International Union for the Protection of New Varieties of Plants

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INVITE - CAN BETTER UNDERSTANDING OF THE GENETIC ARCHITECTURE OF WHEAT DUS CHARACTERISTICS HELP STREAMLINE THE DUS PROCESSES?

Document prepared by an expert from the United Kingdom

The annex to this document contains a copy of a presentation “Invite - Can better understanding of the genetic architecture of wheat DUS characteristics help streamline the DUS processes?”, to be made by an expert from the United Kingdom, at the third session of the TWM.

[Annex follows]

Can better understanding of the genetic architecture of wheat DUS characteristics help streamline the DUS processes?

Dr Camila Zanella

This project has received funding from the European Union’s Horizon 2020 Research and Innovation programme under Grant Agreement No 817970.

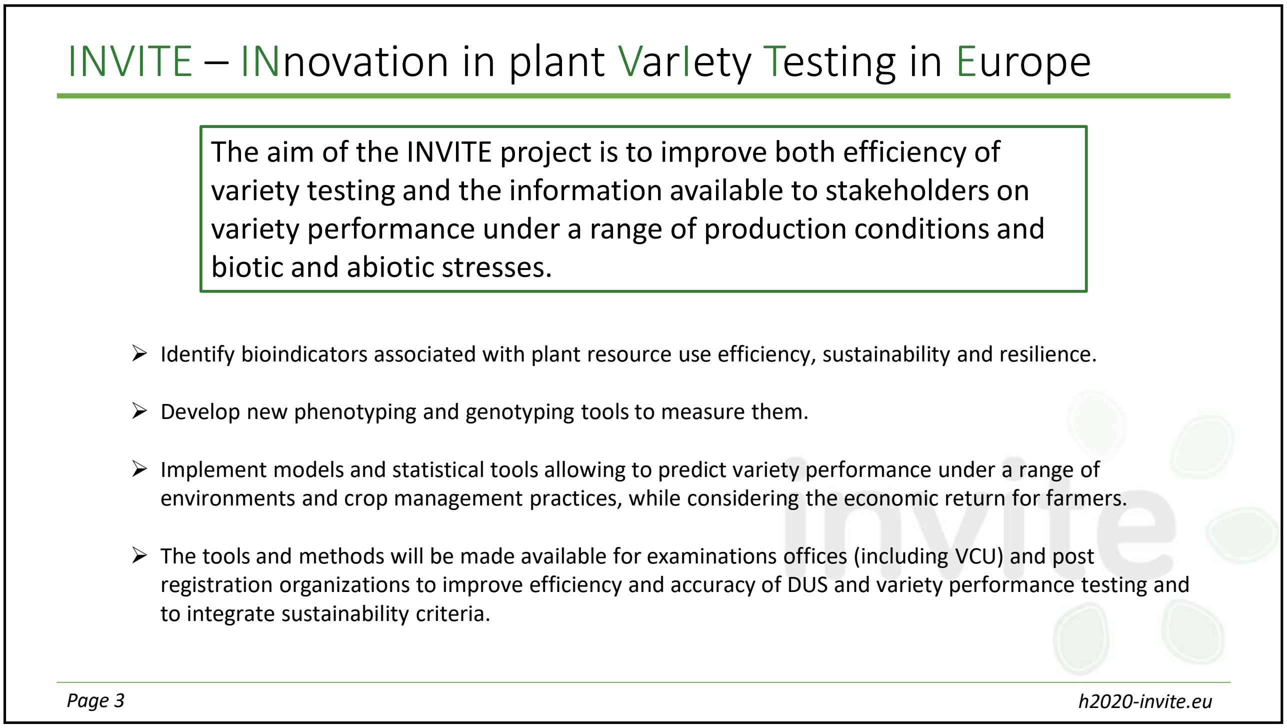
Variety test

Developing a new cereal variety represents a considerable investment by breeders **– 10 years**

