UPOV

International Union for the Protection of New Varieties of Plants

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INVITE GENOMIC PREDICTION FOR REFERENCE COLLECTION MANAGEMENT: WHEAT

Document prepared by experts from the United Kingdom

The annex to this document contains a copy of a presentation “INVITE Genomic prediction for reference collection management: Wheat”, to be made by experts from the United Kingdom, at the third session of the TWM.

[Annex follows]

Genomic prediction for variety collection management

Wheat

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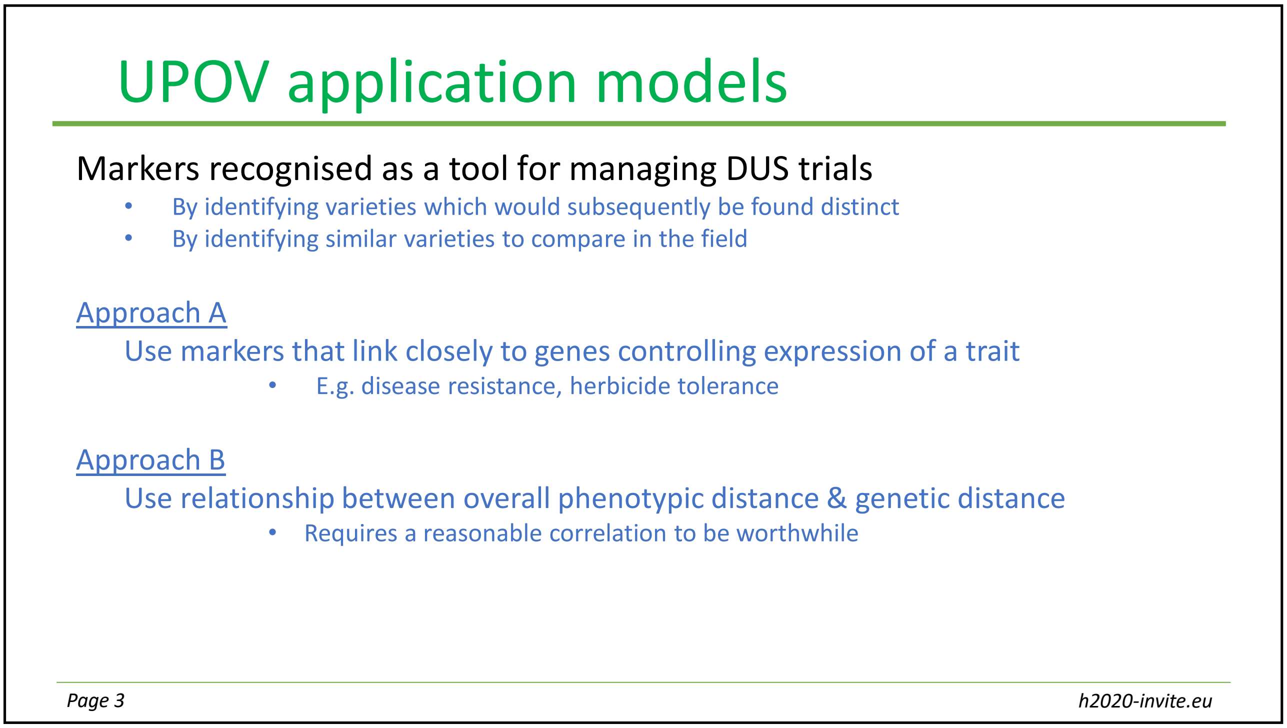
Outline

INVITE project defined a more tailored approach for using markers to manage DUS trial

- Based on modelling the association between markers and characteristics
- Ties more closely with approach used for distinctness assessment

Demonstrate with wheat historical data

In TWM/2/4 demonstrated with perennial ryegrass



UPOV application models

Markers recognised as a tool for managing DUS trials

- By identifying varieties which would subsequently be found distinct
- By identifying similar varieties to compare in the field

