动物遗传学

日本七鳃鳗(Lampetra japonica)口腔腺表达序列标签(EST)分析

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摘要 以日本七鳃鳗口腔腺为材料,构建库容量为2.1×106 pfu/mL的cDNA文库。通过对文库中克隆子的序列测定和生物信息学初步分析,得到1 323条有效EST序列。经BlastX及BlastN软件进行同源对比分析,653条(49.36%)EST可在蛋白质或核苷酸水平上找到同源序列,其中328条与七鳃鳗科物种同源。同源序列功能分类大致分为12类,与蛋白质合成有关的蛋白所占比例最大。1 323条EST进行片段重叠群分析(conting analysis)获得包括547条序列在内的162组片段重叠群并确定了8条全长cDNA。日本七鳃鳗口腔腺cDNA文库以及EST文库的成功构建,为研究日本七鳃鳗口腔腺的功能基因和蛋白质组学奠定了基础。

Expressed Sequence Tags (ESTs) Analysis of the Oral Gland of Lampetra japonica

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Abstract

A cDNA library was constructed from the oral gland of Lampetra japonica. By sequencing the randomly selected clones, 1 323 sequences longer than 100 bp with better chromatogram show were acquired. 653 ESTs shared significant similarity with known sequences in protein or nucleotide databases of NCBI after being analyzed using BlastX and BlastN softwares, and were classified into 11 different functional categories. The highest proportion of the numbers of ESTs was protein synthesis, including 328 ESTs similarity with the known sequences of Petromazonidae animals. With the 1 323 ESTs, 162 non-redundant contings were generated after aligned using software at the threshold of more than 90% homoloy over a minimum of 20 base pairs. There were eight full-length cDNAs had complete ORF. Further studies on the ESTs of the library maybe helpful to elucidate the components of Lampetra japonica oral gland and understand the function of those protein at molecular level.

Key words Lampetra japonica oral gland cDNA library EST

DOI:

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