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Towards genome-wide breeding for yield stability in spring pea

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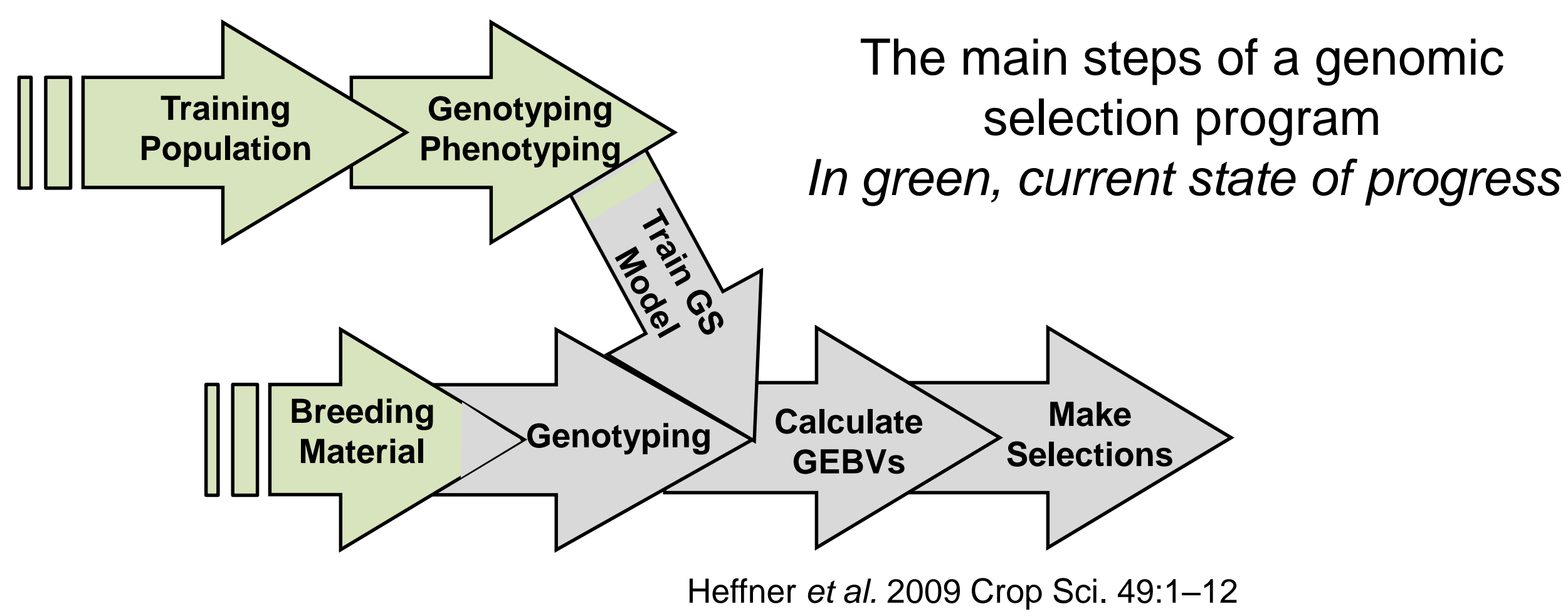
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 8 INRA, UE1375 PHÉNOTYPAGE AU CHAMP DES CÉRÉALES, 5 CHEMIN DE BEAULIEU, 63039 CLERMONT-FERRAND CEDEX, FRANCE

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Field pea (*Pisum sativum* L.) is an attractive crop for human and livestock nutrition and an important contributor to low-input farming systems. Multiple environmental challenges face field pea production and penalize yield regularity. The work-package 1 of the French National ANR project PeaMUST aims at identifying efficient gene combinations for yield stability in low-input cropping systems through genomic selection. Genomic selection is a new breeding method that uses increasingly abundant genomic information and statistical modelling to select superior genotypes based on genomic estimated breeding values (GEBVs). The main goals are: 1- to build a genomic selection prediction equation for yield stability in low-input cropping systems, 2- to implement a genomic selection program and, 3- to evaluate the genetic progress obtained after one and two genomic selection cycles.

