Codon usage bias analysis for the spermidine synthase gene from *Camellia sinensis* (L.) O. Kuntze


Tea Research Institute, Qingdao Agricultural University, Qingdao, Shandong, China

Corresponding author: Z.T. Ding
E-mail: dzttea@163.com

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ABSTRACT. The spermidine synthase (*SPDS*) gene exists widely in all types of plants. In this paper, the codon usage of the *SPDS* gene from *Camellia sinensis* (*CsSPDS*) was analyzed. The results showed that the codon usage of the *CsSPDS* gene is biased towards the T-ended or A-ended codons, which is similar to that observed in 73 genes selected from the *C. sinensis* genome. An ENC-plot for 15 *SPDS* genes from various plant species suggested that mutational bias was the major factor in shaping codon usage in these genes. Codon usage frequency analysis indicated that there was little difference between the *CsSPDS* gene and dicot genomes, such as *Arabidopsis thaliana* and *Nicotiana tabacum*, but significant differences in codon usage were observed between the *CsSPDS* gene and monocot genomes, such as *Triticum aestivum* and *Zea mays*. Therefore, *A. thaliana* and *N. tabacum* expression systems may be more suitable for the expression of the *CsSPDS* gene.

Key words: *Camellia sinensis* (L.) O. Kuntze; Codon usage bias; *SPDS*; ENC-plot; Correlation analysis; Cluster analysis