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Codon usage analysis of prokaryotic mechanosensation genes

Guang B. Liu, Rong Chen, Boris Martinac, Kong-Nan Zhao

Abstract

In the present study, we examined GC nucleotide composition, relative synonymous codon usage (RSCU), effective number of codons (ENC), codon adaptation index (CAI) and gene length for 308 prokaryotic mechanosensitive ion channel (MSC) genes from six evolutionary groups: Euryarchaeota, Actinobacteria, Alphaproteobacteria, Betaproteobacteria, Firmicutes, and Gammaproteobacteria. Results showed that 1). a wide variation of overrepresentation of nucleotides exists in the MSC genes; 2). codon usage bias varies considerably among the MSC genes; 3). both nucleotide constraint and gene length play an important role in shaping codon usage of the bacterial MSC genes and 4). synonymous codon usage of prokaryotic MSC genes is phylogenetically conserved. Knowledge of codon usage in prokaryotic MSC genes may benefit for the study of the MSC genes in eukaryotes in which few MSC genes have been identified and functionally analysed.

Poster Presenter:

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The letter of acceptance from ANGIS:

Guang

With regards to your submission entitled

Codon usage analysis of prokaryotic mechanosensation genes

we would like to invite you to present a poster at the Bioinformatics Australia 2006 conference. A poster space of 1 metre wide x 1 metre high including the heading will be provided. Posters can be put up between 8.00 – 8.45am, or during the breaks on Tuesday November 21. There will be a poster evening session on Tuesday 5.30pm – 7.00pm at which you will be expected to attend.

Please note that this poster acceptance is contingent on the presenting author registering for the conference by October 22. Registration can be made through <http://ba.angis.org.au>

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