**Accurate Detection of Heterogeneity in Chickpeas Using a SNP Array**

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Genomic characterisation of germplasm is critical for making informed decisions in research and breeding. This can range from helping breeders to accelerate the selection of plants with desirable traits, through to asessing genetic diversity and trait dissection. Factors to consider when selecting a genotyping assay include required marker density, turn-around time and budget. For example, while whole genome sequencing provides the most comprehensive information, it is usually only applied for specific research purposes due to the increased complexity of data analysis and higher cost. On the other hand, SNP arrays are robust and cost effective for obtaining a snapshot of the genome.

At Agriculture Victoria, a genotyping tool regularly used by GrainDataGen™ is the Illumina Multispecies Pulse 30K SNP array. To investigate its accuracy for detecting heterogeneity within samples, we genotyped DNA from independent seeds and the same seeds bulked together. High genotype calling accuracy demonstrated its utility for applications such as detecting heterogeneity in genebank accessions, seed purity testing and bulked segregant analysis for QTL detection. Interestingly when utilising the array to genotype hybrid populations derived from crosses between cultivated and wild chickpea species, we observed in some instances higher heterozygosity than expected levels for the familial generation. We hypothesise structural variations between pan-genomes might cause these anomalies.

Our work highlights the high genotype calling accuracy achieved with the Multispecies Pulse 30K SNP array and its suitability for a wide range of applications in research and breeding including the detection of heterogeneity and admixture in plant genetic resources.