



# Identification of resistance gene analogs in Korean wild apple germplasm collections

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**ABSTRACT.** Several plant disease resistance gene (R-gene) classes have been identified on the basis of specific conserved functional domains. Cloning of disease-resistance apple genes would be useful for breeding programs and for studying resistance mechanisms. We used a PCR approach with degenerate primers designed from conserved NBS-LRR (nucleotide binding site-leucine-rich repeat) regions of known R-genes to amplify and clone homologous sequences from six Korean wild apple germplasm collections and an individual plant of the Siberian wild apple, *Malus baccata*. One hundred and twenty-four sequenced clones showed high similarity at multiple NBS motifs with the R-genes of other plants. The clones OLE 2-9, BP 6-11, OLE 1-22, and OLE 5-13 shared 45% identity with the R-gene of other plants. The conserved sequence, which plays an important role in resistance, was found in our isolated resistance gene analogs (RGAs). The sequences of isolated apple RGAs showed more similarity to Toll/interleukin-1 receptor (TIR)-NBS-LRR than non-TIR-NBS-LRR. We suggest using a marker for this resistance gene region as well as for identifying potential material for disease-resistant breeding among Korea wild apple germplasms. This is the first step in preparing a comprehensive analysis of the RGAs in Korean wild apple germplasm.

**Key words:** NBS-LRR; Resistance gene analogs; R-gene