Approach A

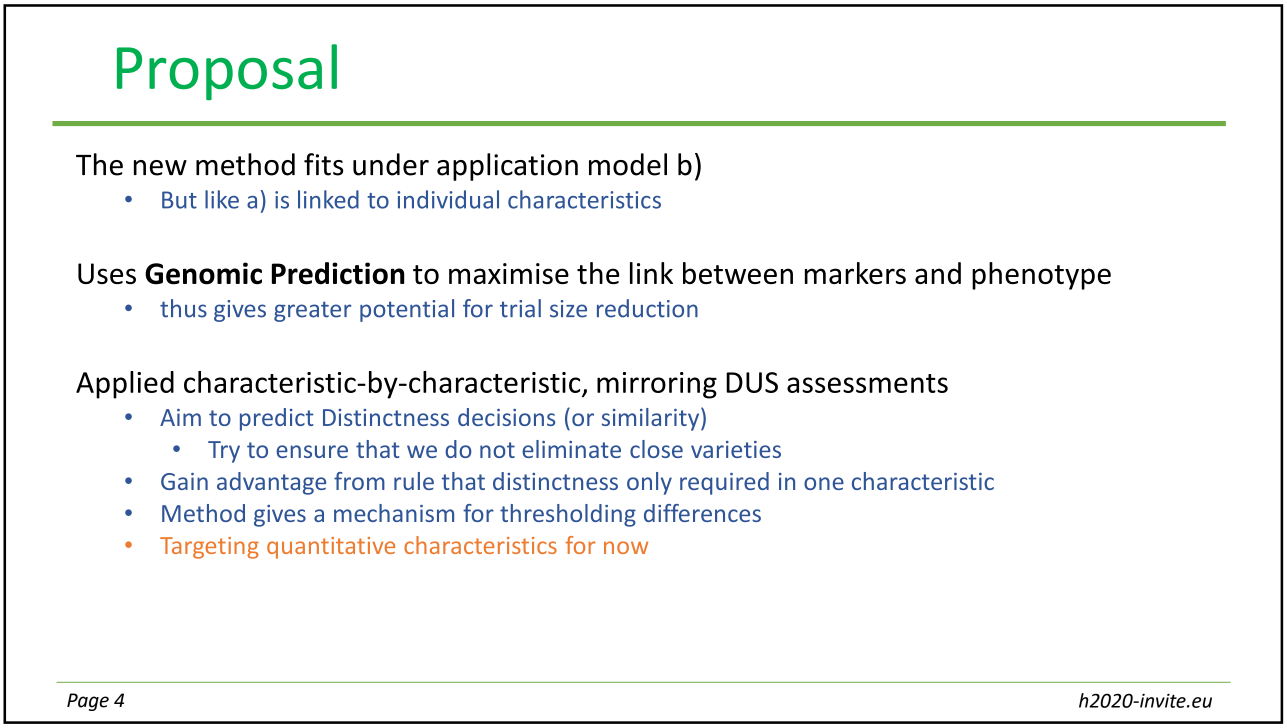
Use markers that link closely to genes controlling expression of a trait

  - E.g. disease resistance, herbicide tolerance

Approach B

Use relationship between overall phenotypic distance & genetic distance

  - Requires a reasonable correlation to be worthwhile



Proposal

The new method fits under application model b)

