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EUCLEG: a foundation to boost legume breeding

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➤ EUCLEG: a foundation to boost legume breeding

Breeding forage and grain legumes to increase EU's and China's protein self-sufficiency

Bernadette Julier – 29 April 2021



INRAE



EUC
LEG



➤ EUCLEG objectives

Enlarge the use of genetic diversity

Develop tools for breeding

- Same strategy for 5 species: alfalfa, red clover, pea, faba bean, soybean
 - Use of genetic resources
 - Phenotyping and genotyping
 - Focus on key phenotypic traits, from establishment to yield and quality, including biotic and abiotic stresses
 - Description of genetic variation, G x E interactions
 - Genetic architecture of traits
 - Software for data management and analyses
 - Strong collaboration with private companies
- Dates : from September 2017 to December 2021



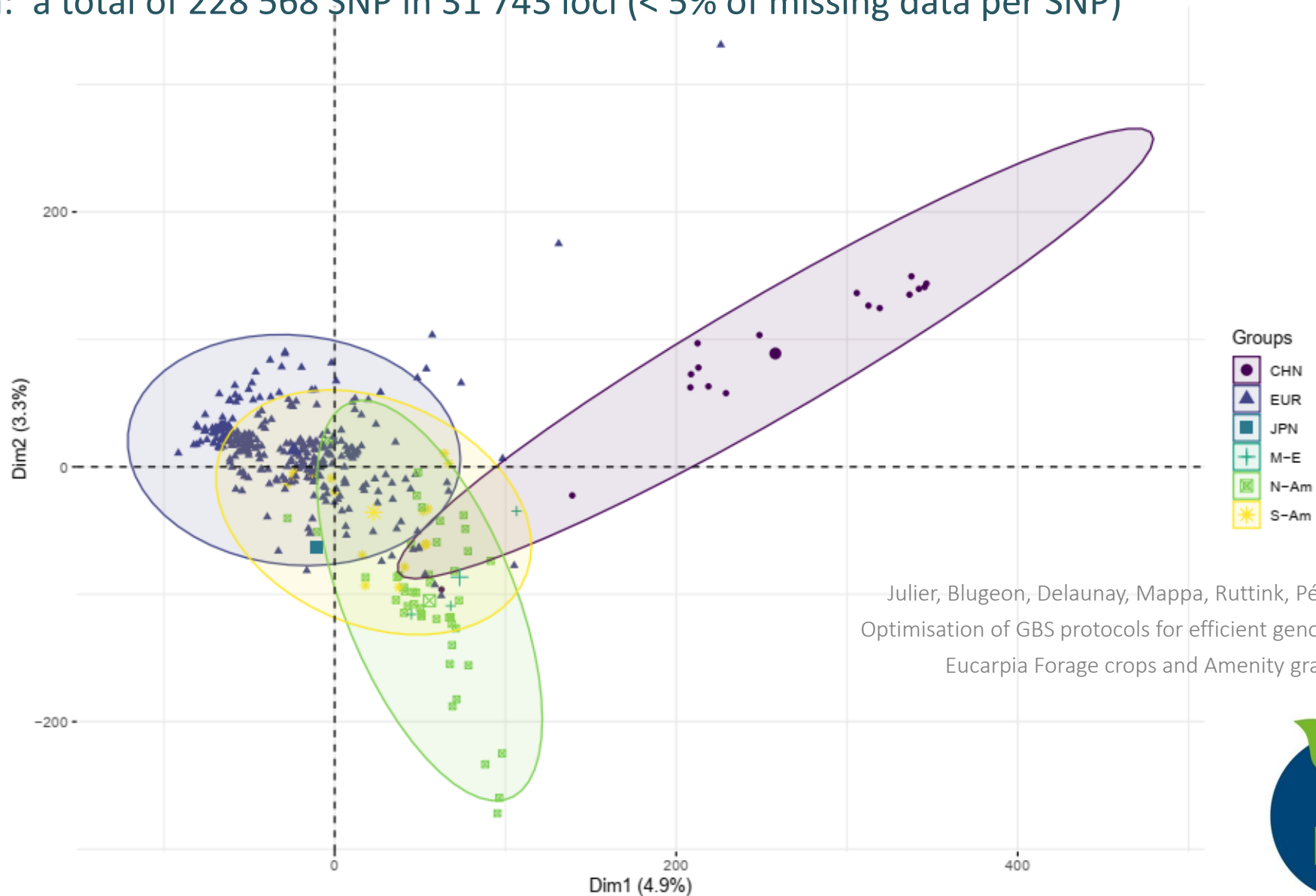
> Genotyping

300 to 1000 accessions/species

- Alfalfa and red clover
 - Accession: synthetic variety or population
 - Genotyping by sequencing GBS
- Pea, faba bean, soybean
 - Accession: pure line
 - Use of SNP arrays

