



HAL
open science

Genetic structure of *Botrytis cinerea* populations from vegetable greenhouses in France

Véronique Decognet, Marc Bardin, Anne Sophie A. S. Walker, Marc Fermaud, Philippe C. Nicot

► **To cite this version:**

Véronique Decognet, Marc Bardin, Anne Sophie A. S. Walker, Marc Fermaud, Philippe C. Nicot. Genetic structure of *Botrytis cinerea* populations from vegetable greenhouses in France. 14. International Botrytis Symposium, Oct 2007, Cape Town, South Africa. hal-02756512

HAL Id: hal-02756512

<https://hal.inrae.fr/hal-02756512>

Submitted on 3 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Genetic structure of *Botrytis cinerea* populations from vegetable greenhouses in France

Véronique Decognet¹, Marc Bardin¹, Anne-sophie Walker², Marc Fermaud³ and Philippe Nicot¹

¹INRA, Unité de pathologie végétale, BP94, Domaine St Maurice, F-84143 Montfavet, France, E-mail: Veronique.decognet@avignon.inra.fr

²INRA, BIOGER-CPP, Route de St Cyr, F-78026 Versailles Cedex, France

³INRA, UMR Santé Végétale, ISVV, F-33883, Villenave d'Ornon, France

Botrytis cinerea can cause severe losses in sheltered crops. Infections are essentially found as stem lesions resulting from infection of the pruning wounds following regular removal of leaves throughout the growing season. 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. The objective of our research was to determine the level of diversity in tomato commercial greenhouses and to study the effect of three factors (geographic scale, cropping system and host) on the structuration of *B. cinerea* populations using 8 microsatellite markers.

In 2002, two greenhouses distant from 300 km were investigated in Provence. In 2003 and 2004, isolates were collected in one of the previous greenhouses and in two other greenhouses located within a 50 km radius. In 2005 and 2006, populations were studied at the national scale, in three tomato greenhouses in each of three regions (Provence, Champagne and Bordeaux). All isolates were sampled from sporulating lesions on tomato plants.

The SSR characterization of isolates in Provence in 2002, 2003 and 2004 revealed the presence of one or several dominant multilocus genotypes in each greenhouse, combined with an extreme diversity of the remaining isolates. A strong geographic structure of populations was suggested because i) the sampling sites shared few common genotypes and ii) none of those genotypes dominant on one site was dominant on the other. Unexpectedly, isolates collected in the three greenhouses in this region in 2005 and 2006 shared the same dominant genotype (more than 80% of all collected isolates). In contrast, in Champagne and Bordeaux regions, none of the repeated multilocus genotypes were dominant.

In the glasshouse sampled repeatedly from 2002 to 2004, in which tomato and lettuce were consecutively produced in a yearly rotation, no dominant genotypes were found among the isolates collected from lettuce, and no genotypes were shared with isolates from tomato. In 2005 and 2006, *Botrytis* populations from tomato greenhouses were compared to those sampled from other substrates (grapevine, litter, or blackberries) collected outside in the close vicinity of the greenhouses. High level of diversity was also observed for these populations which shared few common genotypes with tomato populations.

Our results suggest that migration and exchange of inoculum are frequent among neighbouring greenhouses. Since few genotypes were shared between the populations inside or outside the greenhouses, the results suggest a possible host specialization of *B. cinerea*. Differences in populations sampled from lettuce and tomato in the same greenhouse supports this hypothesis. The systematic occurrence of dominant genotypes in all greenhouses suggests that the cropping system influences the genetic structure and that endogenous secondary inoculum (produced on diseased plants) plays an essential role in the development of grey mould epidemics in commercial tomato greenhouses. All these findings have a direct impact for the management of grey mould in vegetable greenhouses.