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► To cite this version:

Anne Sophie A. S. Walker, Véronique Decognet, Marc Fermaud, Alexandre Bout, Johann J. Confais, et al.. Genetic diversity and structuring factors for *Botrytis cinerea* french populations. 14. International Botrytis Symposium, Oct 2007, Cape Town, South Africa. hal-02757549

HAL Id: hal-02757549

<https://hal.inrae.fr/hal-02757549>

Submitted on 4 Jun 2020

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Genetic diversity and structuring factors for *Botrytis cinerea* French populations

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Botrytis cinerea has long been considered as a very polymorphic fungus, in terms of morphology, host range, pathogenicity, sensitivity to various xenobiotics, ecology and genetic diversity. This plasticity may explain its large geographic distribution and its ability to colonize various environments and to cause important diseases on a large variety of crops. Despite its agronomic importance, little is known about *Botrytis* population dynamics and genetics and the available studies mainly analyse one component, often adaptation to host, as a structuring factor for the populations.

First results will be presented from a multifactorial study of *Botrytis* populations. Samples were collected in 4 distinct French areas (Champagne, Provence, French Riviera and Bordeaux area), on various host plants or decaying substrate (grapevine, tomato, brambles, litter), treated or not with fungicides, in 2 cropping systems (open fields or glasshouses) and during 2 years, in spring and autumn. This sampling plan led to the set up of at least 32 distinct populations per season of collection, and would help to understand the effect of geography and migration at small to large scale, selection by the host-plant and the fungicide programs, effect of the ecological type and of the cropping system on the diversity and genetic structure of *Botrytis* populations. All the isolates were analysed for their diversity according to 8 neutral microsatellite markers, and part of the collection was screened for its sensitivity to various fungicides. These data are managed through the specifically-developed database POPULABOT.

The first results from autumn 2005 confirmed the occurrence of a sibling species living in sympatry with *Botrytis cinerea sensu-stricto*. In France, *B. cinerea* consists of a complex of 2 genetically isolated species: *B. cinerea* Group I (proposed as *B. pseudocinerea*) and *B. cinerea* Group II (or *B. cinerea sensu-stricto*). In our sampling, strains belonging to Group I were highly differentiated from group II strains and exhibited private alleles for 2 microsatellite loci. They were found in any region but their frequencies never exceeded 10%. Genic diversity was regularly high, indicating an equilibrated distribution of the various microsatellites alleles in the populations, due to migration and/or sexual reproduction. The occurrence of regular recombination was confirmed by the low values of multilocus linkage disequilibrium and by the few numbers of repeated multilocus genotypes (clones) in most of the populations. However, in some Provence tomato glasshouses, genic diversity reached very low levels, whereas the multilocus linkage disequilibrium and the number of clones increased significantly, showing a strong effect of the cropping system on the population dynamics. Pairwise F_{ST} s, Factorial Analyses of Correspondences and Molecular Analysis of Variance were used to characterize the respective influence of the different studied factors on population differentiation.

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Walker, A. S., Decognet, V., Fermaud, M., Bout, A., Confais, J., Leroux, P., Gautier, A., Martinez, F., Roudet, J., Nicot, P., Bardin, M., Robin, P., Potron, M., Fournier, E. (2007). Genetic diversity and structuring factors for *Botrytis cinerea* french populations. In: Abstract book (p. 19). Presented at 14. International Botrytis Symposium, Cape Town, ZAF (2007-10-21 - 2007-10-26).