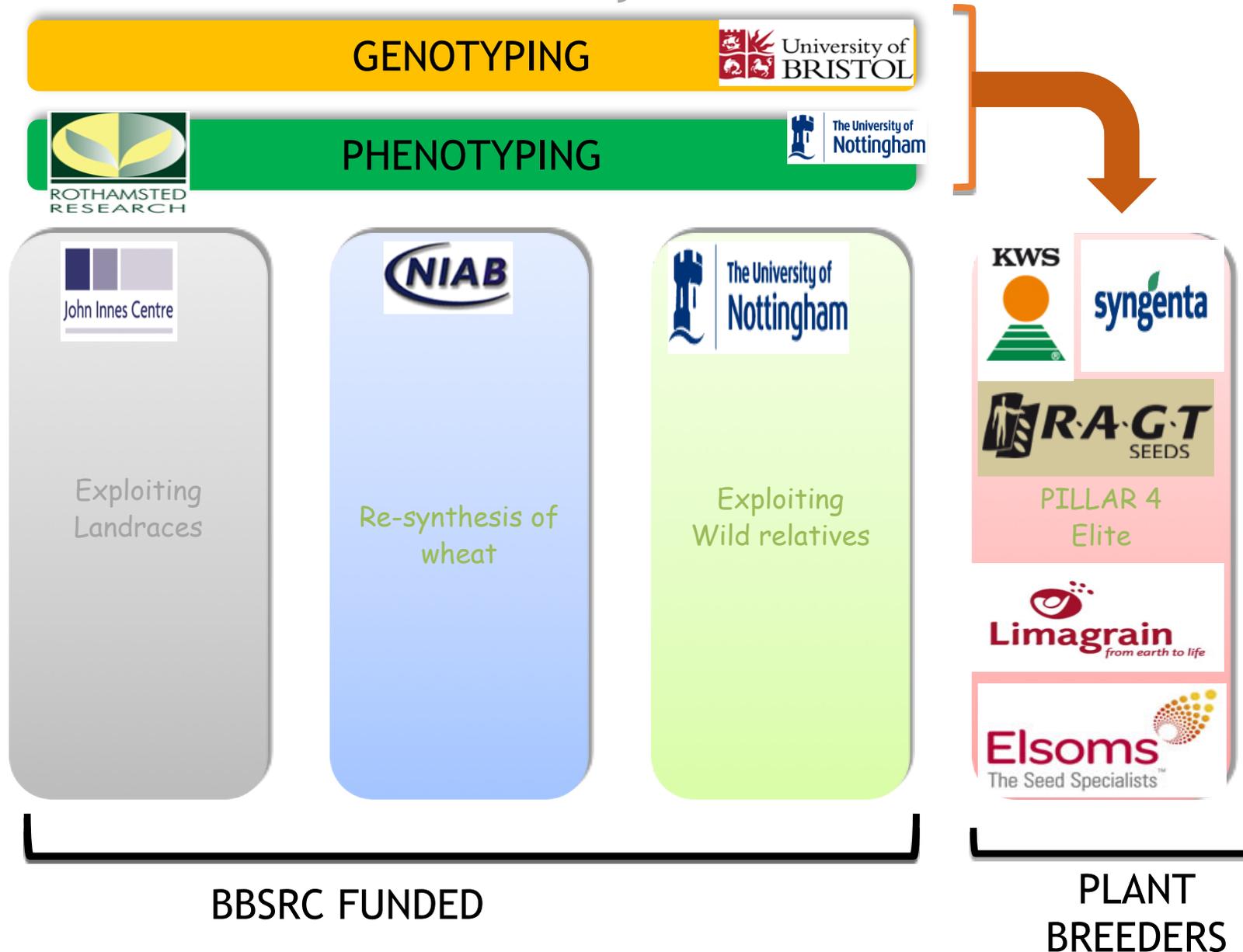


Wheat Pre-breeding Activity

Funded at £15m over 6 years 2011-2017

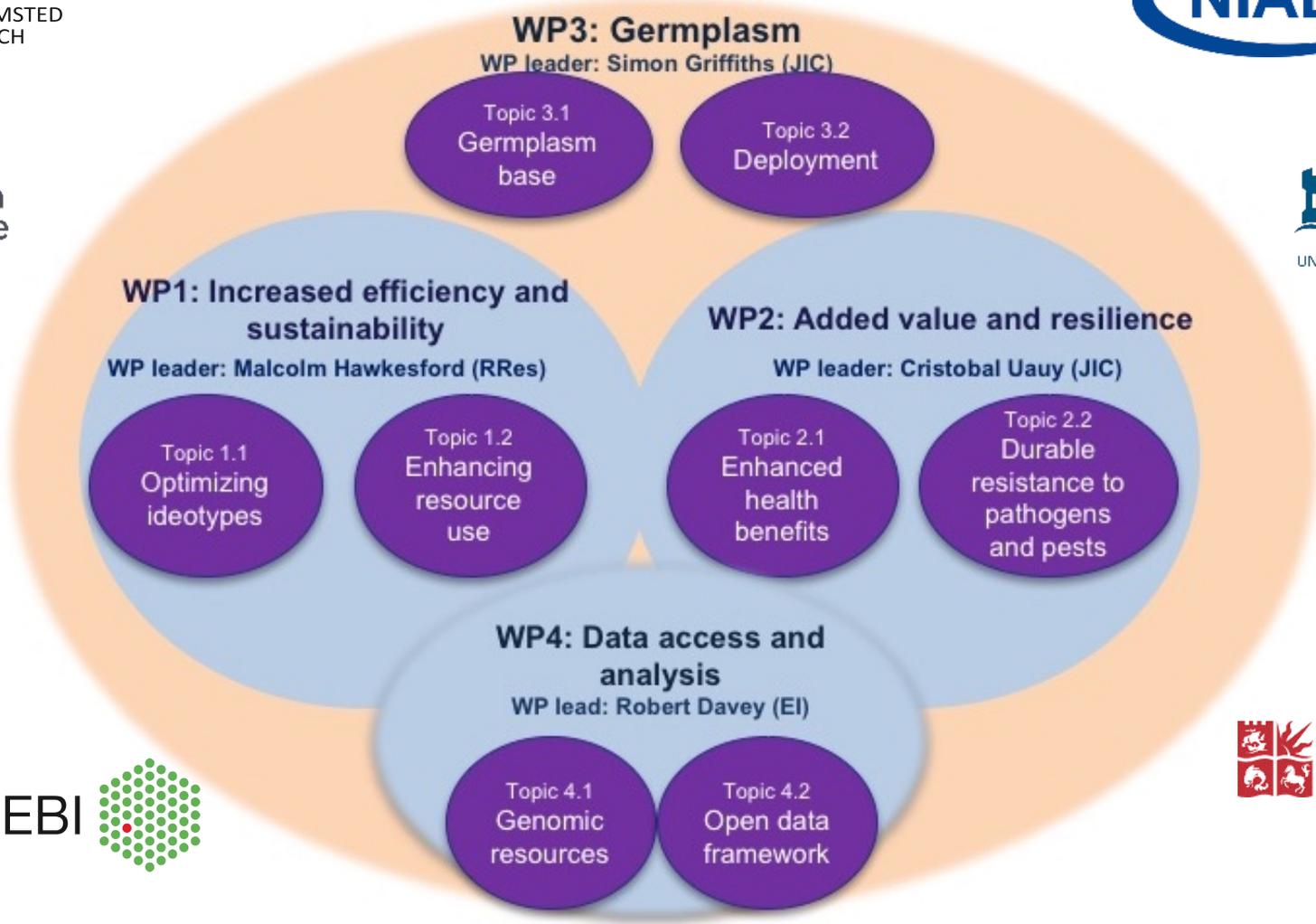


Designing Future Wheat

<https://designingfuturewheat.org.uk>

Funded 2017-2022 (£24 million)
Structure

Eight institutions-36 Project leaders



