A Supertree Analysis Of The Metazoan Phylogeny

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Detailed knowledge of the phylogenetic relationships among the Metazoa and their eukaryotic relatives is critical for understanding the origin of complex life. However, the phylogeny of the metazoan phyla currently remains largely unresolved and has undergone major reorganizations over the past few years. In order to achieve reliable resolution and to avoid stochastic and systematic error, the number and choice of taxa, as well as the quantity of data have to be considered.

We investigated the relationships within the Metazoa by constructing a supertree using multiple gene sequences from a breadth of taxa. To reduce the impact of systematic error, model selection was performed to select adequate substitution models. It was found that not all sequences in the gene families could be accurately described by the optimal model chosen which may have contributed to a lack of resolution in the reconstructed Metazoan phylogeny.