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Characterization of *N* gene homologs in *Nicotiana* species

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We have developed a new variety of *Nicotiana, N. edwardsonii* var. Columbia, that can be used as a bridge plant to move virus resistance genes from *N. glutinosa* to *N. clevelandii*, and have made crosses between *N. edwardsonii*. var. Columbia and *N. clevelandii* to characterize a single dominant gene that specifies resistance to Tomato bushy stunt virus (TBSV). We have also developed a gene silencing assay that specifically targets host resistance genes that fall into the NBS-LRR category and have used this assay to show that TBSV resistance gene has sequence similarity to the *N* resistance gene. As a prelude to cloning the TBSV resistanc gene, it is now important to understand how many *N* gene homologs exist in crosses with *N. glutinosa.* To examine the diversity of *N* gene homolog sequences, we developed PCR primers that amplified a 516 bp DNA segment of Exon 2 of the *N* gene. This PCR reaction yielded multiple products, which were cloned and sequenced. In *N. clevelandii*, two *N* homologs predominated. These sequences differed from the *N* gene by approximately 10%. The analysis of *N* homologs in *N glutinosa* is still being completed, but preliminary results indicate that this *Nicotiana* species contains a broader array of *N* gene homologs than *N. clevelandii.*