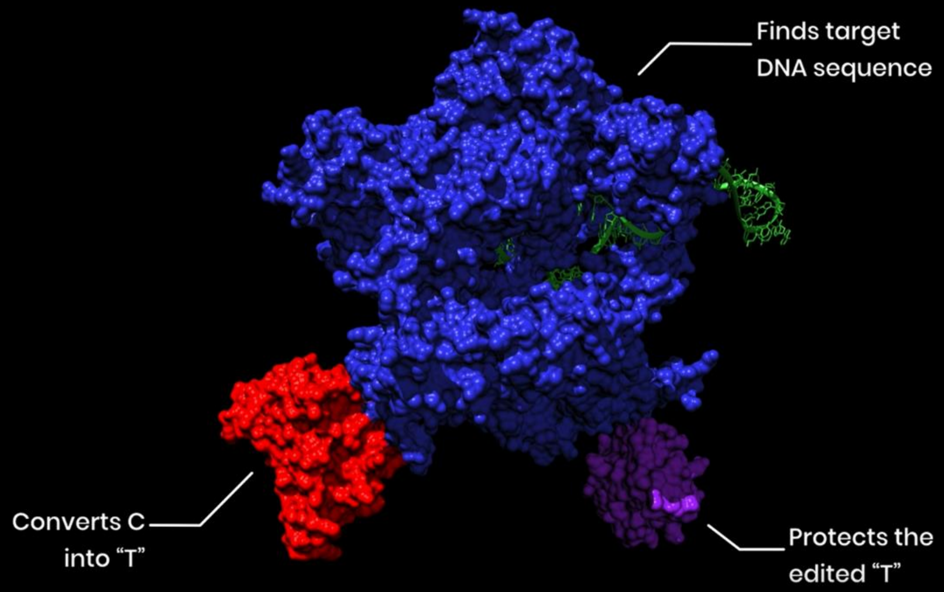
RHT1 CRISPR mutant WATDE0585
NGS confirms perfect 195 bp deletions

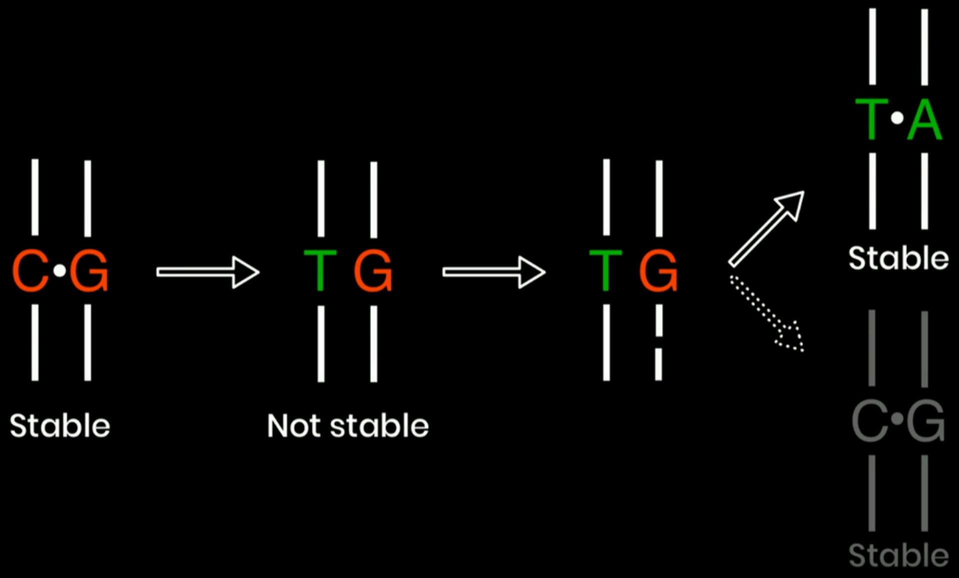
- Until recently transformation was limited to one or two genotypes
- Transformation is now facile
- We are now editing RHT1, PPD1, R, and PIN

WGIN Wheat transformation and GE team

Cytosine base editors

The cytosine BE's comprise of a three-protein fusion





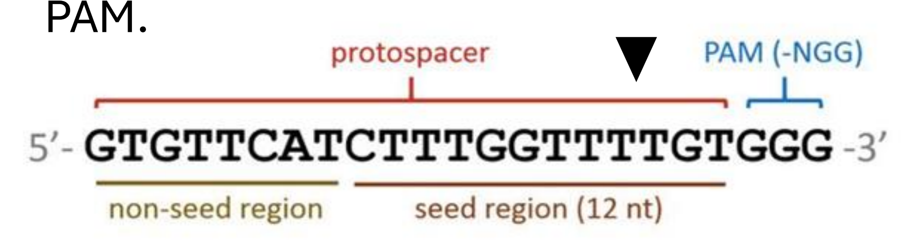
nCas9 or dCas9 and guide complex finds the target sequence

