

研究论文

嗜热泉生古细菌及其他泉古菌同义密码子使用偏向性分析

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摘要

比较分析了嗜热泉生古细菌(*Aeropyrum pernix* K1)和其他两种系统发育相关的泉古菌[嗜气菌(*Pyrobaculum aerophilum* str. IM2)和嗜硫菌(*Sulfolobus acidocaldarius* DSM 639)]的同义密码子使用偏向性。结果表明嗜热泉生古细菌(*Aeropyrum pernix* K1)的密码子偏向性很小,并且与GC3S成高度的相关性。这3种泉古菌的密码子使用模式在进化上很保守。与基因的功能对密码子使用的影响相比,这些泉古菌密码子的使用偏向性更是由其物种所决定的。嗜热泉生古细菌(*A. pernix* K1),嗜气菌(*P. aerophilum* str. IM2)和嗜硫菌(*S. acidocaldarius* DSM 639)生存在不同的极限环境中。推测正是这些极限环境决定了这些泉古菌的密码子使用偏向性模式。此外在这些泉古菌的基因组中并没有发现其正义链和反义链的密码子使用偏向性差别。嗜热泉生古细菌(*A. pernix* K1)和嗜硫菌(*S. acidocaldarius* DSM 639)的密码子偏向性程度与基因表达水平有高度的相关性,而嗜气菌(*P. aerophilum* str. IM2)的基因组并没有发现这种规律。

关键词 [密码子使用偏向性; 密码子使用相对概率\(RSCU\); 嗜热泉生古细菌\(*Aeropyrum pernix* K1\)](#)

分类号

Analysis of Synonymous Codon Usage in *Aeropyrum pernix* K1 and Other Crenarchaeota Microorganisms

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Abstract

<P> In this study, a comparative analysis of the codon usage bias was performed in *Aeropyrum pernix* K1 and two other phylogenetically related Crenarchaeota microorganisms (i.e., *Pyrobaculum aerophilum* str. IM2 and *Sulfolobus acidocaldarius* DSM 639). The results indicated that the synonymous codon usage in *A. pernix* K1 was less biased, which was highly correlated with the GC3S value. The codon usage patterns were phylogenetically conserved among these Crenarchaeota microorganisms. Comparatively, it is the species function rather than the gene function that determines their gene codon usage patterns. *A. pernix* K1, *P. aerophilum* str. IM2, and *S. acidocaldarius* DSM 639 live in differently extreme conditions. It is presumed that the living environment played an important role in determining the codon usage pattern of these microorganisms. Besides, there was no strain-specific codon usage among these microorganisms. The extent of codon bias in *A. pernix* K1 and *S. acidocaldarius* DSM 639 were highly correlated with the gene expression level, but no such association was detected in *P. aerophilum* str. IM2 genomes.</P>

Key words [codon usage bias; relative synonymous codon usage \(RSCU\); *Aeropyrum pernix* K1](#)

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