Phylogenetic Morphology in the Genomic Age: A Review

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Abstract

A phylogeny, or evolutionary tree, is the famous single picture in Darwin's The Origin of Species. In the following century, biologists used similar data to Darwin to reconstruct phylogenies: phenotypic features, particularly morphology. But, beginning in the 1960s, scientists began to use a wider range of genetic and molecular data for phylogenetic inference. Because of the recent exponential increase in our ability to swiftly capture huge amounts of DNA data, phylogenies are now regularly constructed utilising genomic-scale molecular datasets containing hundreds of genes and hundreds of thousands of base pairs. These massive datasets provide computational hurdles, but they often yield completely resolved and well-supported trees.

Keywords: Phylogenomic • Genome • Morphology

Introduction

Molecular phylogenetics has now reached the phylogenomic epoch, and it is widely regarded as the most efficient and powerful method for reconstructing evolutionary trees, at least for living animals. Nonetheless, numerous issues remain, and the assumptions and biases of analytic techniques for dealing with massive genomic datasets are only now being examined. Despite this, morphological data are becoming progressively marginalised in phylogenetic inference: evolutionary trees are frequently formed exclusively on massive genomic datasets, and morphology is frequently considered only in passing, if at all.

The richness of new genetic data has enabled us to recreate evolutionary trees with increasing detail and certainty. While phenotypic (usually physical) features are becoming less relevant in reconstructing evolutionary trees, they continue to play crucial and distinctive functions in phylogenetics, even for living organisms with large amounts of genetic information. Morphology remains a powerful independent source of evidence for evaluating molecular clades, as well as the principal method for time-scaling phylogenies via fossil phenotypes. Morphology phylogenetics is thus necessary for converting undated molecular topologies into dated evolutionary trees.

Literature Review

Laser microscopy and microcomputer-tomography scanning; for example, are increasing the universe of morphological characters gathered from fossil and current organisms. These new data are already being widely shared through image-rich online platforms like MorphoBank. Understanding the evolution of phenotypic features, as well as their connections to the genome, ontogeny, function, and ecology, will always be a central goal of biology. Tracing the evolution of phenotypic features, for example, is critical for determining the molecular foundation of morphological change. Similarly, fossils offer the finest view of broad swaths of vanished biodiversity and accompanying evolutionary dynamics that are mainly or completely unavailable to genetic data.

A much specialised sort of phenotypic analysis that may require additional justification: morphological phylogenetics, and how it improves our understanding of both current and extinct biodiversity. Is there any point in laboriously evaluating and analysing dozens to thousands of features across the phenotypic of living animals in the genomic age, when much larger and more powerful genetic datasets can be gathered much more rapidly and cheaply? Morphology phylogenetics is still important for evaluating molecular phylogenetic trees and time-scaling them using the fossil record, permitting inference of the dynamics of phenotypic and genomic evolution over time and the tree of life [1-3].

Discussion

The growing body of molecular data has revealed the prevalence of convergent evolution of phenotypic traits, revealing that many proposed groupings based on morphological traits are artefacts of homoplasy. Insectivorous mammals, legless reptiles, waterbirds, and metamerically segmented invertebrates are now known to be heterogeneous assemblages of distantly related lineages that have evolved similar traits. While morphology analyses alone may yield erroneous trees, it has been argued that morphology may still have a favourable impact on phylogenetic accuracy when combined with additional (mostly molecular) data [4]. This issue has long been crucial to the debate over whether to analyse morphological and molecular data simultaneously.

These dated trees are also the foundation of modern comparative biology. Several drawbacks in standard methods for putting timelines on phylogenetic trees may be solved by promising tip-dating methodologies that incorporate morphological data and analyses. To achieve these goals, current morphologists must examine phenotypes in a fundamentally new way, morphological evolution must be better modelled, and ways to analysing morphology with genomic data must be improved.

Consilience is a crucial criterion for evaluating scientific hypotheses: evolutionary trees that are supported by several sources of data are more likely to be right. The relative distance between the phenotype and the genome, as well as the highly distinct evolutionary processes of morphology and DNA, strengthen the value of morphology as a test of phylogenomic trees. Only the relative order of divergences between lineages is explicit in molecular phylogenies. The fossil record is usually the primary source of evidence for putting absolute timescales on molecular phylogenies. Nevertheless, this critical temporal information is only valuable if the evolutionary position of the fossils is known precisely. Ideally, this incorporates quantitative analysis of fossil and living taxon morphological datasets in conjunction with Genomic evidence for living species, using simultaneous or scaffold techniques. Molecular data are then used to robustly define the branching pattern of living

taxa, and morphological evolution is traced onto this framework, allowing fossils to be placed in their best places [5].

Inserting fossils into a molecular tree based on a few selected 'key' features may be insufficient because it does not completely account for contradicting evidence and phylogenetic uncertainty. Analysing fossil and living taxa using morphology alone is similarly suboptimal the fossils might be inserted into a morphology-based tree of living taxa that is contradicted by genomic data, such as a phylogeny of mammals that lacks Afrotheria, or a phylogeny of squamate reptiles that unites distantly-related serpentine lineages such as snakes, amphisbaenians and 'legless lizards'. Incorporation of molecular data increases estimations of relationships among extant taxa, which leads to (re-)optimisation of morphological features, which improves their capacity to accurately position fossils. The evolutionary location of the fossils is first identified using topology-only approaches. These fossils are then used to limit specific nodes in a tree in time, either during or after phylogenetic analysis of DNA data. These calibrations take advantage of the axiom that a clade must be at least as ancient as its oldest known fossil. As a result, this fossil establishes the minimum age for the clade's ancestral node. While this is still the most commonly used time-scaling method and has been well tested, it has four major limitations. First, the initial study of the fossil's phylogenetic position ignores temporal information [6,7].

These discussions began when morphological and molecular datasets were frequently roughly equal in terms of number of features and phylogenetic signal, but they are now moot [8]. Morphological features now account for less than 2% of characters in combined analyses, and this number will continue to fall. Because of the growing mismatch between morphological datasets and contemporary phylogenomic datasets,'simultaneous' and'scaffold' analyses will produce increasingly comparable trees. In parallel analysis of some of the largest known morphological datasets and very modest genomic datasets, the genomic data still mainly influenced tree structure.

Regardless of the dating method used, morphological data are critical for connecting the fossil record to time-scale DNA trees of current organisms. These dated phylogenies, in turn, give important light on the dynamics of morphological and molecular evolution over time and the tree of life. In general, dated evolutionary trees considerably improve the power of all comparative phylogenetic inferences. Hence, the temporal information offered by morphological data is ultimately important across biology for inferring diversification dynamics, adaptation, trait connections, and mechanisms of speciation, niche conservatism, and quantifying and prioritising biodiversity.

Conclusion

Conventional morphological phylogenetics, despite being regarded outmoded at times, is so critical for verifying and rigorously dating the tree of life, and ultimately supports much of biology. Yet, the number of taxonomists and morphologists capable of collecting and analysing phenotypic data is declining. The demand for such knowledge is growing because most published morphological datasets are unsuitable for current analysis and integration with genomic data for a variety of reasons, including: Formerly, morphological analyses often scored phenotypic features at the taxonomic level, resulting in many variables being recorded as polymorphic due to between-species variance. In contrast, molecular data is collected at the species or individual specimen level.

Acknowledgement

Not applicable.

Conflict of Interest

There is no conflict of interest by author.

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How to cite this article: Oliviera, Marcia. "Phylogenetic Morphology in the Genomic Age: A Review." J Phylogenetics Evol Biol 11 (2023): 260.