Nucleotide sequence of the *Adh* gene of *Drosophila lebanonensis*

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Drosophila lebanonensis is a member of the victoria group of the *Scaptodrosophila* radiation. A lambda-charon 35 library was constructed and the *Adh* gene was isolated and cloned into the Bluescript +KS, +SK phasmids (Stratagene). A series of nested deletions were generated in order to sequence large regions across the restriction sites (Henikoff, 1984). Sequencing was performed either on a single stranded DNA or double stranded DNA using the dideoxy method (Sanger *et al.*, 1977). The *Adh* coding region has been compared with *D. pseudoobscura* and *D. melanogaster*. The level of homology is 76.9% and 77.5% respectively.

ACKNOWLEDGEMENT

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REFERENCES

1. Henikoff, S. (1984) *Gene* 28, 351-359.
2. Sanger *et al.* (1977) *Proc. Natl. Acad. Sci. USA* 74, 5463-5467.

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1   CGGTCGCTTGTTCATATAGTTTCATACACATACGATACATACGAGTATGTACATACGTGGGCAATTGTATAAGCATTATTACAAAATATAGAATGCAAA
101  ATACACACGAGTCGTCGGGTGGCGATGCTTCAGCTCTTCCGCGTTCATCTGGCTGGGTATTTAAAGCGCGTTATACGCCCTAGGACGACGATTATTGTC
201  AGTGCAGTGGTGGCGTTCGTGTTTCAGCAGCGATTTCGAGACCAACGGCTAATTCTAACGGAATTACGAGTATTACAAAATCTATTATTGGAAGCGGTGAG
301  TTGAGTGTCTAGAAGCGACAGTAAAGTGTGGGAGAACTTTAGAAAGCAGTGATAAAAGAGAACTTTAAATAACCGAAAAATATCAACAAATTGCCGATAAA
401  GAACAATTAAAGTAATAGCTGTAAAAAGCTCTACACTTCGTATGGAATTTGTAGTTAATTTCTACGACTACTTTTGCCAGCACAATAGTGATAGACACCA
501  TTCTTGATTTGTTTCGTTCATCTACTATGACTGCGAGAATTTTTAATGTCTAGGACAATGATAGAGCGATAAAAGCGACTAGACATAGACTAGACACTCTT
601  CCAACAATTAGCGACTAGACACAGACTACACACTCTTCCTAGTAATTCGATAATTTTTTTTTTAAATTTAATAATTAAAGTCAGACGATAAGTTATCGT
701  CTGAAAAGCATTGAAAAAGAAAGCCAGACGAGCTATAGACATCGAACTAGAACTAGAAAAAGTAAGCGTAACATGACCAAGCGATTACATATCGTT
801  CTCGCAGTAAATTCAAATATACAGGAATTTAACGAACTAGTACTAATAATAAAGTCGGCGCGCTCTTTCTGTTTGCTGCCCGCCGACTGATAG
901  CAACAAATGCTTGCCGGCCGCTCGGTCGGCATAACGTAGAAGATTATAATGCTGTGAAAAAACCAAAACAAATAATATGCTGGCGAAGTACTATTTTC
1001 AGGATATTCTTTTCGTTGCGCGACTTCGGCTAGTGTTCATCGAGCACATGTAGAGAGCTACGTAATCGCTATTAACAGAGCTCTGTTAACTTAACATACA
1101 TACATACATACATATGTGTGTATATGATCGTTTGATAAGACATGAATGGTGAGCGTGTTAATGTTGTACCGAAAAGAAATAAATACATACAGACGTTTAC
1201 ATAAAACAAACGACGCGACAGTACGAGGTTGTTTGTCTATTTGTAGCGATAAGAGCGACGCGATGTGTGCAAAATTTTCACATAAATAGCCCGACTAGCT
1301 AACAGATCTCATTCGCATTTTCAGCAGCCAGCAACAAACAGTTAGAGGCACAAGATGGATTGACCAACAAGAACGTTATTTTCGTTGCCGCTCTGGGC
1401 GGTATTGGTCTCGACACGAGTCGGGAGCTCGTCAAGCGTAATCTGAAGGTGAGTCCAACCGTAATCTCTGCTGGAGATGAAACGATTAAACGATTCTG
    MetAspLeuThrAsnLysAsnValIlePheValAlaAlaLeuGly
    GlyIleGlyLeuAspThrSerArgGluLeuValLysArgAsnLeuLys
1501 CGTCCACAGAATTTGTCTATCTTGACAGAGTTGAGAACCGACTGCTCTTGCTGAGCTGAAGGCAATAAATCCCAAGGTGAACATCACCTTCCATACCT
    AsnPheValIleLeuAspArgValGluAsnProThrAlaLeuAlaGluLeuLysAlaIleAsnProLysValAsnIleThrPheHisThrT
1601 ACGATGTGACCGTACCCGTTGCTGAGTCGAAGAAGCTGCTGAAGAAGATTTTCGATCAGCTGAAAACCGTTGACATCTGATCAATGGTGTGCTGATT
    yrAspValThrValProValAlaGluSerLysLysLeuLeuLysLysIlePheAspGlnLeuLysThrValAspIleLeuIleAsnGlyAlaGlyIleLe
1701 GGATGACCATCAGATTGAGCGCACCATTGCCATCACTTCACTGGTCTGGTCAACACCACCACCGCTATTTTGGACTTTTGGGACAAGCGTAAGGGCGGT
    uAspAspHisGlnIleGluArgThrIleAlaIleAsnPheThrGlyLeuValAsnThrThrThrAlaIleLeuAspPheTrpAspLysArgLysGlyGly
1801 CCTGGTGGCATCATTGCCAACATTTGCTCCGTTACTGGCTTCAATGCCATCCACCAGGTGCTGTCTACTCGGCATCCAAGGCTGCTTTGTGACGTTCA
    ProGlyGlyIleIleAlaAsnIleCysSerValThrGlyPheAsnAlaIleHisGlnValProValTyrSerAlaSerLysAlaAlaValValSerPheT
1901 CAAATTCCTGGCGGTAGGAGTATAGCATTGGATTCTCTTATATAATATTAAGAACATTTATAATGTTTTATATAGAACTGGCTCCCATCACTGGC
    hrAsnSerLeuAla
    LysLeuAlaProIleThrGly
2001 GTTACTGCCTATTCGATCAACCTGGCATCACCAGGACCCCTTGGTGCACACTTTCAACTCCTGGCTGGATGTAGAGCCACGTTGTCGCAACTGCTGC
    ValThrAlaTyrSerIleAsnProGlyIleThrArgThrProLeuValHisThrPheAsnSerTrpLeuAspValGluProArgValAlaGluLeuLeuL
2101 TGTCCCATCCAAACCCAGACCTCCGAGCAATGCGGTGAGAACTTTGTCAAGGCCATTGAGGCCAACAAAGAAATGGCGCCATATGGAAATTGGATCTGGGCAC
    euSerHisProThrGlnThrSerGluGlnCysGlyGlnAsnPheValLysAlaIleGluAlaAsnLysAsnGlyAlaIleTrpLysLeuAspLeuGlyTh
2201 CCTTGAGGCCATTGAGTGGACCAAGCACTGGGACTCGCACATCTAAGCATTTCCACGCCATTGTGATAAGATAGACGTGTATACGGAATTGAACAATTAA
    rLeuGluAlaIleGluTrpThrLysHisTrpAspSerHisIle***
2301 TATGAAGTAAGGCTGATTGATAAAGCTTCCATGTTGTCGAACGCTGAATGGTCAATTTGTTATTTTATGAAAATATATCGAAGAGAATTC

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