

载脂蛋白基因家族的密码子空间分析:核苷酸替换的非随机进化选择

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摘要 DNA分子进化中,对核苷酸替换的选择可呈选择中性或选择倾向性。为研究载脂蛋白基因进化过程中对核苷酸变化的选择方式,本文建立了基因的密码子空间分析方法。密码子空间是由密码子3个位置上核苷酸出现机率所组成的矩阵。对该空间中核苷酸分布的非随机性度量可以反映进化过程中核苷酸替换的选择方式。应用该法,我们发现载脂蛋白基因密码子空间第一及第三位的核苷酸分布呈高度非随机性。进一步研究表明:这种核苷酸的非随机分布可能与腺苷酸、胸苷酸对密码子位置的非中性选择有关。此外,还研究了同义密码子的选择使用与分支种系发生的关系。结果显示:载脂蛋白分子演化中存在着同义密码子使用的分子进化钟。这些研究提示密码子空间中核苷酸替换的非随机选择可能是载脂蛋白基因进化的一种特征。

关键词 [分子进化](#) [载脂蛋白](#) [密码子空间](#) [核苷酸非随机分布](#)

分类号

Analysis of Apolipoprotein Gene Family in Codon Space—Non- random Selection of Nucleotide Changes in Evolution

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Abstract

The choice of nucleotide changes in DNA evolution can be either can be either selectively neutral of biased. To study how apolipoprotein gene selects the nucleotide substitutions in the course of evolutionm, a codon space is constructed in which its DNA sequence can be mapped as a matrix of nucleotide frequencies in three codon positions. Accordingly ,a number of mthods that measure the nonrandomnes of nucleotide distribution in codon space are developed based on maximum entropy techniques to define the nature of nucleotide change selection in evolution. By these methods, we demonstrated that the nucleotide composition in 1st and 3rd codon position of apolipoprotein gene is highly nonrandom, which appears to be a result of non-neutral seletion of codon positions by adenosine and thymidine . In additionm this paper is also concerned in the divergence of synonymous condon usage and its correlation to taxonomic distances among species. As a result , a codon usage clock was reported in apolipoprotein A-I. Our studies suggest that non-random selection of nucleotide changes in codon space may represent an evolutionary characteristics of apolipoprotein genes.

Key words [Molecular evolution Apolipoprotein \(Apo\). Codon space Nonrandomness of distribution](#)

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