The Genome-Wide Association Mapping reveals new insights into genome diversity of wild Old World Lupins

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Grain legumes are an important source of nutrients for both animal feed and human food production. Among these legumes are native to the Mediterranean Old World Lupins (OWLs), which are of particular interest to researchers due to their complex flowering regulation, including the requirement for vernalization to promote flowering.

Only three out of 12 OWL species have undergone the domestication process, which required the identification of early-flowering, thermoneutral lines that can be sown independently of temperature and photoperiod. However, this process has reduced their genetic variability, limiting their ability to adapt to climate changes. **Therefore, a major goal of modern lupin genetics is to find new sources of genetic variability that can help improve current varieties and create new ones better suited for the climate of the future1.**

Our research focuses on understanding the mechanisms of flowering induction and regulation in wild OWLs by analyzing homologs of the *FT* gene and potential indels in their promoter region. To achieve this, we conducted a series of glasshouse experiments for 10 species over two years, during which we recorded the dates of the first bud, flower, and pod emergence for approximately 700 accessions. This was supplemented by Genome-Wide Association Mapping using DArT-seq markers generated for three species with at least 100 accessions/genotypes. The next step will involve sequencing both mRNA and whole-genome DNA, as well as conducting Differental Gene Expression analysis to identify the key regulators in the flowering induction pathways of this species.

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***References:***

[1] Bohra, er al., 2022, Trends Biotechnol. 40, 412-431.