Wheat Pre-breeding Activity



Designing Future Wheat



Tools and Resources generated
are all openly and freely available

Landraces

crossed with UK Spring type Elite wheat Paragon

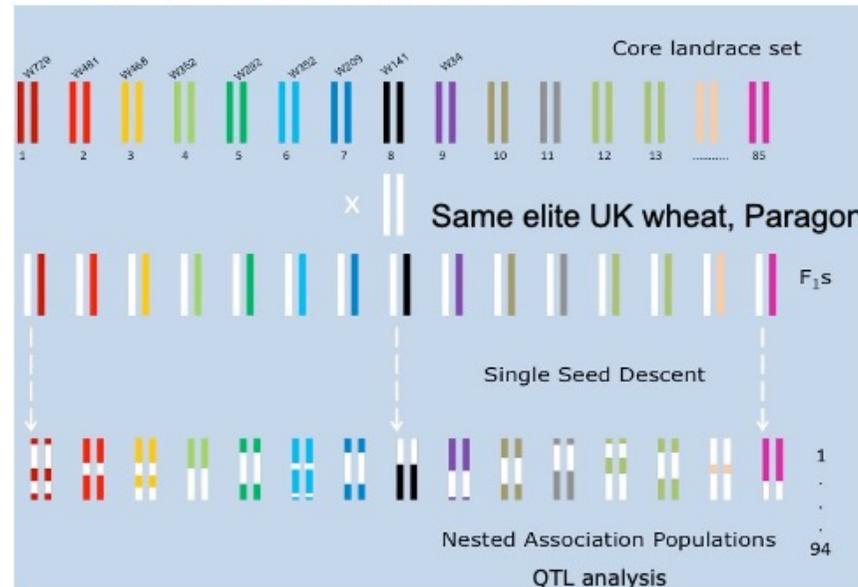
Nearly 1300 landraces from 32 countries

includes 840 landraces from Watkins collection – pre 1930 wheat varieties

↓ Genotyped

Core collection of nearly 120 landraces

capturing most of the diversity in these landraces



>100 F₄:F₆ "off-the shelf"

Watkins-Paragon populations (12,000 segregating lines- genotyped and many phenotyped) → Nearly **800** lines in



