**Advancing predictive breeding methods and capacity building to develop future pulse crops**

Plant breeders are under increasing pressure to improve crop productivity and sustainability to meet future demand. This calls for more efficient breeding approaches to accelerate the introgression and stacking of genetic variation for target traits into elite breeding germplasm. A great source of genetic variation is the genebank, but trait introgression is a time-consuming process and is particularly challenging for multiple traits controlled by multiple genes. To help meet this challenge, we have developed ‘FastStack’, an AI-guided breeding toolkit. Here, we demonstrate the potential of the approach in a pulse crop for the first time. In a mungbean case study, we draw on a global dataset for the minicore collection evaluated in field experiments by collaborators throughout Asia and Africa through the International Mungbean Improvement Network (IMIN) project. Using the FastStack approach we applied a genetic algorithm to identify parental lines for crossing that maximise desirable haplotypes. Then, using genetic simulation we identified the optimal crossing path to rapidly stack haplotypes to improve yield potential by increasing pods per plant and seed weight in mungbean. The FastStack mungbean populations are being created under speed breeding conditions and seed of the lines with stacked haplotypes will be distributed to researchers and breeders to support global yield improvement of mungbean. The toolkit is now being applied and extended in several new investments by the Grains Research and Development Corporation in Australia to accelerate genetic gain for a range of traits in key pulse crops, including chickpea, lentil and faba bean. Finally, we highlight the importance of training and building human capacity in predictive breeding technologies to develop our future pulse crops.

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