Nucleotide sequence of *Salmonella typhimurium* nitroreductase gene

Masahiko Watanabe, Motoi Ishidate Jr and Takehiko Nohmi
Division of Genetics and Mutagenesis, Biological Safety Research Center, National Institute of Hygienic Sciences, 1-18-1, Kamiyoga, Setagaya-ku, Tokyo 158, Japan

Submitted January 5, 1990 EMBL accession no. X17250

'Classical nitroreductase' is an enzyme involved in the intracellular metabolic activation of mutagenic nitroarenes (1). We have already cloned the nitroreductase gene of *Salmonella typhimurium* TA1538 (2) and determined the nucleotide sequence by dideoxy sequence analysis of both strands. Below is shown the nucleotide sequence of 1690 base fragment which contains an open reading frame of 651 nucleotides with potential to encode the nitroreductase. The maxicell technique was used to identify the nitroreductase and its molecular weight was estimated as 28KDa, which is close to the calculated molecular weight of 23,955. Possible sequence of −35, −10, S.D. and rho-independent transcriptional termination signal are indicated.

ACKNOWLEDGEMENT

Supported by a grant-in-aid from the Japan Health Sciences Foundation.

REFERENCES

1. Rosenkranz,H.S. and Mermelstein,R. (1983) *Mutat. Res.* **114**, 217−267.
2. Watanabe,M. *et al.* (1989) *Mutat. Res.* **216**, 211−220.

```
GGATCCCCAAAAGTCCCTGGTAAATCAACAAATTTACCCCAGCATTGCGCCTGGCTATCACATGAATAAGAAACACTGGATTTCAGTCTA   90
TGCGGGCGAGGATATCACCGTCTCGCTACTCAACGATTTGATAAATGACTCATGGAATCTGGTCGTAGACGGGCTGCCTAAAAGAGAGCA  180
ACTGCGCCTGCGGCCGCGCTGATGCAATAACCGTTTCCGCATTTTCCTCCCTTATCTTTTTACCGATAACCCGGTACCCTGCTGATACAA  270
                                                (-35)                (-10)

AAGGGTACTAAACCAACCAGGAGCATTTATGGATATCGTTTCTGTCGCCTTACAGCGCTACTCCACTAAGGCGTTCGATCCCAGCAAAAA  360
                  (SD)     M  D  I  V  S  V  A  L  Q  R  Y  S  T  K  A  F  D  P  S  K  K

ACTGACCGCCGAAGAAGCGGATAAAATAAAAACACTACTACAGTACAGCCCCTCCAGCACCAATTCCCAGCCGTGGCACTTTATTGTCGC  450
 L  T  A  E  E  A  D  K  I  K  T  L  L  Q  Y  S  P  S  S  T  N  S  Q  P  W  H  F  I  V  A

CAGTACGGAAGAAGGCAAAGCGCGCGTAGCAAAATCCGCTGCCGGAAACTACACGTTCAACGAACGCAAAATGCTGGACGCCTCCCATGT  540
 S  T  E  E  G  K  A  R  V  A  K  S  A  A  G  N  Y  T  F  N  E  R  K  M  L  D  A  S  H  V

GGTGGTCTTCTGCGCCAAAACCGCAATGGATGACGCATGGCTTGAGCGCGTCGTCGATCAGGAAGATGCTGATGGCCGTTTCGCTACGCC  630
 V  V  F  C  A  K  T  A  M  D  D  A  W  L  E  R  V  V  D  Q  E  D  A  D  G  R  F  A  T  P

GGAAGCTAAAGCGGCAAATGATAAAGGTCGCCGCTTTTTCGCCGATATGCACCGCGTCTCGCTGAAAGATGACCACCAGTGGATGGCGAA  720
 E  A  K  A  A  N  D  K  G  R  R  F  F  A  D  M  H  R  V  S  L  K  D  D  H  Q  W  M  A  K

GCAGGTTTATCTGAACGTCGGCAACTTTCTGCTGGGCGTCGCCGCGATGGGTCTCGACGCCGTCCCCATTGAAGGTTTCGACGCCGAGGT  810
 Q  V  Y  L  N  V  G  N  F  L  L  G  V  A  A  M  G  L  D  A  V  P  I  E  G  F  D  A  E  V

GCTCGACGCTGAATTTGGTCTGAAAGAAAAAGGCTATACCAGTCTGGTCGTGGTGCCGGTCGGCCATCATAGCGTCGAGGATTTCAACGC  900
 L  D  A  E  F  G  L  K  E  K  G  Y  T  S  L  V  V  V  P  V  G  H  H  S  V  E  D  F  N  A

CGGGCTGCCGAAATCACGTCTGCCGCTTGAAACCACACTGACGGAAGTTTAATCCCCTGCCTAAGCCGGACGCCCGTCCGGCTTTTTTCA  990
 G  L  P  K  S  R  L  P  L  E  T  T  L  T  E  V  *                 -------> <-------******

CCTTTCTGCCAGGTTCCTCAATGATCAATGGCGCGAAGTGCCAGGTTTTACATCGCTAGTGTTAACTTCCTCTTTCAATTTATTGAAAAT 1080
AAATAACATTTAAAACTGGCACGCCGTTTGCCATATCTGGATACCCCCTATCTGGATGAAGGAGAAAACGGGTGAGACATGTTTATGTAG 1170
CCAGCCATGGCCCTTTTGCCCGCGGACTTATTAACAGTCTATCGCTGCTGATTGGCGACGAACACGGCGTGACACCGGTTTGCGCCTACG 1260
ATGGCGATATTGTCACCACGGAGCAGCTTGAACAAACCCTCGAAAATCTGATCGCGCAAGCCAACGGCGAAGAAGTGGTGGTGTTTACCG 1350
ATCTGCTCGGCGGCAGCATCAACAATAGCGCCGCGAAAGTGCTGATGCGTCACCGTCACGTTTTTGTGGTGGCTGGCGTCAACATGACCC 1440
TGTTGCTGGAGTTTTTACTCTGTGAAGAAGAAAGCACAGACGCGGCCATTACCTACGCCACCAATGCGGCGCGTGAATCCATTGTCTTTA 1530
TCAACACGCTAATAACACAACCATCCGCTGACCTACAGGGAGAATCCCATGATCAAATTAGTGCGCATTGATTACCGCCTGCTGCACGGC 1620
CAGGTGGTCTTCGCCTGGACCCGGGCGCTGGATATCGACCATATCATCGTCGCTAACGCCAACGCCGCCG 1690
```