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Sequence of a 1.4 kb *Eco* RI fragment of *Azotobacter vinelandii nif* DNA

Koji Hiratsuka and Kenneth L.Roy*

Department of Microbiology, University of Alberta, Edmonton, Alberta T6G 2E9, Canada

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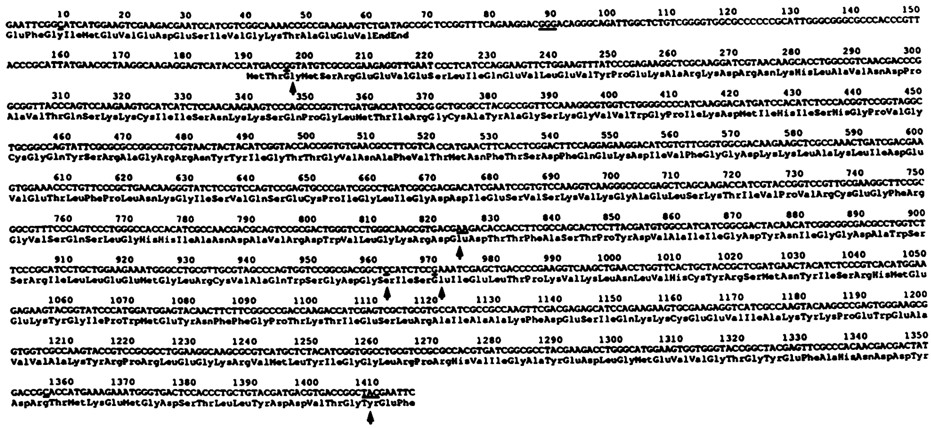
A 28 kb *Hind III* fragment of *Azotobacter vinelandii* UW DNA, identified by its homology to the *Klebsiella pneumoniae nifHDKY* genes in the plasmid pSA30 (1), was cloned into the broad host-range cosmid vector pSa747 (2,3). A 1.41 kb *EcoRI* segment, subcloned into pUC8, was completely sequenced using predominantly the chain termination method of Sanger *et al.* (4). The sequence obtained corresponded to the distal 20 amino acids of the *nifH* gene product (Fe protein), the first 409 amino acids of the *nifD* gene product (MoFe protein α-subunit), and the included intergenic region. When compared with the sequence reported by Brigle *et al.* (5) a total of 13 base changes were found including the C to G change at position 196 which results in the introduction of an *Msp*I site (which is confirmed by digestion). These changes in base sequence result in five amino acid differences including a glycine at position 3 of the *nifD* gene product. This is consistent with the amino acid sequence found by Lundell and Howard (6).



Differences between this sequence and that of Brigle *et al.* (5) are underlined. Arrows indicate changed amino acids.

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*To whom correspondence should be addressed.

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