

Estimation of 12S marker fragment effectiveness for ancient phylogeny reconstruction

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Motivation and Aim: For many years different biopolymer sequences were used to infer the relations of various taxa. Yet few studies were devoted to the estimation of these sequences' effectiveness in phylogeny reconstruction at different taxonomic levels. One of widely used marker fragments is mitochondrial 12S rRNA gene [1]. In present study we tried to determine at which taxonomic levels the use of this gene is justified using Annelida worms as a model taxon.

Methods and Algorithms: We used a set of Annelida 12S gene sequences representing phylogenetic relationships of at various taxonomic levels – from species to class. The sequences were aligned with Clustal Omega globally and with MUSCLE locally. The phylogeny was reconstructed by Maximum Likelihood method implemented in MEGA7 [2] and Bayesian Inference method implemented in BEAST2 [3].

Results: Two different methods of phylogeny reconstruction – Maximum Likelihood and Bayesian Inference – yielded overall similar but slightly different topologies. The bootstrap node supports produced by Maximum Likelihood reconstruction were generally lower than Bayesian posterior supports which may be due to a loss of information during bootstrap resampling [4]. However both methods showed a significant decrease of node support values from tips to root of the trees.

Conclusion: The results suggest the high value of 12S rRNA gene sequences in reconstructing phylogeny at species and genus levels. However, these sequences perform poorly for reconstructing phylogeny at higher levels and can only be used in addition to other gene fragments.

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