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植物诱变育种·农业生物技术

11种植物 $psbA$ 基因的密码子偏好性及聚类分析

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摘要:

植物叶绿体 $psbA$ 基因的启动子是叶绿体基因工程中常用的启动子,研究该基因的编码特点对完善叶绿体基因工程的研究设计、提高外源基因在受体物种中高效、稳定的表达具有重要作用。本研究综合运用了多种分析软件,对11种植物的叶绿体 $psbA$ 基因进行了分析。结果表明,11种植物 $psbA$ 基因的ENC(Effective Number of Codons)值都小于40,显示出了明显的密码子偏好性,即在碱基组成上偏爱以C结尾的密码子。RSCU(Relative Synonymous Codon Usage)值表明共有20个密码子在编码使用上具有偏好性,其中有8个表现出较强的偏好性;另有12个密码子在 $psbA$ 中出现率极低或没有出现。在聚类分析中,基于密码子偏好性参数RSCU的聚类不能正确反映物种间的进化关系,而基于基因序列的聚类更适合作为系统发育分析的参考。

关键词: $psbA$ 基因 密码子偏好性 聚类分析

CLUSTER ANALYSIS AND CODON USAGE BIAS STUDIES ON $psbA$ GENES FROM 11 PLANT SPECIES

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Abstract:

The promoter of $psbA$ gene was frequently used in genetic engineering as the promoter expressed in the chloroplast. Characterization of the codons usage of $psbA$ genes is important to the perfect investigations of genetic engineering in chloroplast. In this study, codon usages of $psbA$ genes from 11 plant species were analyzed by several softwares. The results showed that all the effective number of codons (ENC) were less than 40 in 11 plant species, suggesting that codon usage bias existed in the $psbA$ genes. For example, the codons ending with C were frequently used. Relative synonymous codon usage analyses showed that 20 codons were preferable in the codons of coding DNA sequences (CDS) of $psbA$ gene, whereas 12 codons were seldom used. The cluster tree based on the relative synonymous codon usage (RSCU) could not reveal the evolutional relations among the 11 plant species, whereas that based on CDS of $psbA$ gene could reveal their evolutional relationship much better.

Keywords: $psbA$ genes codon usage bias cluster analysis

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