**Enhancing chickpea tolerance to soil acidity through genomics**

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Australia is the second largest producer of chickpeas, with >95% of production exported. Acid soils with aluminium toxicity is the single largest production constraint for chickpea in Australia after Ascochyta blight. Among the pulse crops, chickpea is the most sensitive to acid soil conditions. Current Australian chickpea varieties do not possess sufficient genetic variation for acid soils tolerance, which has hampered breeding for improved yield and local adaptation beyond the traditional areas of cultivation in southern and northern Australia.

We evaluated 1,100 chickpea accessions including wild cicer introgressions, cultivars and bi-parental crosses using hydroponic assays at 15-20 µM Al3+ concentration, where comparison of root length under normal and stress conditions was used as a measure of acid tolerance. Plant materials were genotyped using the multispecies pulse 30K SNP array. Genomic breeding values for root length and root length index (rootlength\_stress / rootlength\_normal) were estimated using the GBLUP method. Prediction accuracies for root length under stress condition and root length index were 0.42 and 0.32, respectively. Genome-Wide Association Studies (GWAS) and BayesR analysis identified major genes associated with Al3+ toxicity tolerance. Significant trait-marker associations were observed on chromosomes 1, 4, 7 and 8 using GWAS and were consistent with strong marker effects on the same chromosomes in BayesR analysis.

Overall, we observed remarkable genetic variation across accessions for Al3+ toxicity tolerance and achieved a level of genomic prediction accuracy to facilitate early trait selection in breeding. Data obtained from the hydroponic assays will be validated through soil assay and field trials. The novel sources of acid tolerance identified hold promise for providing valuable germplasm to breeding programs aiming to expand chickpea adaptation to acid soils.