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Re-Stating the Origin of Tetrapod Using Measures of Phylogenetic Support for Phylogenomic Data

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Abstract : Whole-genome data from two lungfish species, along with other species, present a valuable opportunity to re-investigate the longstanding debate regarding the evolutionary relationships among tetrapods, lungfishes, and coelacanths. However, the use of bootstrap support has become outdated for large-scale phylogenomic data. Without robust phylogenetic support, the phylogenetic trees become meaningless. Therefore, it is necessary to re-evaluate the phylogenies of tetrapods, lungfishes, and coelacanths using novel measures of phylogenetic support specifically designed for phylogenomic data, as the previous phylogenies were based on 100% bootstrap support. Our findings consistently provide strong evidence favoring lungfish as the closest living relative of tetrapods. This conclusion is based on high internode certainty, relative gene support, and high gene concordance factor. The evidence stems from five previous datasets derived from lungfish transcriptomes. These results yield fresh insights into the three hypotheses regarding the phylogenies of tetrapods, lungfishes, and coelacanths. Importantly, these hypotheses are not mere conjectures but are substantiated by a significant number of genes. Analyzing real biological data further demonstrates that the inclusion of additional taxa leads to more diverse tree topologies. Consequently, gene trees and species trees may not be identical even when whole-genome sequencing data is utilized. However, it is worth noting that many gene trees can accurately reflect the species tree if an appropriate number of taxa, typically ranging from six to ten, are sampled. Therefore, it is crucial to carefully select the number of taxa and an appropriate outgroup, such as slow-evolving species, while excluding fast-evolving taxa as outgroups to mitigate the adverse effects of long-branch attraction and achieve an accurate reconstruction of the species tree. This is particularly important as more whole-genome sequencing data becomes available.

Keywords : novel measures of phylogenetic support for phylogenomic data, gene concordance factor confidence, relative gene support, internode certainty, origin of tetrapods

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