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Genomic selection programs for yield stability in pea

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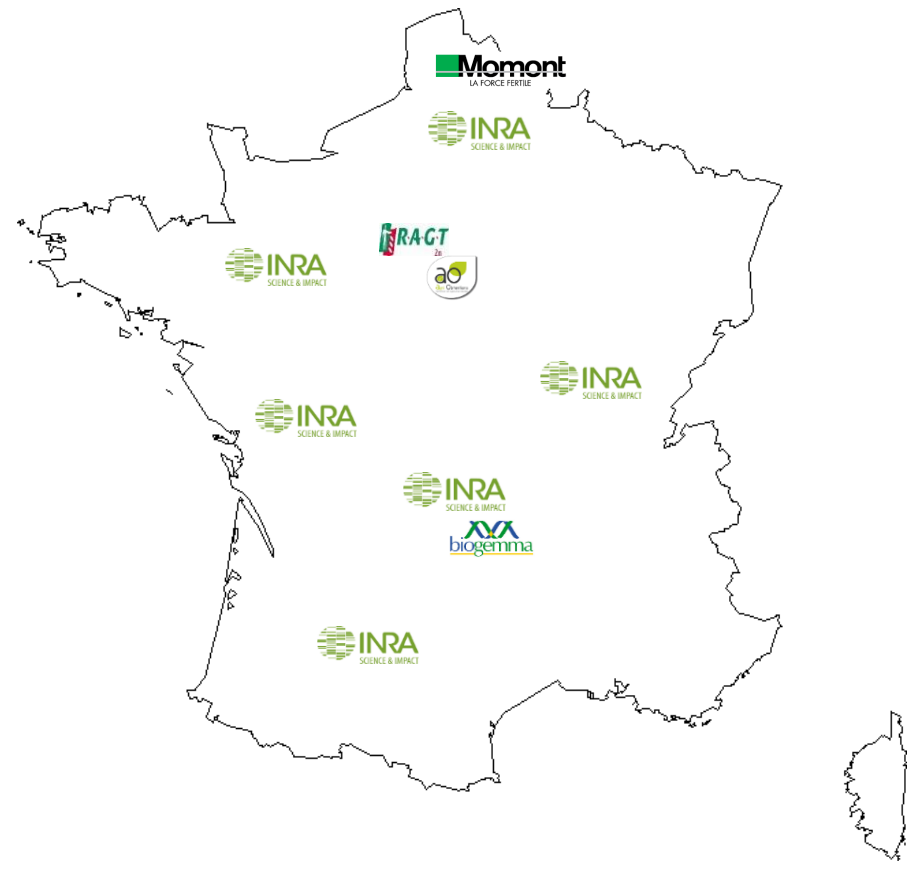
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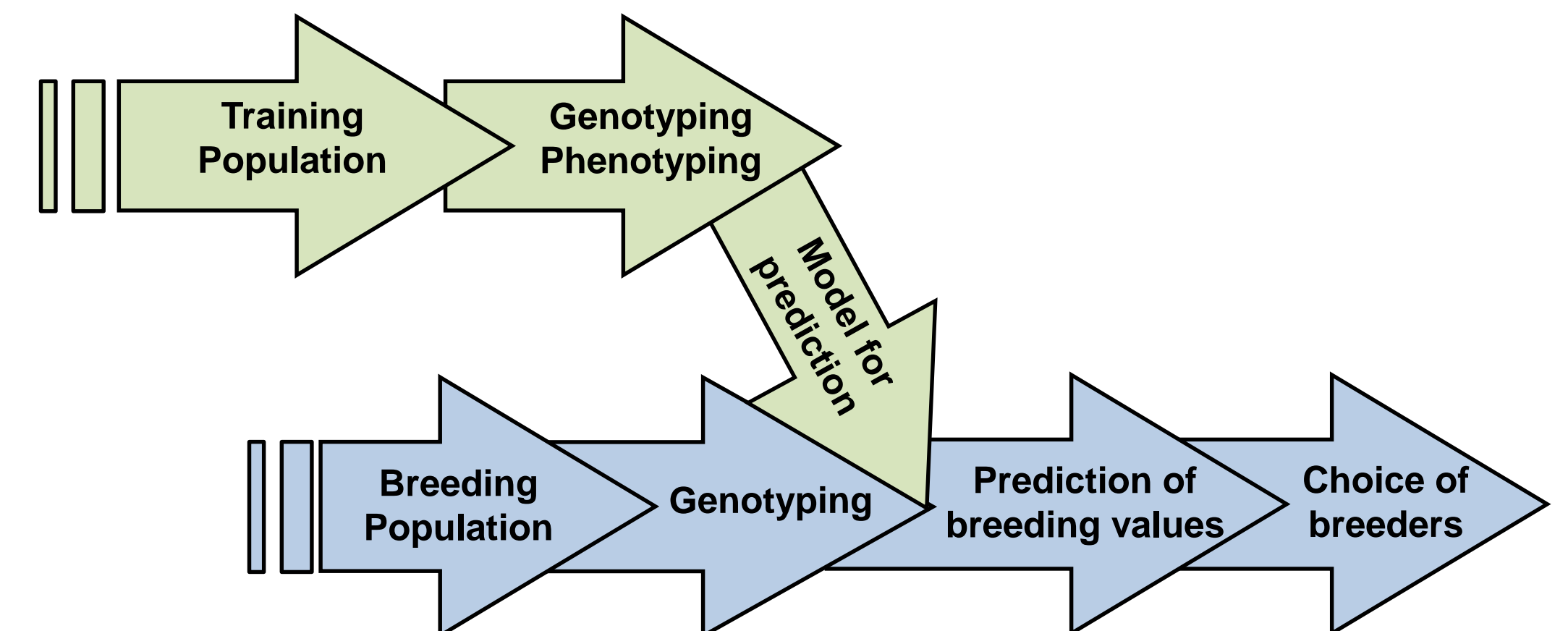


