**Identification of quantitative trait loci for flowering time in chickpea**

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Chickpea (*Cicer arietinum*) is the second most important grain legume, produced in more than 50 countries globally, in diverse environments and production systems. As in most crops, matching the growth cycle to location-specific climatic conditions helps minimise exposure to environmental stresses and maximise yield. Phenology is therefore a key target for adaptation when considering expansion to new production areas or resilience to climate change. Previous studies have reported major loci controlling flowering time but their relationships and functions are not well understood, and only one gene has so far been identified [1,2].

This study aimed to clarify the genetic control of flowering in chickpea and its interaction with growth habit, through QTL analysis. Three F2 populations derived from crosses between a common late flowering line and three distinct early flowering lines were grown under controlled short-day (8-h) conditions and phenotyped for a range of phenology- and architecture-related traits including time and node of flowering, podding and termination of main shoot growth. Most traits varied extensively in the F2 and were found to be controlled by 3-4 QTLs in each cross, explaining up to 60% of the trait variation. Our results confirmed previously reported loci on chromosomes 1, 5, 6 and 8, and identified several novel loci with large effects. Better understanding of the genetic and environmental control of flowering time will be important for future chickpea improvement.

***References:***

*[1] Weller JL, Ortega R (2015) Genetic control of flowering in legumes. Front. Plant Sci. 6, 207*

*[2] Ridge S. et al. (2017) The chickpea early flowering 1 (Efl1) locus is an ortholog of Arabidopsis ELF3, Plant Physiol., 175, 802-815.*