7

Identification of new resistance gene analogs in 33 wild Malus species.

Malnoy, M. [1,2], Baldo, A., [3,4] and Aldwinckle, H.S. [2]

[1] IASMA Research Centre, Via E. Mach 1, 38010 San Michele all'Adige (TN) Italy
[2] Cornell University, Department of Plant Pathology, Geneva, NY
[3] USDA-ARS Plant Genetic Resources Unit, Geneva, NY
[4] Cornell Unversity, Department of Horticultural Sciences, Geneva, NY

Plant R genes are known to confer resistance to a variety of pathogens in a gene-for-gene mode. 800 unique apple genome samples were amplified and sequenced from a variety of wild material and rootstocks using degenerate primers for NBS-LRR Resistance Gene Analogs (RGAs). Forty five differents Malus accessions from the USDA apple gerplasm collection at Geneva, representing 33 Malus species (*MalusXdomestica*, asiatica, baccata, coronaria, florentina, floribunda, fusca, halliana, honanensis, hupehensis, ioensis, kansuensis, micromalus, ombrophila, orientalis, prattii, prunifolia, pumila, robusta, sargentii, sieboldii, sieversii, sikkimensis, sublobata, sylvestris, transitoria, toringoides ,zumi, yunnanensis, zhaojiaoensis), hybrid white angel, and the rootstock Geneva41 were used in this study. Sequences were screened and cleaned of vector sequences and compared with resistance genes previously identified among the Rosaceae and other green plants. Approximately 90 of these matched RGAs previously identified among Malus while an additional 200 are similar to RGAs found in other Rosaceae genera and other plant families. Roughly 30% of the RGA's identified in this study are TIR-type RGAs, while the remaining 70% are Non-TIR-type. These genes will be used to identify novel sources of disease resistance among the wild apples in the USDA apple collection.

Keywords: Apple, gene resistance