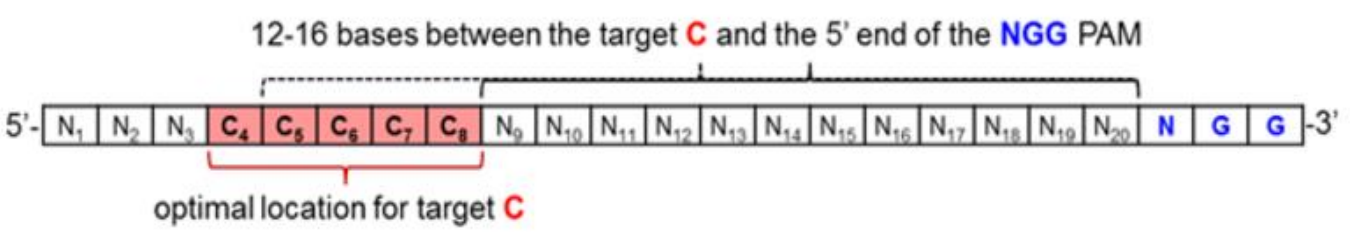
Cytosine deaminase converts Cytosine into Thymine

Uracil DNA glycosylase inhibitor (UGI) protects the T while the target is unstable.

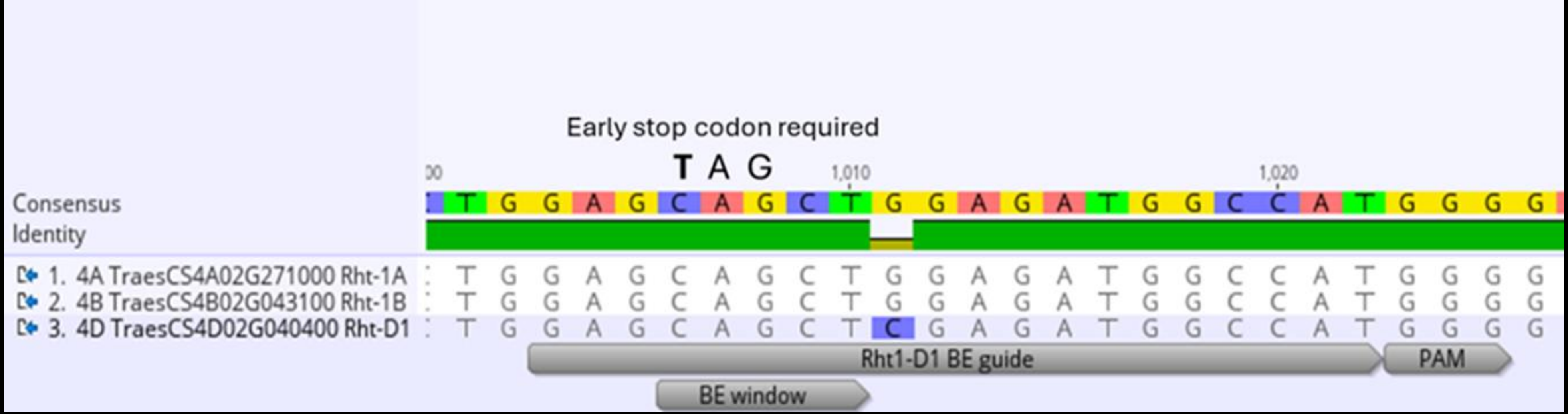
Design guide RNAs for base editing

- Standard Cas9 cuts between the third and forth base from the PAM.

