



Emergence of novel fungal pathogens by ecological speciation: importance of the reduced viability of immigrants

Submitted by Bruno Le Cam on Wed, 06/10/2015 - 12:46

Titre	Emergence of novel fungal pathogens by ecological speciation: importance of the reduced viability of immigrants
Type de publication	Article de revue
Auteur	Gladieux, Pierre [1], Guérin, Fabien [2], Giraud, Tatiana [3], Caffier, Valérie [4], Lemaire, Christophe [5], Parisi, Luciana [6], Didelot, Frédérique [7], Le Cam, Bruno [8]
Editeur	Wiley-Blackwell
Type	Article scientifique dans une revue à comité de lecture
Année	2011
Langue	Anglais
Date	Nov. 2011
Numéro	21
Pagination	4521-4532
Volume	20
Titre de la revue	Molecular Ecology
ISSN	1365-294X
Mots-clés	Adaptation [9], automatic magic traits [10], biological invasions [11], disease emergence [12], ecological speciation [13], Specialization [14], sympatric speciation [15], Virulence [16]

Résumé en
anglais

Expanding global trade and the domestication of ecosystems have greatly accelerated the rate of emerging infectious fungal diseases, and host-shift speciation appears to be a major route for disease emergence. There is therefore an increased interest in identifying the factors that drive the evolution of reproductive isolation between populations adapting to different hosts. Here, we used genetic markers and cross-inoculations to assess the level of gene flow and investigate barriers responsible for reproductive isolation between two sympatric populations of *Venturia inaequalis*, the fungal pathogen causing apple scab disease, one of the fungal populations causing a recent emerging disease on resistant varieties. Our results showed the maintenance over several years of strong and stable differentiation between the two populations in the same orchards, suggesting ongoing ecological divergence following a host shift. We identified strong selection against immigrants (i.e. host specificity) from different host varieties as the strongest and likely most efficient barrier to gene flow between local and emerging populations. Cross-variety disease transmission events were indeed rare in the field and cross-inoculation tests confirmed high host specificity. Because the fungus mates within its host after successful infection and because pathogenicity-related loci prevent infection of nonhost trees, adaptation to specific hosts may alone maintain both genetic differentiation between and adaptive allelic combinations within sympatric populations parasitizing different apple varieties, thus acting as a 'magic trait'. Additional intrinsic and extrinsic postzygotic barriers might complete reproductive isolation and explain why the rare migrants and F1 hybrids detected do not lead to pervasive gene flow across years.

URL de la
notice

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DOI

10.1111/j.1365-294X.2011.05288.x [18]

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Publié sur *Okina* (<http://okina.univ-angers.fr>)