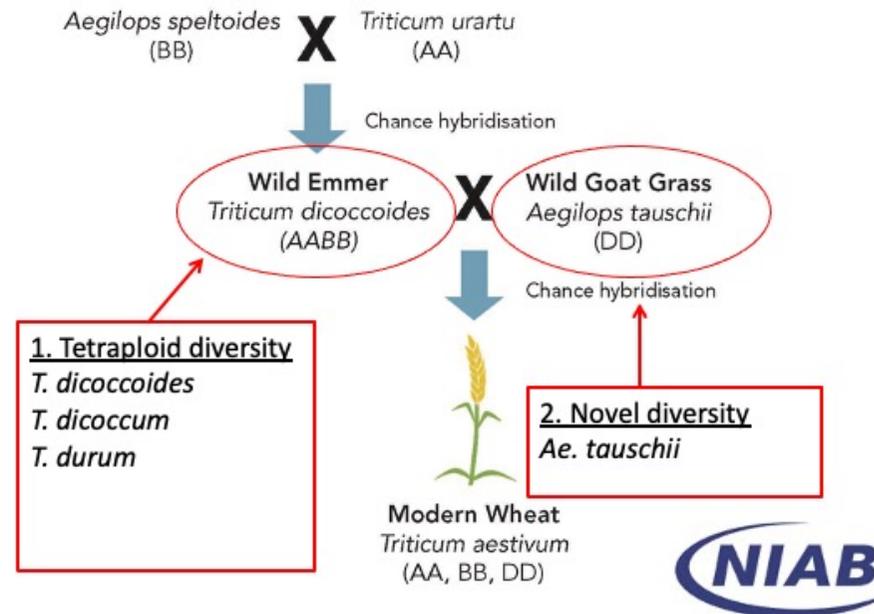
Germplasm Resource Unit

<https://www.seedstor.ac.uk>

Synthetics

crossed with UK 'spring' Elite wheat Paragon

Two streams: incorporating tetraploid AABB (1) and diploid DD (2) diversity



36 (+14) tauschii and 50 tetraploid Synthetics
crossed with Paragon

3050 BC1F₅ lines to be deposited in →

Some lines have been screened in **drought trials**

SeedStor

Germplasm Resource Unit

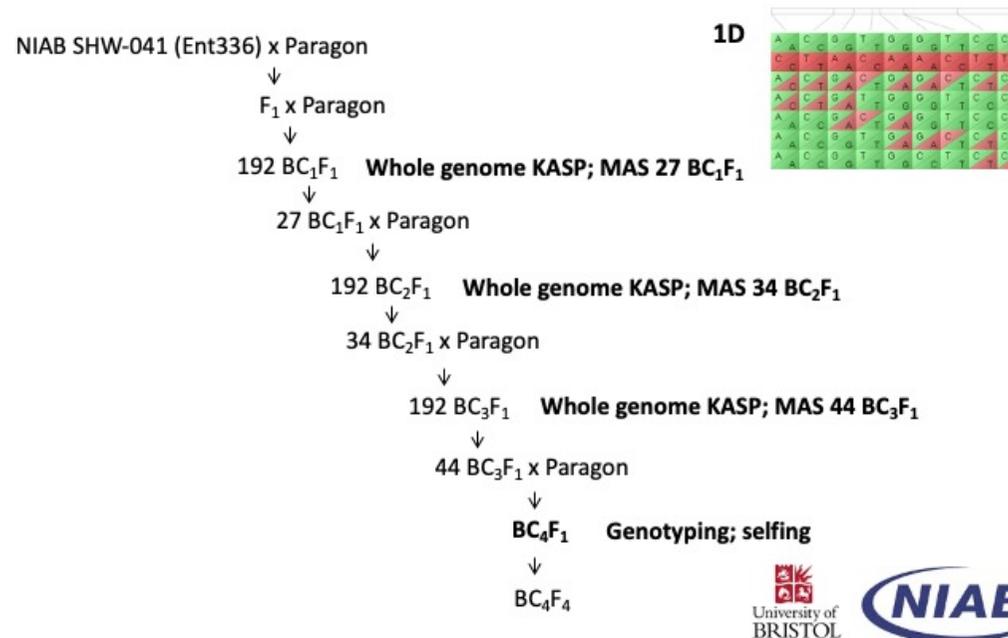
<https://www.seedstor.ac.uk>

CSSLs

Crossed with UK 'Spring' Elite Wheat Paragon

Additional NIAB AABB and DD resources

Chromosome Segments Substitution Lines: lines with small overlapping donor segments of a single AB (TTD-140) and D (Ent-336) donor in a common genetic background (Paragon)



