Work centre:

(1) Crop Development Centre/Dept of Plant Sciences. University of Saskatchewan. Canada

Summary:

Objectives, Description, Main Results & Conclusions

Objectives

We redesigned faba bean nutritional, environmental and economic attributes for economic/ecological adaptation to the Canadian prairie environment to improve crop rotations and global food production systems. Main objectives were (1) reduce seed size (2) eliminate vicine-convicine , (3) reduce tannins and (4) days to maturity and (5) increase economic value of the crop.

Materials and Methods

The F2-derived family method was used to reducing seed size, improve seed shape, reduce vicine-convicine, tannins and and maturity, and increase yield.

Main Results

(1) Seed size reduced from 650 mg per seed to less than 300 mg per seed

in adapted germplasm to reduce seed volume and increase value.

(2) Seed shape altered from the traditional flat shape to almost round.

(3) Molecular marker for the low vicine/convicine (vc1) was discovered and implemented in the entire breeding program.

(4) The white flower (low tannin gene zt1) trait was introduced into the entire

breeding system.

(5) Crop maturity was reduced through genetic, physical and environmental breeding strategies.

(6) Yield potential was maintained or increased depending on the production area, while crop production risks were reduced.

(7) A much greater range of phenotypic and genotypic diversity with economic potential was established for faba bean.

Conclusions (Outcomes)

(1) Effective breeding objectives and methods were established to improve the economic, nutritional, environmental, ecological, agronomic, and culinary attributes of faba bean.

(2) New genetic baseline accelerated production of faba bean

(3) Faba bean protein is now in high demand for expanding plant protein industry in western Canada.

(4) Breeding resulted in greater genetic diversity and production and product diversification.

(5) The economic potential for faba bean in western Canadian crop rotations was increased.

Bibliography

- *Historical review of faba bean improvement in western Canada. Legume Science. Khazaei, Hawkins, Vandenberg Development and validation of a robust, breeder-friendly molecular marker for the vc - locus in faba bean. Khazaei et al.*

606/201. GENOMIC SELECTION FOR PEA GRAIN YIELD AND PROTEIN CONTENT: PREDICTIVE ABILITY FOR INDEPENDENT ITALIAN ENVIRONMENTS AND FOR TARGET AND NON-TARGET GENETIC BASES

Authors:

Margherita Crosta[1], Nelson Nazzicari[1], Barbara Ferrari[1], Luciano Pecetti[1], Tommaso Notario[1], Giovanni Cabassi[1], Paolo Annicchiarico[1]

Work centre:

(1) Council for Agricultural Research and Economics (CREA). Lodi. Italy

Summary:

Objectives

Genomic selection (GS) has special interest for complex polygenic traits, but its actual value for cool-season grain legumes is poorly known. Since GS involves substantial initial phenotyping for model construction, information is needed not only on GS inter-environment predictive ability (as challenged by genotype × environment interactions) but also on the predictive ability penalty suffered by a GS model built for a genetic base (GB) when predicting breeding values for another GB. Pioneer studies were encouraging for pea GS targeting Italian environments for a GB represented by three

recombinant inbred line (RIL) populations issued by connected crosses among three elite cultivars, with average values of inter-environment predictive ability for top-performing GS models of 0.40 for grain yield, 0.53 for protein content, and 0.41 for protein yield (Annicchiarico et al., 2019; Crosta et al., 2022). These values were about halved for inter-population predictions using one RIL population for model construction to predict data of the other populations. This study aimed to provide a thorough assessment of the predictive ability of GS models defined from data of three environments, when applied to data from independent environments and inbred lines from both the target GB (the same three RIL populations) and a non-target GB (three other RIL populations, each including one parent cultivar different from those of the target GB).

Concise description of the work (materials & methods)

While GS model construction was based on data of 276 lines grown in three environments of Northern or Central Italy in the cropping years 2013-14 or 2014-15, GS model evaluation was based on data of 131 independent inbred lines (64 for the target genetic base, and 67 for the non-target base) grown in Northern Italy in the years 2018-19 and 2019-20. All the experiments were autumn-sown and had three replicates. GS predictions relied on 5,537 polymorphic SNP markers made available by ApeKI-based genotyping-by-sequencing.

Main Results

Genotype × year interaction across validation environments was substantial, as indicated by only moderate phenotypic correlation for line values across environments (<0.55 for all focus traits). Grain yield and protein content in each validation environment were poorly correlated (r = 0.10-0.21). On average, GS displayed moderate predictive ability (0.28-0.40) for grain yield, protein content and protein yield of genotypes within individual RIL populations of the target GB or protein content of genotypes of the non-target GB, with minor test year differences (Table 1). Somewhat greater predictive ability was obtained for all focus traits when GS was applied to all genotypes of the RIL populations representing the target GB (Table 1).

Target trait	Cropping year	Within-RIL prediction		Across-RIL prediction
		Target GB	Non-target GB	Target GB
Grain yield per ha	2018-19	0.256	0.113	0.355
Grain yield per ha	2019-20	0.258	0.011	0.444
Grain yield per ha	Average of 2 years	0.292	0.079	0.399
Grain protein content	2018-19	0.313	0.372	0.390
Grain protein content	2019-20	0.425	0.314	0.449
Grain protein content	Average of 2 years	0.403	0.360	0.419
Protein yield per ha	2018-19	0.245	0.085	0.308
Protein yield per ha	2019-20	0.267	-0.089	0.447
Protein yield per ha	Average of 2 years	0.279	0.003	0.378

Table 1. Predictive ability of top-performing Ridge regression BLUP genomic selection models for three pea traits constructed for a genetic base (GB) represented by three connected crosses, when tested on 126 independent inbred lines belonging to the target and a non-target GB grown in two independent environments. Predictions within RIL populations (reporting results averaged across three populations) or across RIL populations

Conclusions

On the whole, these findings confirm and reinforce the usefulness of GS for pea grain yield and protein content of the GB used for model training, while restricting to protein content its interest for a non-target GB.

Bibliography

- Annicchiarico, P., Nazzicari, N., Pecetti, L., Romani, M., Russi, L., 2019. Pea genomic selection for Italian environments. BMC Genomics 20, 603. https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-019-5920-x
- Crosta, M., Nazzicari, N., Ferrari, B., Pecetti, L., Russi, L., Romani, M., Cabassi, G., Cavalli, D., Marocco, A., Annicchiarico, P., 2022. Pea grain protein content across Italian environments: genetic relationship with grain yield, and opportunities for genome-enabled selection for protein yield. Front. Plant Sci. 12, 718713. https://www.frontiersin.org/articles/10.3389/fpls.2021.718713/full