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Véronique Decognet, Marc Bardin, Claire Troulet, Philippe C. Nicot

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Decognet Véronique, Bardin Marc, Troulet Claire, Nicot Philippe
INRA-Unité de Pathologie Végétale, Avignon, France
Veronique.decognet@avignon.inra.fr

Botrytis cinerea can cause severe losses in sheltered tomato crops. Chemical control is the main way to control gray mould, together with preventive cultural methods and climatic control. Information on the genetic structure of the pathogen's population could lead to a better understanding of epidemics and the development of better strategies of disease control.

A total of 1800 isolates of *B. cinerea* were collected from commercial tomato greenhouses in 2002, 2003 and 2004 at different geographical scales in Southern France.

Samples in 2002 were taken once, at the end of the growing season, from two adjacent greenhouses in each of two sites located 300 km apart. Their characterization with 9 SSR markers described by Fournier et al. (2002, Molec. Ecol. Notes 2:253-255) revealed the presence of one or several dominant haplotypes in each individual greenhouse, combined with an extreme diversity of the remaining isolates. The two adjacent greenhouses of a given site shared most of their dominant haplotypes together with several rare haplotypes. Similar results were obtained for isolates collected from sporulating lesions on the plants or from the air spora (ca 100 from each source in each greenhouse). In contrast, a strong geographic structure was suggested at a higher scale by the fact that the sampling sites shared few common haplotypes (7 out of a total of 74), and that none of those dominant on one site was dominant on the other.

In 2003 and 2004, a smaller geographic scale was considered. Isolates were collected on tomato plants over a four-month period in one of the glasshouses examined in 2002 and in two other glasshouses located within a 50 km radius. Again, a few dominant haplotypes together with a high diversity of other isolates were found on each site. Shared haplotypes among sites were also observed at that scale.

In the one glasshouse that was sampled each year, only one haplotype was common to the three successive tomato crops, with highly different frequencies. In that glasshouse, where tomato and lettuce were consecutively produced in a yearly rotation, a few isolates (36) were also collected from diseased lettuce in 2002-2003 and in 2003-2004. Contrary to the situation in the tomato crops, no dominant haplotypes were found among the isolates collected from lettuce, and no haplotypes were shared with isolates from tomato.

The comparison of haplotype frequencies at different geographic and temporal scales suggests that migration and exchange of inoculum are frequent among neighbouring greenhouses (even though they are usually considered as confined). In addition, the systematic occurrence of dominant haplotypes in all greenhouses suggests that endogenous secondary inoculum (produced on diseased plants) plays an essential role in the development of grey mould epidemics in commercial tomato greenhouses. Finally, differences in populations sampled from lettuce and tomato suggest a possible host specialization of *B. cinerea*. These findings have a direct impact for the management of grey mould in vegetable greenhouses.