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EXPLORING THE USE OF GENOMIC PREDICTION APPROACHES FOR VARIETY COLLECTION MANAGEMENT IN BARLEY

Document prepared by an expert from the United Kingdom

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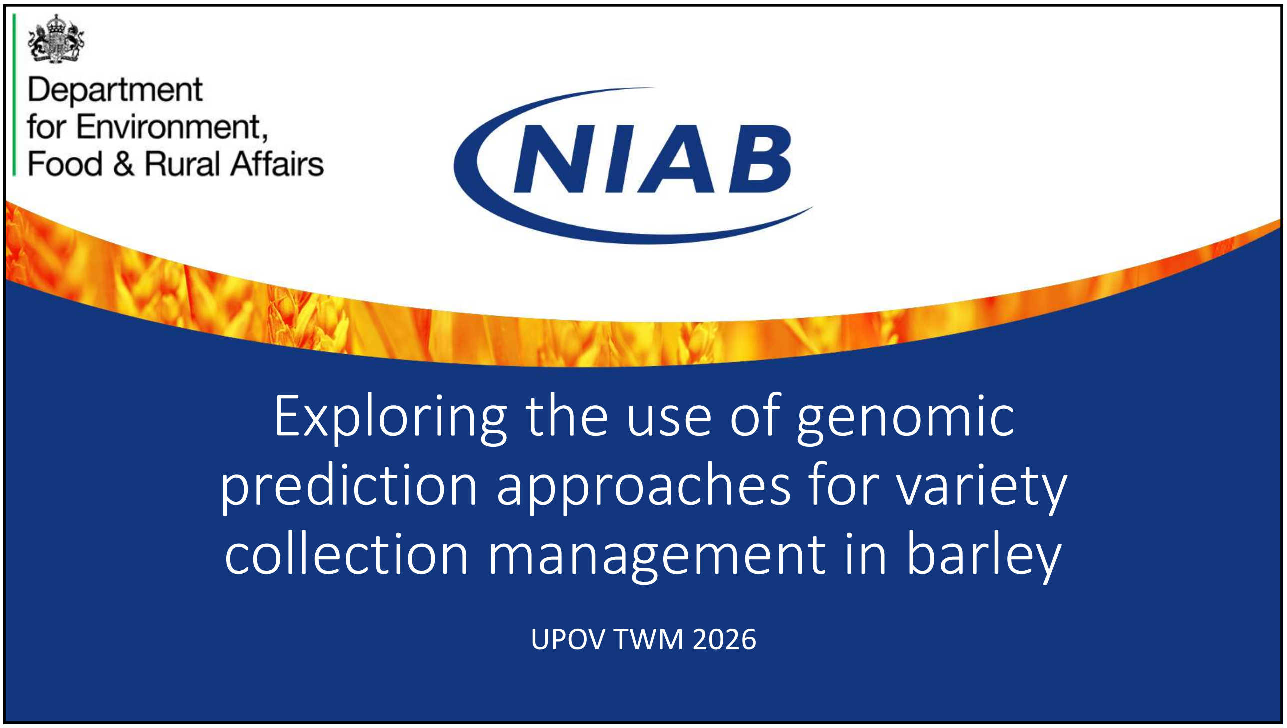
The annex to this document contains a presentation “Exploring the use of genomic prediction approaches for variety collection management in barley”, to be made by an expert from the United Kingdom, at the fourth session of the TWM.

