

Nucleotide sequence of the *Zymomonas mobilis* alcohol dehydrogenase II gene

Ki-Hong Yoon* and M.Y.Pack¹

Genetic Engineering Center, Korea Institute of Science and Technology, PO Box 131, Cheongryang, Seoul and ¹Department of Biological Science and Engineering, Korea Advanced Institute of Science and Technology, PO Box 150, Cheongryang, Seoul, Korea

Submitted December 6, 1989

EMBL accession no. X17065

The structural gene (*adhB*) encoding an alcohol dehydrogenase II from *Zymomonas mobilis* strain ATCC 10988 was cloned into *Escherichia coli* by means of allyl alcohol selection. The complete coding region of *adhB* gene was sequenced on both strands by the Sanger method (1). Juxtaposition of the sequences showed difference in 13 nucleotide bases between the *adhB* gene of *Z. mobilis* ATCC 10988 and that of ZM4 reported previously (2) which causes one amino acid substitution of the enzyme (the small

letters indicate the sequence of ZM4 in Figure). The length of both coding regions was composed of 383 amino acids.

REFERENCES

1. Sanger, F., Nicklen, S. and Coulson, A.R. (1977) *Proc. Natl. Acad. Sci. USA* **74**, 5463–5467.
2. Conway, T., Sewell, G.W., Osman, Y.A. and Ingram, L.O. (1987) *J. Bacteriol.* **169**, 2591–2597.

```

ATGGCTTCTCAACTTTTTATATTCCTTTCGTCACGAAATGGGCGAAGCTTCGGTTGAAAAAGCAATCAAGGATCTTAACGGCAGCGGCTTTAAAAATGCCCTGATCGTTTCTGATGCT
MetAlaSerSerThrPheTyrIleProPheValAsnGluMetGlyGluGlySerLeuGluLysAlaIleLysAspLeuAsnGlySerGlyPheLysAsnAlaLeuIleValSerAspAla
8
120
TTCATGAACAAATCCGGTGTGTGTAAGCAGGTTCGTCACCTGTGAAAACACAGGGTATTAAATCTCGTGTTTATGATGGCGTTATGCCGAACCCGACTGTTACCGCAGTCTGGAAGGC
PheMetAsnLysSerGlyValValLysGlnValAlaAspLeuLeuLysThrGlnGlyIleAsnSerAlaValTyrAspGlyValMetProAsnProThrValThrAlaValLeuGluGly
8
240
CTTAAGATCCTGAAGGATAACAATTCAGACTTCGTCATCTCCCTCGGTGGTGTCTCCCATGACTGCGCCAAAGCCATCGCTCTGGTCGCAACCAATGGTGGTGAAGTCAAAGACTAC
LeuLysIleLeuLysAspAsnSerAspPheValIleSerLeuGlyGlyGlySerProHisAspCysAlaLysAlaIleAlaLeuValAlaThrAsnGlyGlyGluValLysAspTyr
8
480
GAAGGTATGCACAAATCTAAGAAACCTGCCCTGCCTTTGATGTCATCAACACAGCGGTGGTACGGCTTCTGAAATGACGGCTTCTGCATCATCACTGATGAAGTCGTCACGTTAAG
GluGlyIleAspLysSerLysLysProAlaLeuProLeuMetSerIleAsnThrThrAlaGlyThrAlaSerGluMetThrArgPheCysIleIleThrAspGluValArgHisValLys
8
600
ATGGCCATTGTTGACCGTCACGTTACCCGATGGTTTCGTCACAGTCTCTGTTGATGGTGGTATGCCAAAAGGCGCTGACCGCGCCACCGGTATGGATGCTCTGACCCACCGCATTT
MetAlaIleValAspArgHisValThrProMetValSerValAsnAspProLeuLeuMetValGlyMetProLysGlyLeuThrAlaAlaThrGlyMetAspAlaLeuThrHisAlaPhe
8
720
GAAGCTTATTCTTCAACGGCAGCTACTCCGATCACCGATGCTTCCGCTTTGAAAGCAGCTTCCATGATCGCTAAGAATCTGAAGACCGCTTCCGACAAACGGTAAGGATATGCCAGCTCGT
GluAlaTyrSerSerThrAlaAlaThrProIleThrAspAlaCysAlaLeuLysAlaAlaSerMetIleAlaLysAsnLeuLysThrAlaCysAspAsnGlyLysAspMetProAlaArg
8
840
GAAGCTATGGCTTATGCCAAATTCCTCGCTGATGGCTTCAACAACGCTTCGCTTGGTTATGCCATGCTATGGCTCACCAGTTGGGCGGTTACTACAACCTGCCGATGGTCTCTCC
GluAlaMetAlaTyrAlaGlnPheLeuAlaGlyMetAlaPheAsnAsnAlaSerLeuGlyTyrValHisAlaMetAlaHisGlnLeuGlyGlyTyrTyrAsnLeuProHisGlyValCys
8
960
AAGCGTGTCTGCTTCCGCATGTTCTGGCTTATAACGCCTCTGCTGCTGCTGAAAGAGCTGGTGTGCTATGGTCTCGATATCGCCAATCTGGCGATAAAGAAGGGCGCA
AsnAlaValLeuLeuProHisValLeuAlaTyrAsnAlaSerValValAlaGlyArgLeuLysAspValGlyValAlaMetGlyLeuAspIleAlaAsnLeuGlyAspLysGluGlyAla
8
1080
GAAGCCACCATTCAGGCTGTTCGGATCTGGCTGCTTCCATTGGTATTCCAGCAATCTGACCGAGCTGGTGCTAAGAAGAAGATGTCGGCTTCTTCTGCTGACCAAGCTCTGAAAGAT
GluAlaThrIleGlnAlaValArgAspLeuAlaAlaSerIleGlyIleProAlaAsnLeuThrGluLeuGlyAlaLysLysGluAspValProLeuLeuAlaAspHisAlaLeuLysAsp
1149
383
GCTTGTGCTCTGACCAACCGCGTCAGGGTATCAGAAAAGTGAAGAAGTCTTCTGAGCGCTTCTAA
AlaCysAlaLeuThrAsnProArgGlnGlyAspGlnLysGluValGluGluLeuPheLeuSerAlaPhe***

```

* To whom correspondence should be addressed