DUS – Distinct + Uniform + Stable

- For wheat, there are currently 29 characteristics in the UPOV Test Guidelines (TG/3/12 Rev.)
- These phenotypic characters are assessed over a minimum of two growing seasons, with a third year of test sometimes required to unambiguously confirm Distinctness

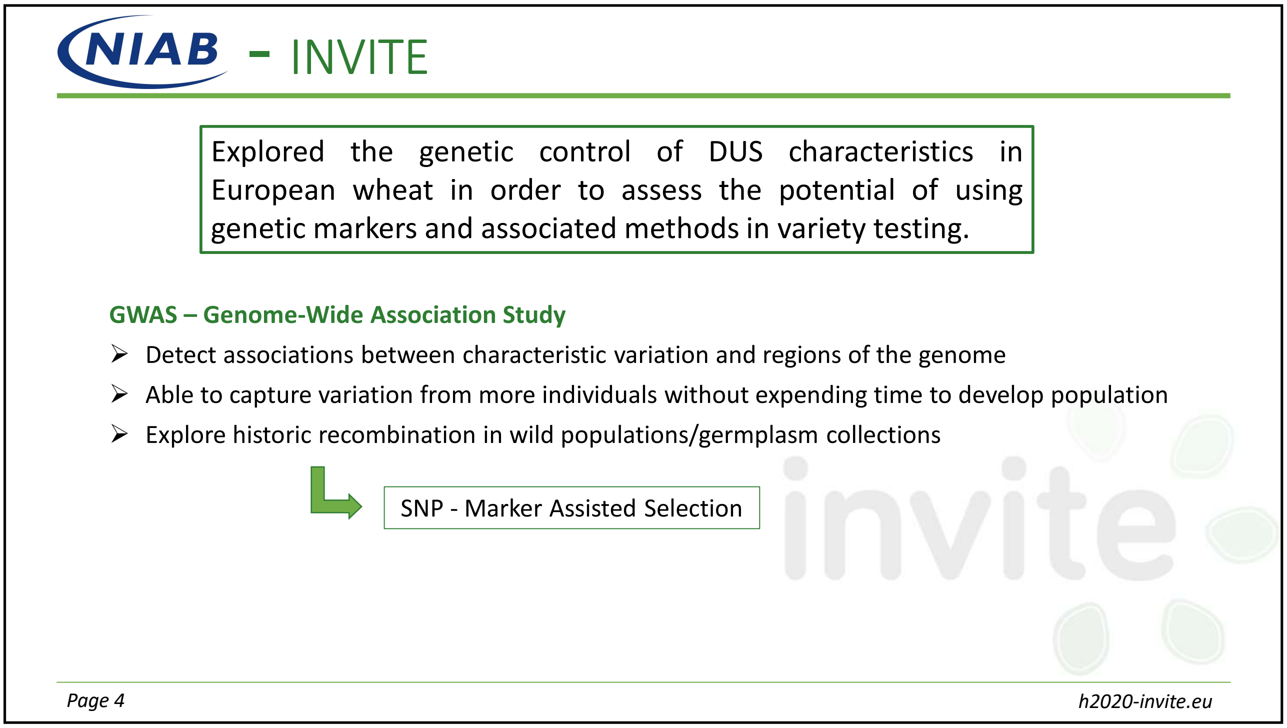
The goal is to develop genetic and analytical approaches for the use of genetic markers within wheat DUS processes



INVITE – INnovation in plant VarIety Testing in Europe

The aim of the INVITE project is to improve both efficiency of variety testing and the information available to stakeholders on variety performance under a range of production conditions and biotic and abiotic stresses.

- Identify bioindicators associated with plant resource use efficiency, sustainability and resilience.
- Develop new phenotyping and genotyping tools to measure them.
- Implement models and statistical tools allowing to predict variety performance under a range of environments and crop management practices, while considering the economic return for farmers.
- The tools and methods will be made available for examinations offices (including VCU) and post registration organizations to improve efficiency and accuracy of DUS and variety performance testing and to integrate sustainability criteria.