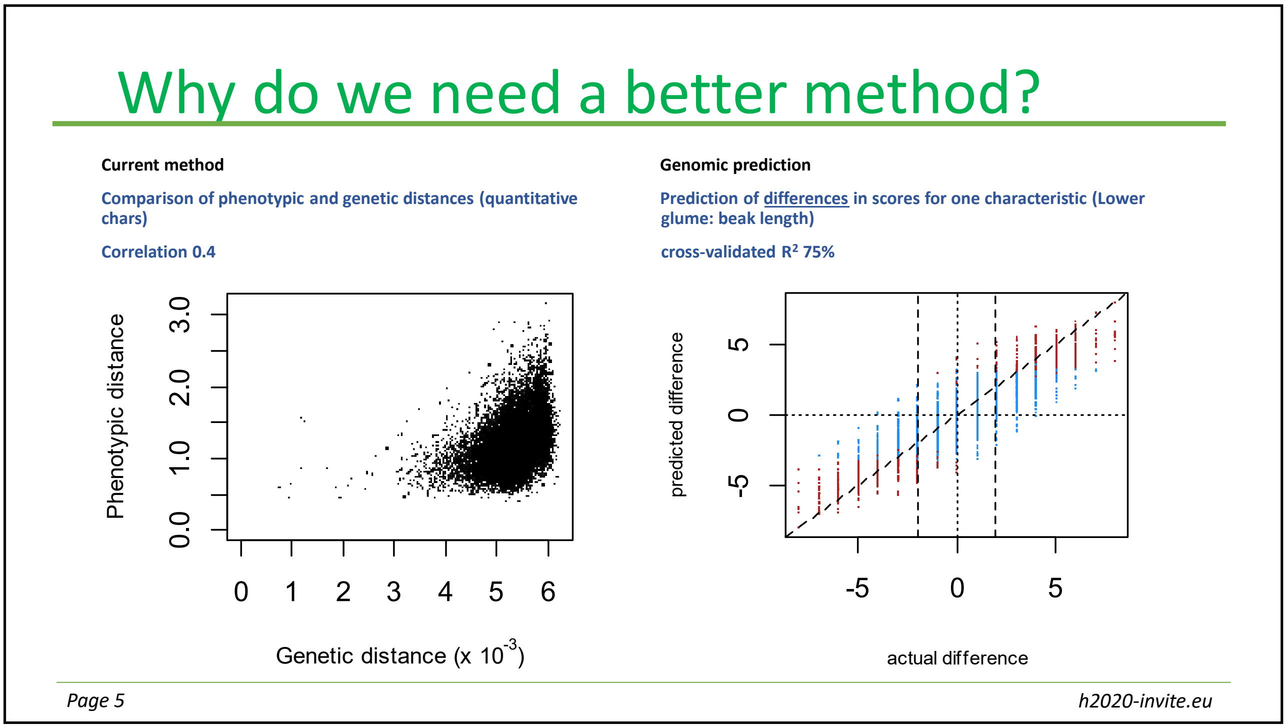
- But like a) is linked to individual characteristics

Uses **Genomic Prediction** to maximise the link between markers and phenotype

- thus gives greater potential for trial size reduction

Applied characteristic-by-characteristic, mirroring DUS assessments

- Aim to predict Distinctness decisions (or similarity)
  - Try to ensure that we do not eliminate close varieties
- Gain advantage from rule that distinctness only required in one characteristic
- Method gives a mechanism for thresholding differences
- Targeting quantitative characteristics for now



Why do we need a better method?

Current method

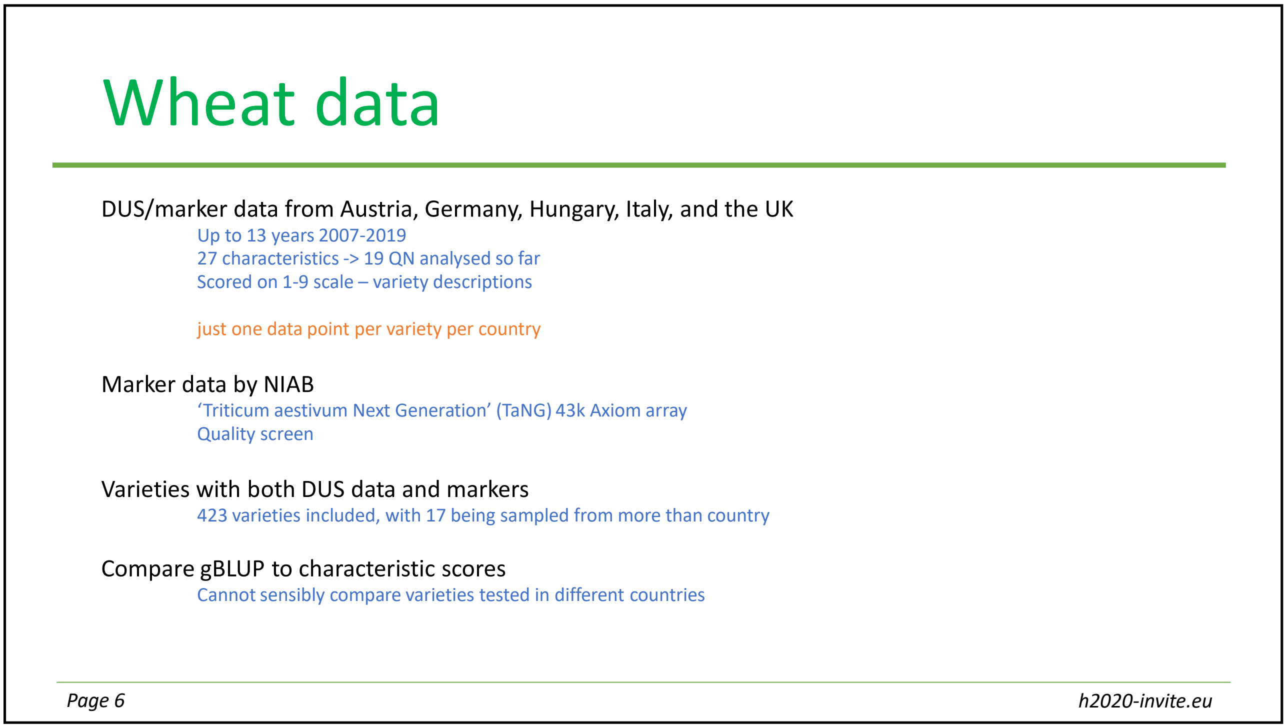
Comparison of phenotypic and genetic distances (quantitative chars)

