

DNA序列进化过程中核苷酸替代的非独立性研究

杨子恒

甘肃农业大学畜牧系, 兰州

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摘要 本文评述了DNA序列间核苷酸替代数的估计方法, 并通过对七个物种中组蛋白基因的比较对DNA进化的模型进行了考察。发现H2A基因第三位点上的碱基组成在物种间变异很大, 并且跟H2A基因第一位点、H4基因第一、三位点及H2A上游、下游序列中的碱基组成有强正相关, 提示DNA序列进化过程中存在着物种特异的区域性约束力。可能的原因是高等真核生物中GC含量升高, 或者是染色体重组使这些同源序列位于不同的等质区段, 从而受到不同的选择突变压。密码内各位点上核苷酸替代的相关性分析表明不同位点的替代是非独立的, 其原因可能是一次替代事件引起多个位点的变化。文中讨论了这些结果对进化树推断的意义。

关键词 [分子进化,核苷酸替代,GC含量,组蛋白基因](#)

分类号

Spatial Association of Nucleotide Substitutions During the Evolution of DNA Sequences

Yang Ziheng

Department of Animal Sciences, Gansu Agricultural University, Gansu

Abstract

Evolutionary models for estimating the number of nucleotide substitutions between n DNA sequences are evaluated with data from histone gene sequences of 7 remote species. It is found that the nucleotide compositions at the third codon position of H2A genes vary greatly among species and are highly correlated with the compositions at the first position of H2A genes, with those at the first and third position of H4 genes and with those in the up- and downstream sequences of H2A genes. This implies the existence of regional constraints over DNA sequences during the evolutionary process, which is different over species. Possible causes for the variations are increment of G+C content in higher eukaryotes, and chromosomal recombination, which brought the histone genes onto different isochores and thus under different selective or mutational pressures. Substitutions at different positions in a codon have been found not to be independent, probably due to multiple substitutions. i.e., single substitution events involving multiple sites. The implication of these results to phylogeny inferring is discussed.

Key words [Molecular evolution](#) [Nucleotide substitutions](#) [G+C content](#) [Histone genes](#)

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