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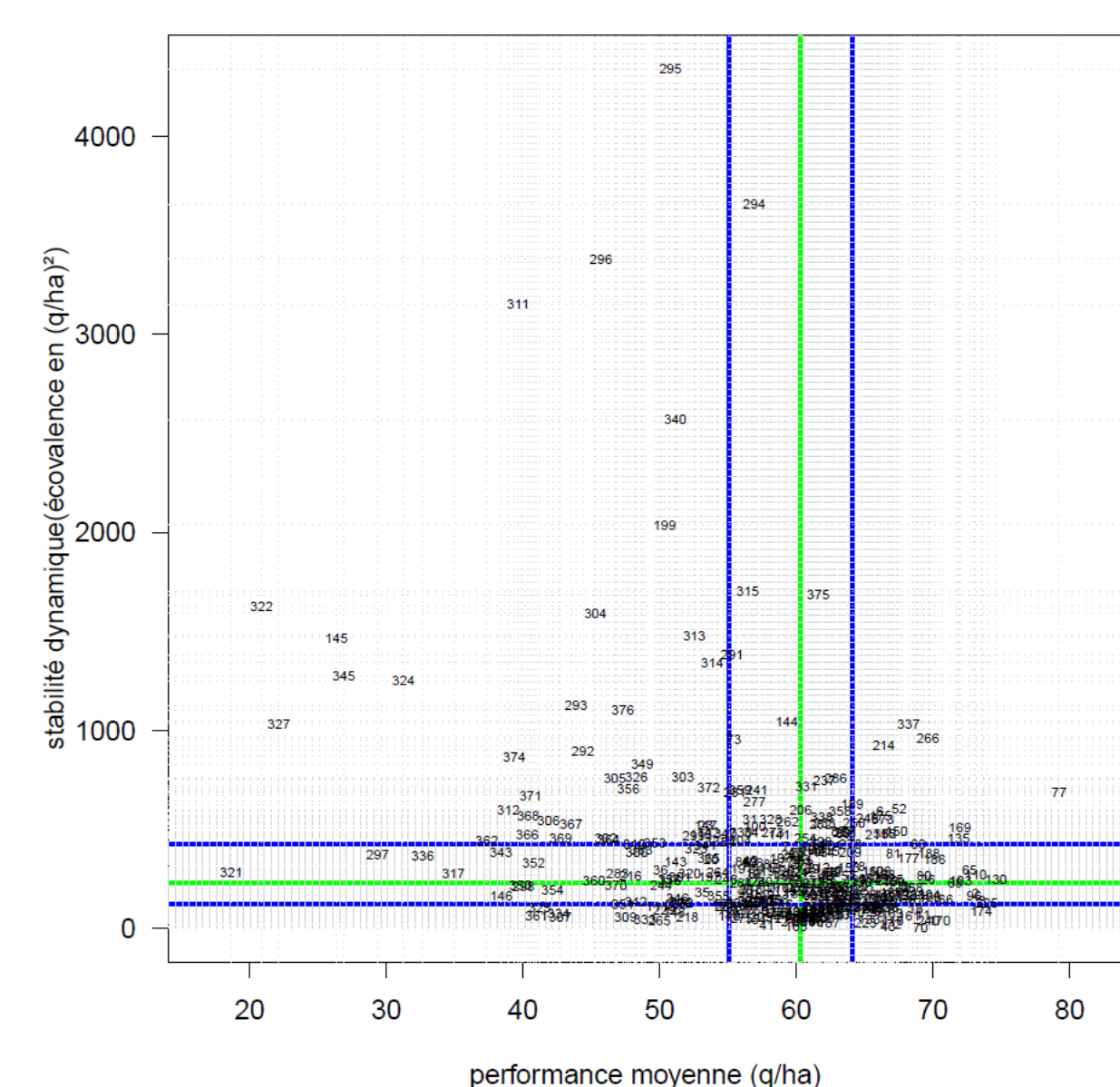
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Genomic selection is a breeding method that uses increasingly abundant genomic information and statistical modelling to select superior genotypes based on genomic estimated breeding values (GEBV). The aims of the PeaMUST work-package 1 are : 1- to 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. A classical GEBV breeding scheme was defined.



