



The threat of wild habitat to scab resistant apple cultivars

Submitted by Emmanuel Lemoine on Thu, 02/12/2015 - 13:03

Titre	The threat of wild habitat to scab resistant apple cultivars
Type de publication	Article de revue
Auteur	Lê Van, Amandine [1], Durel, Charles-Eric [2], Le Cam, Bruno [3], Caffier, Valérie [4]
Editeur	Wiley
Type	Article scientifique dans une revue à comité de lecture
Année	2011
Langue	Anglais
Date	2011
Numéro	4
Pagination	621 - 630
Volume	60
Titre de la revue	Plant Pathology
ISSN	1365-3059
Mots-clés	core collection [5], <i>Malus sieversii</i> [6], <i>Malus sylvestris</i> [7], <i>Malus × domestica</i> [8], quantitative resistance loci [9], quantitative trait loci [10]
Résumé en anglais	<p>Evaluations of plant resistance to pathogens are rarely made using isolates from wild habitats, although the heterogeneity of such habitats may generate pathogen diversity which could be a source of new virulence in cultivated habitats. The aim of this study was to investigate whether scab resistance factors, identified and characterized in apples using isolates of <i>Venturia inaequalis</i> from a cultivated habitat, remained effective against isolates from a wild habitat. Three <i>V. inaequalis</i> core collections originating from the cultivated apple <i>Malus × domestica</i> and from two wild species, <i>M. sieversii</i> and <i>M. sylvestris</i>, were established to maximize pathogen diversity. For each core collection, 10 isolates were inoculated in mixtures onto 51 genotypes from an apple progeny segregating for two qualitative resistance genes and six quantitative resistance loci (QRL). On each apple genotype, isolates that contributed to the scab symptoms were identified within the mixture using microsatellite markers. The most frequently detected isolates were inoculated singly to compare their aggressiveness according to their host origin. The results showed that isolates from a wild habitat were able to infect the susceptible apple genotypes. However, these isolates were never more aggressive than isolates from the cultivated habitat on the resistance factors tested. It can therefore be concluded that the resistance factors used in this study, identified with <i>V. inaequalis</i> isolates from a cultivated habitat, remained effective against isolates from <i>M. sylvestris</i> and <i>M. sieversii</i>.</p>
URL de la notice	http://okina.univ-angers.fr/publications/ua7765 [11]
DOI	10.1111/j.1365-3059.2011.02437.x [12]
Lien vers le document	http://dx.doi.org/10.1111/j.1365-3059.2011.02437.x [12]

Liens

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