Intragenic recombination between pseudogenes as a source of new disease specificity at a simple resistance locus

Huang L1, Brooks SA2, Li W3, Fellers JP4, and Gill BS3

1Department of Plant Sciences and Plant Pathology, Montana State University, Bozeman, MT 59717-3150.
2USDA-ARS, Dale Bumpers National Rice Research Center, 2890 Hwy 130 E., Stuttgart, Arkansas 72160.
3Wheat Genetic and Genomic Resources Center, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506-5502.
4USDA-ARS-PSERU, Department of Plant Pathology, 4008 Throckmorton Hall, Kansas State University, Manhattan, KS 66506-5502

The leaf rust resistance gene Lr21, coding for an NBS-LRR protein, was identified from the wild goat grass Aegilops tauschii Coss, the species that contributed the D-genome to bread wheat (Triticum aestivum L.). Unlike most NBS-LRR type resistance genes that are organized as compound loci, Lr21 is located at a simple locus. We studied the molecular dynamics of this locus in samples of 25 Ae. tauschii accessions and 22 bread wheat cultivars, and discovered at least 13 nonfunctional lr21 alleles existing as truncated expressing pseudogenes and one functional Lr21 allele. The Lr21 specificity arose most likely from two susceptible lr21 alleles through intragenic recombination between the NBS and LRR domains. The discovery suggests plant resistance genes can be generated from the dead alleles. The birth of Lr21 provides new understanding as to why plants keep and often transcribe truncated resistance gene analogs.