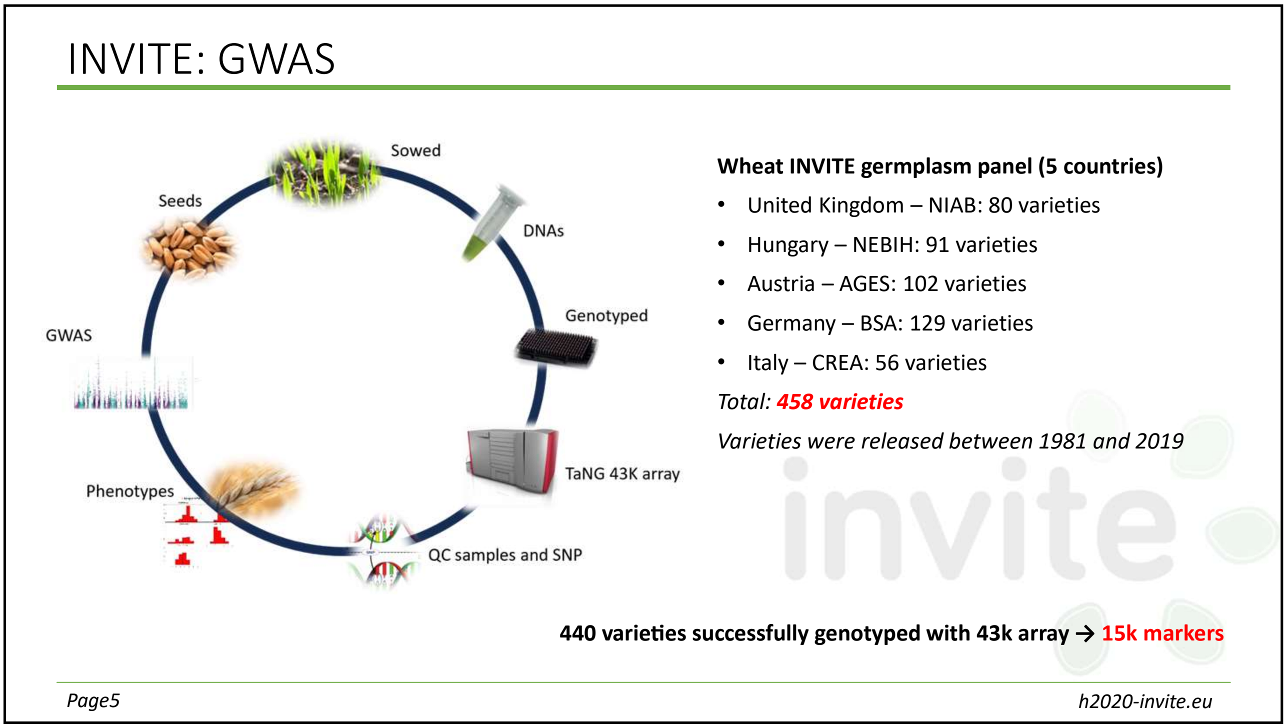
NIAB - INVITE

Explored the genetic control of DUS characteristics in European wheat in order to assess the potential of using genetic markers and associated methods in variety testing.

GWAS – Genome-Wide Association Study

- Detect associations between characteristic variation and regions of the genome
- Able to capture variation from more individuals without expending time to develop population
- Explore historic recombination in wild populations/germplasm collections

