

研究报告

5种鲟鱼免疫球蛋白重链恒定区序列研究

王 荻^{1,3}, 刘红柏^{1,2}

1. 中国水产科学研究院黑龙江水产研究所, 哈尔滨 150070; 2. 东北农业大学博士后流动站, 哈尔滨 150030; 3. 东北林业大学野生动物资源学院, 哈尔滨 150040

收稿日期 修回日期 网络版发布日期 2006-9-29 接受日期

摘要 为了探讨几种鲟鱼免疫球蛋白(IgM)所包含的信息与其亲缘和进化之间的关系, 分别对俄罗斯鲟(*Acipenser. gueldenstaedtii*)、小体鲟(*A. ruthenus*)、施氏鲟(*A. schrenckii*)、中华鲟(*A. sinensis*)和欧鳊(*Huso huso*)的IgM重链(IgH)恒定区进行了研究。采用RT-PCR的方法对IgH核酸序列进行了克隆, 通过软件获得了相应的IgH氨基酸序列。在分别对这5种鲟鱼免疫球蛋白重链恒定区4个区(CH1~CH4)进行研究后发现, 其CH4区氨基酸序列相似性最高。通过对CH4区序列氨基酸变异期望值(Kaa), 物种分化时间(T)及物种间系统进化树(Phylogenetic Tree)等参数的分析, 将克隆的5种鲟鱼IgH恒定区序列与已发表的西伯利亚鲟同源序列比对(源于NCBI序列)后发现: 西伯利亚鲟与俄罗斯鲟、施氏鲟与欧鳊、小体鲟各构成一个分支, 并与中华鲟相对。实验结果从体液免疫系统的演化这个角度, 反映了被研究的鲟鱼物种间的分类地位、地理分布及进化关系之间的联系。

关键词 [免疫球蛋白](#) [重链](#) [恒定区](#) [鲟鱼](#) [进化关系](#)

分类号 [Q953](#)

A Rresearch on Ig Heavy Chain Constant Region of Five Acipenseridae

WANG Di^{1,3}, LIU Hong-Bai^{1,2}

1. Heilongjiang River Fishery Research Institute of Chinese Academy of Fishery Science, Harbin 150070, China; 2. Postdoctoral Research Station of Northeast Agriculture University, Harbin 150030, China; 3. Wildlife Resources College of Northeast Forestry University, Harbin 150040, China

Abstract

Abstract: Analyzed the immunoglobulin (Ig) heavy chain constant regions of Russian sturgeon (*A. gueldenstaedtii*); Sterlte sturgeon (*A. ruthenus*); Amur sturgeon (*A. schrenckii*); Chinese sturgeon (*A. sinensis*) and Great sturgeon (*Huso huso*) with molecular biology and bioinformatics methods. We cloned IgH nucleic acid sequences by RT-PCR using the specific primer, then determined the characteristics and functions of the amino acid sequences and plotted out the sequence into four sub-regions (CH1-CH4), of which CH4 sub-regions one another had the highest identity. According to the analysis of the variation expectation value (Kaa), species differentiation time (T) in the CH4 sub-region phylogenetic tree, we found that Chinese sturgeon and the theoretical common ancestor of the other five sturgeon form the first bifurcation of the tree, while, among the five left, Amur sturgeon and Huso sturgeon, Russian sturgeon and Siberian sturgeon, Siberian sturgeon (sequence from GenBank), Sterlte itself form another three bifurcations respectively. This result can clearly explain the relations of taxonomic status, geographical distribution and evolution among the species studied.

Key words [immunoglobulin](#) [heavy chain](#) [constant region](#) [sturgeons](#) [evolutionary relation](#)

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