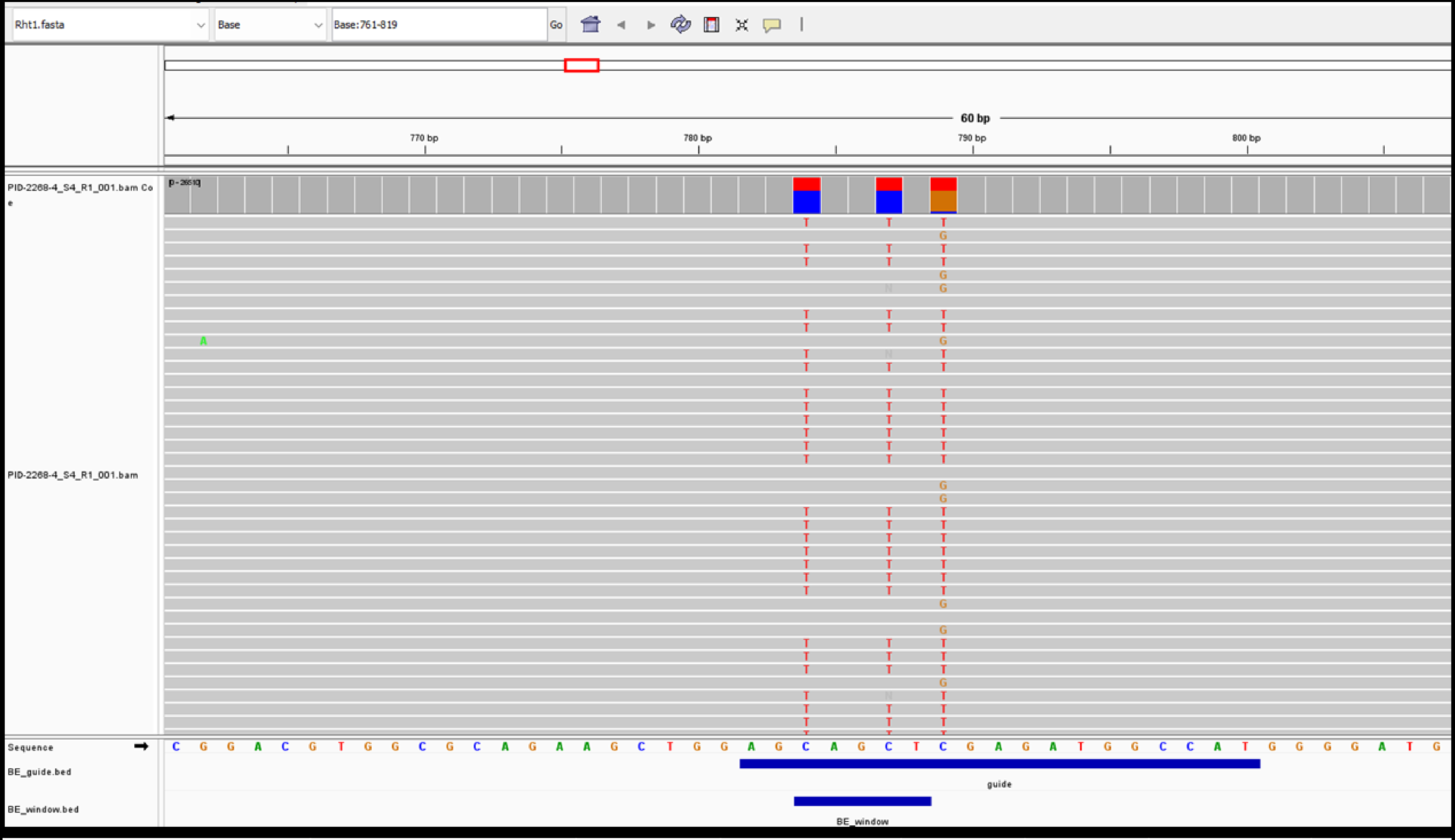




- For BE the activity window in the protospacer is from the 3rd to the 13th base from the 5’ end.
- With an optimal window between the 4th and 8th base.



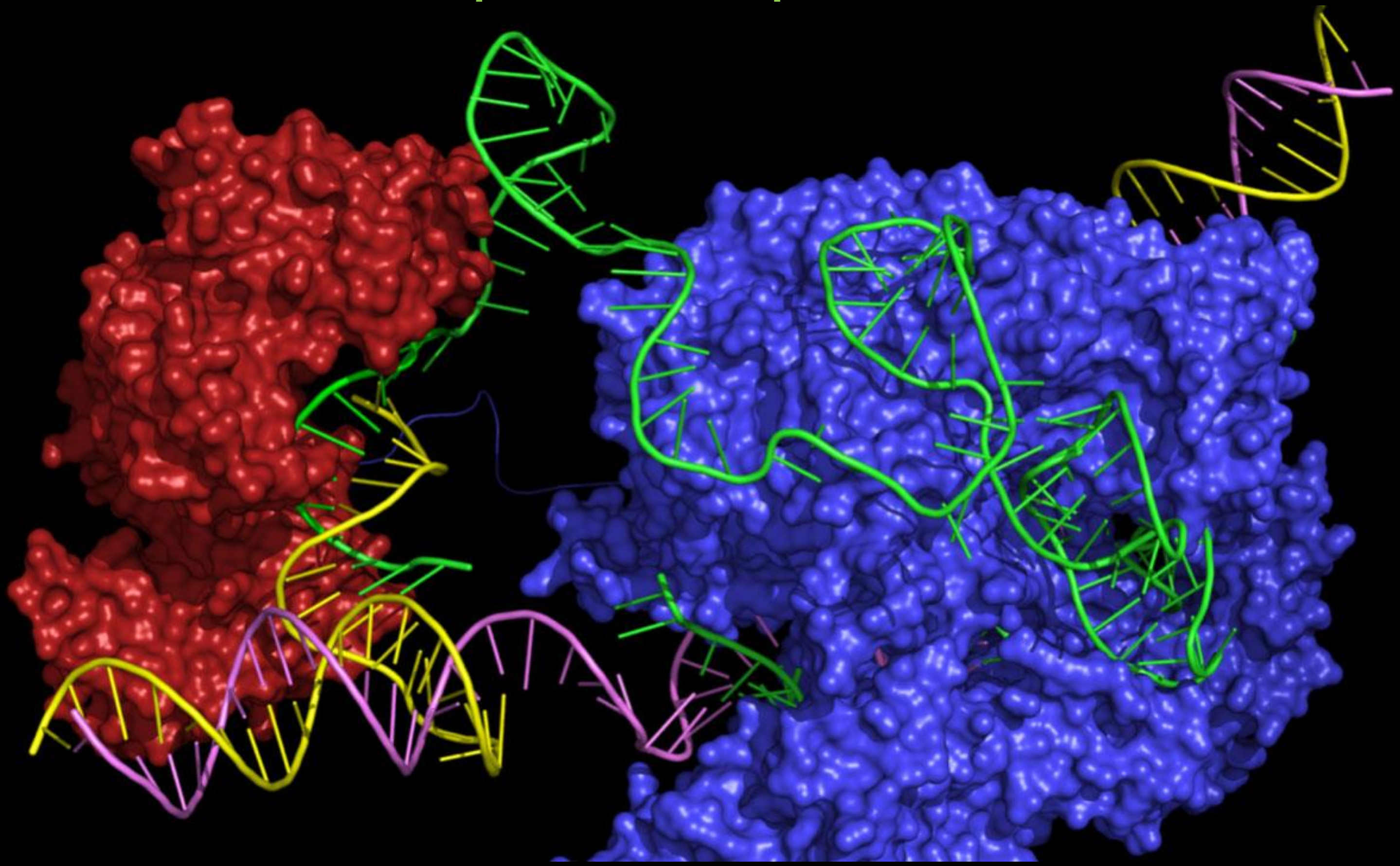
Consensus T G G A G C A G C T G G A G A T G G C C A T G G G G
Identity
1. 4A TraesCS4A02G271000 Rht-1A T G G A G C A G C T G G A G A T G G C C A T G G G G
2. 4B TraesCS4B02G043100 Rht-1B T G G A G C A G C T G G A G A T G G C C A T G G G G
3. 4D TraesCS4D02G040400 Rht-D1 T G G A G C A G C T C G A G A T G G C C A T G G G G



