Identification and characterization of a novel tobacco mosaic virus resistance N gene homologue in Nicotiana tabacum plants

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Abstract

Nicotiana tabacum cv. Xanthi nn plants are susceptible to infection by most tobamoviruses (TMV). However, such plants display a partial hypersensitive resistance response (HR-like response) to TMV-Cg. The genetic mechanism of the HR-like response has yet not been determined, but it may involve a gene with a function similar to that of a resistance gene, responsible for HR in resistant plants. We have cloned a gene homologous to the resistance N gene, named NH, from Nicotiana Xanthi nn plants. The coding region of NH is 5.028 base pairs (bp) long and has 82.6% nucleotide identity with the N gene. In contrast to the N gene, the NH gene lacks intron 4 and does not have sites for alternative splicing of intron 3. Analysis of its sequence revealed that NH belongs to the TIR / NSB / LRR gene class. We were able to detect stable levels of NH-transcript in Nicotiana Xanthi nn plants from 0 to 18 h post-inoculation (hpi) with TMV-Cg. Transcript levels increased slightly at 24 hpi and dropped below basal values at 48 hpi. The NH transcript was also detected in a range of resistant Nicotiana plants (N. tabacum Xanthi NN, N. glutinosa, N. glauca and N. rustica) suggesting that NH is a homologue of the N gene, rather than an allele. We have cloned and characterised the NH gene (GenBank acc. no. bankit598573 AY535010) from nn susceptible plants and postulate that this gene might be involved in the HR-like response seen in these plants.

Keywords: disease resistance, HR-like, hypersensitive response, N gene, TIR / NBS / LRR receptor, TMV-Cg.