



Redefinition of the map position and validation of a major quantitative trait locus for fire blight resistance of the pear cultivar 'Harrow Sweet' (*Pyrus communis* L.)

Submitted by Emmanuel Lemoine on Thu, 02/12/2015 - 13:09

Titre	Redefinition of the map position and validation of a major quantitative trait locus for fire blight resistance of the pear cultivar 'Harrow Sweet' (<i>Pyrus communis</i> L.)
Type de publication	Article de revue
Auteur	Le Roux, Pierre-Marie [1], Christen, Danilo [2], Duffy, Brion [3], Tartarini, Stefano [4], Dondini, Luca [5], Yamamoto, Toshiya [6], Nishitani, Chikako [7], Terakami, Shingo [8], Lespinasse, Yves [9], Kellerhals, Markus [10], Patocchi, Andrea [11]
Editeur	Wiley
Type	Article scientifique dans une revue à comité de lecture
Année	2012
Langue	Anglais
Date	2012
Numéro	5
Pagination	656 - 664
Volume	131
Titre de la revue	Plant Breeding
ISSN	1439-0523
Mots-clés	Erwinia amylovora [12], Malus spp. [13], marker-assisted breeding [14], microsatellite [15], Pyrus spp. [16], synteny [17]
Résumé en anglais	<p>In a previous study, a QTL analysis was conducted on a pear F1 progeny derived from a cross 'Passe Crassane' (PC) × 'Harrow Sweet' (HS). Four genomic regions associated with fire blight resistance were identified, including two main QTL located on linkage groups (LGs), 2A and 4 of 'Harrow Sweet' (HS02A and HS04). In the present study, we report the combination of LGs HS02A and HS02B into a single LG by mapping additional SSR loci from Malus or Pyrus spp. We could thereby precisely identify a single major QTL on LG HS02. We also confirm a putative QTL on LG HS04 by including new SSR markers to the pre-existing LG HS04. Based on SSR marker analysis of 'Harrow Sweet' pedigree, the major HS02 QTL is presumed to originate from the cultivar 'Early Sweet', while the HS04 QTL was traced from 'Harrow Sweet' back to 'Bartlett'. We also describe the validation of the major HS02 QTL for the fire blight severity trait in a second F1 progeny derived from a cross 'Angelys' × 'Harrow Sweet'.</p>
URL de la notice	http://okina.univ-angers.fr/publications/ua7826 [18]
DOI	10.1111/j.1439-0523.2012.02000.x [19]
Lien vers le document	http://dx.doi.org/10.1111/j.1439-0523.2012.02000.x [19]

Liens

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- [19] <http://dx.doi.org/10.1111/j.1439-0523.2012.02000.x>

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