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To a cladist, making a phylogeny is all about constructing a nested hierarchy. The terminal leaves and twigs on a real tree from the forest can of course be classified by doing this, and so can modern species (provided evolution works by branching and sub-branching). Phylogeny, however, is not just about relationships between terminal twigs, it is also about lines of descent (or ancestry) which run up the trunks and branches. If we look at fossil species, we have a high chance of sampling a non-terminal branch from deep within the tree (that is, an ancestor of something else, or even an ancestor of many other things).

The papers referred to by <u>Siddall</u> that he claims "thoroughly debunk" the possibility of finding ancestors in the fossil record merely demonstrate that it is impossible to prove ancestry using a cladistic analysis of a character matrix (see his footnote). However, why should we accept that the cladistic method is the only conceivable approach to the problem? It would be a sad thing if science could really say nothing about the lines of genetic descent that link one species with another through the aeons of Earth history.

### Two types of stratigraphic evidence

To move the debate on, it is helpful to distinguish two categories of stratigraphic evidence that may have a part to play in phylogenetics. The first is information of relative age (as discussed by <u>Marshall</u> and <u>Wagner</u>) and the second is stratophenetic linking as discussed by me. Information of relative age might conceivably be integrated with a cladistic analysis, or less controversially assessed once such an analysis has been performed. Stratophenetic linking, on the other hand, is an entirely alternative methodology that seeks to trace lines of descent (and therefore ancestry) by morphological (phenetic) overlap. However, it has very limited applicability on account of the generally poor fossil record.

#### Let me explain ...

I presume Siddall is content to infer that this year's garden birds belong to the same species as last year's without actually seeing them hatch or making a cladogram. Stratophenetics uses the same common-sense approach. It hinges on whether we can reasonably expect to follow a biological species from one time plane to another, perhaps ten thousand years apart or more, and then on and on, over millions of years, even through branching events and up to extinctions. I believe this can be done for some fossil groups in the light of what we know about their population genetics and the fossil record. I may be wrong in practice, but surely not in principle.

It is empty rhetoric to call this worthy aim "ancestor worship" or a "cult", and it is not true that "stratophenetics begat stratocladistics", which in fact have little in common except the prefix.

#### Uncles and nephews

Finally, it is necessary to clear up one small point. By ancestry, I literally mean lines of genetic descent, parent to offspring, over geological time. It is of course true that many individuals die without issue, or their offspring do, so they themselves are ultimately ancestral to nothing. We have little hope of distinguishing the individuals that were "successful" or "unsuccessful" in this way. But it is a feature of sexual species that if an individual is to be ancestral to anything in the future of its species, it soon (geologically speaking) becomes ancestral to all individuals. So an individual in a species may or may not be literally ancestral to another from the same species in the distant future, but if it is not, it won't be that far off.

Incidentally, it is because of this genetic mixing that we can talk about ancestral links between entire species (gene pools) and their descendants and actually mean what we say. Consequently, if we can resolve individual branching events in the fossil record, we will be able to distinguish "uncle and nephew" species from "father and son" species, which is the point contested by <u>Siddall</u>.

Can it be done? I think so, in certain important instances. If neutrals would like to ponder just a single example, I recommend Sorhannus and others' wonderful work of the planktonic diatom *Rhizosolenia*<sup>1</sup>.

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## References

 Sorhannus, U., Fenster, E.J., Burckle, L.H. & Hoffmann, A. Cladogenetic and anagenetic changes in the morphology of *Rhizosolenia praeburgonii* Mukhina. *Historical Biology* 1, 185-205 (1988).

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