Genomic Selection in pulses

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Genomic selection (GS), which incorporates genome wide marker information to predict the breeding values of individuals in a breeding population, is rapidly becoming an important selection tool in plant breeding. One of the major advantages of using GS in plant breeding is its ability to predict the phenotypic performance of individuals early in the breeding cycle, hence, reducing the generation interval and thus increasing genetic gain. We evaluated its efficacy using c. 2,000 advanced breeding lines from the Australian lentil breeding program. These lines were evaluated annually in a range of environments from 2010-2018 for economically important traits including grain yield, grain weight, disease resistances and abiotic stress tolerances. A genotyping-by-sequencing approach was used to genotype the breeding material and over 200,000 SNPs were identified. The ability to genomically predict the observed phenotypic performance was explored by forward prediction and applying a range of genomic selection models such as GBLUP, BayesA and BayesB as well as incorporating GxE components. Genomic selection has now been fully implemented into the lentil breeding program and prediction equations for yield, grain weight, boron and salt tolerance as well as ascochtya blight and botrytis grey mould resistance have been derived with moderate to high prediction accuracies (0.35-0.70). Optimal crossing schemes have also been designed and applied to increase genetic complementarity, as well as to select elite breeding lines for rapid advancement, reducing the overall generation interval, and increasing genetic gain. Simulation modelling of the lentil breeding program is currently in progress to design a full GS assisted breeding pipeline.