↳ SNP - Marker Assisted Selection



INVITE: GWAS

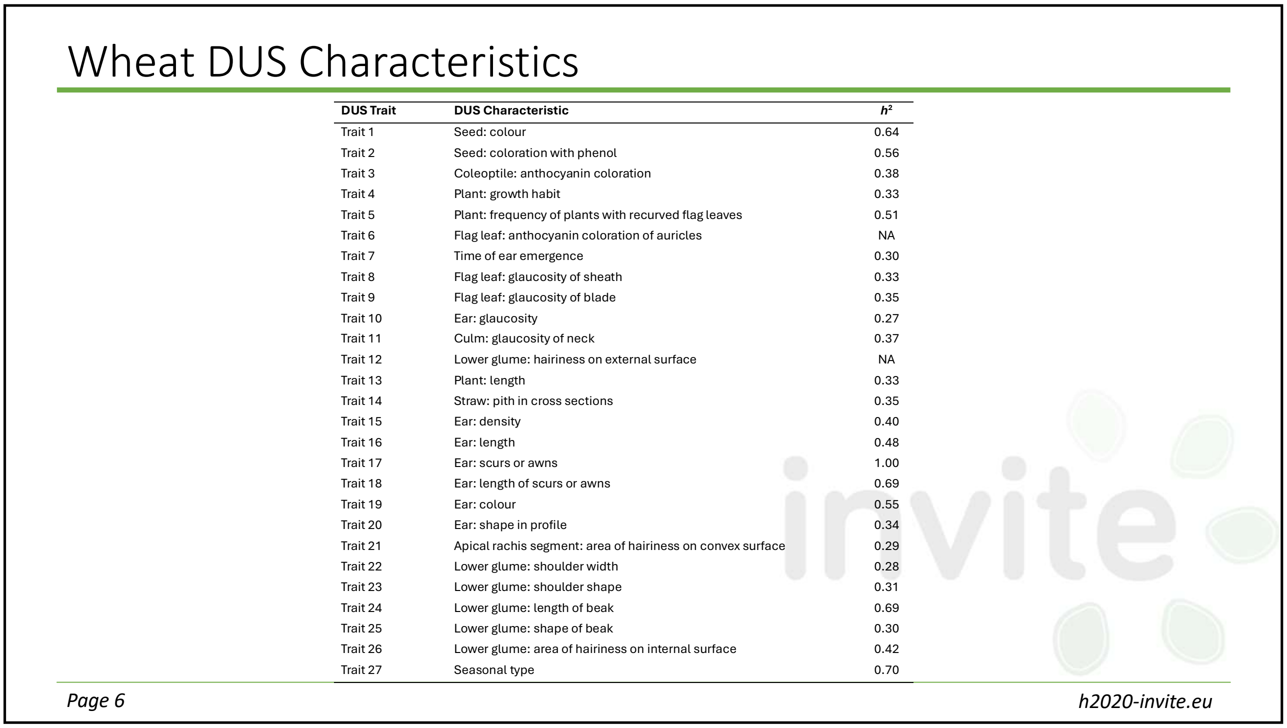
Wheat INVITE germplasm panel (5 countries)

- United Kingdom – NIAB: 80 varieties
- Hungary – NEBIH: 91 varieties
- Austria – AGES: 102 varieties
- Germany – BSA: 129 varieties
- Italy – CREA: 56 varieties

