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PLANT RESISTANCE SUSTAINABILITY

International Conference _____ 2012



La Colle-Sur-Loup (France)
October 16th-19th, 2012



Scientific Programme and Abstracts

Sessions

Session 1: Impact of plant disease resistance on the structure and evolution of pathogen populations

Session 3: From plant-pathogen molecular interactions to the durability of resistance

Session 2: Sustainable and integrated breeding and deployment of genetic resistance

Session 4: Socio-economic issues related to the use of resistant varieties and their deployment in agro-systems

Invited Speakers

Philippe Baret, Université Catholique de Louvain, Belgium - **James Brown**, John Innes Centre, England - **Marion Desquilbet**, INRA, France - **Sylvain Gandon**, CNRS, France - **Benoit Moury**, INRA, France - **Chris Mundt**, Oregon State University, USA - **Laura Rose**, Heinrich-Heine University, Germany - **Walter Rossing**, Wageningen University, The Netherlands - **Peter Thrall**, CSIRO Plant Industry, Australia

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Metaprogramme on Sustainable Management of Crop Health (SMaCH)



Steel, R.G.D. and J.H. Torrie. 1982. Principles and procedures of statistics. A biometrical approach McGraw-Hill Book Co.

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Biological features, positional cloning and validation of the *Ma* gene for high-level and complete-spectrum resistance to root-knot-nematodes in *Prunus*

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Abstract

Stone fruit crops *Prunus* spp. grown under Mediterranean climates are severely damaged by root-knot nematodes (RKN) *Meloidogyne* spp. and breeding for RKN-resistant rootstocks is a promising control alternative to nematicide ban. Resistance (R) genes that confer different spectra have been identified and mapped in plums (*Ma* and *Rjap*), peach (*RMia*) and almond (*RMja*). Thus sustainable resistance in *Prunus* is based on pyramiding of R genes in interspecific rootstock material to take into account the risk of resistance breaking in the durable plant-nematode interaction for perennials. The *Ma* gene from Myrobalan plum has been shown to confer a complete-spectrum, high-level and heat-stable resistance to both mitotic (*M. arenaria*, *M. incognita*, *M. javanica* and *M. enterolobii*) and meiotic (*M. floridensis*) RKN. *Ma* triggers a hypersensitive-like reaction (HLR) in root apices and severe nematode attacks induce the development of subterminal lateral rootlets replacing primary terminal apices and providing an active resistance response to HLR damage (1). Sustainability of resistance conferred by *Ma* has been challenged in multi-year experiments applying a high and continuous nematode inoculum pressure by co-cultivation of RKN-infested susceptible tomato plants together with *Prunus* plants carrying *Ma* or, for comparison, with R tomato plants carrying the *Mi-1* reference gene. Galling and virulent nematode individuals have been observed in *Mi-1* resistant tomatoes but not in *Ma*-carrying *Prunus* plants. The positional cloning of the *Ma* locus in accession P.2175 has been performed using high resolution mapping developed in two successive steps totalling over 3000 segregants. The *Ma* locus interval has been reduced to a 32-kb cluster of three TIR-NB-LRR genes (TNL1 to TNL3) including a pseudogene (TNL2) and a truncated gene (TNL3). Using *A. rhizogenes* transformed hairy roots and composite plants (2), the best candidate gene, TNL1, comprising the genomic sequence and the native promoter region (15.3 kb), has been validated as *Ma* as it conferred the same complete-spectrum and high-level resistance as in the donor accession P.2175. The full-length cDNA (2048 aa) of *Ma* is the longest of all R genes cloned to-date. Its TNL structure is extended by a huge C-terminal post-LRR (PL) region (1088 aa) comprising five repeated PL exons (3).

Keywords: *Meloidogyne*, plant resistance, *Prunus*, root-knot nematode, sustainable resistance

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