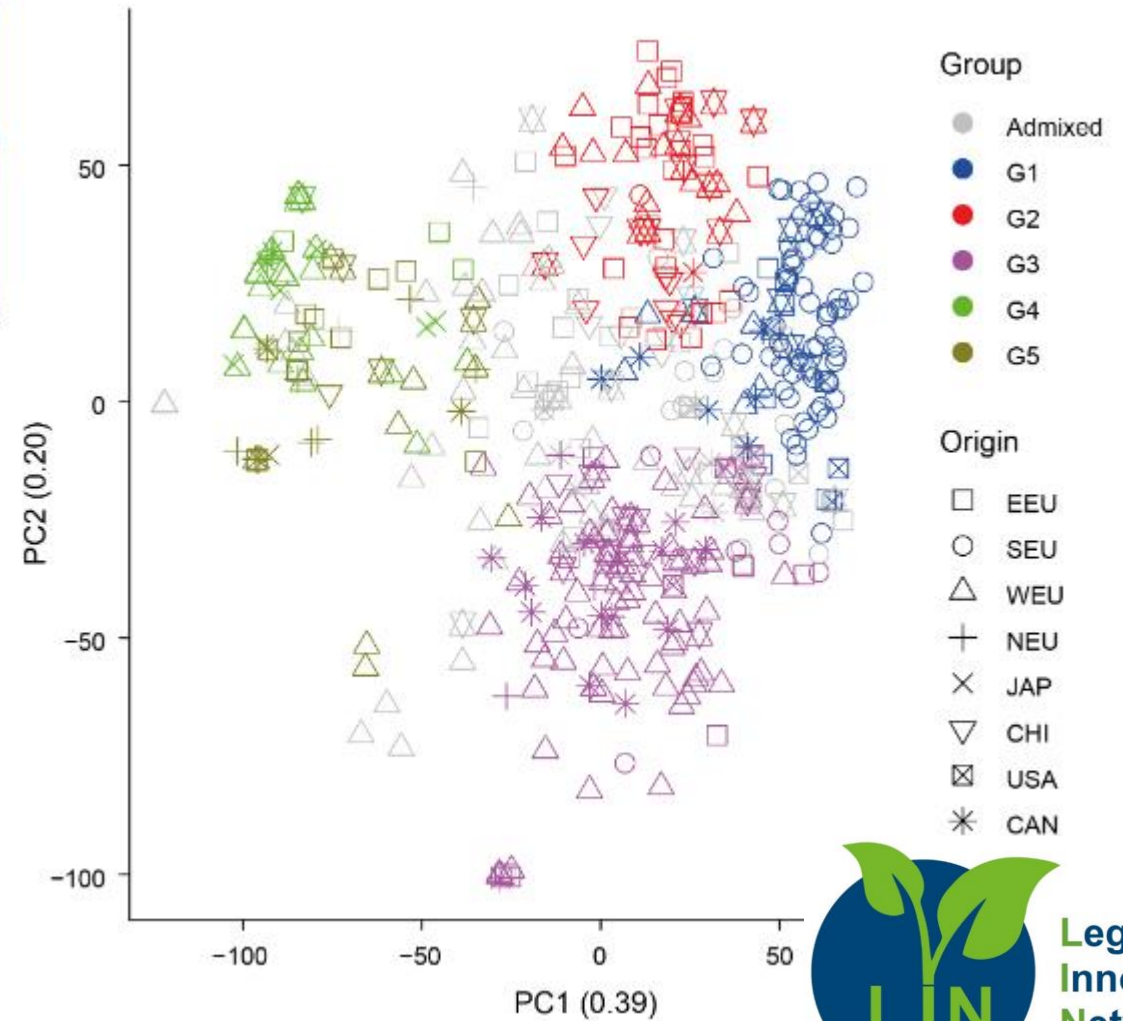
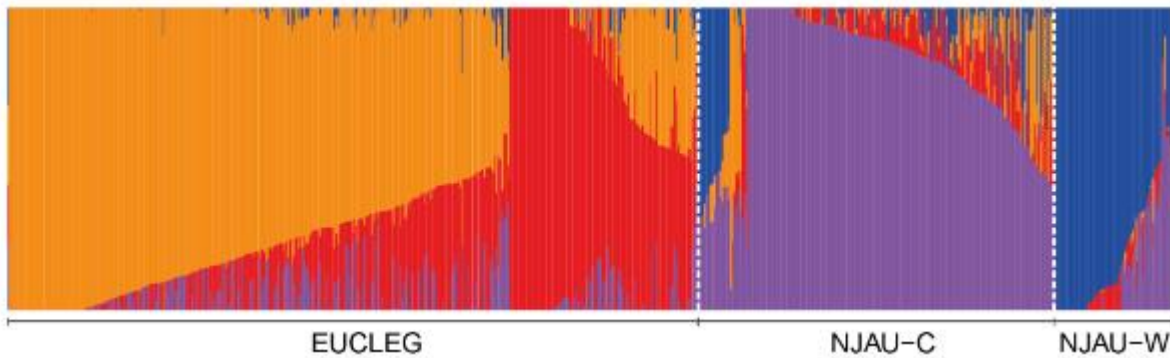
➤ Genetic diversity revealed with markers

