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Nucleotide sequence of the *gyrB* gene of *Pseudomonas putida*

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DNA gyrase is a type II topoisomerase which introduces negative supercoils into closed circular DNA. The two subunits of DNA gyrase are encoded by the genes *gyrA* and *gyrB*. In the course of cloning genes encoding components of the benzoate chemotaxis system of *Pseudomonas putida* strain PRS2000 (1), we cloned the *P. putida gyrB* gene as well as the closely linked genes *dnaA*, *dnaN*, and *recF*. The nucleotide sequence of these latter three genes has been published for *P. putida* strain TN2100 (2). Partial sequence analysis of the corresponding region of the PRS2000 genome indicates that the two strains are very closely related, but not identical. We determined the complete nucleotide sequence of the *gyrB* gene of strain PRS2000 (Fig. 1). The 2418 nucleotide open reading frame codes for a protein of 806 amino acids. The expected molecular weight of 89,900 is in good agreement with the size of the protein produced using the Tabor and Richardson T7 expression system (3). The *P. putida* GyrB protein shares 59% and 68% amino acid identity with the *Bacillus subtilis* (4) and *E. coli* (5) GyrB subunits, respectively, as determined using the analysis programs of Pearson and Lipman (6). Sequence analysis of downstream DNA indicates that *gyrB* is not contiguous with *gyrA*, unlike the gene arrangements in *Staphylococcus aureus* (7) and *Mycoplasma pneumoniae* (8).

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1      TCACCTGTGTAGATCACGAATTACTGAGGGAAGGCTGGCAGACGGAAACGCCAGTTGCTTTGTTCCACGTGGAACAAGGCCGTATCACCC
91     AGACCCACGACCATCGGGAGTGAAGGCATGAGCGAAAATCAAACGTACGACTCCTCCAGCATCAAGGTGCTGAAAGGTTTGGATGCCGTA
                        SD        M  S  E  N  Q  T  Y  D  S  S  S  I  K  V  L  K  G  L  D  A  V
181    CGCAAGCGTCCCGGCATGTACATTGGCGACACCGATGATGGTAGCGGCCTGCACCACATGGTCTTCGAGGTGGTCGACAACTCGATCGAC
        R  K  R  P  G  M  Y  I  G  D  T  D  D  G  S  G  L  H  H  M  V  F  E  V  V  D  N  S  I  D
271    GAAGCCCTCGCCGGTCACTGCGATGACATCACCGTCATCATCCACACGGACGAATCCATCAGTGTGCGCGACAATGGTCGCGGCATTCCG
        E  A  L  A  G  H  C  D  D  I  T  V  I  I  H  T  D  E  S  I  S  V  R  D  N  G  R  G  I  P
361    GTCGACGTGCATAAAGAAGAAGGCGTTTCCGCAGCCGAGGTCATCATGACCGTACTGCACGCCGGCGGTAAGTTCGATGATAACTCCTAC
        V  D  V  H  K  E  E  G  V  S  A  A  E  V  I  M  T  V  L  H  A  G  G  K  F  D  D  N  S  Y