[Annex follows]

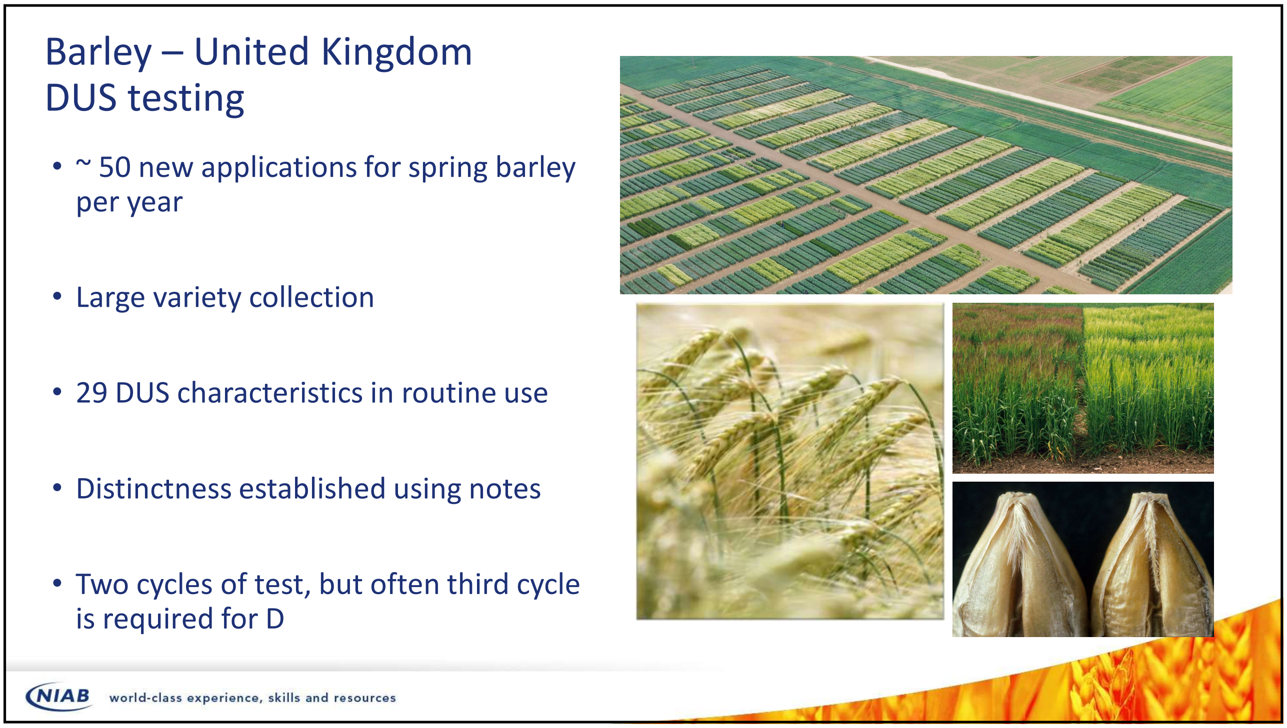


Department for Environment, Food & Rural Affairs

NIAB

Exploring the use of genomic prediction approaches for variety collection management in barley

UPOV TWM 2026



Barley – United Kingdom DUS testing

- ~ 50 new applications for spring barley per year
- Large variety collection
- 29 DUS characteristics in routine use
- Distinctness established using notes
- Two cycles of test, but often third cycle is required for D

