



The genetic structure of a *Venturia inaequalis* population in a heterogeneous host population composed of different *Malus* species

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Mots-clés	Adaptation [5], apple scab [6], Gene flow [7], Isolation-by-distance (IBD) [8], Spatial genetic structure [9] Adaptation, which induces differentiation between populations in relation to environmental conditions, can initiate divergence. The balance between gene flow and selection determines the maintenance of such a structure in sympatry. Studying these two antagonistic forces in plant pathogens is made possible because of the high ability of pathogens to disperse and of the strong selective pressures exerted by their hosts. In this article, we analysed the genetic structure of the population of the apple scab fungus, <i>Venturia inaequalis</i> , in a heterogeneous environment composed of various <i>Malus</i> species. Inferences were drawn from microsatellite and AFLP data obtained from 114 strains sampled in a single orchard on nine different <i>Malus</i> species to determine the forces that shape the genetic structure of the pathogen.
Résumé en anglais	<p>URL de la notice</p> <p>http://okina.univ-angers.fr/publications/ua7892 [10]</p> <p>DOI</p> <p>10.1186/1471-2148-13-64 [11]</p> <p>Lien vers le document</p> <p>http://dx.doi.org/10.1186/1471-2148-13-64 [11]</p>

Liens

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