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To cite this version:

HAL Id: hal-02741945
https://hal.inrae.fr/hal-02741945
Submitted on 3 Jun 2020

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TOWARDS GENOME-WIDE BREEDING FOR YIELD STABILITY IN SPRING PEA

KLEIN A1, TAYEH N1, SIOL M1, HERBOMME Z-JF2, PICHON J-P3, DUARTE J3, DUBORJAL H3, HOUTIN H1, BLANC N1, VALDRINI J-M1, WALCZAK P3, BLERIOT O1, HANOCO E1, CHASSIN A1, BIDON M3, HUART M1, TOURATIER M1, MARTIN C1, JACQUIN F1, AUBERT G1, BURSTIN J1 *

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.

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

Genotyping
The training population was sequenced by performing 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.

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.