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GENOME-ENABLED PREDICTION MODELS FOR GRAIN YIELD, TRANSPIRATION RATE AND BELOW-GROUND TRAITS USING A BARLEY MAGIC POPULATION

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The genome of Multi-parent Advanced Generation Inter-crosses (MAGIC) lines is a mosaic generated shuffling the genetic material of the founderparents. In cereal crops, these experimental populations have beenextensively used to dissect the genetic bases of several traits andepistasis. In plants, genomic prediction (GP) is gaining momentum and isbecoming widely adopted for sustaining crop improvement programs. GP aimsto regress genome-wide molecular markers on phenotypes of individuals tosimultaneously predict their effects.

In the present study, carried out within the framework of the iBarMed project (www.ibarmed.com), we constructed, genotyped and evaluated a barley MAGIC population of 352 individuals developed with a diverse set of eight founder parents. An optimized subset of this MAGIC population was phenotyped for grain yield (GY) in nine field trials organized across an ample range of water regimes and climatic conditions in the Mediterranean and for below-ground traits (seminal roots number or SRN; seminal root angle at juvenile stage or SRA) and transpiration rate (TR) under high evaporative demand in controlled conditions. The adjusted means of GY were combined with genotypic information to develop single-environment and multi-environment GP models including GxE interaction in the set of linear predictors. These GP models were fitted using both genomic best linear unbiased prediction (GBLUP) and reproducing kernel Hilbert space along with a non-linear Gaussian Kernel. Likewise, GP for SRN was carried out using threshold GBLUP and log-normal models as these traits were analyzed as ordinal discrete variable and count data, respectively, while GP models for SRA and TR under high evaporative demand were fitted using standard GBLUP. We included additive and epistatic effects in the set of linear predictors used in GP models for SRA, SRN and TR under high evaporative demand.

Overall, our empirical analyses showed that GP models trained with 90 or more MAGIC lines can be used to predict GY with an accuracy that varies from 0.25 to 0.60 and that beyond QTL mapping and analysis of epistatic effects, MAGIC population might be used to successfully fit GP models. Leave-one out cross-validation of GP models for SRN, SRA and TR under high evaporative demand was used to estimate model accuracy. The accuracy of GP for SRN was computed for threshold GBLUP using Brier Score and was equals to 0.36. Likewise, log-normal GP models for SRN pointed out a Pearson's correlation of coefficient of observed and predicted values equals to 0.58. Using the same cross-validation design, the Pearson's correlation between observed and predicted values of GP models fitted for SRA and TR under high evaporative demand was 0.94 and 0.46, respectively. Our analyses showed that including the epistatic effects in the set of linear predictors

improve both predictive ability and the total variance explained in the models.