Exploring plant defense pathways in the carrot-Alternaria dauci pathosystem, a non-model interaction

Titre	Exploring plant defense pathways in the carrot-Alternaria dauci pathosystem, a non-model interaction
Type de publication	Communication
Type	Communication avec actes dans un congrès
Année	2011
Langue	Anglais
Date du colloque	24/05/2011
Titre du colloque	63rd International Symposium of Crop Protection
Auteur	Lecomte, Mickaël [1], Allenda, Charline [2], Sement, François [3], Berthet, Mathilde [4], Briard, Mathilde [5], Hamama, Latifa [6], Poupard, Pascal [7], Berruyer, Romain [8]
Pays	Belgique
Ville	Ghent

	Most of the molecular mechanisms underlying plant partial resistance QTLs are still unknown. Two competing hypothesis are generally invoked to link observed field resistance with actual molecular gene function. An older hypothesis links partial resistance QTLs with overcome typical R genes encoding classical NBS-LRR or LRR-TM type proteins. In a recent paper (Hu et al., 2008), partial plant resistance was linked with defense mechanisms. These results led us to develop a candidate gene approach to study partial plant resistance of carrot (Daucus carota) towards its main foliar fungal pathogen, Alternaria dauci. Since carrot is a non-model plant, little sequence data is available on public databases. We thus chose to develop a homology-based cloning strategy in order to detect and sequence defense-related genes in carrot. Since A. dauci is a necrotrophic pathogen, we focused this strategy on Jasmonic acid (JA) signaling pathway and JA controlled defense genes (such as JAZ3 or PR4). Since the degenerate primer strategy is not known to be effective on each and every gene, we chose to apply it in a parallel fashion on a rather large set of genes.
Résumé en anglais	Alignments of sequence data from eight already sequenced dicotyledonous plant species were performed for 15 genes. Degenerate primers were defined for 10 genes involved in this JA pathway. Additionally, we defined degenerate primers for two defense genes that are not mainly JA- regulated: the SA-regulated defense gene PR1, and the non host defense gene PAL1. Five out of 12 genes were partially cloned and sequenced. Two strategies are currently deployed to link these defense related genes with partial resistance QTLs observed in the carrot-A. dauci interaction (Le Clerc et al., 2009). SNPs are being found between the resistant and susceptible parents of our mapping populations. They will help us to find potential QTL-candidate co-localizations. Absence of such a co-localization does not mean that a potential candidate is not involved in defense. It is also possible that the QTL influences defense-related genes activation rather than the efficiency of the cognate PR proteins. For this reason, we also plan to study the induction of these genes by A. dauci in both susceptible and resistant backgrounds.
URL de la notice	http://okina.univ-angers.fr/publications/ua8681 [9]

Liens

[1] http://okina.univ-angers.fr/publications?f[author]=157
[2] http://okina.univ-angers.fr/publications?f[author]=15410
[3] http://okina.univ-angers.fr/publications?f[author]=15411
[4] http://okina.univ-angers.fr/publications?f[author]=15412

[5] http://okina.univ-angers.fr/publications?f[author]=166
[6] http://okina.univ-angers.fr/publications?f[author]=159
[7] http://okina.univ-angers.fr/pascal.poupard/publications
[8] http://okina.univ-angers.fr/romain.berruyer/publications
[9] http://okina.univ-angers.fr/publications/ua8681