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

Bielski W1, Rychel-Bielska S2, Surma A3, Belter J3, Nowak S3, Taylor CM4, Kozak B2 and Ksiazkiewicz M3

*wojciech.bielski@up.poznan.pl*

1 Department of Genetics and Plant Breeding, Poznan University of Life Sciences, Dojazd 11, 60-632 Poznan, Poland

2 Department of Genetics, Plant Breeding and Seed Production, Wroclaw University of Environmental and Life Sciences, 50-363 Wroclaw, Poland

3 Department of Gene Structure and Function, Institute of Plant Genetics, Polish Academy of Sciences, 60-479 Poznan, Poland

 4 Agriculture and Food, Commonwealth Scientific and Industrial Research Organisation (CSIRO), 6014 Floreat, Australia

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.

***Funding source:***

This research was funded by the National Science Centre, Poland (SONATINA5, 2021/40/C/NZ9/00075).

***References:***

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