Animal evolution — A fully-resolved phylogenomic tree argues against the Cambrian explosion hypothesis

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Abstract

Recently, Rokas et al. (2005) reported that the animal phylogeny could not be resolved despite the use of 50 genes from 17 animal species. Furthermore, the authors concluded that “the lack of resolution” observed in their tree constitutes a positive signature for “an extreme compression of the metazoan radiation.” Hence, their work apparently supports the Cambrian explosion hypothesis. However, we suspect that the profound influence of taxon sampling on phylogenetic inference was underestimated, thus leading to erroneous conclusions about the mode and tempo of animal evolution.

To substantiate this point of view, we assembled a taxon-rich phylogenomic data set. When including a slowly-evolving nematode we obtained a fully-resolved tree of animals, whereas using a fast-evolving nematode reproduced the genuine phylogenetic signal. Two conclusions of general interest can be deduced from our analyses: (1) based on current data, the animal tree is fully resolved, which argues against the Cambrian explosion hypothesis; and (2) an adequate sampling (i.e. including slowly-evolving species) is crucial to reduce non-phylogenetic signals in genome-scale phylogenetic inference.

Conclusions

1. Phylogenomics allows recovery of an almost fully-resolved animal tree. This needs further testing by including still unsampled taxa. To reduce the non-phylogenetic signals interfering with the phylogenetic signal, slow-evolving taxa should be preferred whenever possible.

2. Since interfering non-phylogenetic signals can be highly uneven, internode recovery does not necessarily correlates with true internode length.

References


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