



Synonymous codon usage patterns in different parasitic platyhelminth mitochondrial genomes

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ABSTRACT. We analyzed synonymous codon usage patterns of the mitochondrial genomes of 43 parasitic platyhelminth species. The relative synonymous codon usage, the effective number of codons (NC) and the frequency of G+C at the third synonymously variable coding position were calculated. Correspondence analysis was used to determine the major variation trends shaping the codon usage patterns. Among the mitochondrial genomes of 19 trematode species, the GC content of third codon positions varied from 0.151 to 0.592, with a mean of 0.295 ± 0.116 . In cestodes, the mean GC content of third codon positions was 0.254 ± 0.044 . A comparison of the nucleotide composition at 4-fold synonymous sites revealed that, on average, there was a greater abundance of codons ending on U (51.9%) or A (22.7%) than on C (6.3%) or G (19.14%). Twenty-two codons, including UUU, UUA and UUG, were frequently used. In the NC-plot, most of points were distributed well below or around the expected NC curve. In

addition to compositional constraints, the degree of hydrophobicity and the aromatic amino acids also influenced codon usage in the mitochondrial genomes of these 43 parasitic platyhelminth species.

Key words: Platyhelminths; Mitochondrial genomes; Optimal codons; Codon usage bias; Correspondence analysis