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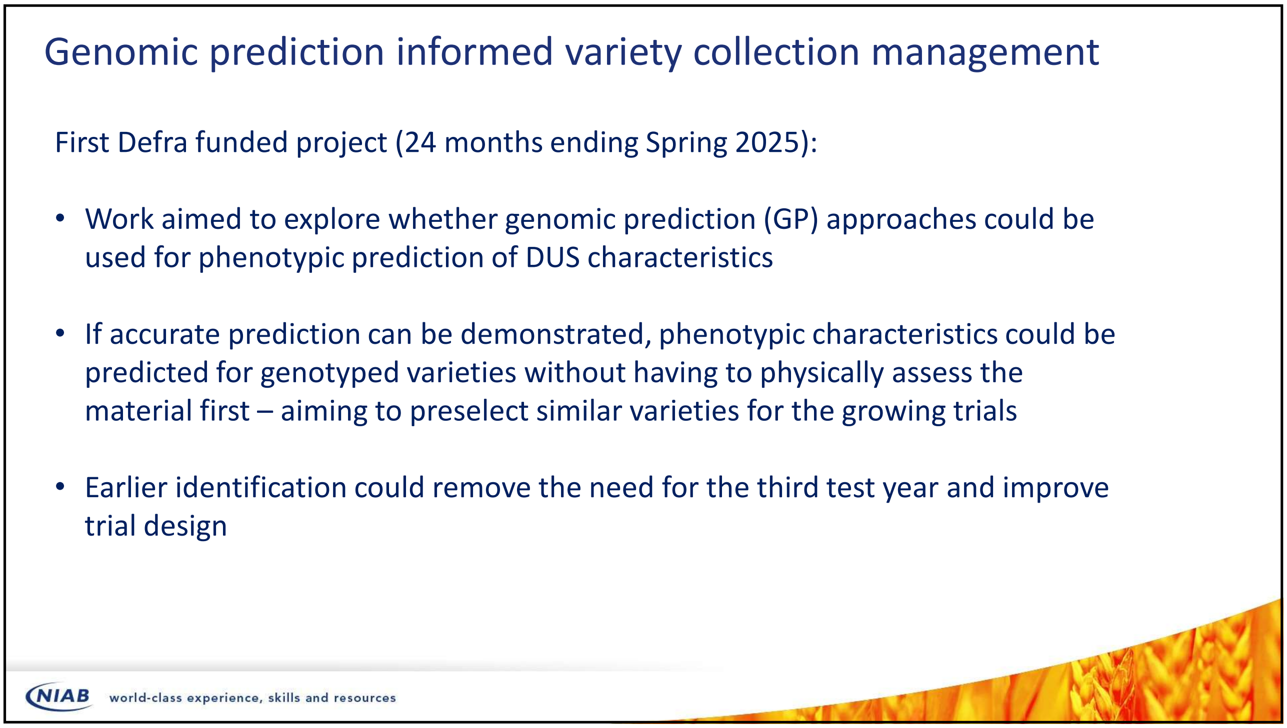

Genomic prediction informed variety collection management

First Defra funded project (24 months ending Spring 2025):

- Work aimed to explore whether genomic prediction (GP) approaches could be used for phenotypic prediction of DUS characteristics
- If accurate prediction can be demonstrated, phenotypic characteristics could be predicted for genotyped varieties without having to physically assess the material first – aiming to preselect similar varieties for the growing trials
- Earlier identification could remove the need for the third test year and improve trial design

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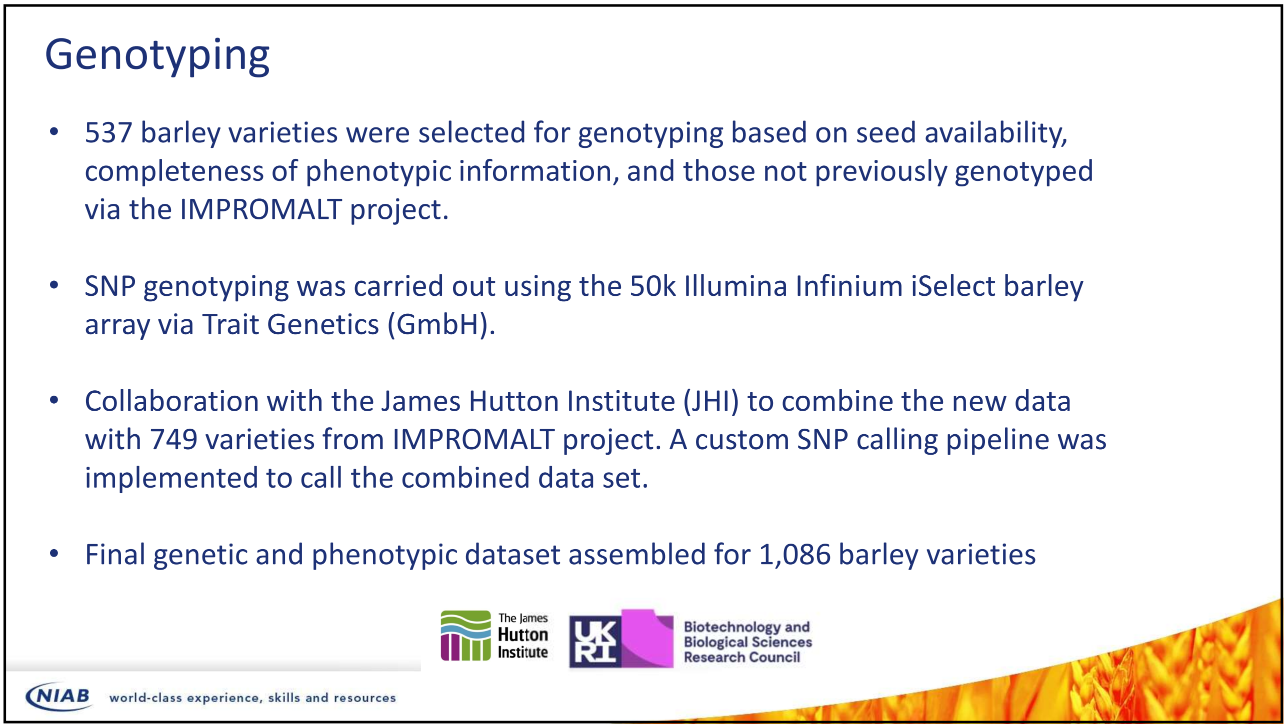

