The main goal of this project is to identify and characterize vernalization pathways of New World Lupins (NWLs) and compare them with the mechanisms described for the Old World Lupins (OWLs). This research aims to understand flowering induction, vernalization response, and adaptation to changing environments in NWLs. It could significantly improve future wild lupin breeding programs and allow for diversifying plant protein sources for food and feed production.

The scientific community is actively seeking alternative protein sources to address the challenges of global climate change and population growth. These changes are expected to lead to crop losses and may necessitate finding new crops in the near future. **As a result, it has become crucial to identify new, sustainable plant protein sources for human consumption and animal feed.** Various protein-rich plants have emerged as promising alternatives, including soybeans, peanuts, common beans, peas, lupins, and other legumes. **These sources have the potential to meet the protein requirements of the growing population while helping to mitigate the impact of climate change on food production. Among these, lupins stand out as one of the most promising alternatives due to their high concentrations of essential amino acids and proteins in dry matter, along with relatively low but rich amounts of monounsaturated (54.2%) and polyunsaturated (28.5%) fatty acids.** Other distinctive features of lupins include the ability to fix atmospheric nitrogen due to the symbiotic relationship with Bradyrhizobium or the taproot system, making them vital in agriculture.

The Lupinus genus has a complex evolutionary history, with various theories about its origins. Most species are found in North and Central America (New World Lupins), with about ten species originating in the Mediterranean region (Old World Lupins). This region is suggested as the ancestral area of the whole genus. It is widely accepted that lupins spread to North and South America around 10-13 million years ago. **Due to geographical barriers, this led to a "super-radiation" event, a rapid increase in new species, particularly in the Andes, resulting in almost 200 new species.** It has been suggested that vernalization pathways evolved during the temperate Cenozoic era (66 million years ago) when global cooling occurred, **leading to substantial genetic differences even among closely related species. Thus, investigating New World Lupins may unveil new, previously unknown regulatory mechanisms of flowering induction or vernalization responsiveness and provide insight into their evolution.**

Our project aims to phenotype all annual and small perennial NWLs found in global germplasm collections. **We are particularly interested in how these species react to vernalization. Additionally, we will study the flowering induction pathways in species with different genotypes in time to flowering (early vs. late).** This research will be the first comprehensive cross-sectional study on NWLs flowering regulation. **Alongside phenotyping, we will analyze differential gene expression to identify candidate genes that regulate flowering and vernalization. Moreover, we will sequence the DNA of representative accessions to construct whole-genome assemblies, crucial for further research and cross-species comparative analyses.** We intend to identify conserved regions of high similarity and regions that differ among all species. We will also perform genome synteny and rearrangement analysis to compare gene order in different genomes and identify colinear blocks, as well as large structural changes in genomes, such as inversions, translocations, duplications, and deletions. **Furthermore, the results will enable the development of a phylogenetic tree representing the evolutionary relationships between species, shedding light on genetic and evolutionary relationships, functional genome elements, and mechanisms driving genomic diversity and adaptation.** These findings may significantly advance the study of this fascinating plant group, helping unveil their evolution comprehensively. **The results could also lay the groundwork for creating new models of flowering and vernalization, potentially leading to the establishment of novel plant protein sources for future feed and food production.**