Alfalfa: a total of 228 568 SNP in 31 743 loci (< 5% of missing data per SNP)



➤ Genetic diversity revealed with markers

Soybean: 224 993 SNP on 874 accessions (< 5% of missing data per SNP)



Saleem A, Muylle H, Aper J, Ruttink T, Wang J, Yu D and Roldán-Ruiz I (2021) A Genome-Wide Genetic Diversity Scan Reveals Multiple Signatures of Selection in a European Soybean Collection Compared to Chinese Collections of Wild and Cultivated Soybean Accessions. *Front. Plant Sci.* 12:631767. doi: 10.3389/fpls.2021.631767

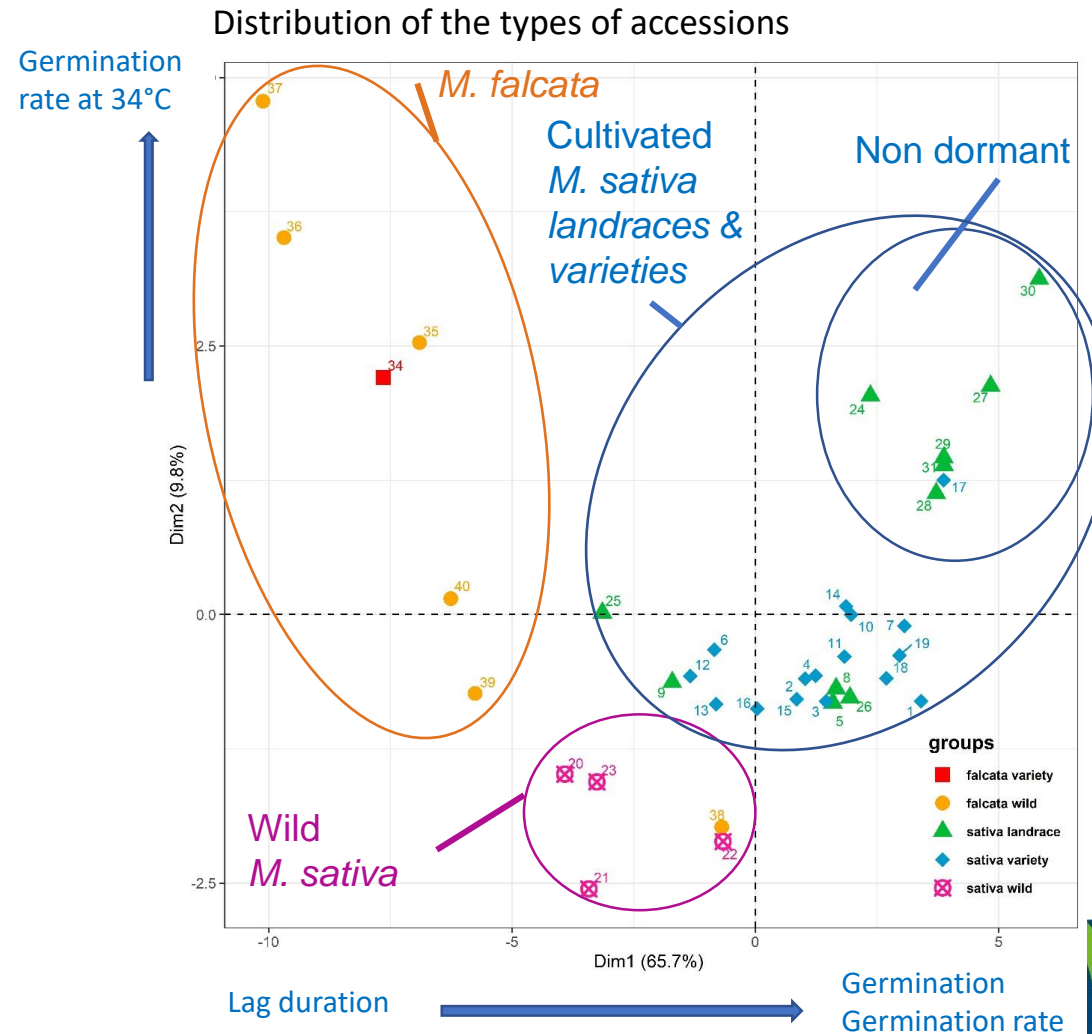
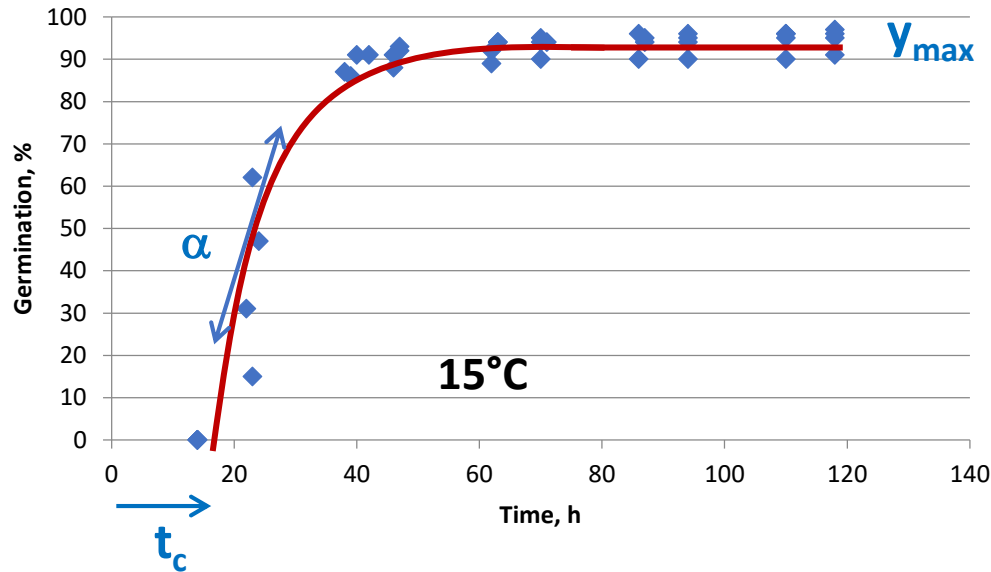
> Phenotyping

Multisite field trials + experiments in controlled conditions

- 3 to 5 locations per species
 - Yield
 - Protein and fibre contents
 - Protein quality
 - Diseases
- Drought, disease, cold tolerance
- Combined stresses: cold x disease, drought x disease
- Germination

➤ Effect of temperature on alfalfa seed germination

38 accessions germinated at 7 temperatures (5 to 40 °C)