Genotyping

- 537 barley varieties were selected for genotyping based on seed availability, completeness of phenotypic information, and those not previously genotyped via the IMPROMALT project.
- SNP genotyping was carried out using the 50k Illumina Infinium iSelect barley array via Trait Genetics (GmbH).
- Collaboration with the James Hutton Institute (JHI) to combine the new data with 749 varieties from IMPROMALT project. A custom SNP calling pipeline was implemented to call the combined data set.
- Final genetic and phenotypic dataset assembled for 1,086 barley varieties

The James Hutton Institute

UKRI Biotechnology and Biological Sciences Research Council

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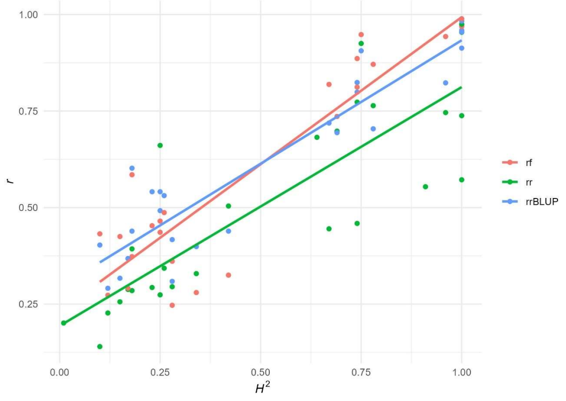
Predicting DUS characteristics – comparison between genomic prediction approaches



Prediction accuracies using three approaches (rf: random forest, rr: ridge regression and rrBLUP: ridge-regression BLUP). The prediction accuracies are regressed on broad-sense heritability (H^2). Prediction accuracies using the ridge-regression approach (rr) and the H^2 values were taken from Jones et al. (2013) and Yang et al. (2023), respectively .

- **Prediction accuracies varied depending on the characteristic and GP methodology used**
- Optimisation of the random forest methodology was explored by using different combinations of hyperparameters within the algorithm and implementing diagnostic marker weighting into the model
- Small improvements could be made to prediction accuracies using diagnostic marker weighting within the model

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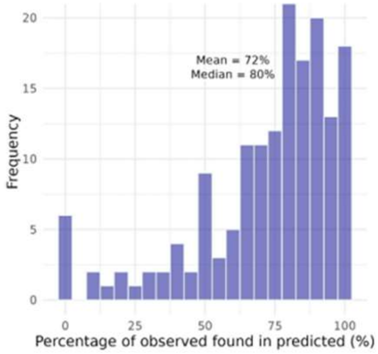
Proof of concept for use of genomic prediction informed approach for variety collection management

