**Quantitative trait locus (QTL) mapping of phenology in lentil**

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Lentil (*Lens culinaris*) is an important pulse crop grown in more than 40 countries worldwide. Current domesticated lentil germplasm is generally considered to form three broad adaptation groups: Mediterranean, South Asian, and northern temperate, corresponding to the main global production regions. Adaptation of lentil from its Mediterranean origins to these other diverse environments involved changes in phenology, reflecting selective pressures that resulted in differential sensitivity to photoperiod and temperature [1,2].

In this study we used a biparental approach to characterize the genetic basis for major differences in phenology across the global lentil germplasm. A total of 940 F2 individuals derived from the cross between the extremely early accession ILL5888 and the photoperiod-sensitive northern temperate accession Indianhead were evaluated for a range of reproductive development and plant architecture traits across two different photoperiods (16h long day and 8h short day). QTL analysis identified three prominent loci: *DFD6a*, *DFD1a* and *NFD5b*. ILL5888 alleles conferred dominant (*DFD6a*) and recessive (*DFD1a*) early flowering under LD and a small but consistent early effect on flowering node in short days (*NFD5b*). Investigation of candidate genes using cross-species synteny analysis indicated the presence of a cluster of florigen (*FTb*) gene orthologs among candidates for *DFD6a.* Relevant candidates for all loci are being further evaluated in F3 and F4 progenies. Ongoing mapping analysis and marker-assisted selection utilizing these resources will expand our understanding of the underlying genetic control of flowering time adaptation in cultivated lentil and inform breeding for diverse environments.

***References:***

*[1] Erskine W et al. (1990) Characterization of responses to temperature and photoperiod for time to flowering in a world lentil collection. Theor Appl Genet. 80, 193-9.*

*[2] Neupane S. et al. (2022) Focusing the GWAS Lens on days to flower using latent variable phenotypes derived from global multi-environment trials. Plant Genome**16:e20269*