Total: ***458 varieties***

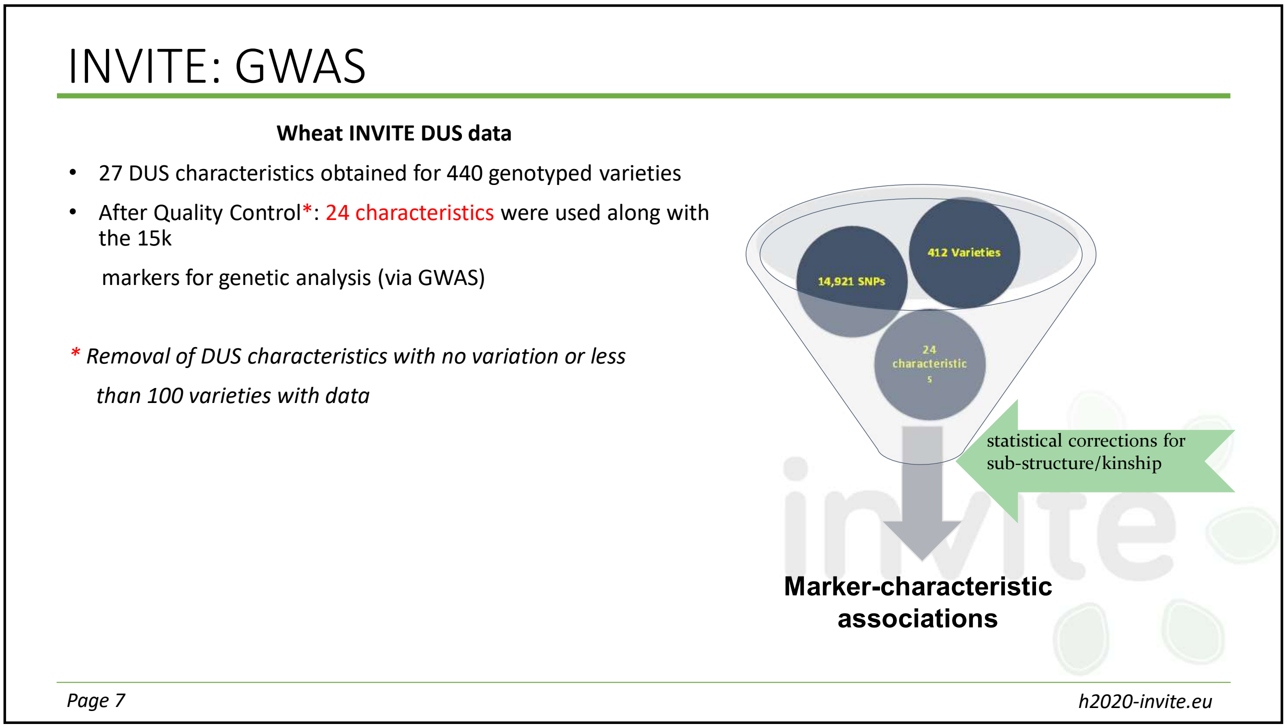
Varieties were released between 1981 and 2019

440 varieties successfully genotyped with 43k array → 15k markers



Wheat DUS Characteristics

DUS Trait	DUS Characteristic	h^2
Trait 1	Seed: colour	0.64
Trait 2	Seed: coloration with phenol	0.56
Trait 3	Coleoptile: anthocyanin coloration	0.38
Trait 4	Plant: growth habit	0.33
Trait 5	Plant: frequency of plants with recurved flag leaves	0.51
Trait 6	Flag leaf: anthocyanin coloration of auricles	NA
Trait 7	Time of ear emergence	0.30
Trait 8	Flag leaf: glaucosity of sheath	0.33
Trait 9	Flag leaf: glaucosity of blade	0.35
Trait 10	Ear: glaucosity	0.27
Trait 11	Culm: glaucosity of neck	0.37
Trait 12	Lower glume: hairiness on external surface	NA
Trait 13	Plant: length	0.33
Trait 14	Straw: pith in cross sections	0.35
Trait 15	Ear: density	0.40
Trait 16	Ear: length	0.48
Trait 17	Ear: scurs or awns	1.00
Trait 18	Ear: length of scurs or awns	0.69
Trait 19	Ear: colour	0.55
Trait 20	Ear: shape in profile	0.34
Trait 21	Apical rachis segment: area of hairiness on convex surface	0.29
Trait 22	Lower glume: shoulder width	0.28
Trait 23	Lower glume: shoulder shape	0.31
Trait 24	Lower glume: length of beak	0.69
Trait 25	Lower glume: shape of beak	0.30
Trait 26	Lower glume: area of hairiness on internal surface	0.42
Trait 27	Seasonal type	0.70