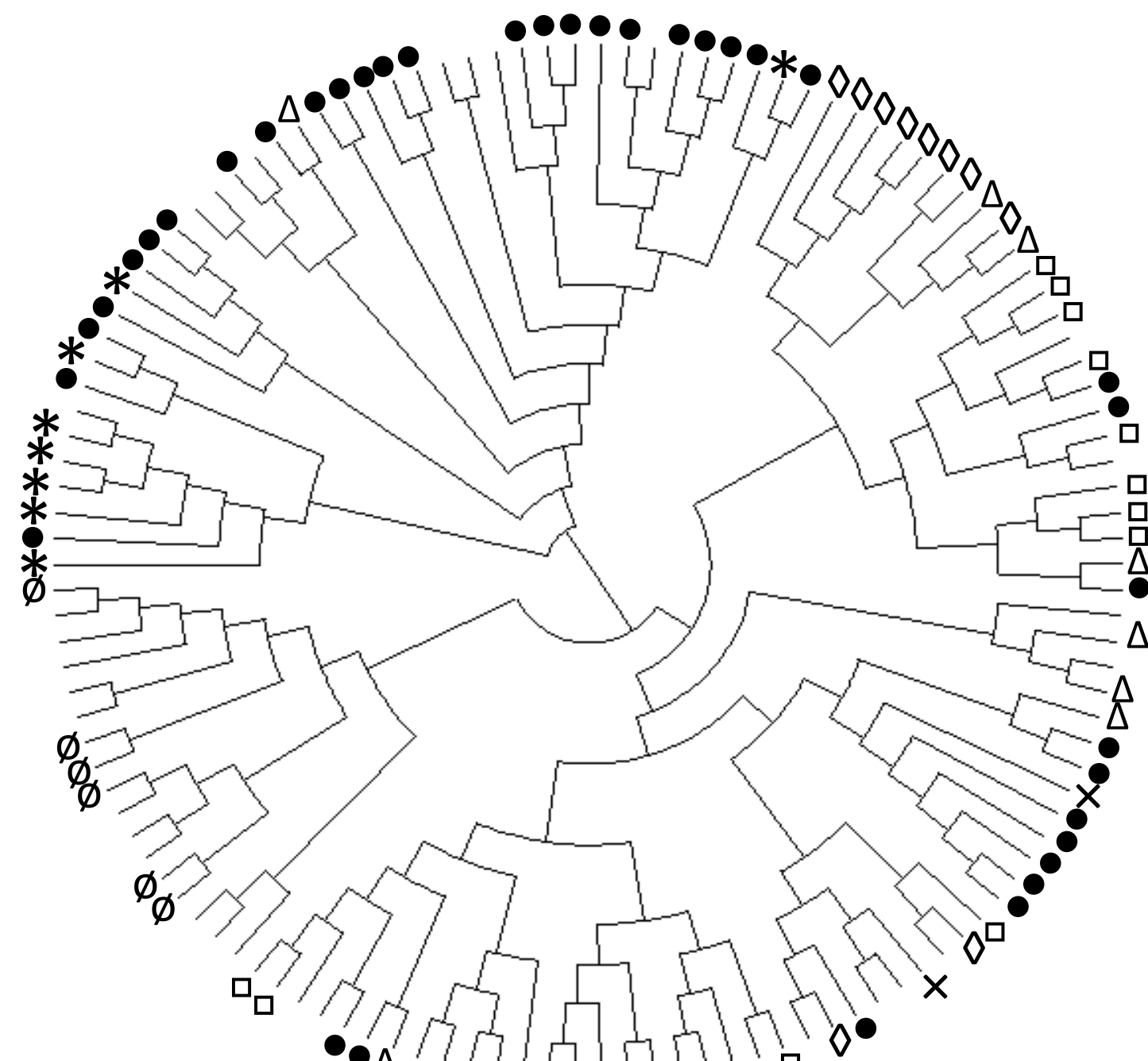


Heffner et al. 2009 Crop Sci. 49:1-12

Defined training population

The PeaMUST spring pea training population includes 300 genotypes:

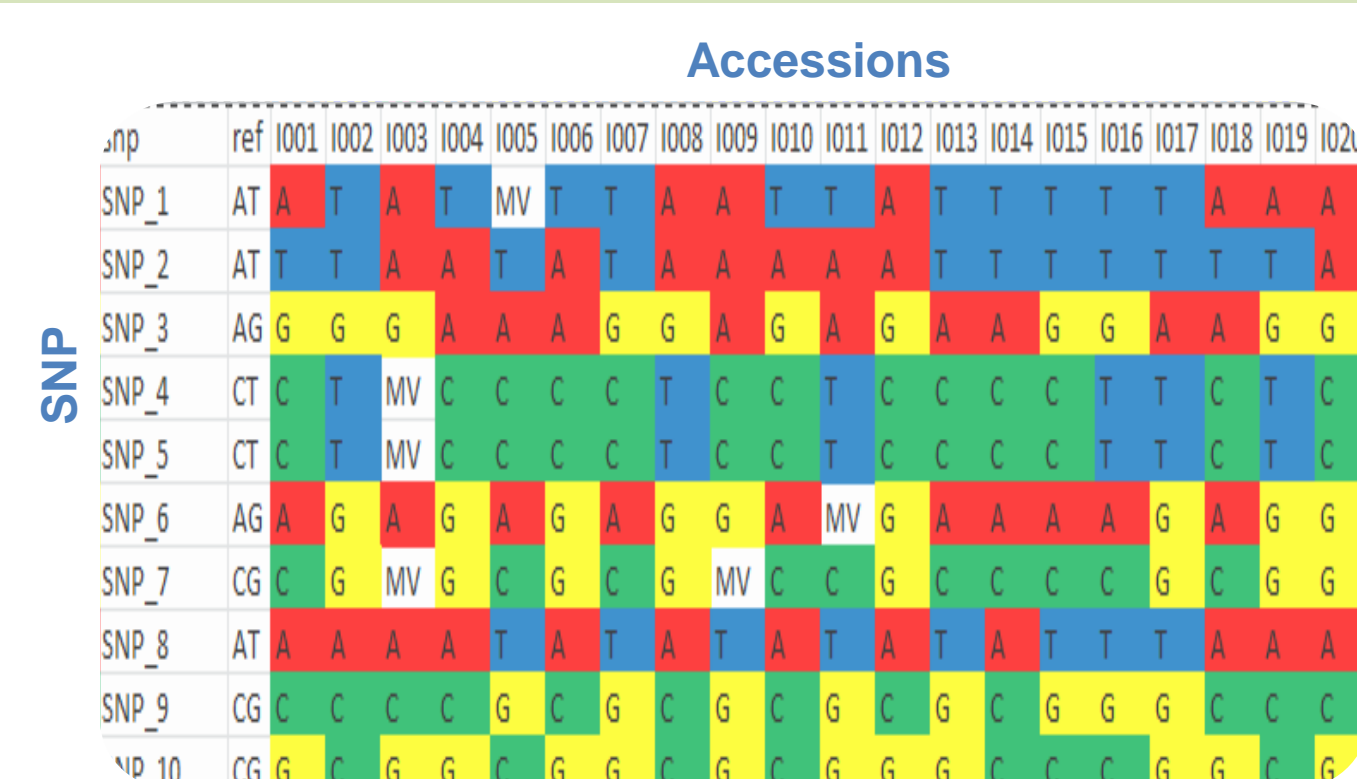
- 203 breeding lines from Momont resulting from 15 crosses (*: parents of crosses);
- 97 accessions from Western (•) and Eastern Europe (◻), Czech Republic (x), Canada (◊), USA (Δ) and donors of *Aphanomyces* root rot resistance from INRA Rennes (∅).



Spring pea dendrogram based on 2621 SNP markers

Genotyping

The training population was genotyped by sequencing genomic DNA after exome capture of ca. 51k gene contexts.