- Taking the registered varieties from the last 10 years, we simulated the similar variety selection using observed vs. Random Forest predicted characteristic values.
- Subsets selected using predicted data were on average larger (observed = 29 varieties and predicted = 49 varieties).
- **There was a good overlap (>70%) between the varieties selected using the predicted approach compared to observed data**



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Next steps towards validation and implementation

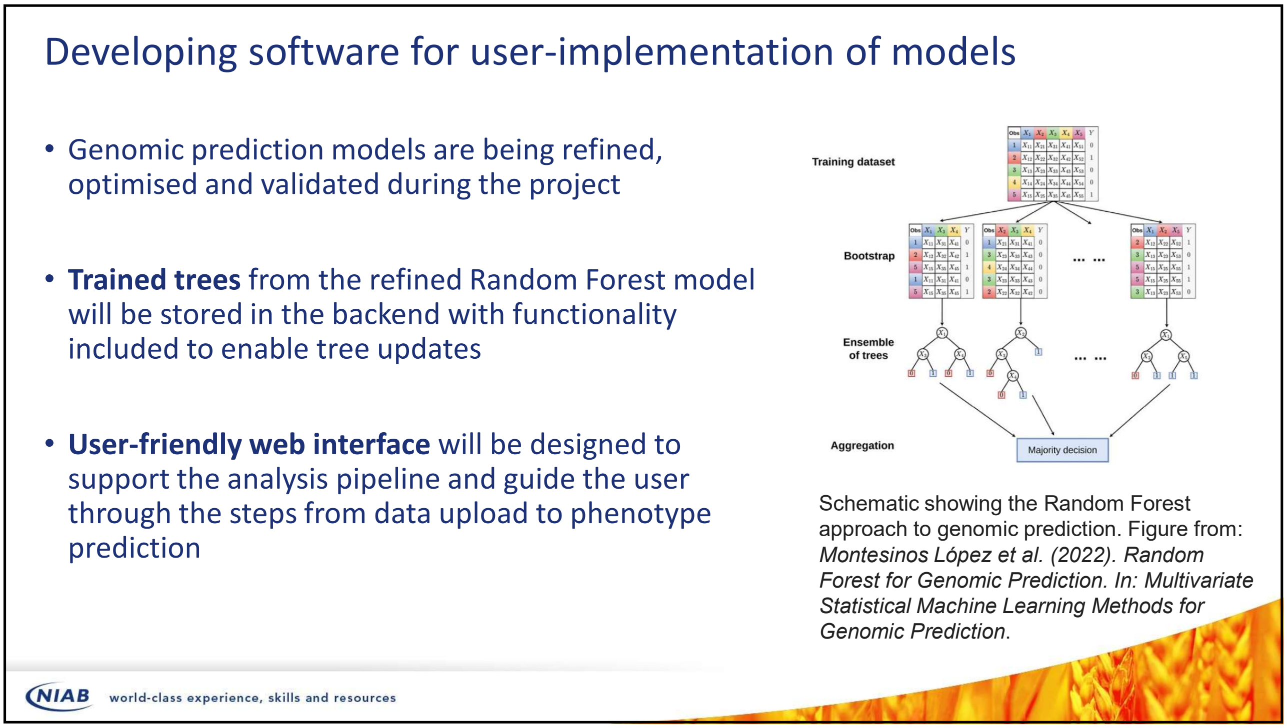
Second Defra funded project (30 months starting September 2025):

- Genotyping remaining spring barley variety collection + new candidate varieties
- Refining and optimising our prediction models
- Testing prediction models in parallel to current DUS testing procedures
- Developing software for user-implementation of the finalised models to support the routine use of the analysis pipeline
- **Considering logistical and technological challenges for future implementation**

Testing predictions in parallel to current DUS testing procedures – current progress

