

The two towers: What do genes and fossils tell us about evolutionary history (of plants)

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The molecular revolution and the advent of “big data” has fundamentally influenced our perception of phylogeny and evolutionary history. Since Darwin’s *Origin of Species*, common ancestry was defined by overall similarity or the sharing of a few unique, derived traits, termed ‘synapomorphies’ in 1950 by Hennig (e.g. the double integument in flowering plants, the angiosperm clade). Already in 1963 Cavalli and Sforza produced the first statistically obtained phylogenetic tree, based on a genetic similarity matrix. Today researches can rely on thousands to ten-thousands of nucleotides or other molecular characters and highly sophisticated mathematical models to infer their evolutionary histories. This led not a few to believe that all other data sets have come out of date.

But there is one place, no molecular data will ever have access to. The evolutionary past. We can obtain fragments of DNA from material that is some thousands and even 10,000 years old, but evolutionary history covers millions of years. Hence, reconstructing the past using genes relies on models but not factual evidence. The only hard evidence for the existence of an organism at a given point in space and time is a fossil, something dug out. Fossils can be (partly) organic but often they are just mineral impressions of a once living and evolving thing. Accordingly, the identification of fossils rely mostly on form; and palaeontology has long ignored the molecular revolution that affected so deeply their neontological sister sciences, systematic biology and biogeography. Using just form, not rarely delinked from function (form-genera and form-species), can be tricky, when it comes to phylogenetic relationships. The first lesson neontologists learned from the analysis of molecular data.

Thus, identifying the “dark spots” of molecular and fossil data is the first step towards a holistic reconstruction of evolutionary history. I will show a number of examples that demonstrate the inadequacy of molecular and morphological data sets when taken alone, and how methodological advances and a bit of thinking-out-of-the box can assist in bridging the still widening gap between the two towers of evolutionary history: the genes and the fossils.