*Beyond congruence: evidential integration and inferring the best evolutionary scenario*

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| **Abstract:**Molecular methods have revolutionised virtually every area of biology, and metazoan phylogenetics is no exception: molecular phylogenies, molecular clocks, comparative phylogenomics, and developmental genetics have generated a plethora of molecular data spanning numerous taxa and collectively transformed our understanding of the evolutionary history of animals, often corroborating but at times opposing results of more traditional approaches. Moreover, the diversity of methods and models within molecular phylogenetics has resulted in significant disagreement among molecular phylogenies as well as between these and earlier phylogenies. How should this broad and multifaceted problem be tackled? I argue that the answer lies in integrating evidence to infer the best evolutionary scenario. I begin with an overview of recent development in early metazoan phylogenetics, followed by a discussion of key conceptual issues in phylogenetics revolving around phylogenetic evidence, theory, methodology, and interrelations thereof. I then argue that the integration of different kinds of evidence (e.g. molecular, morphological, ecological) is necessary for arriving at the best evolutionary scenario (causal explanation) rather than merely the best-fitting cladogram (statistical explanation). Finally, I discuss the prospects of this view in stimulating interdisciplinary cross-talk in early metazoan research and beyond, and challenges that need to be overcome. |  |  |