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P1.1 Evolution of abundance and genetic structure of *Botrytis cinerea* airborne inoculum in the South East of France over 2.5 years

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Botrytis cinerea can be highly damageable for crops cultivated under greenhouse. Understanding the parameters that influence the presence of inoculum and its genetic structure could help to predict the outbreak and prevent the development of epidemics in the greenhouses. Studies in a variety of geographic situations have shown that inoculum can vary greatly both quantitatively and in terms of its genetic structure. However, little is known about the long term evolution of inoculum over a single site. The objective of our study is to characterise such variations and to determine if the abundance and the genetic characteristics of *B. cinerea* airborne inoculum can be linked to local and meso-climatic parameters.

Airborne inoculum of *B. cinerea* was sampled twice a month from September 2007 to March 2010 using a high throughput jet sampler located outdoors, in the vicinity of experimental greenhouses of INRA-Avignon. For each sampling date the airborne concentration was quantified (CFU m⁻³) over a 24-hour period with the help of a selective medium and the climatic data (air temperature, wind speed, relative humidity) were recorded. Isolates were collected and single-spored and their genotype was determined using nine micro-satellites markers designed by Fournier *et al.* (2002).

In total, 65 samplings were carried out over the 2.5-year period. The highest concentrations were encountered in autumn and winter and the lowest during summer, with a 100-fold difference between the highest and the lowest values. Only three sampling dates provided no viable inoculum. These three days (in June and July) were characterized by high temperatures and low relative humidity. Preliminary analyses showed no significant correlation between inoculum concentration and local air temperature, relative humidity and wind speed. Further statistical analyses will be made taking into account parameters of air masses that brought the inoculum on the sampling site.

To date, 222 of the 1355 isolates collected have been characterized. Twenty-two of them were identified as pseudo-cinerea (based on a specific allele at the Bc6 microsatellite marker) and were excluded from further analysis. The microsatellite loci were polymorphic with a number of alleles varying from two (Bc4) to twenty-two (Bc6). We discriminated 156 different multilocus genotypes. Multicopy genotypes were represented by two to six isolates. Airborne population of *B. cinerea* showed a high level of diversity : the Simpson's diversity index was 0.99 and the Simpson evenness index was 0.95. The estimated multilocus linkage disequilibrium was significant but low ($r_d = 0.14$, $P < 0.001$), suggesting a sexual reproductive mode mainly with a low of clonality. The analyses will be pursued with the rest of the isolates collected at others dates and the evolution of the genetic structure of airborne populations of *B. cinerea* will be further characterized.

Reference :

Fournier *et al.* 2002. *Mol. Ecol. Notes* 2 :253-255