Genetic diversity and population structure of the wheat pathogen *Mycosphaerella graminicola* in northern France

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Abstract

Septoria tritici blotch caused by *Mycosphaerella graminicola* is currently one of the most devastating diseases on wheat crops worldwide, especially in northern France, where it causes every year significant yield losses. A collection of 282 single-conidial isolates of the fungus were sampled in June 2009 from 12 fields covering the northern French region Nord-Pas de Calais. All isolates were typed using 8 microsatellite markers and analyzed for mating types in order to assess genetic diversity, population's structure and sexual reproduction of the pathogen in this region. The sampling was performed in most cases using hierarchical sampling and was undertaken from fields non-treated with fungicides and naturally infected by the fungus. Results revealed a very strong genotypic diversity within the population, with the detection of 280 unique haplotypes among the 282 isolates tested (clonal fraction = 1%). A high genic diversity was also found out, as indicated by Ney (0.63) and Shannon (1.40) index values. Although the mating type ratio did not deviate from the 1:1 ratio expected under random mating and regular cycles of sexual reproduction, 14 % of the possible locus-by-locus pairwise comparisons were significant for linkage disequilibrium. Further analyses showed a great population differentiation (G_{ST} = 0.27) and low degree of gene flow (Nm = 1.34) in the population. Both UPGMA and Bayesian clustering methods revealed that this structuration occurred according to the geographical origin of the isolates. The reasons of this genetic structuration and the specificities of the northern French population of *M. graminicola* are discussed.

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