Genomic Selection: a new frontier in Mungbean Breeding

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Genomic selection (GS) is a breeding strategy based on a statistical model that uses molecular markers across the genome to predict the performance of individuals for a trait of interest. The introduction of GS promised to accelerate animal and plant breeding processes while improving their individuals’ performance. However, utilising genomic data to predict the yield potential in plant breeding has some additional challenges that need to be addressed in a GS model. Plant genotypes are tested in replicated trials with spatial variation and genotypes are tested in multi-environment trials (MET) generally, in an unbalanced way, to assess genotype by environment interaction (GxE).

The Australian Mungbean Improvement Program has been testing genotypes for a range of agronomically important traits with primary focus on yield across multiple environments throughout Queensland and New South Wales for many years. Selections for grain yield have relied on factor analytic linear mixed models that use pedigree information and explain GxE [1], helping deliver superior grain yield, reliability, and adaptation to growers. To build on this success, genomic data was collected and implemented in an extension of the previous model which incorporates genomic data in a MET scenario [2]. In this study, we share the details of the GS model as well as the outputs driving selections such as GxE insights, genomic predictions for tested genotypes at all the environments and the potential to predict new genotypes that have not been tested for yield yet only using their genomic marker data profile.

***References:***

[1] Oakey, H., et al (2007) Joint modeling of additive and non-additive (genetic line) effects in multi-environment trials. Theoretical and Applied Genetics, 114, 1319-1332.

[2] Tolhurst, D. J., et al (2019) Genomic selection in multi-environment plant breeding trials using a factor analytic linear mixed model. Journal of Animal Breeding and Genetics, 136(4), 279-300.