

GENOMIC SELECTION IN WHITE LUPIN

Paolo Annicchiarico¹, Nelson Nazzicari², Barbara Ferrari³

¹ Council for Agricultural Research and Economics (CREA), Lodi, Italy, paolo.annicchiarico@crea.gov.it

² CREA, Lodi, Italy, nelson.nazzicari@crea.gov.it

³ CREA, Lodi, Italy, barbara.ferrari@crea.gov.it

Genomic selection, which estimates breeding values by large sets of molecular markers in a statistical model, represented a breakthrough for improving cattle production. Its use for plant breeding has been favoured by the development of Genotyping-by-Sequencing, which can generate large sets of SNP markers at a lower cost than array-based techniques. Genomic selection has shown promise for improving legume crop yield in pioneer studies on soybean, alfalfa and pea.

The main aim of this study was to investigate for the first time the application of genomic selection to lupins, by assessing its ability to predict the grain yield and 10 agronomic traits of white lupin (*Lupinus albus* L.) landraces and varieties grown in Northern Italy. A second aim was to report on on-going work aimed to develop genomic selection models for yield, stress tolerance and grain quality of inbred lines.

The study included 83 landraces from 9 major historical cropping regions (Italy, Egypt, Spain, Portugal, Turkey, Maghreb, Madeira-Canaries, Near East, East Africa), each represented by 3-4 individuals, and 8 French varieties, each represented by 2 genotypes. Phenotypic data of the 91 cultivars are described in Annicchiarico et al. (2010). GBS of the genotypes based on Elshire et al.'s (2011) protocol with modifications issued 6578 polymorphic SNPs. Genomic predictions based on SNP allele frequencies of the cultivars using Ridge regression BLUP or Bayesian Lasso models were assessed by cross validations.

The two models performed comparably. Genomic selection exhibited quite high predictive ability (>0.83) for grain yield, winter survival and onset of flowering, and moderately high predictive ability (0.49-0.63) for plant height, number of leaves on the main stem, leaf size, proportion of seeds on the main stem, number of seeds per pod, and individual seed weight. Only two traits with narrower genetic variation showed modest predictive ability. Our results encourage the genome-enabled identification of promising genetic resources within large germplasm collections. We describe the development a broadly-based sweet-seed reference population from crosses between elite landrace and variety germplasm and its exploitation for defining genomic selection models for inbred lines.

This study was funded by the European Union through the FP 7 project LEGATO (grant agreement no. 613551) and the Horizon 2020 project LIVESEED (grant agreement no. 727230).