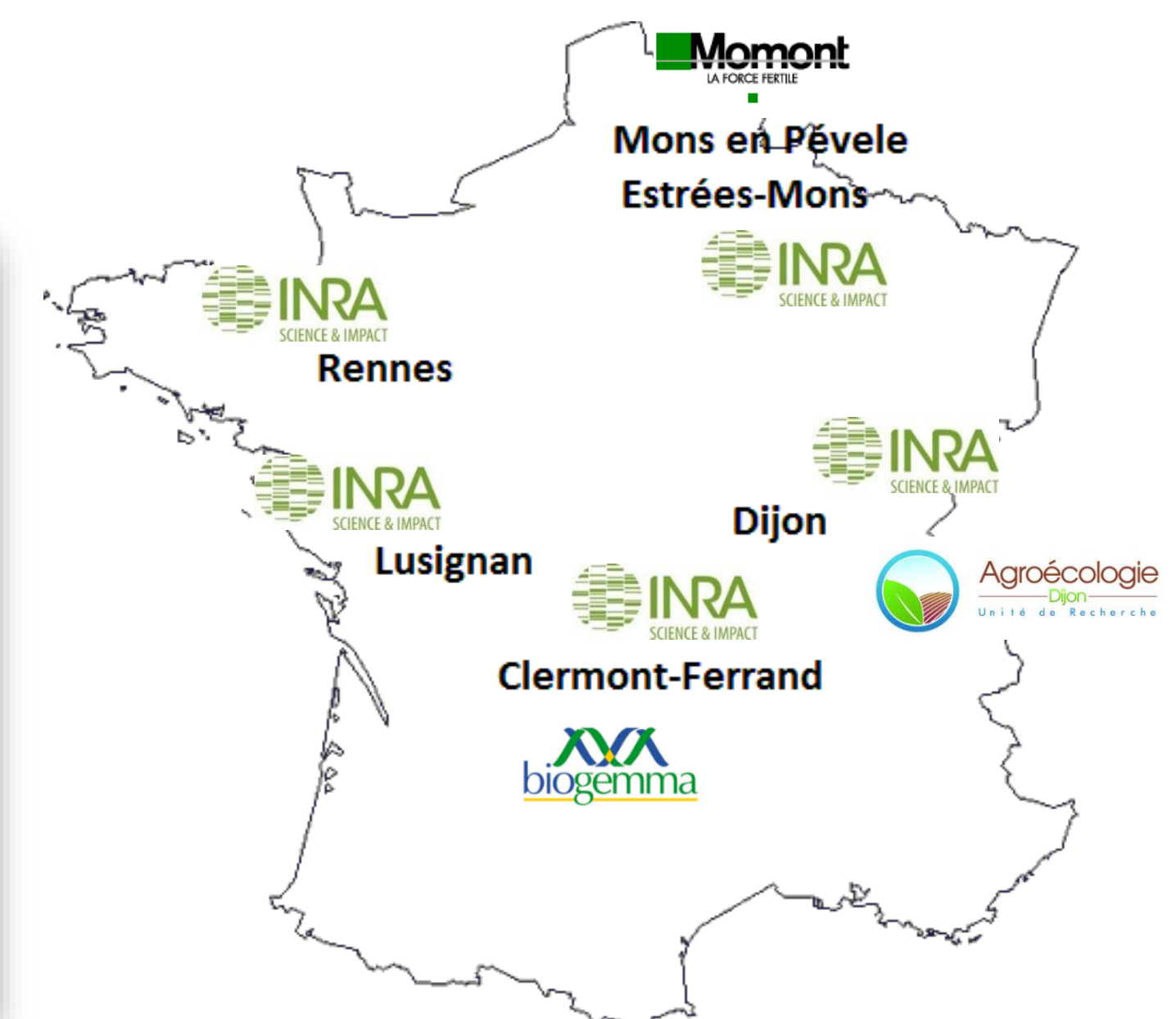


Development of a genomic selection prediction model

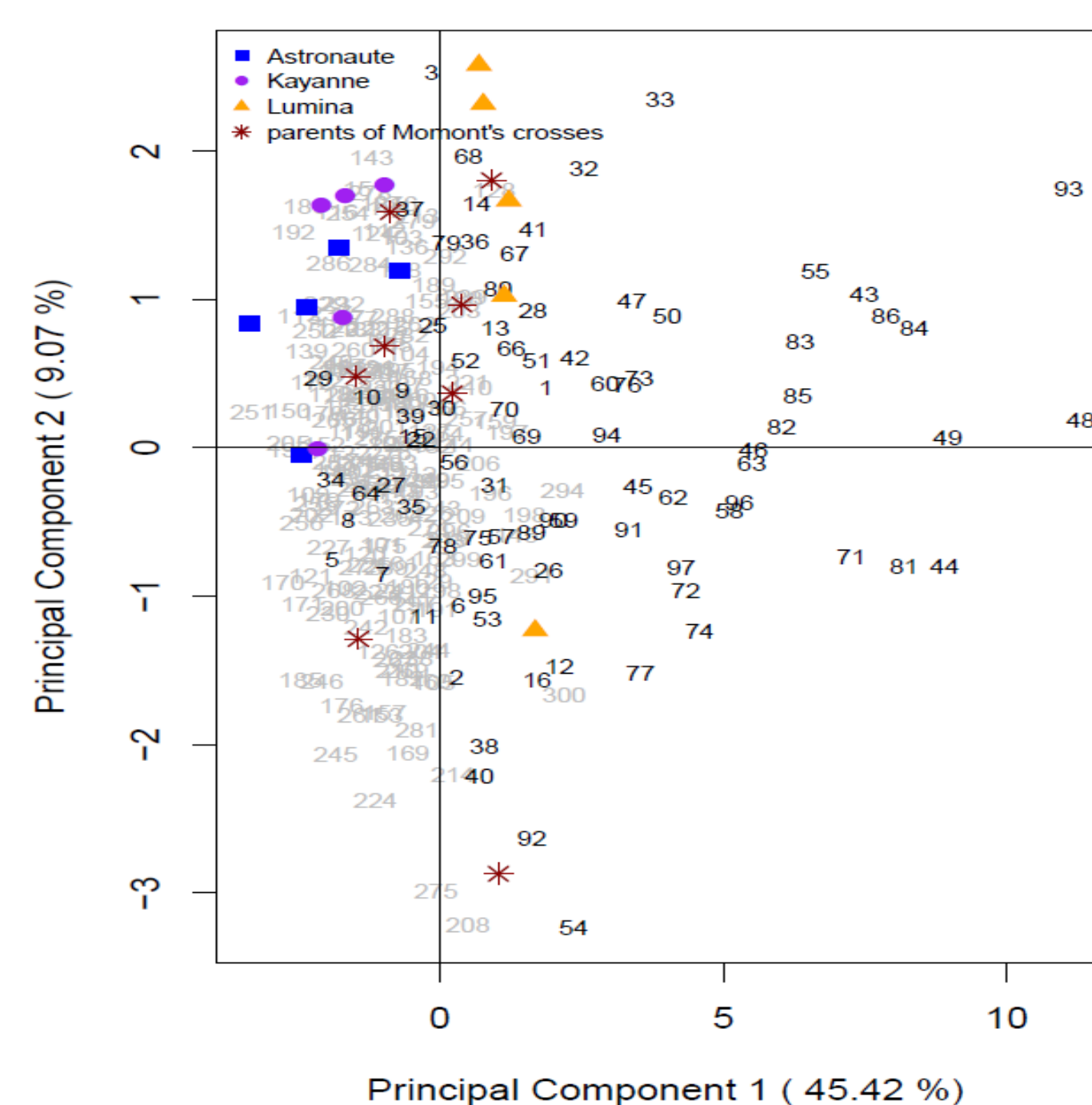
Different statistical methods, namely Partial Least Squares (PLS), Sparse Partial Least Squares (SPLS), Least Absolute Shrinkage and Selection Operator (LASSO), Bayes A, Bayes B and Genomic Linear Unbiased Prediction (GBLUP), have been tested for phenotype prediction in the INRA reference collection (Burstin *et al.*, submitted). They will be evaluated in PeaMUST for producing the GEBV prediction equation.

