

## SL802

### *nif*-Gene Organization and Nucleotide Sequence of *nifV*, *nifH*, D, K and *nifE* from *Frankia* Strain FaCl

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The total size of the pFAH1, a genomic clone of *Frankia* FaCl, was estimated to be about 44Kb by summation of the individual fragment length generated by single or double restriction enzymes. Southern hybridization analyses with *Azotobacter vinelandii nif*-genes as probes and partial sequencing analyses of the subclones revealed that organization of the *nif*-gene in the FaCl strain was *nifV*, H, D, K, E, N, X, W, B. The organization of the structural genes for nitrogenase is the same in this *Frankia* strain as it is in most other nitrogen-fixing prokaryotes but the positioning of the *nifV*-like gene relative to the *nifHDK* cluster differs. A consensus *nif*-promoter-like sequence, found at 5' of *nifH*, was not detected upstream of the *nifV*-like gene. *nifV*-like gene contained a ORF of 1206 NT encoding 401 amino acids. The nucleotide sequence and deduced amino acid sequence of the gene exhibit homology value of 65% and 41% with that from *A. vinelandii*, respectively. The putative Shine-Dargarno sequences were present preceding *nifK*, *nifH*, D, K, and *nifE*, and in *nifK* gene putative start codon GTG was detected instead of ATG. The nucleotide and amino acid sequence of *nifK* of FaCl showed 82% and 76% homolgy with those of *Frankia* HFPCc 13, respectively. Amino acid sequence of *nifK* showed 69% and 61% homology with those of *A. vinelandii*, *Klebsiella pneumoniae*, respectively, while that of *nifE* 73% and 71%, respectively.