

## GENOMIC SELECTION FOR GRAIN YIELD IN DROUGHT STRESS CONDITIONS IN DURUM WHEAT

VITALE P.\*\*\*\*\*, LAIDÒ G.\*, ESPOSITO S.\*, DE VITA P.\*, PECCHIONI N.\*

\*) Research Centre for Cereal and Industrial Crops (CREA-CI), CREA—Council for Agricultural Research and Economics, 71122 Foggia, Italy.

\*\*) Department of Agriculture, Food, Natural Science, Engineering, University of Foggia, Via Napoli 25, 71122 Foggia, Italy.

*genomic selection, durum wheat, grain yield*

Durum wheat (*T. turgidum* ssp. *durum* Desf.) is one of the most important staple crops in the Mediterranean, with areas of cultivation spread worldwide, often in drought-prone areas. Moreover, in the last decades, climate change is having an increasingly significant impact on crop yields due to the increase in temperatures and the decrease in rainfall. Genomic selection (GS) is an attractive method to improve complex quantitative inheritance traits such as grain yield in a climate change scenario. In this study, the prediction accuracy for grain yield was verified in a panel of 250 durum wheat varieties using several GS models, then the most fitting model was chosen to select the best parents for higher grain yield progenies. Specifically, the durum wheat panel was phenotyped for grain yield in two consecutive growing seasons (2017-18 and 2018-19) at the CREA-CI, Foggia under two different crop management in replicated field trials: “Not stressed” (nStr) (with nitrogen and water supply), and “Stressed” (Str) (without any supply). The entire panel was genotyped using the “Axiom TaBW420” SNP array. Best linear unbiased estimates (BLUEs) between year and SNP matrix filtered at different MAF levels were used to verify the accuracy at different percentages of training (TP) and validation (VP) populations using RR-BLUP. Therefore, the best setting was used to train four Bayesian models (BayesA, BayesB, BayesC, and BayesLASSO). The most suitable model was chosen to estimate marker effects to select the crosses. Grain yield BLUEs ranged from 3.7 to 8.8 t/ha and from 3.5 to 8.3 t/ha for nStr and Str, respectively. Relatively low heritabilities were found in both treatments 0.32 (nStr) and 0.53 (Str). After filtering, an SNP matrix of about 63K markers was produced. The best setting resulted with MAF at 5% and 70-30% of TP and VP. Medium-high prediction accuracies were detected for all models in both treatments. The accuracies for nStr were found higher than Str for each model up to 6%. The prediction accuracy ranged from 0.56 to 0.58 for nStr and from 0.52 to 0.53 for Str. The RR-BLUP model was the one with best accuracies, therefore it was used to weigh marker effect to perform parent selection. The best ten crosses were selected from both field conditions. The predicted average yield of progenies was up to 7.5 and 7.3 t/ha for nStr and Str respectively, with the best predicted lines potentially reaching a grain yield of 9.5 t/ha for nStr and 9.2 t/ha for Str. In this work, the accuracy of five models was estimated to select the best fitting model to predict the best crosses for grain yield in low input (drought and nitrogen) and standard field conditions. Wheat predicted families will be genotyped, and the best lines will be selected based on genomic estimated breeding values (GEBVs). In addition, a representative fraction of them will be phenotyped for grain yield to validate the model.