Morphology and Molecules: An Integrated Comparison of Phenotypic and Genetic Rates of Evolution

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Fossil species are based on the preservable portion of the phenotype (morpho-species). Although the benchmark of a biological species remains reproductive isolation, in practice extant species are described in terms of their broader phenotype (skeletal and soft tissue phenotype and behavior) and properties of their genotypes (molecular distance). Molecular methods are now a routine, if not mandatory part of modern systematics. Because the theory behind molecular phylogenies is simple, resulting in relative and numerical estimates of the amount of time since the last common ancestor (tLCA), molecular data have risen in importance in both the applied, practical identification of species as well as the theoretical concepts behind the process of speciation. When molecular differences between species are at odds with morphologic differences, terms such as "cryptic species" or "ecophenotypic variation" are used to describe the apparent disconnect between morphology and molecules. Because changes in the genes used for phylogenetic-molecular clock applications (PhyMol DNA, e.g. COI, 16S,12S mitochondrial and 18S, 28S nuclear) are fixed in the genome at rates different than the genes responsible for morphogenesis (Morph-DNA), a disconnect between the two can be expected, regardless of the absolute rates of change in either.

Speciation rates and patterns can be modeled by the timing of four events 1) Differentiation of populations (Most Recent Common Ancestor, tMRCA); 2) Reproductive isolation (Last Common Ancestor, tLCA); 3) Successful Fixation in a change of Morphologic-DNA (tMorphFix); 4) Time of observation (present day or other). These events define four intervals, A) Variation among populations and potential hybridization; B) Molecular distance greater than morphologic distance = cryptic species; C) Molecular distance proportional to morphologic = equilibrium; D) Morphology unchanged with molecular divergence. Variable timing of these events and resulting intervals will produce the familiar patterns associate with microevolution and speciation.

Using this model, relationships between morphology and molecules and any resulting influences on fossil and biological species concepts are more clearly defined and consequences for practical species identification can be evaluated. Published data from Neogene bryozoans by M. Dick, A. Herrera-Cubilla are used to demonstrate the viability of this method and to explore implications of initial results for six species.