Nucleotide sequence of the *luxA* and *luxB* genes of the bioluminescent marine bacterium *Vibrio fischeri*

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Luminescence in marine bacteria is catalyzed by the heterodimeric enzyme luciferase, whose alpha and beta subunits are encoded by the *luxA* and *luxB* genes respectively (1). In *Vibrio harveyi*, these genes have been sequenced (2,3). We have determined the nucleotide (nt) sequence of both strands of a cloned DNA fragment that contains these genes from a second species, *V. fischeri* strain MJ-1 (4). Start and stop codons are underlined. *luxA* (start=289) and *luxB* (start=1392) are 1065 and 981 nt in length (355 and 327 aa), respectively, and are separated by 38 nt. The 3' end of an open reading frame encoding an aldehyde gene (4) is 30 nt upstream of *luxA* (position 256). The purine ambiguity at position 1445 in the *luxB* sequence, silent with respect to amino acid (aa) replacement, was unresolvable by repeated sequencing. Because the first four aa's of the alpha and beta subunits are identical in both *V. harveyi* and *V. fischeri*, it was proposed that *luxA* and *B* resulted from a gene duplication (5). Our data strengthen this conclusion. When aligned, the derived aa sequences for *luxA* and *luxB* of *V. fischeri* are identical at 28.5% of their positions and their hydrophathy profiles are similar. The aa sequences derived from *luxA* of *V. harveyi* and *V. fischeri* are 63% identical, those for *luxB* are 52% identical, and those derived from the portions of the upstream aldehyde gene are 62% identical.

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GAGCTCATTGATAGCATTGAATCTAGTAATTTGAAGCTCTATTGCGCTAATTGGAAAGTTACATGATCTTGGGGAAAAATTTGGTTGTATTAAGAAATTTTATCAATCAGTGACGAAGGCA 120
GCCTTAGCATTAGATGATGGTTTATTTGGATTAGAGATAGACATTATGAACCTCGATTGGAGACGTTACAAGTATTACTGTTAAGGAGCGTAGATTAAGAAATGAATGAAATGAA 240
TTATTAGAATTTGGCTTAATAAACAGAAATCACCAAAAAGGAATAGAGATGAAGTTTGGAAATATTTGTTTTCGTATCAACCCAGGTTGAACCTCTAAGCTAAGTAAGTGAATCGCTT 360
TGTTCCGGCTGGTATCGCTCAGAGAAGATGGGTTTGATACATATTGGACCTTGAAGACATCATTTTACAGAGTTTGGCTTACCGGGAATTTATTTGTTGCTGGCGTAACTGTTAGGA 480
AGAACATAAACATTAAATGTTGGCAGTATGGGGTTGTTATTCGACAGCACCCAGTTCGACAGTTAGAAGACGTTTATTAATAGATCAATGTGGAAGGCTGTTTAAATTTTGA 600
ACCGTTCGAGGGCTATACCATAAAGATTTTCGAGTATTTGGTGTGATATGGAAGAGTCTCGAGCAATTACTCAAAATTTCTACAGATGATAATGGAAGCTTACAGACGGAACCAT 720
AGCTCTGATAGTGATTACATTCATTTCCTAAGGTTGATGTATATCCCAAGGTGACTCAAAAATGTACCAACCTGTATGACTGCTGAGTCCGCAAGTACGACAGATGGCTAGCAATA 840
CAAGGGCTACCAATGGTTCTAGTTGGATTATTTGGTACTAATGAAAAAAGGACAGATGGAACCTATATAAGAAATGGCAGCAAGATGGTCTATGATATATCTAAATAGATCATTTG 960
ATGACTTATATTTGTTCTGTTGATGATGACCAAAAAGGCGCAAGATGTTTGGGGAGTTTCTGAAAAATTTGGTATGACTCATATGTAATGGCAACCAATCTTTAATGATAGCAAT 1080
CAAACTCGTGTTTATGATTATCATAAAGGTCAATGGCGTATTTGTTTACAAGGACATACAACACCAATCGACGTGTTGATTATAGCAATGGTATTAAACCTGTAGGCACTCTGAG 1200
CAGTGATTGAAATCATCAACGTGATATTGATGCAACGGGATTTACAAACATTACATGCGGATTTGAAGCTAATGGAAGTGAAGATGAAATTAATGCTTCCATGCGACGCTTTATGACA 1320
CAAGTCGCTCTTCTTAAAGAACCTAAATTAATTACTTATTTGATGACTAGAGATAATAAGGAACAAGTTATGAATTTGGATTATTTTCTAACTTTGAGAAGATGGAATAACAT 1440
CTGARGAAACGTTGGATAATATGGTAAAGACTGTACCGTTAATTTGATTCACCTAAATATCATTTTAATACTGCCCTTTGTTAATGAACATCACTTTTCAAAAATGGTATTGTTGGAGCAC 1560
CTATTACCGCAGCTGGTTTTTATTAGGGTTAAACAAATAAATACATATTTGGTTCATTAATCAAGTAATACCACCCATCACTTGTACGTGTAGCAGAGAAGACCGCTTTATTAGATC 1680
AAATGTCAGAGGGGCGCTTCACTCTTGGTTTATGAGTCTGCGAAAGTGATTTGCAAAATGGAAATTTTATAGACGTATATCTCATCAAGGCAACAACATTTGAAGCATGCTATGAATAA 1800
TAAATGACGCAATTAATACAGGTTATTTGTCATCCCCAAACGACTTTTATGATTTTCCAAAGTTTCAATTAATCCACACTGTTACAGTGAGAATGGACCTTAAGCAATATGATCCGCTA 1920
CATCAAAAAGTGCATGCTGTTGGGCGCAAAAAGGCACTGCTTTTAACTTTAAGTGGGAGGATAATTTAGAACCAAGAAGACGCTATGCAATCTATATAATAAAGACAGCAACAAT 2040
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TTCCTTTTAAATTTCTGTTGATATTAGGATATTACGAGAGGGTATGACTGCTCATCTGAATATAAAGAAATCAATCATTGCTAGTTGAGAAATGATGATCTTATGAC 2520
GAACCCACAGAGTGGTCTATTGAAGAGCAAAAAGAAATACGGGATAAAT

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