

Genome-wide codon usage bias analysis in *Beauveria bassiana*Prajna Muthabathula^{1,*}, Saragadam Suneetha¹, J. Ratna Grace²¹Department of Botany, Andhra University, Visakhapatnam, Andhra Pradesh, India; ²Department of Botany, Dr. V. S. Krishna Government Degree College, Visakhapatnam, Andhra Pradesh, India; Prajna Muthabathula - Email: prajna.muthabathula@gmail.com; *Corresponding authorReceived October 12, 2018; Revised October 27, 2018; Accepted October 27, 2018; Published December 28, 2018
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Abstract:

Codon usage bias analysis allows in identifying the factors that are influencing and contributing to shape the evolution of the organisms. Therefore, it is of interest to analyze 10363 gene sequences from *Beauveria bassiana*. The GC content with 51.50% is higher than the AT content (48.50%) in *B. bassiana*. The fungal nuclear genes tend to be GC rich and predominantly G/C ending. Codon usage bias exhibited by *B. bassiana* is based on the Relative Synonymous Codon Usage (RSCU) values of 61 sense codons, of which 28 codons are with RSCU value larger than 1. Other factors like Nucleotide composition, mutational pressure and selection also has a role in shaping the codon usage bias. We identified 24 optimal codons that end with G or C. Correlation analysis suggests existence of translational efficiency of amino acids. Based on the GC3s distribution evolution of the *B. bassiana* genes is by the contribution of mutation pressure. ENC may be the major factor in shaping the codon usage bias. This study provides insights into the compositional selection pressure of the genes in *B. bassiana*.

Keywords: *Beauveria bassiana*, codon usage, translational efficiency, mutational pressure

Background:

The probability of the codon used for an amino acid over a different codon, which codes for the same amino acid is regarded as codon bias. Different codons that encode the same amino acid are known as synonymous codons. Even though synonymous codons encode the same amino acid it has been shown that for a wide variety of organisms different synonymous codons are used with different frequencies. This phenomenon is termed as codon bias [1]. It is found in all eukaryotic and prokaryotic genomes. Codons used more often are referred to as optimized codons or preferred codons. Synonymous codon usage identity may be varying or similar in the genome or among different genes within the genome. Several factors that influence the variations in the codon usage patterns which include genetic drift, mutational pressure and natural selection [2] and these factors are highly responsible for differences in codon usage variations among different organisms. Multiple forms of selection may act resulting

in different clusters of synonymous codon usage patterns among genes within the genome [3].

An analysis of genome-wide codon usage bias patterns investigates their consequences and causes and helps in identifying the selective forces that are involved in shaping the evolution of the codon usage patterns, which help in understanding the perspectives of genome biology [4]. Codon usage bias of several organisms have been analyzed however, very little is known about codon usage bias in *B. bassiana* entomopathogen, belonging to Hypocrealean fungi (cordycepsaceae, Ascomycota) that is used as a potential biopesticide. It is an environmental friendly mycoinsecticide, which is commercially available whose genome was sequenced and light has shed on its differential gene expression and adaptability to different niches [5]. It has diversifying roles apart from bio-pesticidal activity, also found as