Training population phenotyping

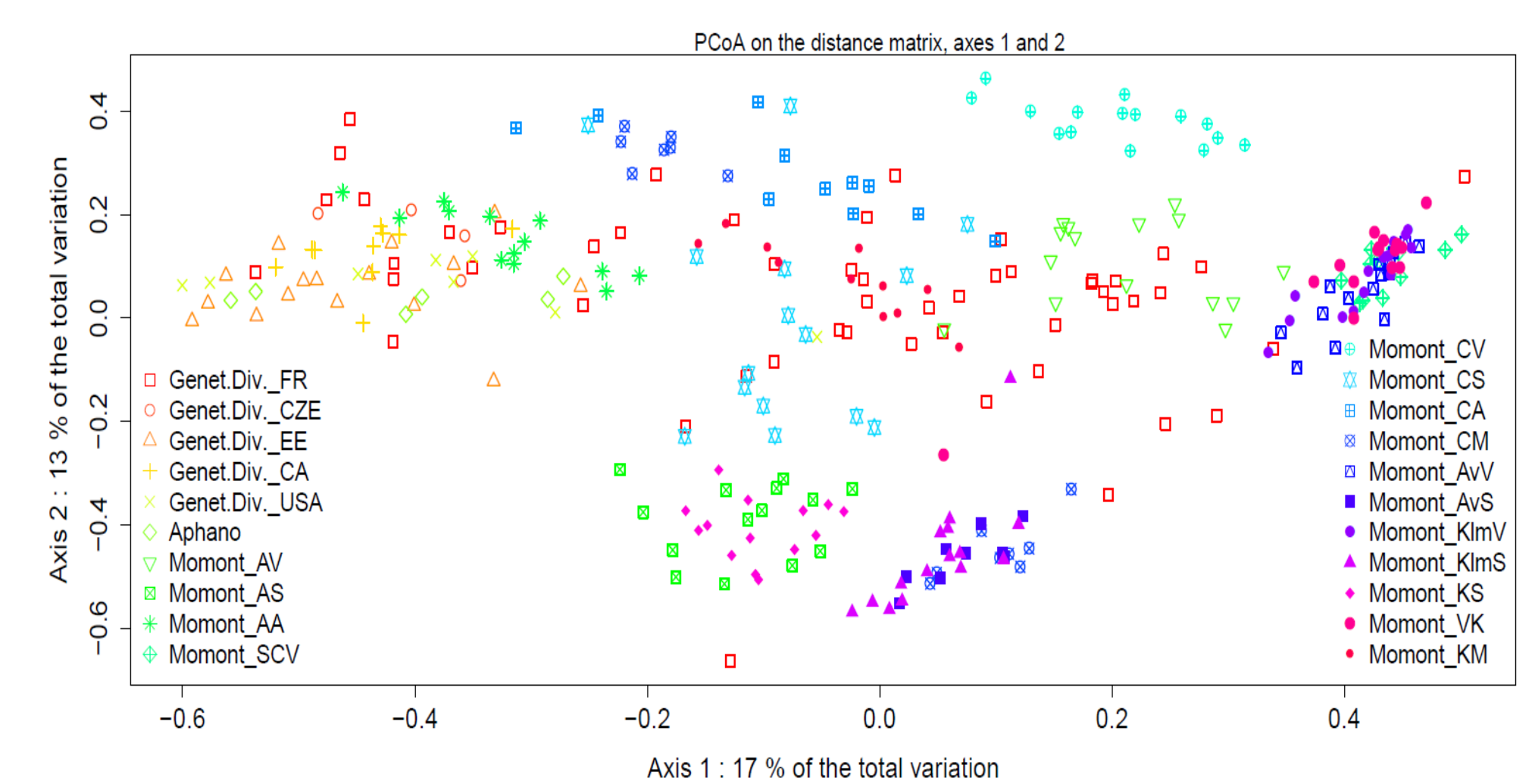


Yield dynamic stability of winter pea population in 2016

A spring dry pea and a conventional winter pea population were phenotyped in multi-site field yield trial networks between 2013 and 2016. The DIAGVAR method was used to model G x E interactions and evaluate the impact of environmental covariates on yield stability.

