**Characterisation of the Chickpea Germplasm for Vigour-related traits**

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Chickpea (*Cicer arietinum* L.) is a valuable protein source and is currently ranked as the second-largest produced pulse worldwide. Often, chickpea cultivation experiences a range of biotic and abiotic stresses and thus increasing pressure has been put on breeders to develop high-yielding varieties that are resistant/tolerant to stress and resilient to climate change. The development of crop varieties with improved vigour is a strategy that promotes strong early establishment to overcome weed competition and also improves plant growth and performance under unfavourable conditions. But plant vigour is a genetically complex trait.

This research aimed to perform a SNP-Chip-based genomic characterization of advanced chickpea breeding lines for the presence of early vigour alleles using the genotypic data (from pulse multispecies 30K SNP-Chip) and published literature [1,2]. Based on the known early vigour QTL (Quantitative trait loci) regions, positions of the QTL-linked markers on chromosomes Ca1, 3 and 4 associated with vigour-related traits were used.

Results showed that of the 16,931 advanced chickpea breeding lines genotyped through 30K SNP-Chip, 113 have early vigour alleles present for all three QTL regions. Also, unique SNPs to accessions were identified from these locations. In the close vicinity of SNPs on chromosomes Ca3 and 4, 140 and 39 genes respectively, are found that may be associated with plant vigour. The results obtained may provide a roadmap for further research to support chickpea breeding for increased vigour.

***References:***

[1] Nguyen DT. et al, The genetics of vigour‑related traits in chickpea (Cicer arietinum L.): insights from genomic data. Theor Appl Genet. 2022;135(1):107-124.

[3] Nguyen DT. et al, Fine mapping of a vigor QTL in chickpea (Cicer arietinum L.) reveals a potential role for Ca4\_TIFY4B in regulating leaf and seed size. Front. Plant Sci. 2022;13:829566.