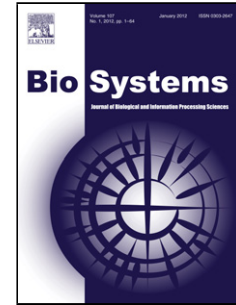


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Unique features of nucleotide and codon usage patterns in mycoplasmas revealed by information entropy

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Abstract:

Currently, the comparison between GC usage pattern at the 3rd codon position and codon usage index is commonly used to estimate the roles of evolutionary forces in shaping synonymous codon usages, however, this kind of analysis often loses the information about the role of A/T usage bias in shaping synonymous codon usage bias. To overcome this limitation and better understand the interplay between nucleotide and codon usages for the evolution of bacteria at gene levels, in this study, we employed the information entropy method with some modification to estimate roles of nucleotide compositions in the overall codon usage bias for 18 mycoplasma species in combination with Davies-Bouldin index. At gene levels, the overall nucleotide usage bias represents A content as the highest, followed by T, G and C for mycoplasmas, resulting in a low GC content. This feature is universal across these species derived from

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