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► **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 tomato greenhouses in France. 9. International Congress of Plant Pathology, Aug 2008, Turin, Italy. , Journal of Plant Pathology, 90, 2 (Supplement), S2-83-84, 2008. hal-02755640

**HAL Id: hal-02755640**

**<https://hal.inrae.fr/hal-02755640v1>**

Submitted on 3 Jun 2020

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### Genetic structure of *Botrytis cinerea* populations from tomato greenhouses in France

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The effect of three factors (geographic scale, cropping system and host plant) on the structure of *B. cinerea* populations was investigated using 8 microsatellite markers. Strong genetic differentiation was observed between populations in tomato greenhouses and those collected outside in close vicinity (grapevine, litter, or blackberries). Great differences were also repeatedly observed within a greenhouse between tomato and lettuce populations consecutively produced in yearly rotations. Among populations sampled on tomato stem lesions, geographic differentiation was observed at a national scale (comparison of Bordeaux area, Champagne and Provence) and at a regional scale, for glasshouses sampled in Provence from 2002 to 2004. In Provence, populations from tomato were characterized by the presence of one or several dominant genotypes in each greenhouse, combined with an extreme diversity of the remaining isolates. The sampling sites shared few common genotypes and none of the genotypes dominant on one site were dominant on another site. Unexpectedly, isolates collected in three greenhouses in Provence in 2005 and 2006 shared the same dominant genotype (more than 80% of all collected isolates). Our results suggest frequent exchange of inoculum among greenhouses and a possible host specialization of *B. cinerea*. 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 tomato greenhouses. All these findings have a direct impact for the management of grey mould in vegetable greenhouses.

Comment citer ce document :

Decognet, V., Bardin, M., Walker, A. S., Fermaud, M., Nicot, P. (2008). Genetic structure of *Botrytis cinerea* populations from tomato greenhouses in France. *Journal of Plant Pathology*, 90, 2 (Supplement), S2-83-84 . Presented at 9. International Congress of Plant Pathology, Turin, ITA (2008-08-24 - 2008-08-29).