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► **To cite this version:**

Anne-Sophie Walker, Alex Mercier, Marguerite Cuel, Jean-Marc Pradier, Adeline Simon, et al.. Population structure and host specialization in *Botrytis cinerea*. 10. French Society for Plant Pathology (SFP), May 2017, Dunkerque, Malo-les-Bains, France. , 236 p., 2017, Deepen Knowledge in Plant Pathology for Innovative Agro-Ecology: Book of Abstracts. hal-01603401

HAL Id: hal-01603401

<https://hal.science/hal-01603401>

Submitted on 2 Jun 2020

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Session 2
Poster 51

Population structure and host specialization in *Botrytis cinerea*

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The *Botrytis* genus encompasses more than 30 species, most of them being able to infect a restricted range of host plants. Nevertheless, *B. cinerea* is considered a generalist pathogen, recently found to infect 586 plant genera. 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 and, for pathogens, may help forecasting disease emergence and implementing sound management strategies. 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, carried out *in vitro* on detached leaves. 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. Population genomics analysis used to compare variation between and within lines of strains provided promising sets of genes that may induce 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 genomes and small RNA sequencing are required to definitely identify the determinants of host specialization. Our findings open up new perspectives for disease control by managing *Botrytis* hosts in agricultural landscapes, and reinforcing prophylactic measures.

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