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**Population structure and host specialization in *Botrytis cinerea***

Alex Mercier<sup>1\*</sup>, Adeline Simon<sup>1</sup>, Clémentine Duplaix<sup>1</sup>, Marguerite Cuel<sup>1</sup>, Jean-Marc Pradier<sup>1</sup>, Muriel Viaud<sup>1\*\*</sup>, Pierre Gladieux<sup>2\*\*</sup> and Anne-Sophie Walker<sup>1\*\*</sup>

1UMR BIOGER, INRA, AgroParisTech, Université Paris-Saclay, Thiverval-Grignon, France

2UMR BGPI, INRA, CIRAD, Montpellier, France

\*alex.mercier@inra.fr

\*\*Thesis co-directors

The *Botrytis* genus encompasses more than 30 species, most of them being able to infect a narrow range of host plants. However, the *B. cinerea* species is considered a generalist pathogen, found to infect more than 1600 plant species. This makes *B. cinerea* an interesting candidate to study ecological specialization. This was first approached while describing population structure in France, from strains collected on greenhouse tomato, grapevine, blackberry, strawberry and hydrangea. Understanding the causes of population subdivision is of fundamental importance, as studying barriers to gene flow between populations may reveal key aspects of the process of adaptive divergence. Population genetics analyses revealed a weak association between population structure and geography, but a clear differentiation according to the host plant of origin, and especially for greenhouse tomato and grapevine. Host specialization was validated by cross-inoculation experiments. Genomes from strains contrasting for their specialization on tomato, grapevine, blackberry and hydrangea were Illumina-sequenced and genomic phylogeny analysis confirmed the similarities between genomes from strains collected on the same host. McDonald-Kreitman's test used to compare variation within lines of strains with variation against a common *B. fabae* outgroup provided promising sets of genes that may play a role in host specialization. In addition to coding sequences, analysis of small RNAs from strains collected either on tomato or grapevine was initiated. Preliminary sequencing data suggest that these two populations have contrasted repertoires of small RNAs. Further analysis and additional PacBio-sequenced genomes and small RNA sequencing are required to definitely identify the determinants of host specialization.

**Keywords:** *Botrytis cinerea*, adaptation, population structure, host specialization, genome sequencing, cross-inoculation test