Special Section on Reticulate Evolution

Foreword

Reticulate Evolution: From Bacteria to Philosopher

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Reticulate evolution refers to evolutionary processes that cannot fully be represented by the classical (bi)furcating tree model. In a provocative paper in Science, Doolittle (1999) stressed the importance of reticulate evolution in the form of lateral gene transfer (defined below) for the evolution of bacteria and higher groups of organisms.

During my years of formation as an evolutionary biologist, I came across such phenomena as hybridization and allopolyploidy, which did not fit and could not be represented using the classical evolutionary tree model. At the time, these phenomena were considered to be exceptions in the evolutionary process rather than the rule. In the mid-1970s, two important contributions appeared which demonstrated the generality of reticulation as an evolutionary process: Sneath (1975) summarized the biological evidence from various fields and showed for the first time how reticulate evolution could be represented using modified cladograms, while Sonea and Panisset (1976, 1981) showed that lateral gene transfer was a very general method of

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evolution among bacteria. Sonea and Mathieu (2000) have reviewed the more recent evidence from the world of prokaryotes.

The biological reticulate evolution concepts developed during the 1970’s and 1980’s awaited the development of mathematical methods for the reconstruction of reticulograms; a reticulogram is a network capable of representing a reticulate evolutionary structure. Without them, the concepts could not be implemented using, in particular, the molecular data that are becoming increasingly available. Such methods have started to appear in the numerical classification literature; they include statistical methods for reconstructing reticulate patterns as well as methods for testing the goodness-of-fit of reticulate models. In June 1993, during the joint meeting of the Classification Society of North America and the Numerical Taxonomy Group held at the University of Pittsburgh, reticulate models for evolution were presented by Philippe Casgrain, John A. Hartigan, and Arthur R. Lee. The papers included in this Special Section discuss the biological concepts that form the foundation of this type of analysis as well as the methods presently available for the reconstruction of reticulograms.

Reticulate patterns of relationships are found in nature in the following phylogenetic situations:

(1) In bacterial evolution, lateral gene transfer (LGT) is the mechanism by which bacteria can exchange genes across “species” through a variety of mechanisms which are described in a contribution to this Special Section written by Sneath (2000). Lateral gene transfer can be studied either in the deep phylogeny, as in the classical work of Margulis (1981) which summarized the endosymbiont hypothesis (Figure 1; see also Doolittle 1999, Figure 3), or in presently evolving groups.

(2) Reticulations appear as the result of allopolyploidy in plants, which leads to the instantaneous appearance of a new species possessing the chromosome complement of its two parent species.

(3) Reticulate evolution also appears during micro-evolution within species, in sexually reproducing eukaryotes, after genetic differentiation of allopatric populations followed by gene exchange through migration. This point is developed in the contribution of Smouse (2000) to this Special Section.

(4) Homoplasy, which is the portion of phylogenetic similarity resulting from evolutionary convergence (i.e., parallel evolution and reversals), can be represented by reticulations added to a phylogenetic tree.

Reticulate patterns are also found in such non-phylogenetic problems as:

(5) Host-parasite relationships involving host transfer.
(6) Vicariance and dispersal biogeography.