Genomic Prediction for Rust Resistance in Pea

Genomic selection (GS) has grown rapidly in recent years as a marker-assisted tool for plant breeding, especially for disease-related traits that are difficult to measure. One such trait is rust (*Uromices pisi*) resistance in pea (*Pisum sativum* L.), which is difficult to assay because it is strongly influenced by the environment. We report a study of the efficacy of GS for predicting rust resistance in pea, as represented by data collected from field and controlled conditions in a 320 accessions panel. Genotyping was carried out using 24,279 DArT-Seq markers developed through genotyping-by-sequencing. The effects on prediction accuracy of different GS models including the genomic relationships approach were compared using cross-validation. Additionally, the marker × environment (MxE) interactions were included in a genomic best linear unbiased prediction (GBLUP) model as covariate to evaluate the prediction efficiency. Finally, different ways of combining trait data from environments using single traits or multi-trait index (MTI) combining traits from controlled conditions were compared. The best predictive ability achieved in rust disease was 0.633 through MTI, obtained using GBLUP analysis. GBLUP and Bayesian LASSO performed slightly better than the other model tested. The predictive abilities of testing/training Cross-Validation strategies were highly variable, highlighting the effect of the GxE interaction. The inclusion of marker × environment interactions did not increase the prediction accuracy for lines that had not been phenotyped but did improve the results significatively of prediction across environments. This study report that predictive abilities increased thanks to combining several traits into one using an MTI, both to predict breeding values for lines that have not been evaluated, and to provide better estimated breeding values for lines phenotyped. Thus, GS is potentially useful for pea breeding programs searching rust resistance, providing a good approach when Genotypic x Environment interactions are challenging.