

TOMATO R-GENES GENOME-WIDE SORTING

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A complete set of candidate disease resistance (R) genes was identified in the genome sequence of tomato (*Lycopersicon esculentum* var. Hein 1706). These putative R genes were characterized with respect to structural diversity, phylogenetic relationships and chromosomal distribution, and compared with R genes that have now been cloned from different monocot and dicot plant species. We found more than 700 coding sequences, including TNL proteins, CNL proteins, RLP proteins RLK proteins, as well as, other different domains arrangements. Genes were not uniformly distributed on chromosomes. Many of them remain in clusters, containing highly similar gene members. Fifty-four per cent of predicted R-genes were located in 121 gene clusters, and 81 of these gene clusters showed extensively gene duplications. The structural and genetic diversity that exists among R-proteins in tomato is remarkable and suggests that diversifying selection has played an important role in the evolution of R genes in this agronomically important species.