- Genomic prediction accuracies assessed for the current spring barley variety collection dataset
- Predictions completed using Random Forest-based classification or regression depending on the DUS characteristic
- Predictions for candidate varieties used to select similar variety subsets from the variety collection for field distinctness evaluation
- **Seventy-four additional varieties required for field evaluation based on the predicted data**

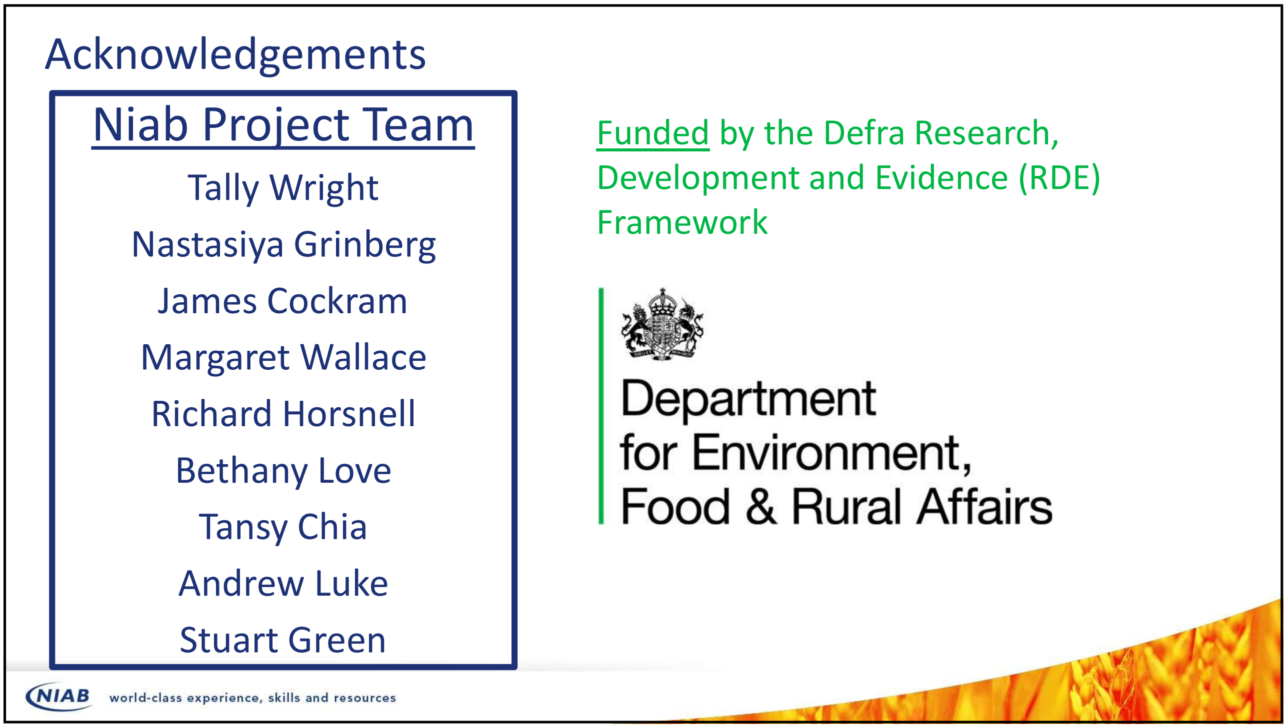
17th April 2026, plant emergence



Developing software for user-implementation of models

- Genomic prediction models are being refined, optimised and validated during the project
- **Trained trees** from the refined Random Forest model will be stored in the backend with functionality included to enable tree updates
- **User-friendly web interface** will be designed to support the analysis pipeline and guide the user through the steps from data upload to phenotype prediction

Schematic showing the Random Forest approach to genomic prediction. Figure from: *Montesinos López et al. (2022). Random Forest for Genomic Prediction. In: Multivariate Statistical Machine Learning Methods for Genomic Prediction.*



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Niab Project Team

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