Genomic-enabled prediction model with genotype × environment interaction in elite chickpea lines

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Genomic selection (GS) allows safe phenotyping and reduces cost and shortening selection cycles. Incorporating of genotype × environment (G×E) interactions in genomic prediction models improves the predictive ability of lines performance across environments and in target environments. Phenotyping data on a set of 320 elite chickpea breeding lines on different traits (e.g., plant height, days to maturity, and seed yield), from three consecutive years for two different treatments at two locations were recorded. These lines were genotyped on DArTseq(1.6K) and Genotyping-by-Sequencing (GBS; 89K SNPs) platforms. Five different models were fitted, four of which included genomic information as main effects (baseline model) and/or G×E interactions. Three different cross-validation schemes that mimic real scenarios that breeders might face on fields were considered to assess the predictive ability of the models (CV2: incomplete field trials; CV1: newly developed lines; and CV0: new previously untested environments). Different prediction models gave different results for the different traits; however, some interesting patterns were observed. For CV1, analyzing yield seed interaction models improved baseline counterparts on an average between 55 and 92% using DArT and DArT combined with GBS data, respectively [between 9 and 112% for all traits]. While for CV2 these improvements varied b tween 65 and 102% [between 8 and 130% remaining traits]. In CV0, no clear advantage was observed considering the interaction term. These results suggest that GS models hold potential for breeder's applications on chickpea cultivar improvements.