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# Resistance to fungicides and genetic diversity among *Botrytis cinerea* populations

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*Botrytis cinerea* is responsible for grey mould and induce quantitative and qualitative losses on various crops, such as grapevine and tomato. In many cropping systems, control against *Botrytis* is mainly achieved by the use of chemical fungicides, which can enable the selection of a wide range of resistances, either specific to one fungicide (e.g. benzimidazoles, phenylcarbamates, dicarboximides, anilino-pyrimidines, hydroxyanilides) or multiple to several unrelated modes of action (MDR : multidrug resistance). Global evolution of the *Botrytis* populations, assessed by population genetics methods, may help to understand the evolution and distribution of resistances to fungicides in natural populations.

Isolates of *Botrytis* were collected in France in 2005 and 2006 from homogeneous treated/untreated grapevine plots in Champagne and Bordeaux areas, and from untreated plots in Provence and in the French Riviera areas. Additional samples were collected from brambles and litter in these vineyards, and from treated tomato glasshouses in the four regions. These isolates were all characterized for their microsatellite profile (8) and resistance profiles to the main botryticides were assessed with *in-vitro* tests for part of them.

Phenotype analysis showed a large variety of resistance profiles, highly representing the fungicide selective pressures applied locally. For example, in Champagne, glasshouses isolates showed mainly specific resistance to benzimidazoles, phenylcarbamates and dicarboximides, whereas in the vineyard, MDR strains represent at least half of the populations. Frequencies of resistances, maximal at vintage, tend to decrease after winter but are still detectable at spring time. More generally, resistant isolates are issued from untreated grapevine plots as well as untreated substrates (brambles, litter), maybe suggesting migrations between the various hosts.

Genic and genotypic diversity indexes within these populations showed a possible effect of recombination and migration. At last, pairwise  $F_{ST}$ s, Factorial Analysis of Correspondances and Molecular Analysis of Variance enabled to estimate the genetic differentiation between (1) treated and untreated plots, at several geographical scales and (2) between the main resistant phenotypes, MDR for example, showing regularly significant but low levels of differentiation.

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