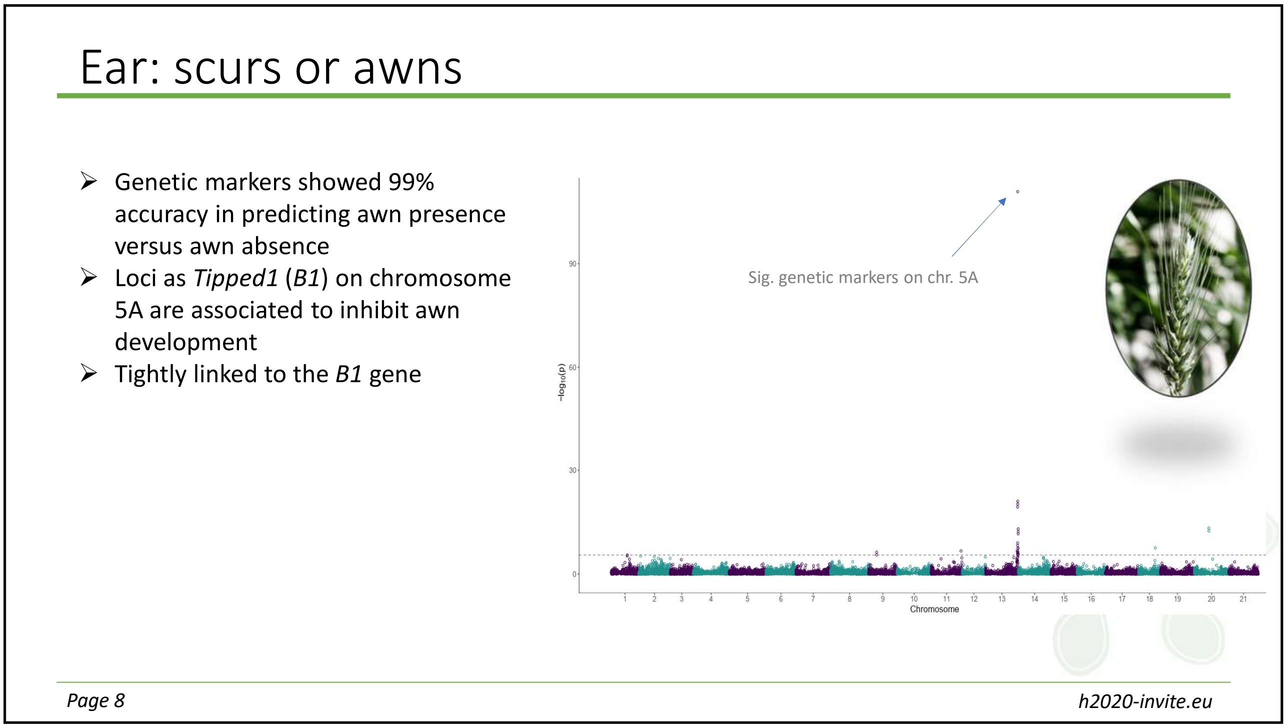
INVITE: GWAS

Wheat INVITE DUS data

- 27 DUS characteristics obtained for 440 genotyped varieties
- After Quality Control*: 24 characteristics were used along with the 15k markers for genetic analysis (via GWAS)

** Removal of DUS characteristics with no variation or less than 100 varieties with data*

Marker-characteristic associations



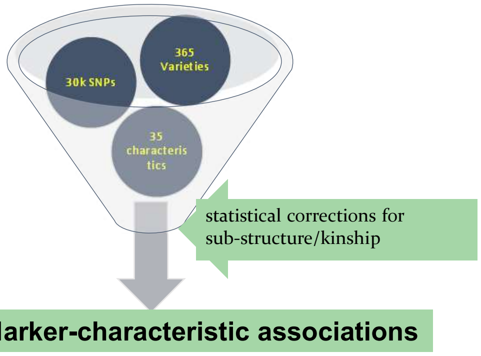
Ear: scurs or awns

- ➢ Genetic markers showed 99% accuracy in predicting awn presence versus awn absence
- ➢ Loci as *Tipped1* (*B1*) on chromosome 5A are associated to inhibit awn development
- ➢ Tightly linked to the *B1* gene