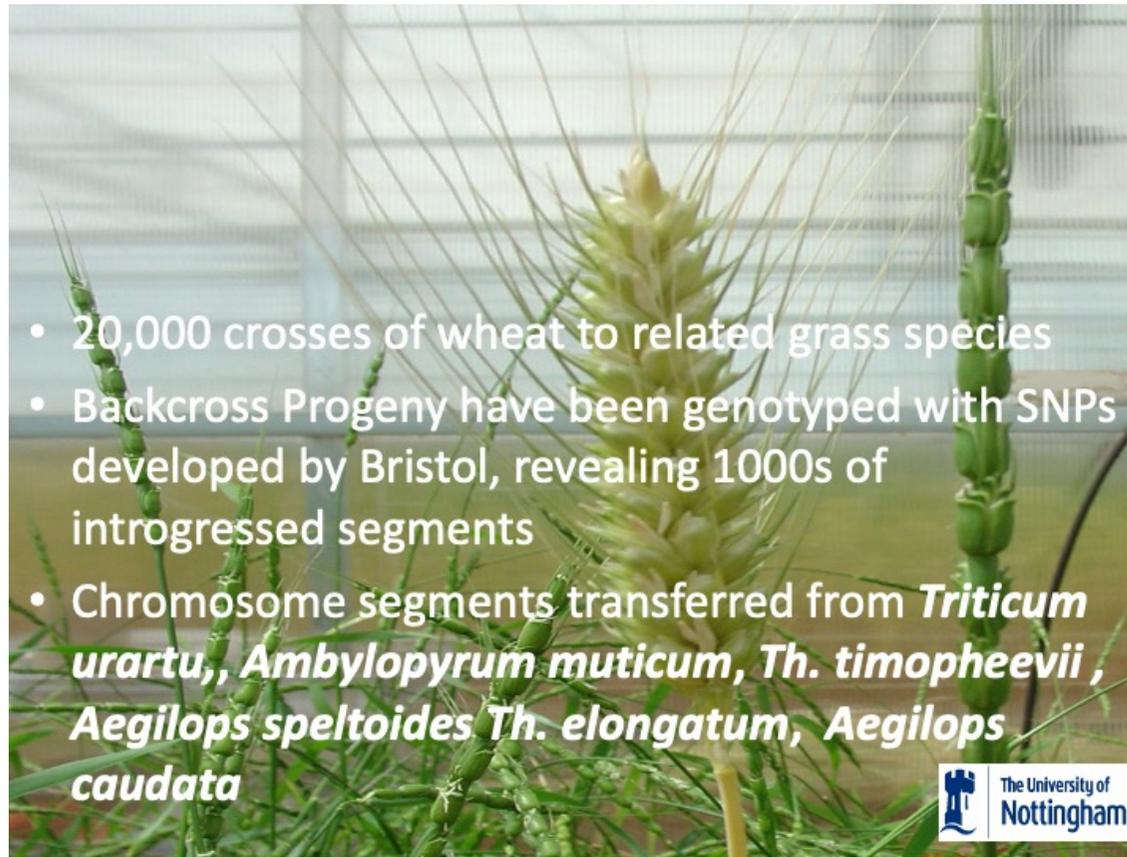
Complete segment tiling covering
the whole genome

109 CSSL lines to be deposited in  Germplasm Resource Unit

SeedStor 

<https://www.seedstor.ac.uk>

Wild relatives



300 Paragon lines carrying homologous segments from either *urartu*, *muticum*, *timopheevii*, *speltoides*, *elongatum* and *caudata* to be deposited in

SeedStor 

Germplasm Resource Unit

<https://www.seedstor.ac.uk>

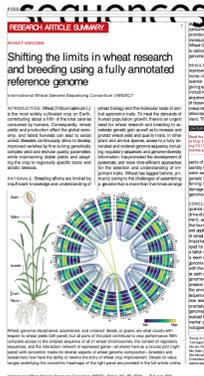


Tools for Gene functional characterisation

multiple wheat genome

Wheat gene expression-Science-2018

Targeted gene mutagenesis
Sequenced
TILLING-201
CRISPR-2018



RESEARCH ARTICLE SUMMARY
Shifting the limits in wheat research and breeding using a fully annotated reference genome
Introduction: Wheat is a major global food crop. The wheat genome is highly complex, with three sub-genomes (A, B, and D) and a high level of polyploidization. This complexity has hindered the identification of genes underlying important wheat traits. A fully annotated reference genome is essential for understanding the genetic architecture of wheat and for identifying candidate genes for breeding.



