



Genome-wide identification and evolutionary analysis of nucleotide-binding site-encoding resistance genes in *Lotus japonicus* (Fabaceae)

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Genet. Mol. Res. 14 (4): 16024-16040 (2015)

Received August 10, 2015

Accepted October 22, 2015

Published December 7, 2015

DOI <http://dx.doi.org/10.4238/2015.December.7.16>

ABSTRACT. Nucleotide-binding site (NBS) disease resistance genes play a crucial role in plant defense responses against pathogens and insect pests. Many NBS-encoding genes have been detected in *Lotus japonicus*, an important forage crop in many parts of the world. However, most NBS genes identified so far in *L. japonicus* were only partial sequences. We identified 45 full-length NBS-encoding genes in the *L. japonicus* genome, and analyzed gene duplications, motifs, and the molecular phylogeny to further understand the NBS gene family. We found that gene duplication events rarely occur in *L. japonicus* NBS-encoding (LjNBS) genes. In addition, LjNBS genes were subjected to selection pressure, and codon usage bias was evident. We tested for purifying selection (specifically in the CC-NBS-LRR and TIR-NBS-LRR groups), and found strong purifying selection in the TIR-domain-containing sequences, indicating that the CC-NBS-LRR group is more likely to undergo expansion than the TIR-NBS-

LRR group. Moreover, our results showed that both selection and mutation contributed to LjNBS codon usage bias, but mutational bias was the major influence on codon usage.

Key words: *Lotus japonicus*; Nucleotide-binding site disease resistance genes; Gene duplication; Selection pressure; Codon usage bias