Seq ID	Construct	Plant ID	Ref Pos	Type	Ref Base	Called Base	SNP %
PID-2268-4_S4_R1_001	pGGG TaCBE6int Rht1	106.03.01	784-787-789	SNP	C	T	37-36-37

Prime Editing

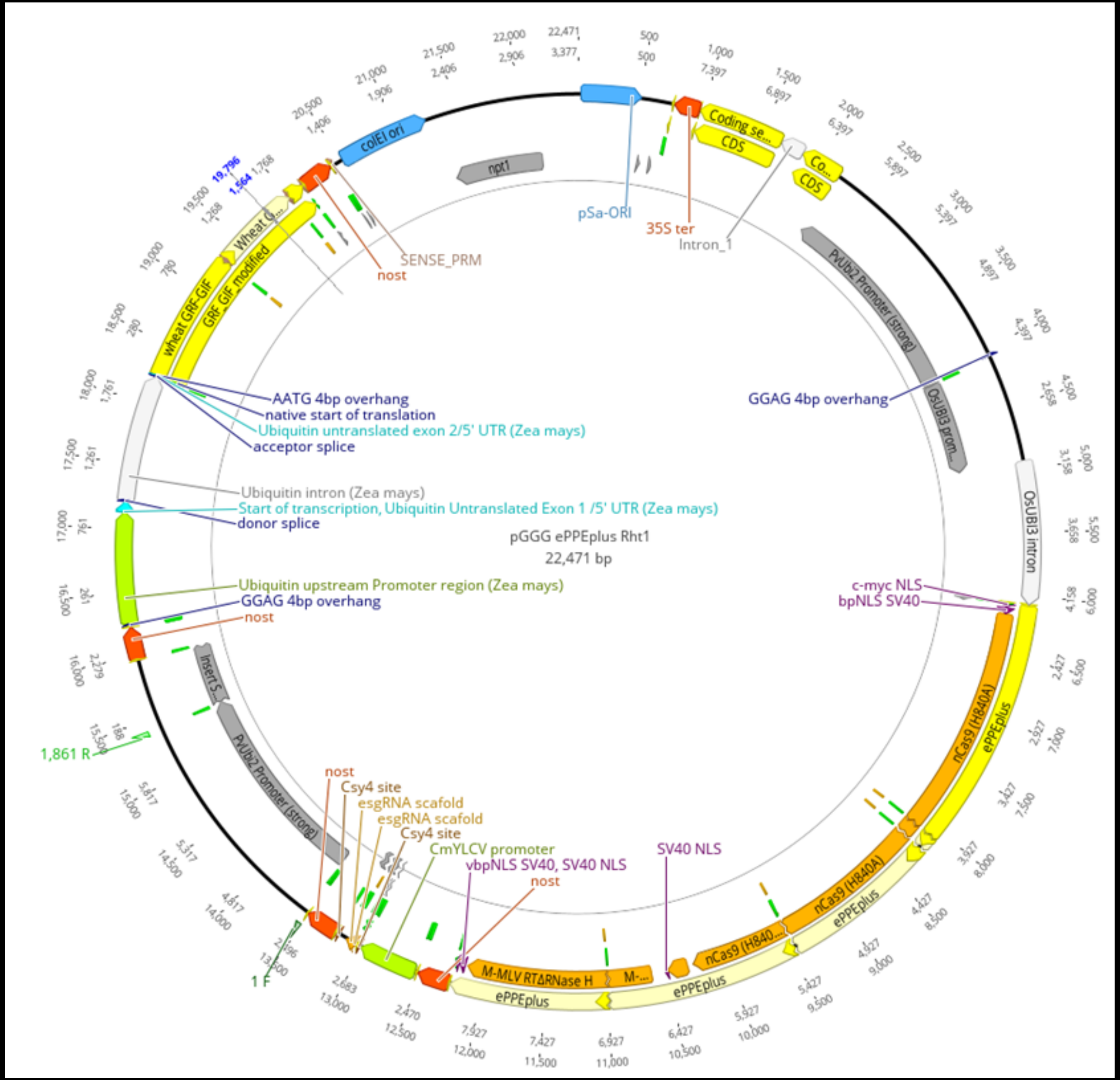
Prime editors comprise of a two-protein fusion



