

A Comprehensive Analysis of the Phylogenetic Signal in Ramp Sequences in 211 Vertebrates

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Abstract : Background: Ramp sequences increase translational speed and accuracy when rare, slowly-translated codons are found at the beginnings of genes. Here, the results of the first analysis of ramp sequences in a phylogenetic construct are presented. Methods: Ramp sequences were compared from 211 vertebrates (110 Mammalian and 101 non-mammalian). The presence and absence of ramp sequences were analyzed as a binary character in a parsimony and maximum likelihood framework. Additionally, ramp sequences were mapped to the Open Tree of Life taxonomy to determine the number of parallelisms and reversals that occurred, and these results were compared to what would be expected due to random chance. Lastly, aligned nucleotides in ramp sequences were compared to the rest of the sequence in order to examine possible differences in phylogenetic signal between these regions of the gene. Results: Parsimony and maximum likelihood analyses of the presence/absence of ramp sequences recovered phylogenies that are highly congruent with established phylogenies. Additionally, the retention index of ramp sequences is significantly higher than would be expected due to random chance (p-value = 0). A chi-square analysis of completely orthologous ramp sequences resulted in a p-value of approximately zero as compared to random chance. Discussion: Ramp sequences recover comparable phylogenies as other phylogenomic methods. Although not all ramp sequences appear to have a phylogenetic signal, more ramp sequences track speciation than expected by random chance. Therefore, ramp sequences may be used in conjunction with other phylogenomic approaches.

Keywords : codon usage bias, phylogenetics, phylogenomics, ramp sequence

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