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Genetic structure and diversity of *Botrytis cinerea* populations in French vineyards at regional and national scales

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Botrytis cinerea is a haploid, filamentous, Ascomycete fungus which can exhibit great phenotypic and genetic diversity. This necrotrophic fungus causes grey mould on numerous plants and, in grapevine, the disease can drastically reduce yield at harvest and wine quality.

The population genetic structure was investigated by using eight polymorphic microsatellite markers within Group-II in *B. cinerea*, *i.e.* by excluding the genetically isolated strains of Group-I (proposed as *B. pseudocinerea*). The spatial distribution of the genetic variability was assessed i) at the regional scale, by sampling 10 vineyard sites in the Bordeaux region in September 2004 ii) at the national scale, on the basis of three sites in Champagne vineyards, three near Bordeaux and two in Provence (sampling periods: autumn 2005 and spring 2006). All the corresponding populations (sites x season) included from 21 to 49 monoconidial isolates and the sites were not sprayed by specific fungicides during the sampling season.

At the regional scale, a high genotypic variability was found within Group II. This was illustrated by the occurrence of few repeated multilocus genotypes within the populations tested. Low levels of linkage disequilibrium were detected within most of the populations suggesting that recombination events occur. These results would bring indirect evidence that sexual reproduction may predominate over clonal reproduction within the populations considered. Such results will be discussed according to the population definition which is, in particular, dependent upon both the sampling strategy and plot size. A weak, but significant, genetic structure was found among populations ($F_{st} = 0.02$), but no significant pattern of isolation-by-distance was detected across the Bordeaux populations. The results from similar analyses performed at the national scale will be presented and compared with the previous ones. The hypotheses of isolation-by-distance and possible barriers to gene flow at a larger geographic scale will be discussed in relation to dispersal ability of the pathogen in the French populations.