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# Isolation and characterization of NBS-LRR-resistance gene candidates in turmeric (*Curcuma longa* cv. surama)

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**ABSTRACT.** Turmeric (*Curcuma longa*), an important asexually reproducing spice crop of the family Zingiberaceae is highly susceptible to bacterial and fungal pathogens. The identification of resistance gene analogs holds great promise for development of resistant turmeric cultivars. Degenerate primers designed based on known resistance genes (R-genes) were used in combinations to elucidate resistance gene analogs from *Curcuma longa* cultivar surama. The three primers resulted in amplicons with expected sizes of 450-600 bp. The nucleotide sequence of these amplicons was obtained through sequencing; their predicted amino acid sequences compared to each other and to the amino acid sequences of known R-genes revealed significant sequence similarity. The finding of conserved domains, viz., kinase-1a, kinase-2 and hydrophobic motif, provided evidence that the sequences belong to the NBS-LRR class gene family. The presence of tryptophan as the last residue of kinase-2 motif further qualified them to be in the non-TIR-NBS-LRR subfamily of resistance genes. A cluster analysis based on the neighbor-joining method was carried out using *Curcuma* NBS analogs together with several resistance gene analogs and known R-genes, which classified them into two distinct subclasses, corresponding to clades N3 and N4 of non-TIR-NBS sequences described in plants. The NBS analogs that we isolated can be used as guidelines to eventually isolate numerous R-genes in turmeric.

**Key words:** Resistance gene analogs; Multiple sequence alignment; NBS-LRR; R-genes