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Analysis of codon use features of stearoyl-acyl carrier protein desaturase gene in *Camellia sinensis*



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HIGHLIGHTS

- The CsSAD gene has similar codon usage bias with *C. sinensis* genome genes.
- The CsSAD gene is biased toward codons ending with A/T.
- The *E. coli* expression system is superior to yeast expression system for the CsSAD gene.
- Clustering model was validated to be the optimal one with the jackknife test method.

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ABSTRACT

The stearoyl-acyl carrier protein desaturase (SAD) gene widely exists in all kinds of plants. In this paper, the *Camellia sinensis* SAD gene (CsSAD) sequence was firstly analyzed by Codon W, CHIPS, and CUSP programs online, and then compared with genomes of the tea plant, other species and SAD genes from 11 plant species. The results show that the CsSAD gene and the selected 73 of *C. sinensis* genes have similar codon usage bias. The CsSAD gene has a bias toward the synonymous codons with A and T at the third codon position, the same as the 73 of *C. sinensis* genes. Compared with monocotyledons such as *Triticum aestivum* and *Zea mays*, the differences in codon usage frequency between the CsSAD gene and dicotyledons such as *Arabidopsis thaliana* and *Nicotiana tobacum* are less. Therefore, *A. thaliana* and *N. tobacum* expression systems may be more suitable for the expression of the CsSAD gene. The analysis result of SAD genes from 12 plant species also shows that most of the SAD genes are biased toward the synonymous codons with G and C at the third codon position. We believe that the codon usage bias analysis presented in this study will be essential for providing a theoretical basis for discussing the structure and function of the CsSAD gene.

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1. Introduction

As we all know, nucleic acids are templates of protein synthesis and the genetic code chooses 61 codons to represent 20 standard amino acids. Each amino acid can be coded by 1–6 codons and these alternative codons for the same amino acid are termed as synonymous codons (Prabha et al., 2012). Research showed that genes prefer to use some codons in synonymous codon usage, namely existing as codon usage biased (Zhou et al., 2007). Codon usage is highly variable among different species and principally related to gene function (Ma et al., 2002; Fuglsang, 2003), and these variations are also found within the related species and genes (Ma et al., 2009). It indicates these genomes and genes bear different pressure in evolution process. Codon usage bias analysis

has important significance in many aspects. It helps to reveal the genetic evolution law in some pertinent species or between gene families of a certain species (Sorimachi, 2009, 2010a, 2010b) and contributes to understanding the regulatory mechanism in the process of transcription and translation. It also can improve the gene expression level by predicting the optimum host of the exogenous gene and ameliorating the exogenous gene (Wu et al., 2007).

At present, there are two kinds of theories accounting for codon bias phenomenon, namely the Neutral theory and the “Selection–Mutation–Drift” theory (Bulmer, 1991). The Neutral theory holds that the mutations occurring in the third base position of a codon is the result of neutral selection, and synonymous mutations do not affect survival fitness; this kind of selection on codons only related to mutation, which are not affected by natural selection pressure. The “Selection–Mutation–Drift” theory considers that the occurrence of mutation has direction; synonymous codon usage bias reflects effects on both

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