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## Unique evolutionary pattern of NBS-LRR genes among five Rosaceae species

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### **Abstract:**

Disease resistance (R) genes from different Rosaceae species have been identified by map-based cloning for resistance breeding, and most disease resistance genes encode NBS-LRR protein. However, reports describing evolutionary pattern of R-genes in Rosaceae species are rare because several Rosaceae genome sequences have only become available in last several years. We performed a systematic genome-wide survey of NBS-LRR genes among five Rosaceae plants, including *Fragaria vesca* (woodland strawberry), *Malus × domestica* (apple), *Pyrus bretschneideri* (Asian pear), *Prunus persica* (peach) and *Prunus mume* (mei, or Japanese apricot) with 144, 748, 469, 354 and 352 NBS-LRR genes. The high proportions of multi-genes and similar Ks peaks ( $K_s = 0.1-0.2$ ) of gene families in the four woody genomes indicate that recent duplications played an important role in the four woody perennial Rosaceae species. Subsequently, 385 species-specific duplicate clades were dominant in the phylogenetic tree constructed by all 2067 NBS-LRR genes. High percentages of NBS-LRR genes involved in species-specific duplication were found among the five genomes (54.86% in woodland strawberry, 68.05% in apple, 57.56% in pear, 44.07% in peach and 45.74% in mei). It might be inferred that species-specific duplication mainly contributes to the expansion of NBS-LRR genes in the five Rosaceae species. In addition, the  $K_s$  and  $K_a/K_s$  values of TIR-NBS-LRR (TNL) were significantly greater than those of non-TIR-NBS-LRR (non-TNL), suggesting that rapidly evolved TNLs have different evolutionary patterns to adapt to different pathogens compared with non-TNL genes. In addition, some of the RPW8 domain-containing NBS-LRRs had  $K_a/K_s$  ratios less than 1, suggesting that they were driven by positive selection.

**Keywords:** NBS-LRR genes, Rosaceae species, disease resistance genes, species-specific duplication