

Nucleotide sequence of wild-type and mutant *nifR4* (*ntrA*) genes of *Rhodobacter capsulatus*: identification of an essential glycine residue

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The *nifR4* gene of *Rhodobacter capsulatus* has been sequenced and found to be homologous with the *ntrA*(*rpoN*) genes of other bacteria (1). A large number of mutations have been mapped to this locus, including many spontaneous mutations (2). A 2.1kb *Hind*III fragment containing the wild-type gene from *R. capsulatus* strain B10 (3) was cloned in pUC18 and sequenced enzymatically with Sequenase, using synthetic oligonucleotides as primers. Both strands were sequenced completely. The nucleotide sequence of the presumed coding region shown below differed in three places from the previously published sequence, and the resulting changes in the amino acid sequence are underlined. The altered base sequence between positions 1762 and 1777 gave an improved amino acid sequence homology with the products of other *ntrA* genes, due to the presence of a glutamate residue at position 377 (1).

The *nifR4* genes from four mutant strains (2) were isolated and sequenced. In three strains, RC18 (G-1705 → A), RC19 (C-683 → T) and RC23 (C-683 → T), the mutation resulted in the formation of a nonsense codon. In the fourth strain, RC20 (G-966 → A), the mutation resulted in the substitution of Asp for Gly-108. The glycine residue at this position, corresponding to position 152 in *Klebsiella pneumoniae*, is conserved in all the *ntrA* genes sequenced (4).

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644 ATGGAACCTCGCGCAGACGCTTCCCAAAGACAGCATGCAGATGGCGGGGCGAGTGCCTCCATCCCTCGCCATCCTTGGCATGTGTCGCGAGGATTTGT
 1 M E L A Q T L S Q R Q T M Q M A G Q M L H S L A I L G M S S Q D L

744 CCGAGCATCTGACCGAACAGGCCACATCGAAACCCCTTTCTGACCTACCGCGCCCGGCCCTTCATCGCCCGGGCGCGAGGATTTGACGCGCGTGGG
34 S E H L T E Q A T S N P F L T Y R A P P A F I A R G G E D F D A V G

844 CGCGGTGGCGCGCACAAAGCCGCTGATGGCCCATGTGGTCGATCAGATCGAGATGGCCTTCAACGAGACCCCGACCGGCTGCTGGCGCTCGCCTTT
68 A V A A H K P S L M A H V V D Q I E M A F T E T P D R L L A L R F

944 GCGGAGCGCTGGAGCGCGAGCGCTGGCTGGCGCAGAGCCTCGACAGCATCGCGCTGGCGGGCGGGGTGTCGCTTTCGCGCGCGCAATCGATGCTGGCGG
101 A E A L E P S G W L G Q S L D S I A L A A G V S L S R A E S M L A

1044 TCCTCGAGGGCTTCGAGCCTACCGGCCCTTTTCGCGCGGACCTGTGCGATTGCGTGTGCTGCTGCAGCGCGCGAGGCGGACATCCTGACCTGGGAAGTCGA
134 V L Q G F E P T G L F A R D L S D C L I L Q A R E A D I L T W E V E

1144 AACGCTGATCCGCAACATTCGGCTGATCGCGAAAACCGGCTGTCGATCTGGCCGATCTTTGGCATTGCGACATCCCGGACATCCCGAAATCATCAAG
168 T L I R N I R L I A E N R L S D L A D L C D C I G D I P E I I K

1244 CAGATCCGGCACTTGAACCGGAAGCCGGGCTTGCCTTCGACCATCAGCCGACGCGCGTTTTCGCGCGGATCTGATCGCGCTGCGCGGGCGCGAGGGCT
201 Q I R H L N P K P G L A F D H Q P T P V F P P D L I A V R G A E G

1344 GGAACGTTGGAACCTCAACCGGCCCACTCGCCCAAGATCACCCTGCGCGAAGATCGTTTTCGCGATGGCACCCCGATGCGAAGGCGCGCGCGGAACCGGG
234 W T V E L N R A T S P T I T V R E D R F A D G T A D A K A R A E R R

1444 AAGCGTGGCGAGGCGCGGGCGCTGGGAGGCGCTGGAGCGAGCGCGGATACGCTGTTGCGCACCGCCGCGCTGCTGGTGGCGCGGAATCGCGCCTTC
268 R R G R G P G A G E A L E R R G D T L L R T A A V L V A R Q S A F

1544 CTCGACAAAGGGCCCGCCATCTGTTGCGCGTACGCTGGAGGATGTGGCTCGGAACCTGGCCTGCATGCTCGACGATTTGCGCGCGGCTCGCGGGC
301 L D K G P A H L V P L T L E D V A S E L G L H A S T I S R A V S G

1644 GGATGATOCAGACCCAGAACCGGGCGCTCGCGCTGCGGGCGTCTTTTCCGCGCGGCTCGAACCAGGCGGTTGGCGAGGCGGTTGCGCGGACCGCT
334 R M I Q T Q T R A L P L R A F L F S R A V S T Q G G G E A V S R D S L

1744 TGATTTGCTGACGCGCACCGTGGCGGGCGAAGATCGCGAAAACCGCTGTCGGATGATGCGATCGTAGCCTCGCGAAGCGCGGGCTGCGGATCGCG
368 D F V Q R T V G G E D R Q N P L S D D A I V T L A E R A G L R I A

1844 CGGCGGACGTTGGCGAAATACCGCTCGACGCTGGGCTTGCCTCCTCCTACGAGCTCGCGCGCCGCGCGCGCGCTGA
401 R R T V A K Y R S T L G L A S S Y E R R R A A A A R *
    
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