

Evolutionary and functional studies of the variability of reproductive modes in the poplar rust fungus, *Melampsora larici-populina*

Ammar ABDALRAHEM, Pascal FREY, Sébastien DUPLESSIS, Fabien HALKETT

Université de Lorraine, INRAE, IAM, F-54000 Nancy, France

ammar.abdalrahem@inrae.fr

The variability of reproductive modes is a long-standing enigma in evolutionary biology because it drives the evolutionary trajectories of populations and the morphological or physiological characteristics of the individuals that compose them. The phytopathogenic fungus *Melampsora larici-populina*, causing the poplar rust disease, is particularly interesting for the study of the polymorphism of reproduction modes. Indeed, this phytopathogenic fungus exhibits a complex heteroecious life cycle, typical of rust fungi (Pucciniales), alternating between a sexual reproduction phase on larch trees (*Larix* spp., aecial host) and an asexual multiplication phase on poplar trees (*Populus* spp., telial host). This alternation of sexual and asexual reproduction exhibits some similarities with the cyclical parthenogenesis of aphids and daphnia.

In addition to the predominant sexual lineages of *M. larici-populina*, previous population genetics studies have identified several lineages where certain genotypes persist in the population through years via asexual reproduction. Our aim is to investigate the evolutionary implications of asexual reproduction in *M. larici-populina*, with a particular focus on the potential drivers of the distribution and evolution of asexual lineages.

To address this, our study employs an evolutionary ecological approach that utilizes a large dataset of genotypes sampled over many years from different locations across France. Our study reveals a distinct pattern in the distribution of sexual and asexual lineages in France. While sexual lineages are predominant throughout the country, asexual lineages are more frequent in southern France. This pattern suggests that ecological and environmental factors may be shaping the distribution of asexual lineages. We aim to clarify the evolutionary history of these asexual lineages by including assessments of genetic structure and gene flow between sexual and asexual lineages. Our analyses will provide valuable insights into the diversification and timing of the emergence of asexual lineages. We will also investigate the expression patterns of genes associated with sexual and asexual reproduction modes through comparative genomic and transcriptomic analysis to identify if and how the regulation of these genes differs according to reproduction modes in *M. larici-populina*.

To further investigate this complex phenomenon, we will conduct a complementary phenotype field experiment to monitor the developmental stages of sexual reproduction. This will allow us to compare the developmental stages of the sexual and asexual lineages and determine the extent of investment of asexual lineages in sexual reproduction and its implications for the evolutionary trajectories of populations.

Overall, this study aims to contribute to our understanding of the complexity of reproductive mode variability in *M. larici-populina* and how it affects the evolution and adaptation of this important phytopathogenic fungus. Conducting a comprehensive study that investigates various aspects of asexual reproduction in *M. larici-populina*, provides valuable insights into

the mechanisms underlying the persistence of asexual lineages and the factors that drive their distribution and evolution.

Keywords: Asexual reproduction, sex-asex transitions, evolution, genotypes, life cycle.