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Abstract – SY32

PREDICTION OF GRAIN YIELD AND COMPLEX TRAITS TO ASSESS THE POTENTIAL OF A MAGIC POPULATION FOR GENOMIC SELECTION IN BARLEY

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Seed traits (ST) are targets of barley breeding programs as they are crucial components of yield and quality [1]. Climate change is increasing drought episodes and heat waves in the Mediterranean, which in turn are causing important yield losses in this cereal crop [2]. Therefore, new breeding strategies are needed to sustain barley yield and quality since this cereal plays a relevant role in poorer communities of the Mediterranean, for ensuring food security, especially in North Africa and developing countries. This work carried out in the framework of the iBarMed project (www.ibarmed.com) aims at selecting high-yielding barley lines with enhanced grain quality adapted to Mediterranean environments using genomic prediction and a MAGIC population, which was previously developed inter-crossing eight founder lines. The MAGIC population used in this study was sown in several temperate and semi-arid environments (Annoucer - Morocco, Fiorenzuola d’Arda - Italy, Adana and Konya - Turkey) using alpha lattice experimental designs and phenotyped for grain yield (GY) and heading date (HD). Moreover, grains of MAGIC lines were scanned to phenotype several STs as grain length, width, area, perimeter, diameter, eccentricity, circularity, compacity, rugosity and thousand-kernel weight (TKW) using Optomachine. To create genomic prediction (GP) models and compute “Genomic Estimated Breeding Values” (GEBVs), training and breeding populations, composed by 90 MAGIC lines and 323 individuals, respectively, were fingerprinted using the Illumina 50K barley iSelect SNP array [3]. Using linear mixed models, Best Linear Unbiased Prediction (BLUPs) of GY and STs were computed. GP models were fitted using BGLR (Bayesian Generalized Linear Regression) package implemented in R software, which allowed to combine adjusted means (BLUPs) of GY and STs with genotypic data of the training population using ridge regression method. Different single and multi-environments models have been fitted and cross validated using different schemes and used to select lines for temperate and semi-arid environments. Fitted prediction models show high accuracy for field trials carried out in the same environments and different years. Moreover, prediction models for STs were created and for grain width and TKW, model accuracy of 0.41 and 0.26, were obtained respectively.

[1] Q. Wang et al., “Dissecting the genetic basis of grain size and weight in barley (*Hordeum vulgare* L.) by QTL and comparative genetic analyses”, Front. Plant Sci., vol. 10, p. 469, 2019, doi: 10.3389/fpls.2019.00469.

[2] W. Xie et al., “Decreases in global beer supply due to extreme drought and heat”, Nat. Plants, vol. 4, no. 11, p. 964-973, 2018, doi: 10.1038/s41477-018-0263-1.

[3] M. M. Bayer et al., “Development and evaluation of a barley 50k iSelect SNP array”, Front. Plant Sci., vol. 8, pp. 1–10, 2017, doi: 10.3389/fpls.2017.01792.