**Genomic** **prediction for Grain yield and other key traits in field pea**

Riaz A1, Pandey B2, Sudheesh S1, Gebremedhin A1, Lin Z1, Fanning J2, Hayden MJ1,3, Rosewarne G2, Kaur S1,3

*E-mail of the corresponding author:* [*adnan.riaz@agriculture.vic.gov.au*](mailto:adnan.riaz@agriculture.vic.gov.au)

1. *Agriculture Victoria, AgriBio, Centre for AgriBioscience, Department of Energy, Environment and Climate Action, 5 Ring Road, Bundoora, VIC 3803, Australia*

*2 Agriculture Victoria, Grains Innovation Park, Department of Environment, Energy &*

*Climate Action, Horsham, VIC 3400, Australia*

*3 School of Applied Systems Biology, La Trobe University, Bundoora VIC 3086, Australia*

Field pea (*Pisum sativum* L.) is an important pulse crop grown worldwide for its protein-rich seeds and economic value. Pea breeding programs have used traditional methods to improve yield and yield stability. However, the rate of genetic gain is not enough to meet the increasing demand for protein, especially with the changing climate and increasing population, necessitating the deployment of modern tools and technologies in breeding programs. Genomic selection (GS) is an innovative approach that uses whole genome markers to predict the breeding values of individuals early in the breeding cycle to reduce the generation interval and increase the genetic gain per unit of time. In this study, we developed and implemented GS for the Australian National Field Pea breeding program. The training population comprised 2,889 advanced breeding lines and was evaluated in multi-environment trials over 2013-2023 for 15 traits, including grain yield, phenological traits, biotic resistance, abiotic stress tolerance, and seed quality. The narrow sense heritabilities ranged from 0.26 - 0.67, confirming the polygenic inheritance. We used 39,659 high-quality SNPs and phenotypic data to train GBLUP model for genomic prediction. Three prediction accuracy validation scenarios, leave-one-out, forward, and five-fold cross-validations, were used: leave-one-out, forward, and five-fold cross-validations. The prediction accuracies for all traits ranged from 0.12 to 0.78. The GS was utilized in two phases within the field pea breeding program, namely, F1 and F4:5. These stages aimed to enhance the selection process for parental lines in the subsequent breeding cycle and selecting lines for field trials. Our results showed that GS could improve prediction accuracy and intensity and help in early parental selection. Implementing GS would enable an increased rate of genetic gain and the development of better-adapted pea varieties.