Correlation 0.4

Genomic prediction

Prediction of <u>differences</u> in scores for one characteristic (Lower glume: beak length)

cross-validated R^2 75%



Wheat data

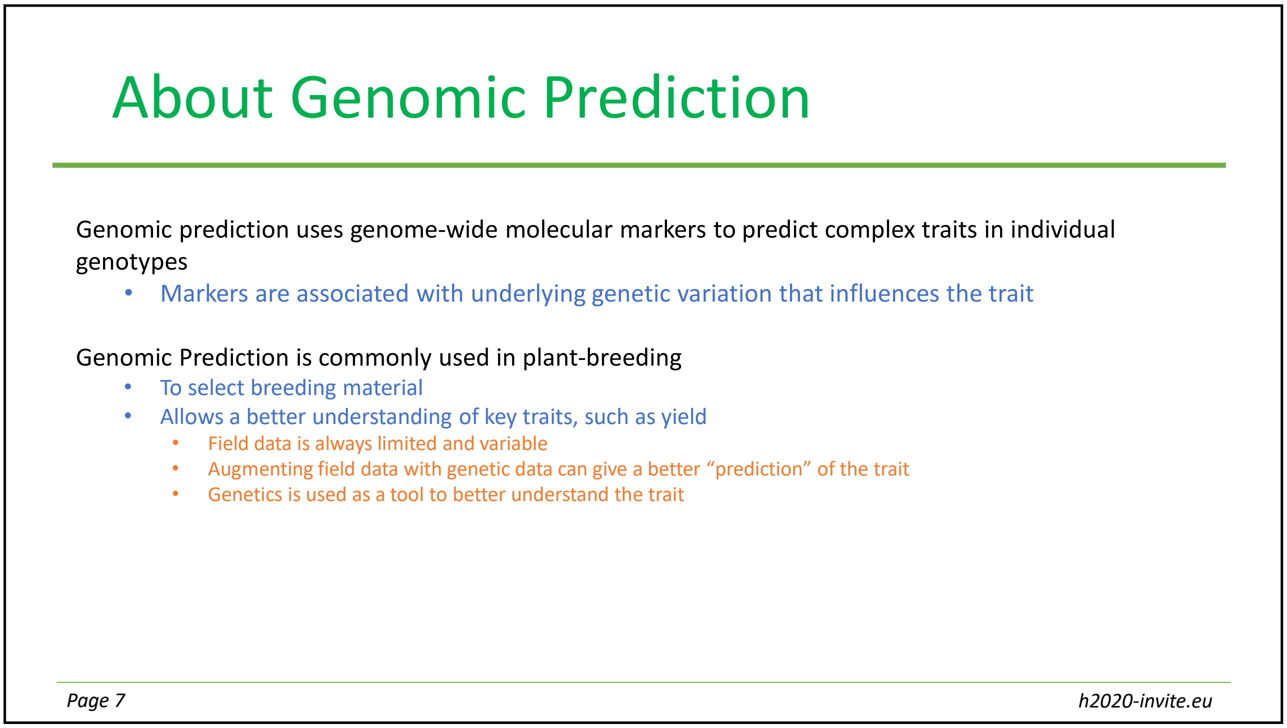
DUS/marker data from Austria, Germany, Hungary, Italy, and the UK
- Up to 13 years 2007-2019
- 27 characteristics -> 19 QN analysed so far
- Scored on 1-9 scale – variety descriptions

