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Codon usage patterns in Nematoda: analysis based on over 25 million codons in thirty-two species.

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ABSTRACT: BACKGROUND: Codon usage has direct utility in molecular characterization of species and is also a marker for molecular evolution. To understand codon usage within the diverse phylum Nematoda, we analyzed a total of 265,494 ESTs from 30 nematode species. The full genomes of Caenorhabditis elegans and C. briggsae were also examined. A total of 25,871,325 codons were analyzed and a comprehensive codon usage table for all species was generated. This is the first codon-usage table available for 24 of these organisms. RESULTS: Codon usage similarity in Nematoda usually persists over the breadth of a genus but then rapidly diminishes even within each clade. Globodera, Meloidogyne, Pristionchus, and Strongyloides have the most highly derived patterns of codon usage. The major factor affecting differences in codon usage between species is the coding sequence GC content which varies in nematodes from 32-51%. Coding GC content (measured as GC3) also explains much of the observed variation in the effective number of codons (R = 0.70), a measure of codon bias, and even differences in amino acid frequency. Codon usage is also affected by neighboring nucleotides (N1 context). Coding GC content correlates strongly with estimated non-coding genomic GC content (R = 0.92). Examining abundant clusters in five species, candidate optimal codons have been identified which may be preferred in highly expressed transcripts. CONCLUSIONS: Evolutionary models indicate that total genomic GC content, likely the product of directional mutation pressure, drives codon usage rather than the converse, a conclusion supported by examination of nematode genomes.

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