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First Middle Last^{1,2}, First-Name Last^{1,2}, Chorng-Horng Lin³, Jong-Kang Liu⁴, Tit-Yee Wong⁵, Chung-Hsin Yeh⁶ and Xxxx Xxx^{1,6,*}

¹National Museum of Marine Biology and Aquarium, Checheng, Pingtung 94450, Taiwan, R.O.C.

²Institute of Marine Biodiversity and Evolution, National Dong Hwa University, Checheng, Pingtung 944, Taiwan, R.O.C.

³Department of Bioresources, DaYeh University, 112 Shan-Jiau Road, Da-Tsuen, Chang-Hua 515, Taiwan, R.O.C.

⁴Department of Biological Sciences, National Sun Yat-sen University, Kaohsiung 804, Taiwan, R.O.C.

⁵Department of Biology, Bioinformatics program, The University of Memphis, Memphis, TN, USA

⁶Institute of Marine Biotechnology, National Dong Hwa University, Checheng, Pingtung 94450, Taiwan, R.O.C.

*Corresponding author. E-mail: xxxxx@nmmba.gov.tw.

Abstract

Just type your abstract here. For example, unicellular cyanobacteria *Synechococcus* are ubiquitous, abundant, and extremely competitive phytoplankton in the marine ecosystem. In this study, synonymous codon usage in the genome of *Synechococcus* sp. WH8102 was analyzed.

Key words: Key, words, *Synechococcus*

Introduction

Type your introduction here. Reference should be cited this way (Grocock and Sharp, 2002), or like this (Singer and Hickey, 2003; Peixoto et al., 2003; Gupta et al., 2004), and the factors governing synonymous codon preferences are not the same in different organisms.

Materials and Methods

The complete genome sequences and coding sequences of *Synechococcus* sp. WH8102 (accession no. BX548020) (Palenik et al., 2003) were obtained from the GenBank sequence database.

Subsection if you have one

The frequency of (Russell and Sharp, 2001; Palenik et al., 2003).

Correspondence analysis (CA) is a multivariate analysis used to summarize data structures in multidimensional space by projecting onto low-dimension subspaces, while losing as little information as possible (Grocock and Sharp, 2002; Peixoto et al., 2003; Gupta et al., 2004).

Results

Results here. You may also combine your results and discussion in one section.

Discussion

And the discussion here.

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References

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Tab. 1. Overall codon usage of *Synechococcus* sp. WH8102 genes. AA: amino acid; N: number of codons. The preferentially used codons for each amino acid are displayed in bold.

Fig. 1. Distribution of (a) GC3s and (b) Nc values in *Synechococcus* sp. WH8102.

Fig. 2. Nc-plot (Nc vs. GC3s values) of the *Synechococcus* sp. WH8102 genes. The curve represents the expected curve between GC3s and Nc under random codon usage.