Prime editing (PE) has broad applications as it can rewrite small strips of DNA code

nCas9 and guide complex finds the target sequence

Reverse Transcriptase transcribes DNA from an RNA template on the 3’ end of the PegRNA

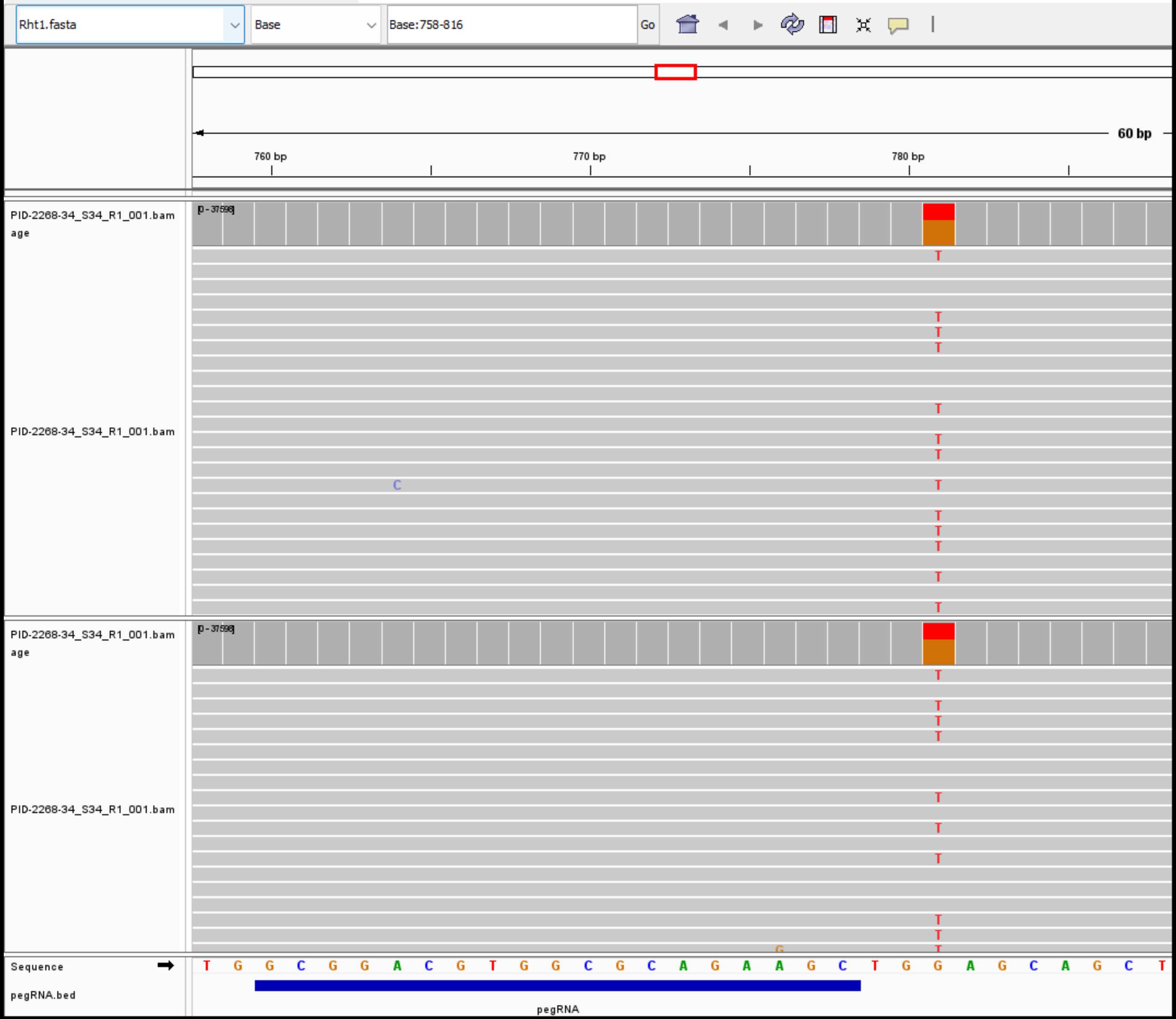


- The pGGG ePPEplus Rht1 vector containing the Rht1 prime editing guide which includes the template RNA for the reverse transcriptase, the enhanced plant prime editor plus nCas9 M-MLV reverse transcriptase fusion (Ni et al., 2023) , the Csy4 pegRNA processing system.
- The Csy4 pegRNA processing system is reported to minimise the circularisation of the pegRNAs.
- PegRNA driven by polymerase II promoter Cestrum yellow leaf curling virus (CmYLCV) for high transcription.
- Most up-to-date plant prime editor ePPEplus driven by the strong rice ubiquitin promoter.

PPE Tang et al.,2020, ePPE Lin et al., 2020, ePPEmax Ni et al., 2023

Rht1 Prime edited WATDE0549

The perfect recreation of Rht-D1b as adopted by the PBI in 60s-70s for the UK green revolution

