One of the key questions in population genetics is how organisms adapt to new environmental conditions, and artificial selection is a powerfull tool for studying this phenomenon. Comparing varieties from different breeding eras provides insight into how species have gradually adapted to contemporary cultivation conditions. Numerous species in modern agriculture are grown under similar conditions characterized by dense planting and high nitrogen availability.

Maize and wheat are among the most important agronomic species. Despite their biological differences, there are significant similarities in the evolutionary histories of these two species. Both were domesticated about 10,000 years ago in tropical climates: maize in Mexico and wheat in the Middle East. Subsequently, both species spread and are now cultivated almost worldwide. Despite differences in breeding strategies, both species have undergone transformations since the Green Revolution. They currently occupy a similar ecological niche: the modern agricultural field. Although modern agriculture has effectively adapted plants to current cultivation conditions, this progress has come with a loss of genetic diversity in modern varieties. This loss may limit the ability to develop new varieties capable of adapting to changing environmental conditions.

Conventional genetic methods for analyzing agronomic traits, such as genome-wide association studies, are likely insufficient in terms of speed to meet the potentially impending food deficit predicted for 2050. Evolution, on the other hand, represents the ultimate field study. In particular, the occurrence of convergent evolution among populations inhabiting similar environments provides strong evidence that selection, rather than neutral processes, shapes trait variability. Given the similarities in the adaptation of maize and wheat to modern field conditions, they constitute an attractive system for studying convergent evolution. Examining the molecular processes that have undergone parallel selection in both species during their adaptation to these conditions can provide valuable insights into the mechanisms of adaptation to new environments.

Metabolites, the intermediate and end products of biological processes, play a key role in plant adaptation to new environments and offer an alternative approach to studying plant evolution compared to genomes and transcriptomes. Additionally, compared to morpho-developmental traits such as yield, metabolites often have simpler genetic architectures, allowing the study of genetic factors controlling them in relatively small populations. This makes them a promising avenue for understanding the genetic factors underlying the adaptation of maize and wheat to modern cultivation conditions. In the proposed project, the research hypothesis that m**aize and wheat undergo convergent evolution at the metabolic level during modern breeding** will be tested. To do this, we will analyze varieties from different breeding periods using association, transcriptomic, metabolomic, and population genetics methods. Identifying alleles, including those potentially lost in modern varieties of quantitative trait loci (QTL) for metabolites, has dual purpose. Firstly, it may broaden our understanding of the mechanisms of adaptation to new environments. Secondly, it can provide valuable information to facilitate the development of plant varieties better suited to survive in today's and future changing climatic conditions.