just one data point per variety per country

Marker data by NIAB
- ‘Triticum aestivum Next Generation’ (TaNG) 43k Axiom array
- Quality screen

Varieties with both DUS data and markers
- 423 varieties included, with 17 being sampled from more than country

Compare gBLUP to characteristic scores
- Cannot sensibly compare varieties tested in different countries



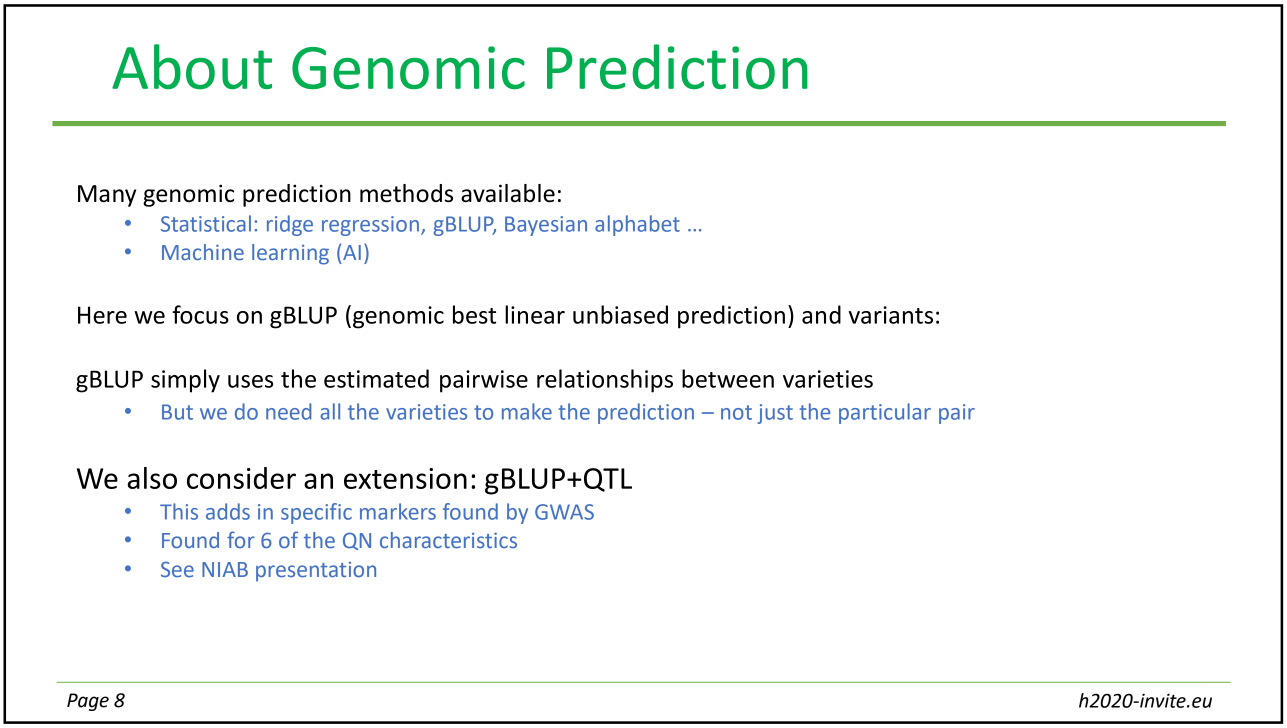
About Genomic Prediction

Genomic prediction uses genome-wide molecular markers to predict complex traits in individual genotypes

