**AI- Augmented Rapid Allele Stacking to Breed for Durable Ascochyta Blight Resistance in Chickpea**

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Ascochyta Blight (AB) is one of the most devastating fungal diseases of chickpea. The genetic architecture of AB resistance is moderately complex, involving a combination of a few major genes (qualitative) and numerous minor (quantitative) genes. Breeding for AB resistance has traditionally involved pyramiding major genes, however it is prone to failure due to the rapid evolution of the pathogen, which results in pathogen shifts every 5-7 years. Chickpea varieties experience a decline in AB resistance over time. A different approach is therefore needed to breed for durable AB resistance in chickpea. One potential solution is the use of genomic selection (GS), which considers both major and minor genes to predict breeding values. In this study, we implemented an AI-augmented and genomic-assisted speed breeding approach to develop germplasm with enhanced qualitative and quantitative AB resistance. Phenotypes were collected from 2,962 chickpea lines using terrace screens (outdoor pot-based, screen from 2016 to 2023, using different single *Ascochyta rabiei* isolates) and field nurseries (2020-2023, using a mixture of isolates). All material was genotyped using a multi-species pulse 30k SNP chip. A strong genetic correlation (0.91) was observed between the terrace and field data, indicating a close relationship. High genetic correlations (c. 0.8) were also observed between different isolates. The results demonstrate the potential of developing durable AB-resistant chickpea lines that can withstand multiple isolates. Using our fast-track breeding approach, we generated improved germplasm in < 3 years with c. 30% less disease severity than the diverse germplasm as predicted from genetic values. Our study offers a fast approach to breed for durable AB resistance in chickpea that can be applied to any breeding program to breed for durable disease resistance.