451    AAAGTATCTGGCGGCTTGCACGGCGTAGGTGTTTCTGTTGTGAACGCCCTGTCCGAGAAGCTCGTGCTGACCGTTCGCCGTAGCGGCAAG
        K  V  S  G  G  L  H  G  V  G  V  S  V  V  N  A  L  S  E  K  L  V  L  T  V  R  R  S  G  K
541    ATCTGGGAGCAGACCTACGTTCACGGCGTACCACAAGCGCCGATGGCTGTTGTCGGTGAAAGCGAAACCACCGGTACCCACATCCACTTC
        I  W  E  Q  T  Y  V  H  G  V  P  Q  A  P  M  A  V  V  G  E  S  E  T  T  G  T  H  I  H  F
631    AAGCCGTCGGCTGAGACCTTCAAGAATATCCACTTCAGCTGGGACATCCTGGCCAAGCGTATTCGCGAGTTGTCGTTCCTCAACTCGGGC
        K  P  S  A  E  T  F  K  N  I  H  F  S  W  D  I  L  A  K  R  I  R  E  L  S  F  L  N  S  G
721    GTTGGCATTCTGCTGAAGGATGAGCGCAGCGGTAAGGAAGAGTTCTTCAAATACGAAGGCGGCCTGCGTGCGTTCGTCGAGTACCTGAAC
        V  G  I  L  L  K  D  E  R  S  G  K  E  E  F  F  K  Y  E  G  G  L  R  A  F  V  E  Y  L  N
811    ACCAACAAGACGCCAGTCAACTCCCAGGTGTTCCACTTCAGCGTTCAGCGTGAAGACGGCGTGGGCGTGGAAGTTGCTTTGCAGTGGAAC
        T  N  K  T  P  V  N  S  Q  V  F  H  F  S  V  Q  R  E  D  G  V  G  V  E  V  A  L  Q  W  N
901    GACAGCTTCAACGAAAACCTGCTGTGCTTCACCAACAACATTCCACAGCGCGACGGTGGCACCCACTTGGTGGGCTTCCGTTCTTCGCTG
        D  S  F  N  E  N  L  L  C  F  T  N  N  I  P  Q  R  D  G  G  T  H  L  V  G  F  R  S  S  L
991    ACCCGTAGCCTGAACAGCTACATCGAACAGGAAGGCCTGGCGAAGAAGAACAAGGTGGCGACCACGGGTGACGACGCCCGTGAAGGCCTG
        T  R  S  L  N  S  Y  I  E  Q  E  G  L  A  K  K  N  K  V  A  T  T  G  D  D  A  R  E  G  L
1081   ACCGCGATCATCTCGGTGAAGGTACCGGACCCCAAGTTCAGCTCGCAGACCAAAGACAAGCTGGTTTCCTCGGAGGTGAAAACCGCCGTG
        T  A  I  I  S  V  K  V  P  D  P  K  F  S  S  Q  T  K  D  K  L  V  S  S  E  V  K  T  A  V
1171   GAACAGGAGATGAACAAGTACTTCTCTGACTTTCTGCTGGAAAACCCGAACGAGGCCAAGGCCGTCGTTGGCAAGATGATCGATGCCGCT
        E  Q  E  M  N  K  Y  F  S  D  F  L  L  E  N  P  N  E  A  K  A  V  V  G  K  M  I  D  A  A
1261   CGTGCGCGTGAAGCAGCTCGTAAAGCCCGCGAGATGACTCGCCGCAAAGGTGCGCTGGATATCGCCGGACTGCCAGGCAAGTTGGCGGAC
        R  A  R  E  A  A  R  K  A  R  E  M  T  R  R  K  G  A  L  D  I  A  G  L  P  G  K  L  A  D
1351   TGCCAGGAGAAGGACCCTGCCCTTTCCGAACTGTACCTGGTGGAGGGTGACTCCGCAGGTGGCTCGGCCAAGCAAGGTCGTAACCGTCGT
        C  Q  E  K  D  P  A  L  S  E  L  Y  L  V  E  G  D  S  A  G  G  S  A  K  Q  G  R  N  R  R
1441   ACCCAGGCGATCTTGCCGCTGAAGGGTAAGATCCTCAACGTCGAGAAAGCACGCTTCGACAAGATGATCTCGTCCCAGGAAGTGGGCACG
        T  Q  A  I  L  P  L  K  G  K  I  L  N  V  E  K  A  R  F  D  K  M  I  S  S  Q  E  V  G  T
1531   CTGATCACTGCGCTTGGCTGTGGTATCGGCCGCGAAGAGTACAACATCGACAAGTTGCGTTATCACAACATCATCATCATGACCGATGCT
        L  I  T  A  L  G  C  G  I  G  R  E  E  Y  N  I  D  K  L  R  Y  H  N  I  I  I  M  T  D  A