- Markers are associated with underlying genetic variation that influences the trait

Genomic Prediction is commonly used in plant-breeding

- To select breeding material
- Allows a better understanding of key traits, such as yield
  - Field data is always limited and variable
  - Augmenting field data with genetic data can give a better “prediction” of the trait
  - Genetics is used as a tool to better understand the trait



About Genomic Prediction

Many genomic prediction methods available:

- Statistical: ridge regression, gBLUP, Bayesian alphabet …
- Machine learning (AI)

Here we focus on gBLUP (genomic best linear unbiased prediction) and variants:

gBLUP simply uses the estimated pairwise relationships between varieties

- But we do need all the varieties to make the prediction – not just the particular pair

We also consider an extension: gBLUP+QTL

- This adds in specific markers found by GWAS
- Found for 6 of the QN characteristics
- See NIAB presentation

Framework for using genomic prediction for trial management

Fit a genomic prediction model to existing data

Predict the difference between a candidate and another variety

- Varieties in collection have genetic data + historic phenotypic data
- Candidate variety has genetic data only

Assess whether the **difference is significant**

- Can use same probability values as COYD (eg 1%)
- For wheat, distinctness may be based on a fixed difference in UPOV notes (commonly 2 notes)

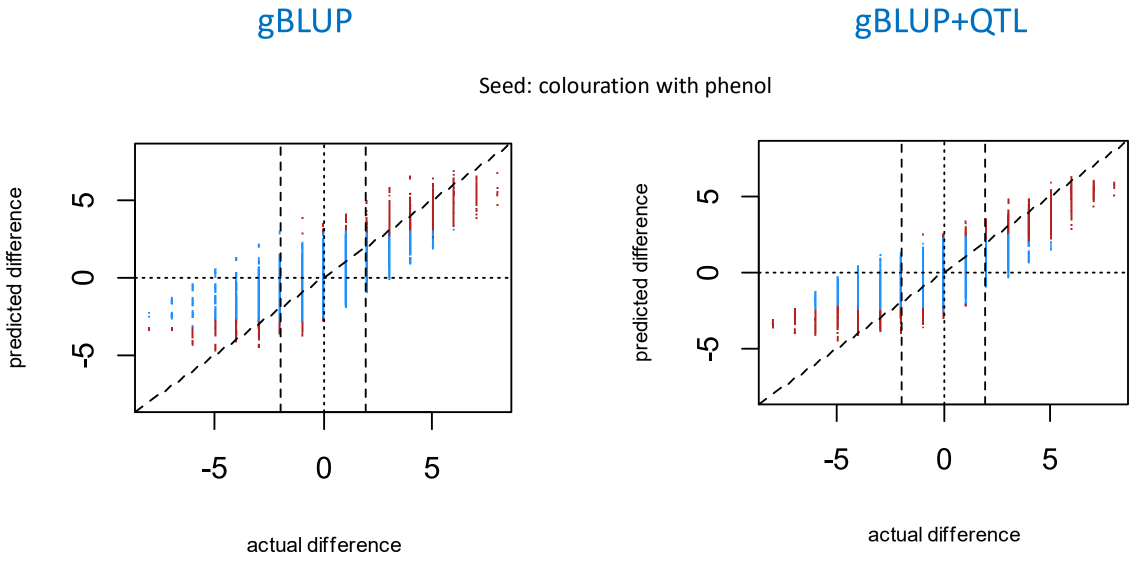
In some crops, including wheat, emphasis may be on finding similar varieties

Assessing how well GP works

Using historical data set

1. Take each variety in turn and treat as candidate
    - try to predict its over-year mean (like COYD)
2. Predict differences between “candidate” and reference variety
    - *Reference* based on phenotype data (and genetic data)
    - *Candidate* based on genetic data (no phenotypic data) – LOO (Leave-One-Out)
3. Assess whether this predicted difference is significant at 1% (using gBLUP model)
4. Compare with actual differences in phenotypic means

Note: we do not have failed candidates in the data set



black lines denote two notes difference
red points show sig dif (0.01) for gBLUP prediction