Exome capture resequencing

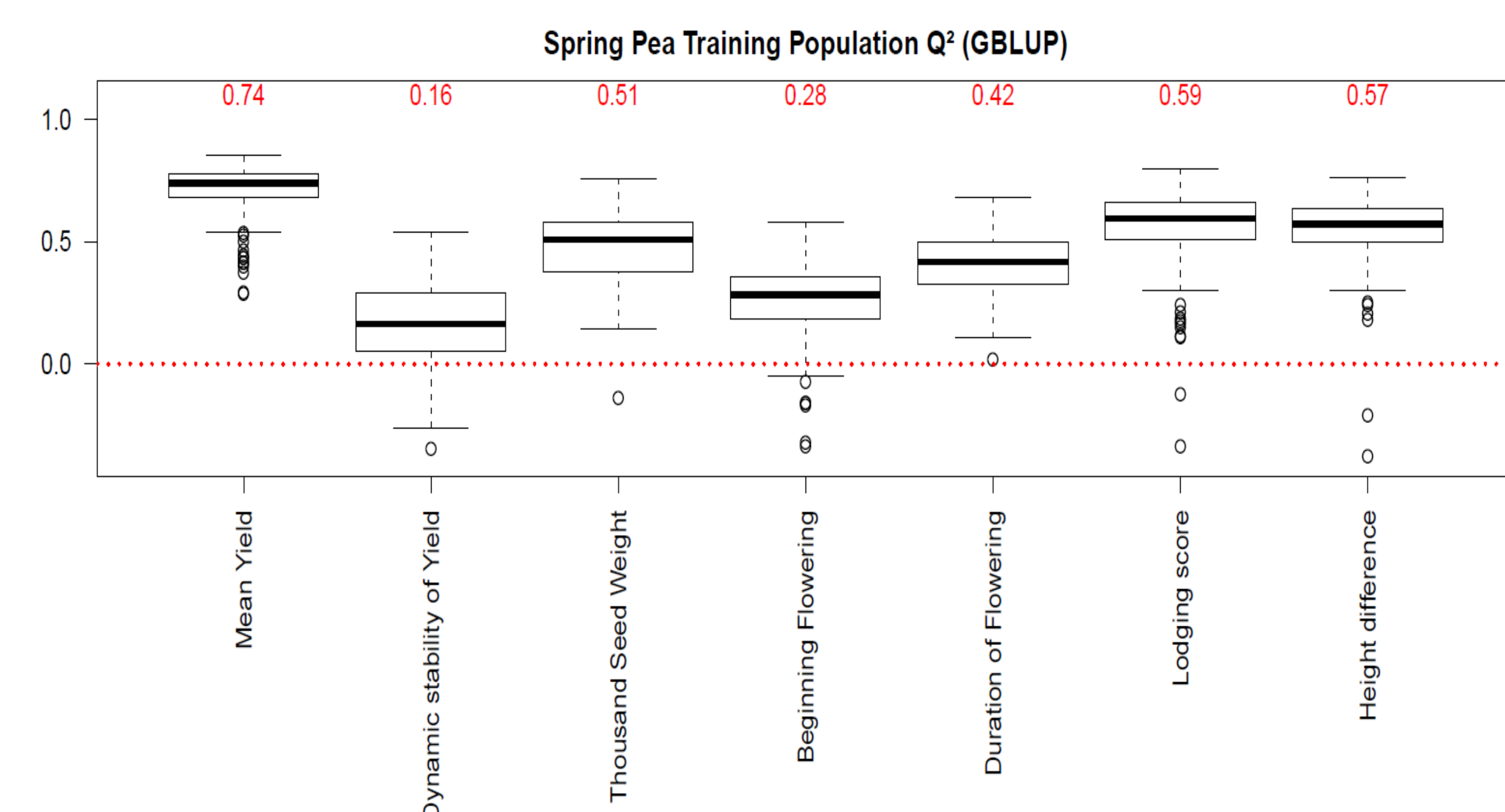
Training populations were genotyped using exome capture resequencing. 746k and 1.2 M SNPs were discovered in the spring and the conventional winter pea populations, respectively.



Genetic diversity in spring pea training population

GEBV prediction equation

The GBLUP statistical method was selected to develop the GEBV prediction equation. 9 traits were retained for prediction based on their prediction accuracies (Q^2) and importance in the breeding scheme.



Prediction accuracies (Q^2) in spring pea training population for 7 traits - 16 environments 2013-2014-2015 - 300 genotypes

GEBV prediction in breeding population

Genomic estimated breeding values have been computed for the 1262 individuals of the spring pea breeding population. 20 lines were selected based on GEBV as potential breeders for next generation in 2017.



Correlations	5kkm_GBLUP
Seed weight observed vs predicted	0.46
Thousand Seed Weight observed vs predicted	0.31
Flowering date observed vs predicted	0.53
Duration of Flowering observed vs predicted	0.20
Height difference observed vs predicted	0.52

Genomic selection programs are currently developed in spring pea, conventional winter pea and photoperiodic winter pea. Implementation in spring pea has provided the first GEBV equation and a selection index built from 9 important traits. Based on the GEBV, the superior genotypes were selected as progenitors for the second generation of genomic selection. They will be evaluated under field conditions in 2017-18 to measure the genetic gain and the breeding method efficiency.