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COMMENTS ON WÄGELE'S REPLY

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I have referred to Wägele's (1994) method as "idiosyncratic" because it is not Hennig's (1966) method. Hennig (1966) did not use groundpatterns in his phylogenetic system, and even suggested (p. 10) that bauplan research, which is similar to Wägele's groundpatterns, is essentially typological. Hennig (1966), moreover, did not provide a heuristic method for dealing with conflicting characters (homoplasy) using maximum parsimony.These features of empirical cladistics, which came after Hennig's work (see reviews of Felsenstein, 1982, and Edwards, 1996), are largely ignored by "neohennigian" phylogenetists. Wägele's method for estimating phylogenetic trees, which I find to be ineffective and unparsimonious, involves inferring *ad hoc* groundpatterns from presumed monophyletic groups and then assembling these groundpatterns, building block style, into more inclusive groundpatterns. Wägele (above) does not address this central criticism directly.

Wägele (above) misses the significance of my discussion of synapomorphy vs. autapomorphy, which meant to illuminate the mechanics of his method. Of course, a character state may be either, *depending on the analytical universe*. Empirical cladistic methods do not change the terminal taxon number during tree estimation, so a character state cannot change from presumptive synapomorphy to autapomorphy. In Wägele's method, the synapomorphic state can coalesce into an autapomorphy, as a result of his building groundpatterns from groundpatterns. Empirical cladistics is clear about this distinction : if you change the number of terminals, you have a different analysis because the relationships of the characters are also changed. As mentioned above, the changing set of terminal taxa in Wägele's method allows him to ignore global parsimony.

Wägele's reply suggests that empirical cladists do not recognise the linkage between the "probability of homology" and the "probability of monophyly". I'm certain that the average cladist is familiar the underlying theory associated with the terms "monophyly" and "homology". Wägele's references to "probability" and "data quality", however, imply *ad hoc* weighting algorithms, where monophyly and homology become confounded, such as in his dubious DNA alignment procedures (Wägele, 1995; Wägele and Stanjek, 1995). Wägele also suggests that tree lengths may not be relevant, while at the same time espousing the use of parsimony in character analysis. Clearly Wägele is not interested in parsimony.

Finally, a critical evaluation of Wägele (1994) can determine whether his ideas have been distorted or used out of context. Further discussion here is not essential.

REFERENCES (not included above)

EDWARDS A.W.F., 1996. The origin and early development of the method of minimum evolution for the reconstruction of phylogenetic trees. *Systematic Biology* **45** : 79-91.

FELSENSTEIN J., 1982. Numerical methods for inferring evolutionary trees. *Quarterly Review of Biology* **57** : 379-404.