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Identification and sequence analysis of putative *Sulla* species Nod factor receptor.

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Abstract

In legumes, LysM domains of receptors-like kinases (RLKs) mediate rhizobial NFs perception; which are required for infection and establishment of symbiosis without triggering the host immune response. In this study, we identify the LysM extracellular domain sequences of putative *Sulla* species Nod factor receptors (*S. pallida*, *S. capitata* and *S. coronaria*). The Blast search displayed high identity percentages with genes encoding LjNFR5-like of several legumes. Phylogenetic trees were built using the partial nod factor receptor and predicted amino acid sequences, which grouped *Sulla* in a separate clade. The multiple alignments of the LysM2 domains revealed that amino acids found to be important in other legume species are not conserved in *Sulla* species. Further examination of the predicted proteins sequences (LysM2 domain) showed that the three species were different in the two crucial sites for Nod factor perception.

Keywords: *S. pallida*; *S. capitata*; *S. coronaria*; LysM domains; Nod factor receptor proteins; Molecular analysis.

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