Phenotyping

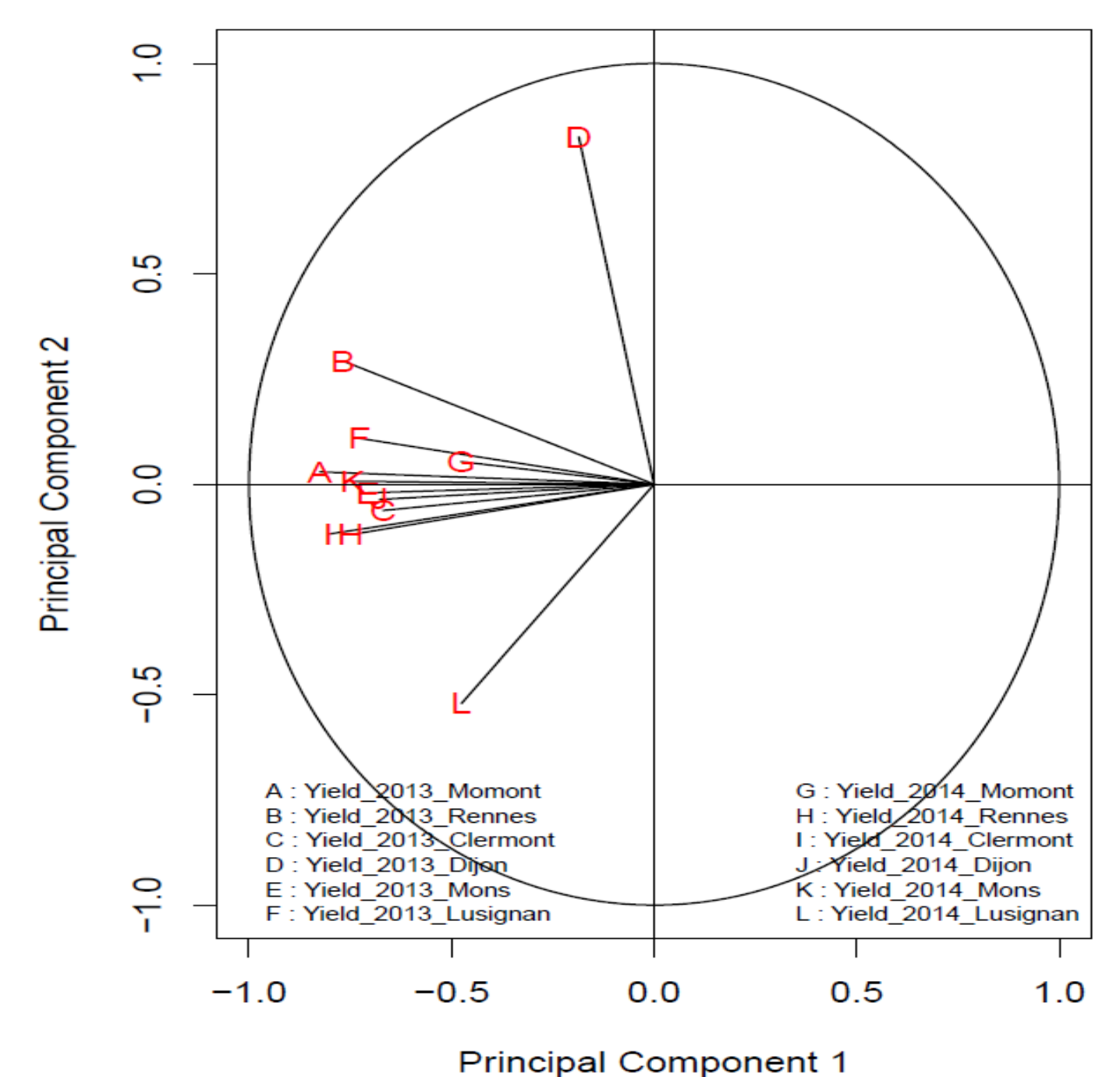
The training population was phenotyped in 12 field environments for phenology, yield-related traits, seed protein content, lodging and disease resistance.



Phenotyping network



Principal component analysis of yield showing variability between accessions and across environments



Selection of superior lines based on predictions

A breeding material composed of ca. 2000 lines derived from 7 different crosses is currently under construction. Genotyping by sequencing is planned for the end of 2015. Genotypic information on the breeding material will be then fed into the prediction model to determine the overall predicted value of individual lines and identify those carrying the best gene combinations for yield stability.

Conventional phenotype-based selection can take several years which limit the rate of variety improvement and breeder's ability to respond to new challenges. By using genomic selection, we look forward to rapidly select superior genotypes with improved genetic gain and efficiency. Efforts currently conducted on spring pea, described in this poster, will be further applied to "hr" and "Hr" winter pea. Selected genotypes all along the project of different types of pea will be evaluated under field conditions starting in 2017. This will pave the way to draw comparisons between the conventional and the revolutionary breeding methods in the particular case of field pea.