1621   GACGTTGACGGTTCGCACATCCGTACCCTGCTGCTGACCTTCTTCTTCCGTCAGTTGCCGGAACTGGTCGAGCGTGGCTACATCTACATT
        D  V  D  G  S  H  I  R  T  L  L  L  T  F  F  F  R  Q  L  P  E  L  V  E  R  G  Y  I  Y  I
1711   GCCCAGCCGCCACTGTACAAGGTGAAAAAAGGTAAGCAGGAGCAGTACATCAAGGACGACGAGGCCATGGAAGAATACATGACCCAGTCG
        A  Q  P  P  L  Y  K  V  K  K  G  K  Q  E  Q  Y  I  K  D  D  E  A  M  E  E  Y  M  T  Q  S
1801   GCCCTGGAAGACGCAAGCCTGCACCTGGACGAGTCGGCCCCAGCGGTTTCTGGCGTGCAGCTGGAAAGCCTGGTGAACGAATTCCGTAGT
        A  L  E  D  A  S  L  H  L  D  E  S  A  P  A  V  S  G  V  Q  L  E  S  L  V  N  E  F  R  S
1891   GTCATGAAGACCCTTAAGCGCCTGTCGCGGTTGTACCCGGAAGAGCTGACCGAGCACTTCGTGTACCTGCCTGAGGTGACCCTGGAGCAG
        V  M  K  T  L  K  R  L  S  R  L  Y  P  E  E  L  T  E  H  F  V  Y  L  P  E  V  T  L  E  Q
1981   TTGGGTGACCACGCGGTGATGCAAGCCTGGCTGGCCAAGCTGCAGGAGCGTCTGAACTCCAGCCAGAAGTCTGGCCTGGCTTACAACGCG
        L  G  D  H  A  V  M  Q  A  W  L  A  K  L  Q  E  R  L  N  S  S  Q  K  S  G  L  A  Y  N  A
2071   AGCCTGCGTGAAGACAAAGAACGCAACGTATGGCTGCCGGAAGTGGAAATCACCTCCCACGGCCTGGCCAGCTACATCACGTTCAACCGT
        S  L  R  E  D  K  E  R  N  V  W  L  P  E  V  E  I  T  S  H  G  L  A  S  Y  I  T  F  N  R
2161   GACTTCTTTGGCAGCAATGACTACCGGACCGTCGTCAACATCGGTGCCAAGCTCTCCAGCCTGTTGGGTGAAGGTGCTTACGTACAACGT
        D  F  F  G  S  N  D  Y  R  T  V  V  N  I  G  A  K  L  S  S  L  L  G  E  G  A  Y  V  Q  R
2251   GGTGAACGCCGTAAGGCAATTGTCGAGTTCAAGGAAGGCCTGGACTGGCTGATGAATGAGACCACCAAGCGTCACACCATCCAGCGATAC
        G  E  R  R  K  A  I  V  E  F  K  E  G  L  D  W  L  M  N  E  T  T  K  R  H  T  I  Q  R  Y
2341   AAAGGGCTGGGTGAGATGAACCCGGACCAGCTGTGGGAAACCACCATGGACCCGACCGTTCGCCGTATGCTCAAGGTCACCATCGAGGAT
        K  G  L  G  E  M  N  P  D  Q  L  W  E  T  T  M  D  P  T  V  R  R  M  L  K  V  T  I  E  D
2431   GCGATCGCTGCTGACCAGATCTTCAACACCCTGATGGGTGATGCAGTCGAGCCGCGTCGTGAGTTCATCGAAAGCAACGCGTTGTCGGTG
        A  I  A  A  D  Q  I  F  N  T  L  M  G  D  A  V  E  P  R  R  E  F  I  E  S  N  A  L  S  V
2521   TCGAACCTGGACTTCTGATCAGGTGTAGGTTCACAGAAAAGCTGCACGCTTTCACAAATAGATGACCGGCCGGGCTTCAACCATGGCCCC
        S  N  L  D  F  *
2611   TGTCGGTCACCATCAAGCCCGCCTTCGCGGGCTTTTTTTGCCTGGAATTC
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Figure 1. Nucleotide sequence of the *gyrB* gene and deduced amino acid sequence of the GyrB protein from *Pseudomonas putida* strain PRS2000. SD indicates a possible Shine-Dalgarno site. Arrows indicate a putative transcription terminator.

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