Nucleotide sequence of the Rhizobium etli nos gene*

(Nodulation genes; symbiosis; methyltransferase phylogenetic analysis; NodS alignment)

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SUMMARY

The complete nucleotide sequence of the nos gene from the bean-nodulating Rhizobium etli, presumably encoding a methyltransferase, was determined. A phylogenetic analysis of five different Nos proteins from three genera of Gram soil bacteria, Azorhizobium, Bradyrhizobium and Rhizobium, was performed.

Bacteria of the genera Rhizobium, Bradyrhizobium and Azorhizobium can develop nitrogen-fixing nodules on leguminous plants in a host-specific way. The first stage of this interaction leads to the activation of bacterial nodulation (nod) genes by plant flavonoids. The nod genes code for Nod factors, which act as host-specific signals to trigger nodule formation. The Nod factors are oligomers of β-1,4-linked glucosamine residues, N-acylated on the terminal non-reducing sugar and N-acetylated on the other residues (Dénaire et al., 1993).

The nodABC genes are involved in the biosynthesis of the core of the Nod factors. Recently, we have proposed (Vázquez et al., 1993) that NodI and NodJ proteins are members of a polysaccharide secretion system that could be involved in the export of the Nod factors. Other nod genes, mediate the “decoration” of the core with various substituents (N-acyl chain, sulfate, acetate, methyl and carbamoyl groups, sugars) in order to make them host-specific.

Recently, nos and nodU genes have also been identified in A. caulinodans (Geelen et al., 1993). An analysis of the deduced aa sequences of nos gene products from R. sp. NGR234, B. japonicum and A. caulinodans, revealed consensus sequences with high similarity to SAM-utilizing enzymes. In A. caulinodans, nos has been proposed to encode for a Mtase involved in the modification of the Nod factor (Geelen et al., 1993).

We reported a unique organization of the common nod genes in R. leguminosarum bv. phaseoli strain CE3 (Vázquez et al., 1991), reclassified as belonging to a new species, R. etli (Segovia et al., 1993). At present we are reporting that immediately downstream from the R. etli common nodC gene (38 bp), we found a 205-aa ORF (GenBank accession No. L11750) that encodes a 2728-Da Nos showing a strong similarity to the R. sp. strain NGR234 Nos, as well as to the deduced aa sequences of R. japonicum, R. fredii and A. caulinodans Nos that have been described as SAM-utilizing enzymes (Geelen et al., 1993). At the aa level, the ORF shows 66, 55, 54 and 31% identity with R. sp. strain NGR234, B. japonicum, R. fredii USDA257 and A. caulinodans Nos aa sequences, respectively (Fig. 1).

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*On request, the authors will supply detailed experimental evidence for the conclusions reached in this Brief Note.

Abbreviations: A., Azorhizobium; aa, amino acid(s); B., Bradyrhizobium; bp, base pair(s); GCG, Genetics Computer Group (Madison, WI, USA); kb, kilobase(s) or 1000 bp; Mtase, methyltransferase, nod, nodulation genes; Nos, nodulation factors; ORF, open reading frame; R., Rhizobium; SAM, S-adenosylmethionine.