➤ Genetic architecture of breeding traits

QTL and genomic prediction

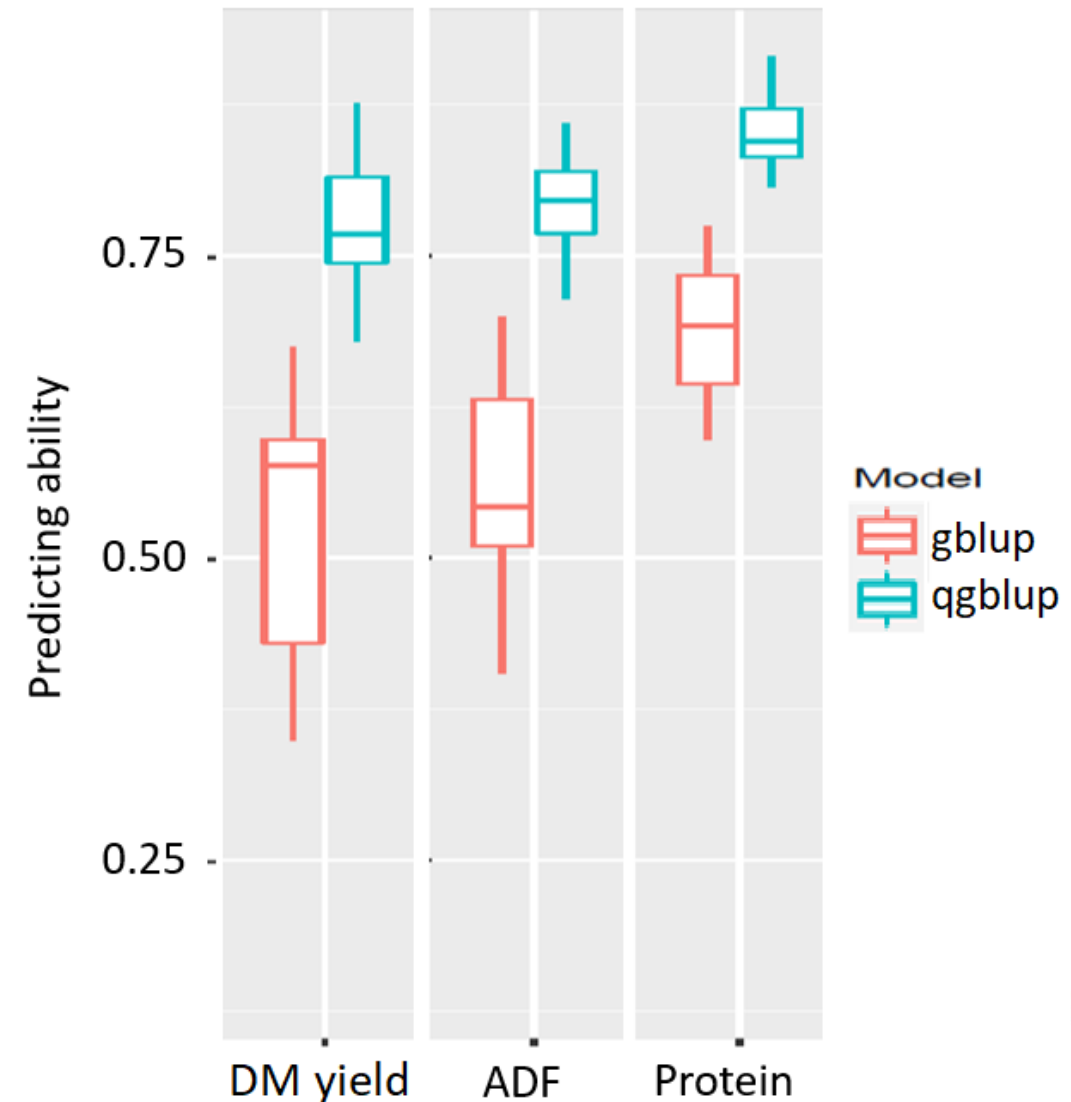
- 2021 work
- Illustration for two species, yield and quality



➤ Is it possible to predict traits from markers?

Alfalfa, all markers, traits recorded in 3 locations x 2 years

- We are able to predict 60-70% of genetic variation with 'simple' genomic prediction (gblup)
- Predictions reached 76-85% when taking into account the QTL (qgblup)