Wheat: Proportion of varieties distinguished by characteristic

Characteristic	gBLUP	gBLUP+QTL
Seed: colouration with phenol	5.8%	16.3%
Coleoptile: anthocyanin colouration	1.7%	5.9%
Growth habit	1.4%	
Frequency of plants with recurved flag leaves	7.1%	
Ear emergence	2.6%	
Flag leaf: glaucosity of sheath	1.0%	
Flag leaf: glaucosity of blade	3.8%	
Ear: glaucosity	1.6%	
Culm: glaucosity of neck	1.1%	
Plant: length	4.2%	
Ear density	2.3%	2.9%
Ear length	3.7%	
Awn or scur length	11.9%	23.3%
Area of hairiness on convex surface	1.1%	
Lower glume: shoulder width	1.3%	
Lower glume: shoulder shape	0.1%	
Lower glume: beak length	13.8%	19.8%
Lower glume: beak shape	0.9%	
Area of hairiness on internal surface	2.5%	4.5%

Proportion of varieties distinguished over all the QN characteristics

	Proportion distinct	
	GBLUP	GBUP+QTL
Wheat	38%	55%

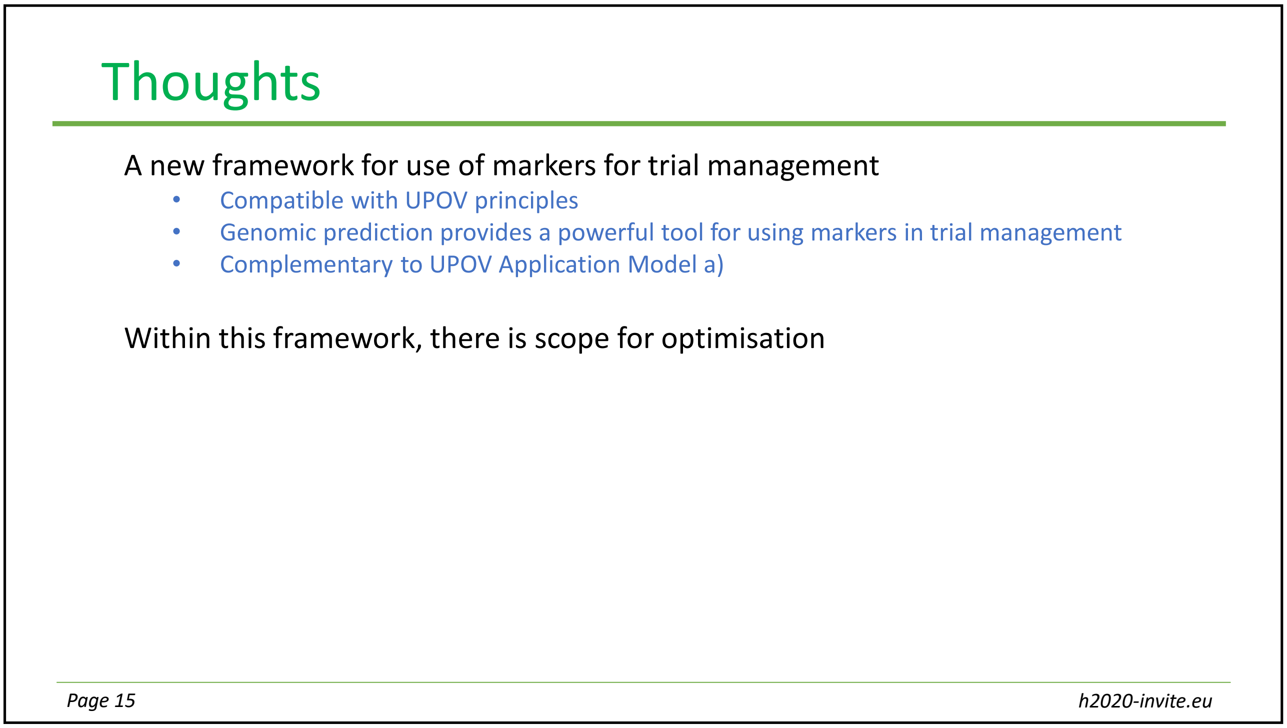
Summary

New method is clearly more effective than the current UPOV application model b)

