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The nucleotide sequence of 3-isopropylmalate dehydrogenase gene from *Bacillus subtilis*

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FEATURES: The genes coding for 3-isopropylmalate dehydrogenase from Bacillus coagulans (facultative thermophile) and B. caldotenax (obligate, moderate thermophile) were sequenced (1,2). The B. subtilis leu gene has already been cloned in Escherichia coli by Nagahari and Sakaguchi (3). In order to compare the amino acid and nucleotide sequences of the mesophile to those of the thermophiles, the B. subilis gene was sequenced.

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TTGAAGAAACGTATTGCTCTATTGCCCGGAGACGGGATCGGCCCTGAAGTATTAGAATCAGCGACAGACGTACTGAAAAGTGTTGCCGAACGCTTTAACCATGAATTTGAATTTGAATAT  120
 M  K  K  R  I  A  L  L  P  G  D  G  I  G  P  E  V  L  E  S  A  T  D  V  L  K  S  V  A  E  R  F  N  H  E  F  E  F  E  Y

GGCCTGATTGGAGGGGCGGCTATTGATGAACATCATAACCCCCTCCCGGAGGAAACCGTTGCTGCTTGTAAAAATGCAGACGCGATATTGCTTGGTGCTGTCGGCGGACCGAAATGGGAT  240
 G  L  I  G  G  A  A  I  D  E  H  H  N  P  L  P  E  E  T  V  A  A  C  K  N  A  D  A  I  L  L  G  A  V  G  G  P  K  W  D

CAAAACCTTTCGGAACTGAGACCGGAAAAAGGGCTGCTCAGCATCAGAAAACAGCTTGATTTGTTTGCGAATTTGCGGCCTGTGAAGGTATTTGAAAGCCTTTCTGACCGTTCGCCTTTG  360
 Q  N  L  S  E  L  R  P  E  K  G  L  L  S  I  R  K  Q  L  D  L  F  A  N  L  R  P  V  K  V  F  E  S  L  S  D  R  S  P  L

AAAAAAGAATATATAGATAATGTTGATTTCGTTATCGTTCGTGAGCTCACAGGCGGCTTGTATTTCGGCCAGCCGAGCAAACGTTATGTAAACACTGAAGGTGAGCAGGAAGCAGTAGAT  480
 K  K  E  Y  I  D  N  V  D  F  V  I  V  R  E  L  T  G  G  L  Y  F  G  Q  P  S  K  R  Y  V  N  T  E  G  E  Q  E  A  V  D

ACACTGTTTTATAAGCGAACGGAAATTGAACGAGTGATCAGAGAGGGCTTCAAAATGGCGGCAACCAGAAAAGGCAAAGTGACCTCTGTAGATAAAGCGAATGTTCTTGAATCAAGCCGG  600
 T  L  F  Y  K  R  T  E  I  E  R  V  I  R  E  G  F  K  M  A  A  T  R  K  G  K  V  T  S  V  D  K  A  N  V  L  E  S  S  R

CTGTGGCGTGAAGTGGCTGAGGACGTTGCACAAGAATTTCCTGATGTGAAGCTTGAGCACATGCTTGTGGATAACGCGGCCATGCAGCTAATTTATGCACCGAATCAATTTGATGTCGTG  720
 L  W  R  E  V  A  E  D  V  A  Q  E  F  P  D  V  K  L  E  H  M  L  V  D  N  A  A  M  Q  L  I  Y  A  P  N  Q  F  D  V  V

GTGACTGAAAATATGTTCGGTGATATTTTAAGCGATGAAGCGTCCATGCTTACAGGCTCGCTCGGAATGCTCCCGTCAGCCAGCCTATCAAGCTCTGGCCTTCATCTGTTTGAACCTGTT  840
 V  T  E  N  M  F  G  D  I  L  S  D  E  A  S  M  L  T  G  S  L  G  M  L  P  S  A  S  L  S  S  S  G  L  H  L  F  E  P  V

CATGGCTCCGCGCCTGATATTGCCGGTAAAGGGATGGCAAATCCGTTCGCAGCCATATTGTCAGCGGCAATGCTTTTGAGAACATCTTTCGGGCTTGAAGAGGAAGCGAAAGCTGTAGAA  960
 H  G  S  A  P  D  I  A  G  K  G  M  A  N  P  F  A  A  I  L  S  A  A  M  L  L  R  T  S  F  G  L  E  E  E  A  K  A  V  E

GATGCGGTAAACAAAGTCTTGGCTTCTGGAAAAAGAACAAGAGACTTGGCACGGAGTGAAGAGTTCAGCAGCACTCAGGCCATTACAGAGGAAGTTAAGGCAGCAATCATGAGTGAAAAT 1080
 D  A  V  N  K  V  L  A  S  G  K  R  T  R  D  L  A  R  S  E  E  F  S  S  T  Q  A  I  T  E  E  V  K  A  A  I  M  S  E  N

ACAATTTCTAATGTGTGA
 T  I  S  N  V  ***
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COMMENTS: The G+C contents of coding region and third letter of the codon for the B. subtilis enzyme were 46.5 and 44.1%, respectively. The values were lower than those for the B. coagulans (53.1 and 55.7%, respectively) (1) and the B. caldotenax (56.7 and 65.2%, respecctively) (2).

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