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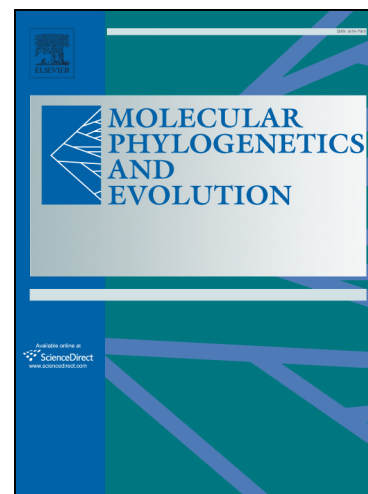
Assessing the utility of transcriptome data for inferring phylogenetic relationships among coleoid cephalopods

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## Assessing the utility of transcriptome data for inferring phylogenetic relationships among coleoid cephalopods

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### Highlights

- The stability of topologies generated by transcriptome data is impacted by taxon sampling, ortholog number and the amount of missing data.
- Analyses of our combined dataset recover a sister-group relationship between Sepiida and Myopsida, with this clade sister to Oegopsida.
- No trees generated by any analyses supported monophyly of Sepioidea, a group containing all sepioid orders (Idiosepiida, Sepiida, Sepiolida and Spirulida).
- Trees in the present study include higher levels of branch support than recovered by multigene datasets, but differ from trees in other recent phylogenomic studies.

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