Use of single step factor analytic linear mixed model to develop a pipeline for genomic selection of resistance to new aggressive *Ascochyta rabiei* isolates in chickpea breeding lines

Asif A1\*, McGarty A2, Cullis B.R2 and Hobson K1

*\*E-mail: ahsan.asif@dpi.nsw.gov.au*

*1 Chickpea Breeding Australia, New South Wales Department of Primary Industries, Tamworth, NSW 2340, Australia*

*2 Mixed Models and Experimental Design Lab, National Institute for Applied Statistics and Research Australia, School of Mathematics and Applied Statistics, University of Wollongong,Wollongong, NSW 2522, Australia*

Ascochyta blight (AB), caused by the fungal pathogen *Ascochyta rabiei*, is a major chickpea disease in Australia and worldwide. Identification of new aggressive isolates and the breakdown in resistance of most Australian cultivars have put an enonrmous pressure on breeders to deliver new AB resistant varieties to growers. The latest techniques, such as genomic selection (GS) can be an ideal solution to develop new varieties with improved resistance in a shorter time frame. In this study, we phenotyped a diverse set of 14,836 Australian chickpea breeding lines in 11 environments, including controlled, semi controlled and field conditions, across three Australian states. Of the 14,836 phenotyped lines, 14,629 were genotyped using a Multispecies Pulse 30K SNP Array. This panel was then used to fit a factor analytic linear mixed model (FALMM), using a single step approach. The model incorporated all sources of variation relating to genetic and non-genetic effects, and the additive and non-additive genotype by environment interactions were modelled using factor models of order 2 and 1 respectively. The interaction classes (iClass) approach identified measurable, though small differences in resistance betweeen field and controlled/semi controlled environments. These results provide the basis for genomic selection of unphenotyped lines.