RESEARCH ARTICLE SUMMARY
A haplotype-led approach to increase the precision of wheat breeding
Introduction: Wheat is a major global food crop. The wheat genome is highly complex, with three sub-genomes (A, B, and D) and a high level of polyploidization. This complexity has hindered the identification of genes underlying important wheat traits. A haplotype-led approach to wheat breeding can increase the precision of gene selection and improve the efficiency of breeding programs.



RESEARCH ARTICLE SUMMARY
The transcriptional landscape of polyploid wheat
Introduction: Wheat is a major global food crop. The wheat genome is highly complex, with three sub-genomes (A, B, and D) and a high level of polyploidization. This complexity has hindered the identification of genes underlying important wheat traits. Understanding the transcriptional landscape of polyploid wheat is essential for understanding gene expression and regulation in this complex genome.

RESEARCH ARTICLE SUMMARY
Uncovering hidden variation in polyploid wheat
Introduction: Wheat is a major global food crop. The wheat genome is highly complex, with three sub-genomes (A, B, and D) and a high level of polyploidization. This complexity has hindered the identification of genes underlying important wheat traits. Uncovering hidden variation in polyploid wheat is essential for understanding the genetic architecture of wheat and for identifying candidate genes for breeding.

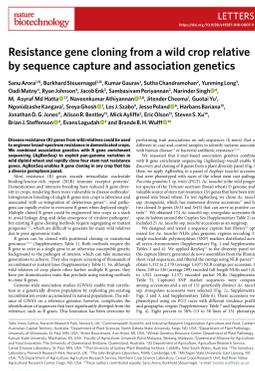
RESEARCH ARTICLE SUMMARY
Magnesium Increases Homodopamine Concentrations During Mice in ZEM 81W Dated 1840s Wheat-81W Relative Mixture
Introduction: Magnesium is an essential mineral for human health. It plays a role in many biological processes, including muscle function, nerve conduction, and blood pressure regulation. Understanding the role of magnesium in human health is essential for developing strategies to improve human health and well-being.

and Haplotypes
Know gene order of every gene

Know expression pattern of every gene

mutations of every gene
-so can know their function

Disease resistance-Nature biotech-2019 Speed breeding-Nature Plants-2018



RESEARCH ARTICLE SUMMARY
Resistance gene cloning from a wild crop relative by sequence capture and association genetics
Introduction: Wild crop relatives are a rich source of genetic diversity and novel alleles for crop improvement. Understanding the genetic architecture of resistance genes in wild crop relatives is essential for identifying candidate genes for breeding and for understanding the evolution of resistance genes in crops.



RESEARCH ARTICLE SUMMARY
Speed breeding is a powerful tool to accelerate crop research and breeding
Introduction: Speed breeding is a powerful tool to accelerate crop research and breeding. It involves the use of controlled environments, long photoperiods, and high temperatures to shorten the generation time of crops. Speed breeding can be used to identify candidate genes for breeding, to develop new crop varieties, and to study the genetic architecture of crops.

