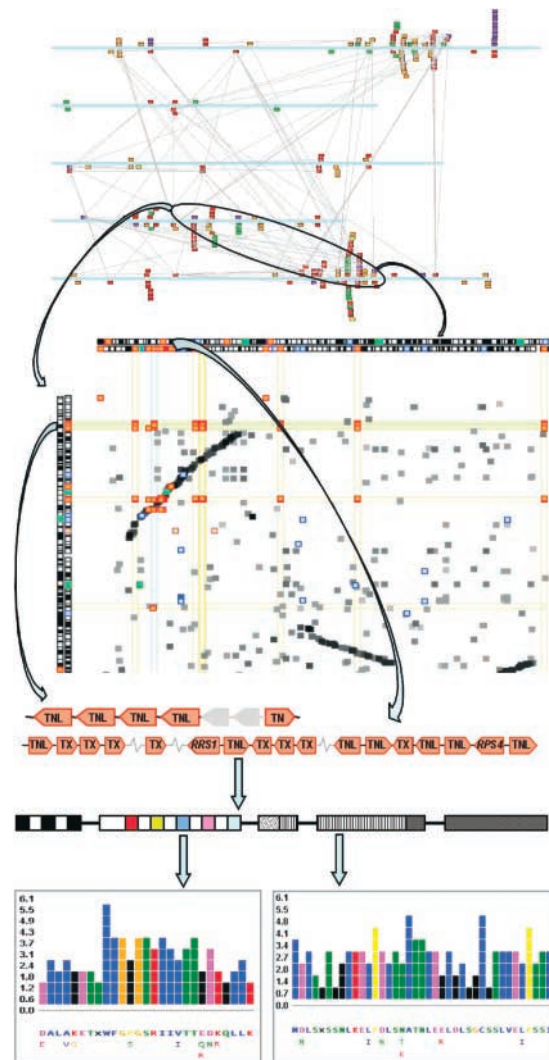


**HIGHLIGHT**

# Resistance Rodeo: Rounding up the Full Complement of Arabidopsis NBS-LRR Genes

Plant resistance (*R*) genes encode proteins that mediate the recognition of corresponding pathogen-encoded avirulence (*Avr*) proteins, triggering localized cell death (the hypersensitive response) and systemic acquired resistance. A large number of *R* genes have been characterized from numerous plant species that collectively confer resistance to a wide range of pathogens, including viral, bacterial, and fungal pathogens, and even to some nematodes and insects. Plant nucleotide binding site–Leu-rich repeat (NBS-LRR) proteins appear to function principally (perhaps exclusively) in signaling associated with the recognition of and resistance to pathogens and represent the largest of five known classes of *R* proteins (reviewed by Dangl and Jones, 2001). In this issue of *The Plant Cell*, **Meyers et al. (pages 809–834)** present an analysis of the structure, arrangement, and phylogeny of the full complement of 149 NBS-LRR genes in the Arabidopsis ecotype Columbia genome (Figure 1). Despite the wealth of information on the structure and function of NBS-LRR genes that has come from numerous primary research and review articles in recent years, this comprehensive analysis offers novel insights into genome evolution in general and *R* gene evolution in particular and provides a useful World Wide Web–based resource for other researchers in the field.

Meyers et al. started their analysis by manually reannotating all previously identified NBS-LRR genes and searching the genome sequence for genes missed in the earlier annotations. An important outcome of this work was a change in annotation of some 36% of previously identified NBS-LRR genes, suggesting the weakness of current automated annotation methods. This work also identified 11 new pseudo-genes, which tend to be annotated as full-



**Figure 1.** Lassoing and Branding *R* Genes: Progressively More Fine-Scale Analysis of NBS-LRR–Encoding Genes.

From top, distribution of NBS-LRR–encoding genes over the five chromosomes of Arabidopsis; pairwise Basic Local Alignment Search Tool (BLAST) comparison of two *TNL*-containing regions of chromosomes 4 and 5; gene organization of two paralogous *TNL* clusters; motif and domain configuration of an individual *TNL* gene; and MEME analysis of motifs within the NBS and LRR domains of *TNL* proteins. (Figure courtesy of Blake Meyers and Richard Michelmore.)

## HIGHLIGHT

length open reading frames by automated methods that simply create introns surrounding frameshift or nonsense mutations. With corrected annotations in hand, Meyers et al. proceeded to catalog the conserved domains of all of the NBS-LRR proteins and conducted phylogenetic analyses to ascertain their relationships.

NBS-LRR proteins can be subdivided into proteins that contain a Toll/Interleukin-1 receptor-like (TIR) region and those that contain a coiled-coil (CC) region near the N terminus. Meyers et al. found 51 CC-NBS-LRR-encoding (CNL) genes and 92 TIR-NBS-LRR-type (TNL) genes in the Columbia genome, plus 6 additional genes that lacked a TIR or a CC region but were classified as having TIR-type (2 genes) or CC-type (4 genes) NBS regions. In addition, 58 genes were found that contain *R* gene-related TIR, CC, and/or NBS regions but lack an LRR region; thus, they were not included in the final tally of 149 *NBS-LRR* genes.

Several interesting and important conclusions can be gleaned from the current work of Meyers et al. First, the CNL and TNL classes can be divided into a number of subgroups within each class, and there appears to be little or no recombination among genes of different subgroups. This runs contrary to the proposal of Richly et al. (2002) that recombination between diverse *NBS-LRR* genes may drive the acquisition of resistance specificities. Even the most highly conserved motifs of the *NBS-LRR* genes display considerable sequence variation among subgroups. Another ramification of this observation is that the isolation of *NBS-LRR R* genes from other species based on degenerate primers may miss entire subgroups of *R* genes. A second insight provided by this work, and by the related work of Cannon et al. (2002), is that CNL genes appear to

represent a more ancient subgroup than TNL genes. In Arabidopsis, TNL genes represent the larger subgroup and appear to have undergone recent amplification relative to the CNL subgroup. This is different from the patterns of evolution of these genes in other plant species. In fact, TNL genes appear to be completely absent from the grass family, apparently as a result of gene loss (Bai et al., 2002; Cannon et al., 2002; Meyers et al., 2002). In addition, TNL genes in Arabidopsis typically contain long C-terminal extensions beyond the LRR regions, whereas CNL genes do not, which suggests a fundamental difference in function between the two classes of protein. A third insight of interest is that *NBS-LRR R* genes appear to be underrepresented in duplicated segments of the Arabidopsis genome, suggesting that duplicated *R* gene clusters were deleted selectively after polyploidization events (Simillion et al., 2002). Although segmental duplication of large portions of the genome may be responsible for some amplification of these genes, there is clear evidence of microscale chromosomal duplications and deletions. It was concluded that small translocation events involving individual *NBS-LRR* genes or small sets of genes are a common phenomenon.

Finally, Meyers et al. present a useful World Wide Web-based resource (<http://www.niblrrs.ucdavis.edu>) that includes a database of NBS sequences that contains the complete list of Arabidopsis *NBS-LRR* genes with alignments of the NBS regions, sequence analyses of other motifs, gene locations, EST matches, and links to other resources. The work of Meyers et al. is a valuable addition to the study of *R* gene evolution and provides a solid framework for future investigations into *NBS-LRR* gene function.

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