Modern populations of organisms face increasingly rapid environmental changes, including climate shifts, habitat loss, and the spread of invasive pathogens. These forces impose strong selective pressures, requiring swift adaptive responses. One key mechanism facilitating such adaptation is polygenic adaptation, characterized by subtle, coordinated shifts in allele frequencies across multiple genes. Detecting this process in natural populations poses a challenge for traditional quantitative genetic methods. Consequently, advanced genomic approaches—such as whole-genome population resequencing and genome-wide association studies (GWAS)—combined with genomic prediction tools have become essential for accurately forecasting adaptive potential and responses to selection. Examining allele frequency changes before and after new selective pressures, as well as across different age classes within populations, offers valuable insights into the dynamics of polygenic adaptation. This perspective is particularly relevant for long-lived forest trees, which allow the observation of multiple generations coexisting in their natural environment.

European ash (*Fraxinus excelsior* L.) provides an ideal model for applying these advanced genomic approaches. It currently faces two severe threats: ash dieback (ADB), caused by the invasive fungus *Hymenoscyphus fraxineus*, and the impending invasion of the emerald ash borer (*Agrilus planipennis*). First detected in Poland in 1990, *H. fraxineus* has since devastated ash populations across Europe, with mortality rates approaching 100% in some natural stands. Because resistance to ADB is heritable and varies among age classes, European ash populations offer a rare opportunity to investigate evolutionary processes driven by intense selective pressure and the resulting shifts in resistance-related allele frequencies.

This study aims to uncover and characterize the evolutionary mechanisms underlying the adaptive responses of European ash populations to the intense selective pressure exerted by *H. fraxineus*. We will integrate genomic and environmental data to achieve a comprehensive understanding of these dynamics. Our work will focus on three natural Polish populations (Czerwony Dwór, Jawor, and Kwidzyn), examining seedlings, juveniles, and mature trees. By analyzing a broad spectrum of genomic polymorphisms—SNPs, InDels, and structural variants (CNVs, PAVs, inversions, translocations, and segmental duplications)—we will assess age-related adaptive responses both within and among populations. To achieve our goals, we propose two key innovations.

The first innovation is the use of Genomic Estimated Breeding Values (GEBVs) to detect polygenic adaptation. We will compare predicted GEBVs (based on genetic relatedness) with observed GEBVs (derived from resistance-associated markers) within and across populations. This comparison will reveal whether allele frequency changes are driven by selective pressures acting consistently across populations or reflect population-specific genetic structure. In addition, we will estimate the heritability of resistance to *H. fraxineus* using genomic relatedness matrices, providing a deeper understanding of the genetic architecture of resistance.

The second innovation integrates genomic and environmental data to assess how environmental variability influences adaptive responses in European ash. By correlating tree health measures with environmental variables, we will identify how local conditions modulate genetic responses to selective pressures, particularly from *H. fraxineus*. This approach will help uncover genotype-by-environment interactions that either facilitate or limit the adaptive potential of these populations.

Together, these innovations offer a comprehensive view of the adaptive processes shaping European ash populations, encompassing genetic variability, environmental factors, and their interactions. In contrast to previous studies focusing solely on genomic analysis or environmental components, our integrated approach captures the complex interplay of genetics, environment, and adaptation in a long-lived tree species. The insights gained will inform conservation strategies and management practices aimed not only at mitigating the impacts of ash dieback but also at anticipating and preparing for future threats such as the emerald ash borer. Ultimately, the results will support the development of more resilient ash populations through the application of genomic tools in breeding programs and sustainable forest management.