Sig. genetic markers on chr. 5A

WAGTAIL: GWAS

- Existing genome wide marker sets for wheat – Wagtail - **402** north-west European cvs (predominantly UK, FRA, DEU)
  - Sourced existing wheat **genotypic data** (90k SNP array) and **DUS data** from UK academic-industrial project 'WAGTAIL'



statistical corrections for sub-structure/kinship

Marker-characteristic associations

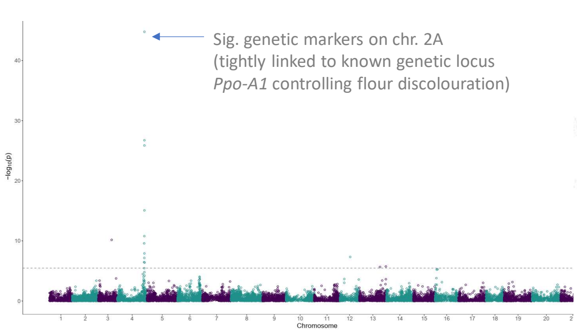
Genotyping: Illumina iSelect 90k chip

60k work

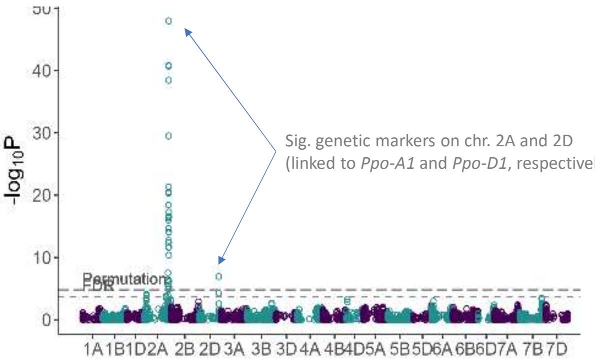
30k polymorphic in WAGTAIL

Camila Zanella, Bethan Love, Tally Wright, James Cockram

Seed: coloration with phenol



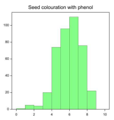
Sig. genetic markers on chr. 2A (tightly linked to known genetic locus *Ppo-A1* controlling flour discolouration)



Sig. genetic markers on chr. 2A and 2D (linked to *Ppo-A1* and *Ppo-D1*, respectively)

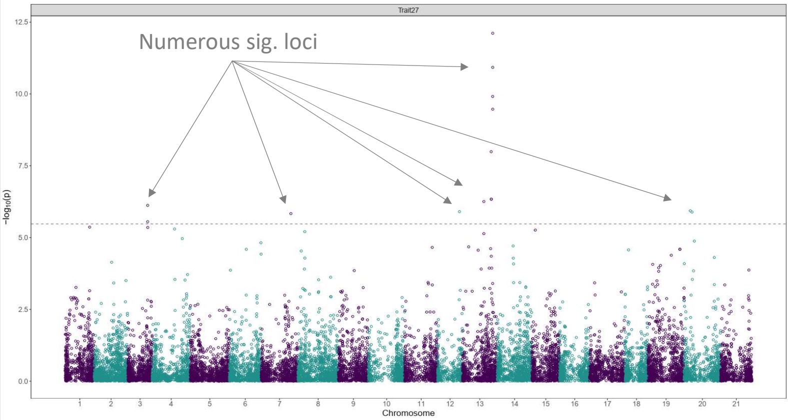
INVITE GWAS

WAGTAIL



- Characteristic scored on a 1-9 (quantitative) scale.
- Few genetic loci identified, but highly significant.

Seasonal type



Characteristic controlled by numerous genetic loci

Outcomes & relevance to variety testing

- Characteristic heritability and the number of genetic loci underpinning the characteristics are key for the establishment of markers associated to a DUS characteristic
- More heritable/qualitatively scored characteristics are more feasible to identify loci linked to the characteristic and stablish markers associated
- For implementation:
  - **Highly heritable characteristics** controlled by one or a low number of loci will be best suited for a like-for-like replacement of genetic markers
  - **Lowly heritable characteristics** with complex genetic architecture will require alternative methods for marker-based prediction of phenotype, such as genomic prediction approaches combined with decision thresholding that takes into account the number of notes on the phenotypic scale that is required for Distinctness to be called.

invite

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