



Analysis of synonymous codon usage in *FAD7* genes from different plant species

Q.P. Ma, C. Li, J. Wang, Y. Wang and Z.T. Ding

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

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

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ABSTRACT. In this study, the codon bias of the *FAD7* genes among 10 different plant species was analyzed to identify general patterns of codon usage in the *FAD7* genes. Our results showed that U-ended or A-ended codons were preferentially used in *FAD7* for dicots, whereas G-ended or C-ended codons were preferentially used in *FAD7* for monocots. An ENC-plot showed that some other factors may influence the codon usage of *FAD7*, except mutation bias in plant species. A correlation analysis between the codon adaptation index and GC or GC3s contents demonstrated that the codon usage bias of the *FAD7* gene in plant species could be influenced by the gene expression level. The cluster analysis of relative synonymous codon usage values and phylogenetic trees of protein sequences for *FAD7* genes confirm that the codon preference of *FAD7* is influenced by genetic relationships. Moreover, *Arabidopsis thaliana* and *Nicotiana tabacum* were predicted to be the most appropriate expression hosts for the *FAD7* genes from dicots, and *Zea mays* may be suitable for the expression of the *FAD7* genes from monocots. Our results provide useful insights into the evolutionary relationships of plant species.

Key words: *FAD7*; ENC-plot; Correlation analysis; Cluster analysis; Codon usage frequency