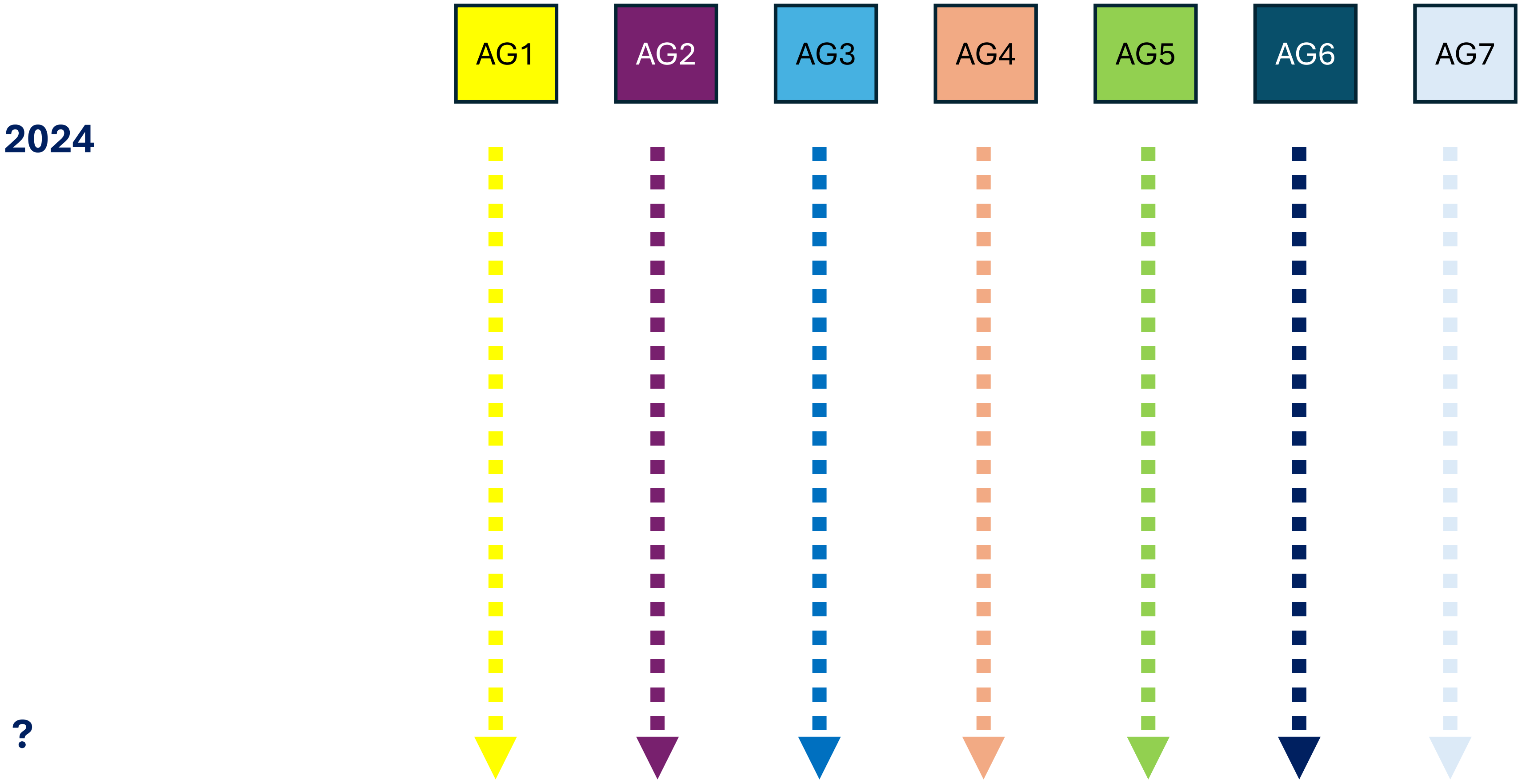


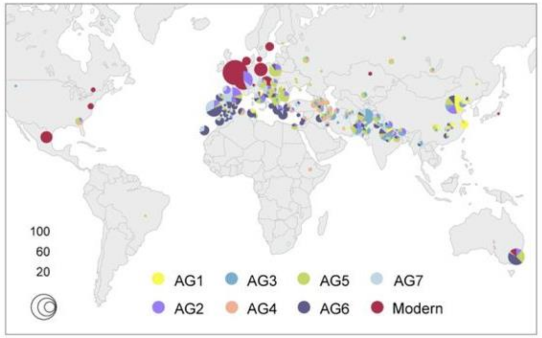
Prime editing results

- Of 14 transgenic Watkins plants tested 11 showed prime editing activity
- 5 of which showed high prime editing activity with more than 30% SNP calls (G to T) within the total NGS reads.

Seq ID	Construct	GRU Code	Plant ID	Ref Pos	Type	Ref Base	Called Base	SNP %
PID-2268-25_S25_R1_001	pGGG ePPEplus Rht1	WATDE0394	80R2.03.02	781	SNP	G	T	32%
PID-2268-28_S28_R1_001	pGGG ePPEplus Rht1	WATDE0394	80R2.03.06	781	SNP	G	T	33%
PID-2268-29_S29_R1_001	pGGG ePPEplus Rht1	WATDE0394	80R2.03.07	781	SNP	G	T	35%
PID-2268-33_S33_R1_001	pGGG ePPEplus Rht1	WATDE0549	81R1.02.01	781	SNP	G	T	42%
PID-2268-34_S34_R1_001	pGGG ePPEplus Rht1	WATDE0549	81R1.02.04	781	SNP	G	T	42%

Watkins pedigrees could capture immense adaptive variation