For Wheat:

- Three QN characteristics well predicted by markers
- QL characteristics will add to overall discrimination – especially if model a) is possible

- Prediction of similarity is important for laying out first year trial
- Markers could also be used to improve information for laying out second year trial

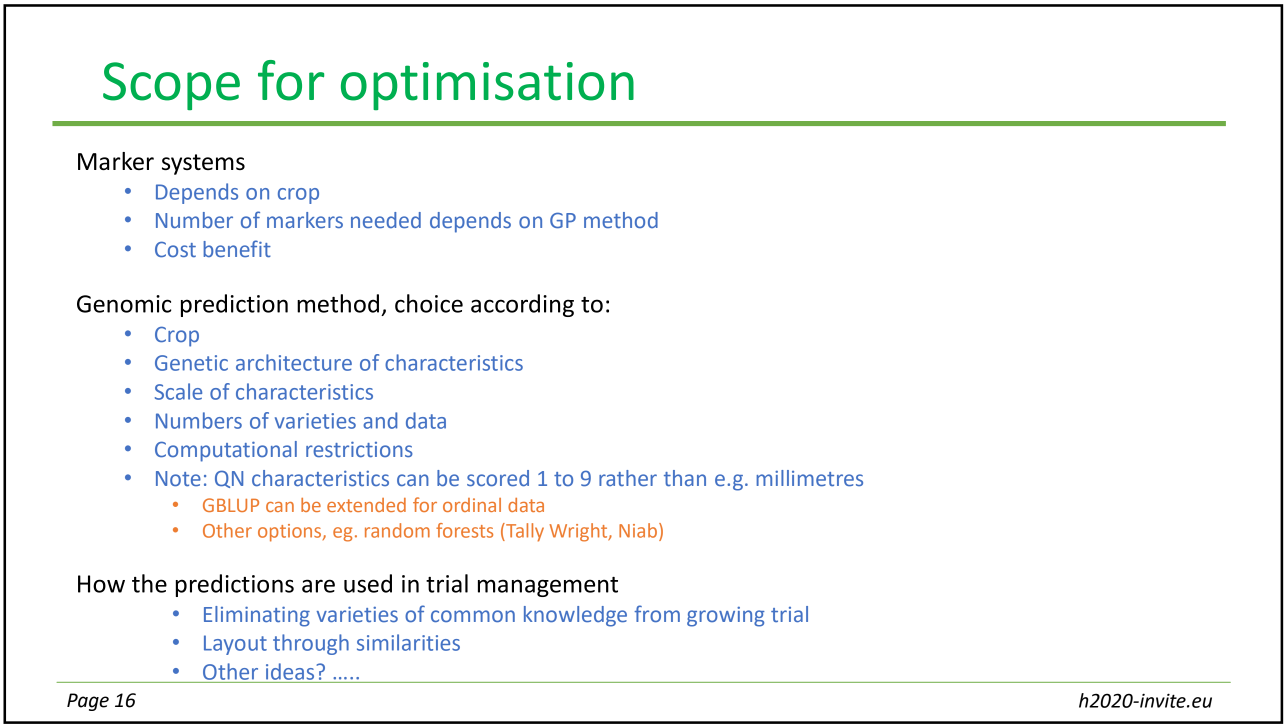


Thoughts

A new framework for use of markers for trial management

- Compatible with UPOV principles
- Genomic prediction provides a powerful tool for using markers in trial management
- Complementary to UPOV Application Model a)

Within this framework, there is scope for optimisation



Scope for optimisation

Marker systems

- Depends on crop
- Number of markers needed depends on GP method
- Cost benefit

Genomic prediction method, choice according to:

- Crop
- Genetic architecture of characteristics
- Scale of characteristics
- Numbers of varieties and data
- Computational restrictions
- Note: QN characteristics can be scored 1 to 9 rather than e.g. millimetres
  - GBLUP can be extended for ordinal data
  - Other options, eg. random forests (Tally Wright, Niab)

How the predictions are used in trial management

- Eliminating varieties of common knowledge from growing trial
- Layout through similarities
- Other ideas? …..

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[End of Annex and of document]