Advances in understanding genomic diversity and adaptive evolution of the plant pathogenic model system *Colletotrichum*.

Fungi pose a major threat to global crop production. Several factors, including current farming practices, fungicide resistance, increased trade, and climate change, are likely to worsen this problem. As we move towards more sustainable agriculture and phase out fungicides, we urgently need better ways to manage plant diseases. This requires a deeper understanding of how fungal populations evolve and how they interact with plants at the molecular level.

Colletotrichum species are among the top ten most important fungal plant pathogens globally (Dean et al., 2012). This diverse genus includes over 340 currently recognized species grouped into 20 complexes (Talhinhas and Baroncelli, 2021). Within the Acutatum and the Gloeosporioides species complex we find a wide diversity of important traits such as host range and host preference, mode of reproduction and differences in the strategy used to infect their hosts.

One of the main challenges in studying Colletotrichum is the reliability of past taxonomic assignments. The genus has undergone continuous taxonomic rearrangements in recent decades, primarily due to unclear species boundaries and a lack of coordination within the scientific community. Over the past 15 years, several species have been split, while others have been merged, creating considerable confusion and unreliable taxonomic information. An example is provided by Colletotrichum species belonging to the Acutatum and the Gloeosporioides complexes associated with Malus domestica (apple) and responsible for apple bitter rot (ABR) and glomerella leaf spot (GLS) worldwide.

The project aims to improve the knowledge on the European and global distribution of plant pathogenic species of the genus *Colletotrichum*, recently subject to taxonomical changes

To achieve this objective, the following activities are planned:

- to depict the identity, under current terms, of *Colletotrichum* isolates stored in culture collections of different countries. Taking in consideration the host, location and date of isolation, this approach will provide an overview of the geographical and temporal dissemination of *Colletotrichum* in crop and non-crop hosts, providing an historical approach that better enables understanding the present distribution of these fungi depicted in new surveys and to the information generated on the current global distribution of *Colletotrichum*;

- to reallocate taxonomically past records and to investigate host association patterns and the global distribution of *Colletotrichum* spp. and to build a user-friendly tool/protocol for the correct and solid characterization of *Colletotrichum* species;
- to collect and examine samples of anthracnose, bitter decay, or leaf blemishes from selected host plants in the EU, known to be significant hosts of the mentioned fungi. The focus should be on major crops associated with each *Colletotrichum* species, even if still not reported in EU countries, using appropriate identification techniques. The findings will feed the discussions on the occurrence and distribution of various plant-pathogenic *Colletotrichum* species within the EU territory.

Activities plan

Computational

- creation of genetic databases of Colletotrichum spp.
- Primer design
- Phylogenetic analyses
- Genome assembly and annotation
- Identification and characterization of repetitive elements
- Population genomic analyses

Biology and Molecular Biology

- fungal cultivation and conservation
- DNA and RNA extraction
- Amplification by PCR