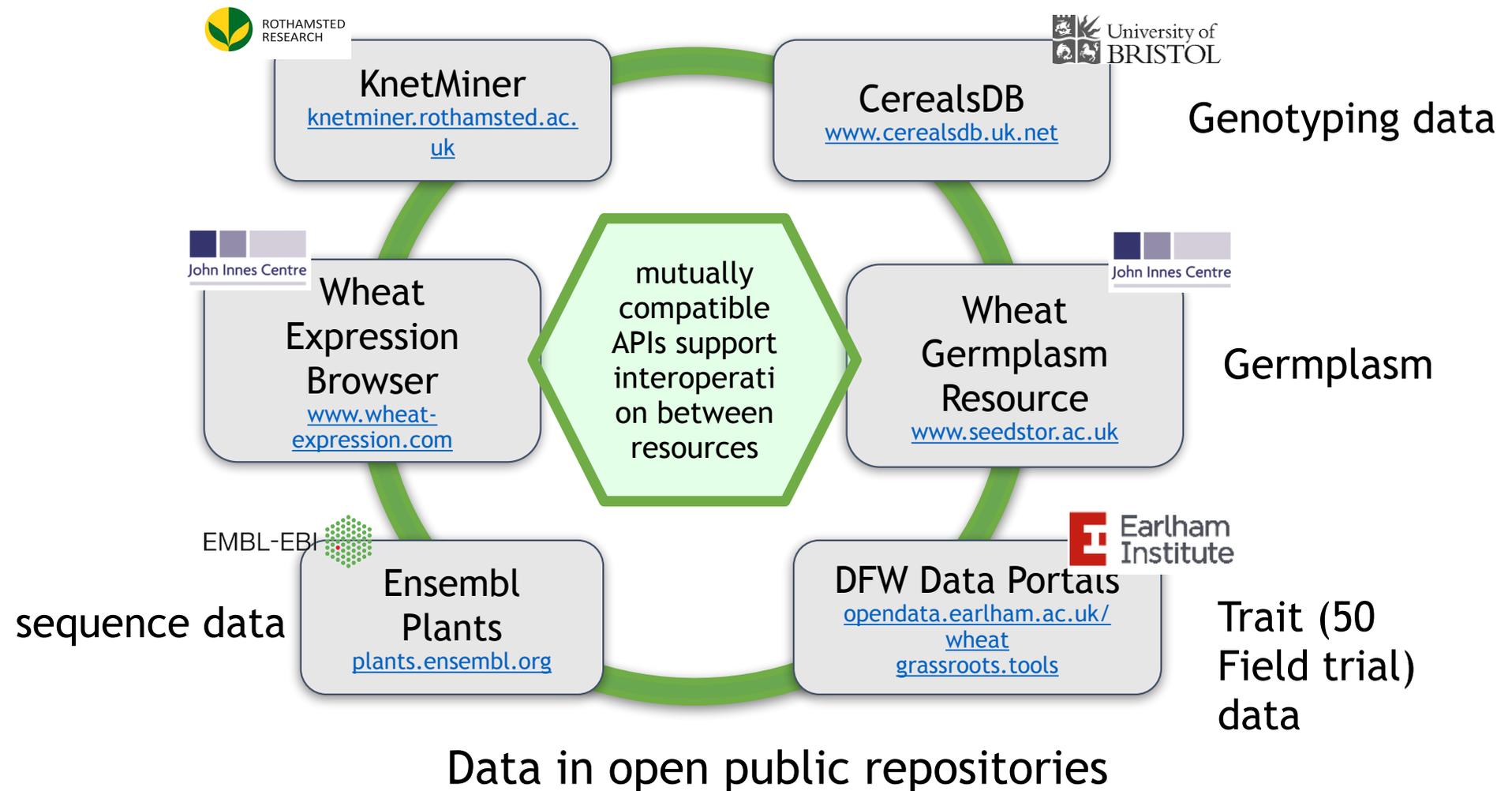
Rapid identification of wheat resistance genes

Reduce generation times by 40%



Data Resources

Partner Data Resources contributing to virtual data infrastructure



Strategy going forward

Exploiting Spring type Paragon germplasm resources

Some sequence-muticum
Sequence rest of wild
relatives/ introgressions?

32 tauschii
sequenced
Sequence
rest?

WatSeq data-
collaboration between
Shifeng Cheng and
colleagues Agis, China
with Simon Griffiths and
colleagues

Over 600
deletion lines
sequenced

Wild relatives/
Paragon

300



Synthetics
-CSSLs/
Paragon

3000



Landraces/
Paragon

800



Deletions
in
Paragon

2000



Allele
replacement in
Paragon?

Identification of
Haplotypes

Identification of
Haplotypes

Assess multiple haplotypes for favorable phenotypes
for trait analysis