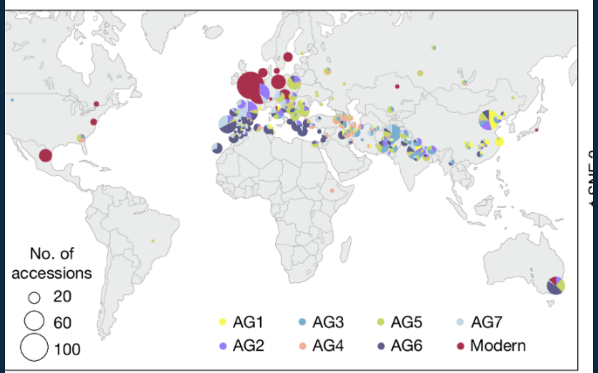


By maintaining AG identity in pedigrees the adaptive traits accumulated for diverse environments over 10000 years will be maintained

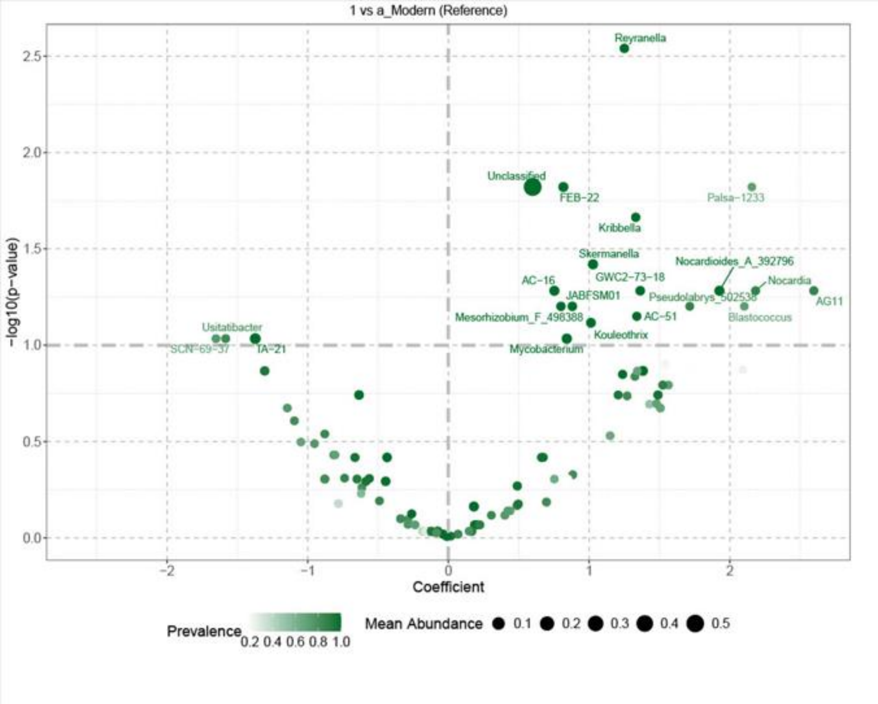
Well adapted high performing lines built on different trait networks

Restarting breeding pedigrees allows the selection for new traits from day 1

Maria
Hernandez
Soriano



- AG2 and AG5 are the founding groups of modern wheat
- AG2 and AG5 show no differences in microbial recruitment compared to modern wheat (only AG2 comparison shown below)
- Others, most notably AG1 (China) do show significant differences in recruitment compared to modern wheat: Reyranella, Kribella, Skermanella, many unclassified
- Do these interactions confer benefit for the crop?



