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P.3.4: GENETIC DIVERSITY AND INOCULUM EXCHANGE OF *Botrytis cinerea* BETWEEN TOMATO GREENHOUSES IN NORTHERN ALGERIA

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To estimate the genetic diversity for a better understanding of the spread of *Botrytis cinerea*, we genotyped with nine microsatellite markers 174 isolates collected from four greenhouses during three growing seasons in the region of Bejaia. Four of these isolates were detected as *Botrytis pseudocinerea* according to the allele size at locus Bc6. For all other isolates further studied, all loci were polymorphic, with the mean number of alleles per locus ranging from 2.77 to 5.22. Considerable genetic variability was detected in all subpopulations ($D^* > 0.87$; $H_{nb} > 0.40$). Based on the standardized index of association analysis, significant but low levels of clonality occurred, not excluding the possibility of recombination ($r_D = 0.07$, $P < 0.001$). A total of 109 haplotypes were characterized among the isolates, few of which were shared between subpopulations. This, together with moderate genetic differentiation among subpopulations according to the geographical origin ($0.080 < F_{ST} < 0.167$), suggested a low level of inoculum exchange among greenhouses and little carry-over of inoculum from one sampling season to the next. The importance of genetic structure of *B. cinerea* populations is discussed and should be taken into consideration for the management of grey mould.



ABSTRACT BOOK

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