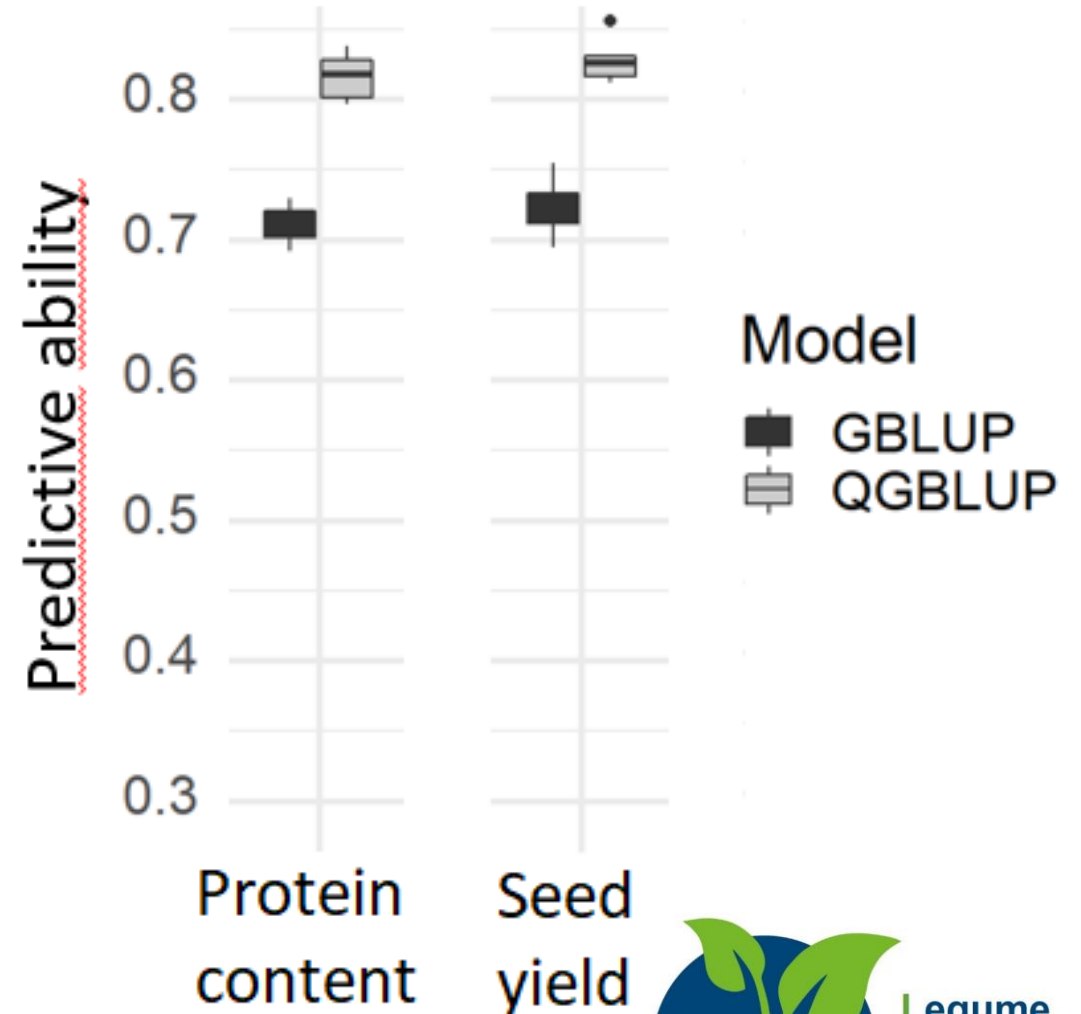
Pégard, Leuenberger, Julier, Barre (2021)
 Genomic prediction of lucerne yield and quality
 Eucarpia Forage crops and Amenity grasses, submitted



➤ Is it possible to predict traits from markers?

Soybean, 348 accessions, 126 860 markers

- We are able to predict > 70% of genetic variation with 'simple' genomic prediction (gblup)
- Predictions reached > 80% when taking into account the QTL (qgblup)



➤ Communication, dissemination

Researchers, breeders, partitionners



- Special issue of Frontiers in Plant Science

<https://www.frontiersin.org/research-topics/11418/breeding-forage-and-grain-legumes-for-sustainable-protein-production>

- Workshop in Brno (CZE) in Nov 2019:
 - Training course on methodologies for genotyping and data analyses
 - Videos available: <http://eucleg-trainings.ikbks.com/videos-from-trainings/>
- Website www.eucleg.eu, newsletters
- To be announced:
 - Webinar « post-EUCLEG legume breeding »: September 2021



➤ Innovations

To be used in breeding

- Genetic resources and related data
- Genotyping tools
- QTL and equations of genomic prediction



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Thanks for your attention