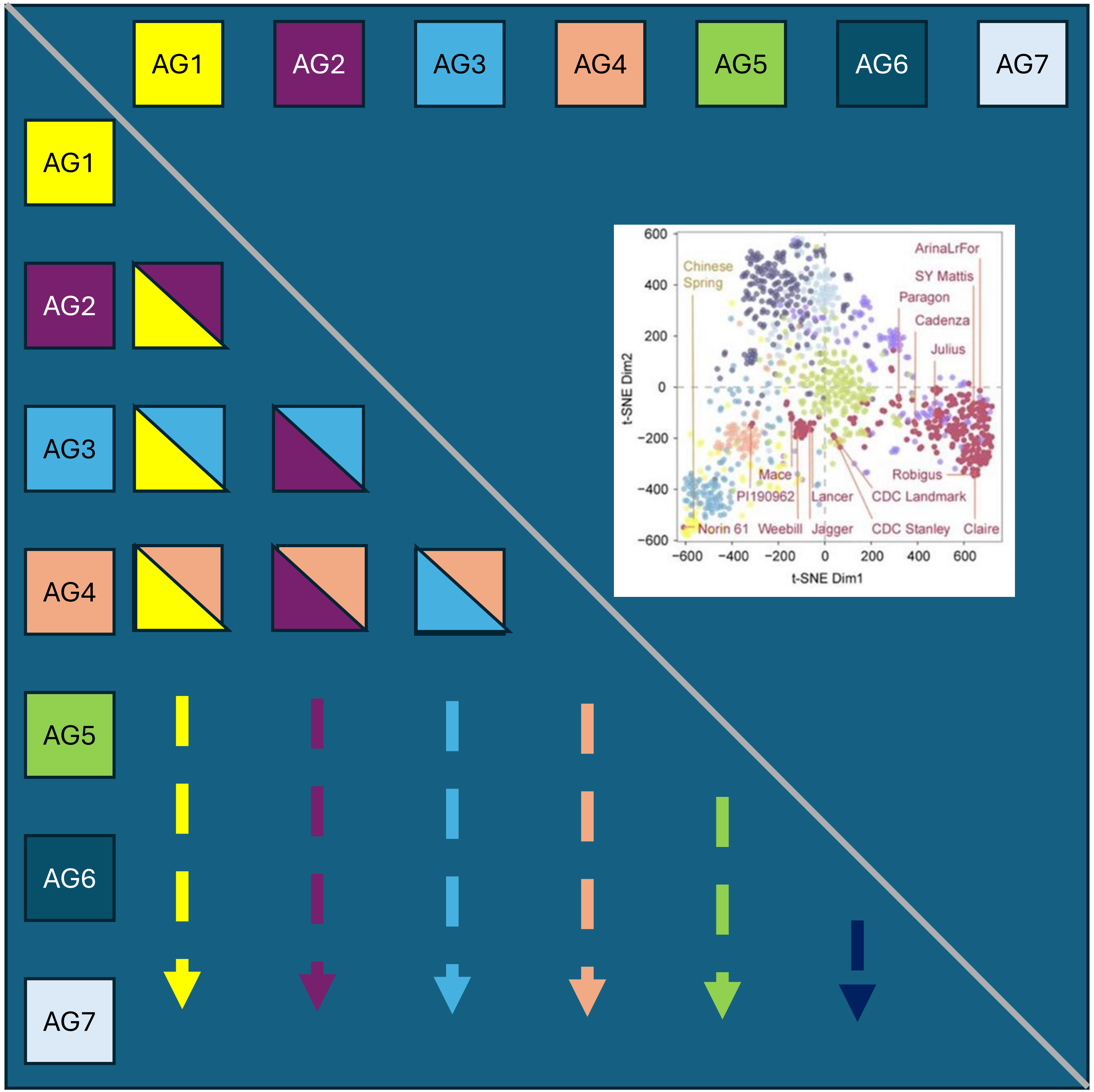
Ancestral group 1 versus modern

Unearthing the rhizosphere microbiome recruited by ancestral bread wheat landracesMaria C HERNANDEZ SORIANO, Frederick James Warren, Falk Hildebrand, Luzie U Wingen, Anthony J Miller, Simon Griffiths

bioRxiv 2025.05.08.652585; doi: https://doi.org/10.1101/2025.05.08.652585

Volcano plots, taxa above threshold on right of plot shows increase in landraces

Maintaining selection within ancestral groups will maximise heterosis



- For many crops the advent of hybrid varieties has been a step change
- In spite of many (extremely expensive) attempts this has not been the case for wheat
- Insufficient dispersed dominance?
- The primary goal of the Watkins PBO pedigree is to produce lines with improvements achieved by inbreeding
- But they will also be used to test newly diverse heterotic pools

Thanks

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Wheat Breeders Toolkit Companies
RAGT
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NPZ

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