

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

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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.

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ATGGCTTCTCAACTTTTTATATTCCTTTCGTCACGAAATGGGCGAAGCTTCGGTTGAAAAAGCAATCAAGGATCTTAACGGCAGCGGCTTTAAAAATGCCCTGATCGTTTCTGATGCT      8      120
MetAlaSerSerThrPheTyrIleProPheValAsnGluMetGlyGluGlySerLeuGluLysAlaIleLysAspLeuAsnGlySerGlyPheLysAsnAlaLeuIleValSerAspAla
TTCATGAACAAATCCGGTGTGTGTAAGCAGGTTCGTCACCTGTGAAAACACAGGGTATTAAATCTCGTGTTTATGATGGCGTTATGCCGAACCCGACTGTTACCGCAGTCTGGAAAGGC      8      240
PheMetAsnLysSerGlyValValLysGlnValAlaAspLeuLeuLysThrGlnGlyIleAsnSerAlaValTyrAspGlyValMetProAsnProThrValThrAlaValLeuGluGly
CTTAAGATCCTGAAGGATAACAATTCAGACTTCGTCATCTCCCTCGGTGGTGTCTCCCATGACTGCGCCAAAGCCATCGCTCTGGTCGCAACCAATGGTGGTGAAGTCAAAGACTAC      8      360
LeuLysIleLeuLysAspAsnSerAspPheValIleSerLeuGlyGlyGlySerProHisAspCysAlaLysAlaIleAlaLeuValAlaThrAsnGlyGlyGluValLysAspTyr
GAAGGTATGCACAAATCTAAGAAACCTGCCCTGCCTTTGATGTCATCAACACAGCGGTGGTACGGCTTCTGAAATGACGGCTTTCTGCATCATCACTGATGAAGTCGTCACGTTAAG      8      480
GluGlyIleAspLysSerLysLysProAlaLeuProLeuMetSerIleAsnThrThrAlaGlyThrAlaSerGluMetThrArgPheCysIleIleThrAspGluValArgHisValLys
ATGGCCATTGTTGACCGTCACGTTACCCGATGGTTTCGTCACAGTCTCTGTTGATGGTGGTATGCCAAAAGGCGCTGACCGCGCCACCGGTATGGATGCTCTGACCCACCGCATTT      8      600
MetAlaIleValAspArgHisValThrProMetValSerValAsnAspProLeuLeuMetValGlyMetProLysGlyLeuThrAlaAlaThrGlyMetAspAlaLeuThrHisAlaPhe
GAAGCTTATTCTTCAACGGCAGCTACTCCGATCACCGATGCTTCCGCTTTGAAAGCAGCTTCCATGATCGCTAAGAATCTGAAGACCGCTTCCGACAAACGGTAAGGATATGCCAGCTCGT      8      720
GluAlaTyrSerSerThrAlaAlaThrProIleThrAspAlaCysAlaLeuLysAlaAlaSerMetIleAlaLysAsnLeuLysThrAlaCysAspAsnGlyLysAspMetProAlaArg
GAAGCTATGGCTTATGCCAAATTCCTCGCTGTTGCGCTTCAACAACGCTTCGCTTGGTTATGTCATGCTATGGCTCACCAGTTGGGCGGTTACTACAACCTGCCGATGGTCTCTCC      8      840
GluAlaMetAlaTyrAlaGlnPheLeuAlaGlyMetAlaPheAsnAsnAlaSerLeuGlyTyrValHisAlaMetAlaHisGlnLeuGlyGlyTyrTyrAsnLeuProHisGlyValCys
AAGCTGTTCTGCTTCCGCATGTTCTGGCTTATAACGCCTCTGCTGTTGCTGCTGAAAGAGTGGTGGTCTATGGTCTCGATATCGCCAATCTGGCGGATAAAGAAGGGCGCA      8      960
AsnAlaValLeuLeuProHisValLeuAlaTyrAsnAlaSerValValAlaGlyArgLeuLysAspValGlyValAlaMetGlyLeuAspIleAlaAsnLeuGlyAspLysGluGlyAla
GAAGCCACCATTCAGGCTGTTCGGATCTGGCTGCTCCATTTGGTATTCCAGCAAACTGACCGAGCTGGTGCTAAGAAGAAGATGTCGGCTTCTTCTGCTGACCAAGCTCTGAAAGAT      8      1080
GluAlaThrIleGlnAlaValArgAspLeuAlaAlaSerIleGlyIleProAlaAsnLeuThrGluLeuGlyAlaLysLysGluAspValProLeuLeuAlaAspHisAlaLeuLysAsp
GCTTGTGCTCTGACCAACCGCGTCAGGGTATCAGAAAAGTGAAGAAGTCTTCTGAGCGCTTCTCTAA      1149
AlaCysAlaLeuThrAsnProArgGlnGlyAspGlnLysGluValGluGluLeuPheLeuSerAlaPhe***      383
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* To whom correspondence should be addressed