

## I. Research project objectives

White lupin is a grain annual legume plant, widespread in the Mediterranean region. It's a valuable crop due to its high protein and oil content in seeds. Mostly it's used as animal feeds component, but can also be **a potential healthy human food and alternative source of proteins instead of soybean**. *L. albus* is a long day plant and in comparison to soybean (short day) it is better adapted to Polish climate, and as a result is an excellent perspective for a new source of protein. However it still needs genetic improvement to maximise its agronomic potential, due to the short growing season and frequent occurrence of terminal drought.

**One of the major breeding limitation of *L. albus* is the time of flowering and maturing.** Analysis of mapping population derived from the cross between Kiev Mutant (early) and Ethiopian landrace P27174 (late) revealed the presence of two Quantitative Trait Loci - QTLs (localised in LG01 and LG03), explaining 52% of total flowering time variation. Additional genes (*Ef1*, *Ef2*) as well as three other recessive alleles (*floridus*, *festinus* and *contractus*) conferring early flowering phenotype were identified in *L. albus* collection i.a. in early lines P28283 and Start. So far attempts to introduce the early flowering qualities to the new variety failed, due to low percentage of flowering plants in the progenies. These obstacles may be avoided by using different donor of the early flowering trait. **Further studies proved that early flowering in *L. albus* is controlled by several QTLs, however candidate genes responsible for early flowering phenotype have not yet been found.**

The general objective of this proposal is **to decipher molecular mechanism of flowering induction in white lupin (*Lupinus albus* L.) and to determine the main genes involved in this process.** It will be followed by the development of methodology for molecular markers-assisted selection of collection lines.

## II. Describe the research to be carried out

Set of molecular markers anchored in identified QTLs will be designed and used for genotyping of *L. albus* core germplasm collection to identify different, new alleles. To estimate flowering time and the impact of the vernalization process, greenhouse experiments will be carried out. Lineage Disequilibrium within all identified flowering QTLs will be estimated. RNA sequencing of selected lines and analysis of gene expression patterns will be performed to confirm the participation of candidate genes in flowering induction of white lupin. Expression patterns of all genes in plant samples collected in different time points and vernalization treatment will be compared.

## III. Reasons for choosing the research topic

Nowadays **Europe has become heavily dependent on soybean imports** (even for 70% of its plant protein requirements), which has become the prevalent source of plant proteins for food and feed. **White lupin is native European legume that can become major alternatives to soybean due to its high-quality protein content** – about 34–45% of dry matter, as well as 10–13% content of oil with excellent nutritional characteristics. **Lupins are relatively more tolerant to several abiotic stresses than other legume species, and have a proven potential for the recovery of poor and contaminated soils.** Resistance to diseases such as anthracnose and phomopsis stem blight as well as late flowering and maturing are probably the main limiting factor in the crop expansion.

**The recognition of expression profiles of main floral pathway integrators in response to low temperature and day length in *L. albus* lines will be the first major step for deciphering the complex pattern of flowering regulation pathway crosstalks in plants.** The drawn conclusions will constitute a cornerstone not only for further flowering studies on different *Lupinus* species but most importantly will facilitate the development of new markers, suitable for selection genotypes for genetic cross to develop a new *L. albus* variety, with all agronomically important traits.