**Multi-Trait, Multi-Environment GBLUP Improves Genomic Prediction in Mungbean**

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Mungbean is a culturally and economically important grain legume crop, and accelerating its genetic improvement is crucial. While genomic prediction has been shown to accelerate genetic gain in many other crops, there has been limited application in mungbean. This study reports the application of genomic unbiased best linear prediction (GBLUP) to enable genomic selection in mungbean. With the aim of maximising the accuracy of genomic predictions, we have investigated the use of a multi-trait, multi-environment GBLUP (MT-ME-GBLUP) approach, which exploits genetic correlations between traits within and across environments[1]. Here, yield, plant height and days-to-50%-flowering data from the Mini-Core, a set of diverse mungbean germplasm[2], collected from four trials in different environments in Australia, was used. MT-ME-GBLUP was compared with single-trait, single-environment GBLUP (ST-SE-GBLUP) under four cross-validation schemes which varied based on how the validation population was masked for traits (complete or yield only), and environments (balanced or sparse). Masking yield only represents a strategy wherein yield is predicted by a correlated trait which can be measured early or cheaply, while sparse testing across environment allows testing of more genotypes at lower cost. Models were validated on yield only. ST-SE-GBLUP had an average prediction accuracy of 49.2%. MT-ME-GBLUP didn’t perform better under complete-balanced scheme. The genomic prediction accuracies from MT-ME-GBLUP did increase by 6.3%, 7%, and 8.1% under complete-sparse, yield-balanced, yield-sparse schemes, repectively. Overall, these results suggest the benefits of adopting genomic selection in mungbean breeding. Moreover, MT-ME-GBLUP, with an appropriate breeding strategy, could further increase efficiency of mungbean breeding programs.

***References:***

[1] Calus M et al, Accuracy of multi-trait genomic selection using different methods, Genetics Selection Evolution, 2011, 43, p.26.

[2] Schafleitner R. et al, The AVRDC – The World Vegetable Center mungbean (Vigna radiata) core and mini core collections, 2015, BMC Genomics, 16, 1, p.344.