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In the third week of contributions to the debate, [Forey](#) and [MacLeod](#) criticized the foraminiferal fossil record and its stratigraphic analysis, interpreting our views and results in a largely oversimplified and erroneous manner.

Good in parts

Contrary to [Forey's](#) comments, it was not at all our intention to glorify the foraminiferal fossil record. Rather, we wanted to show that when this record is good (which is not true for all foraminifera) it can be useful to study the tempo and mode of molecular evolution.

We are, of course, aware of factors responsible for the incompleteness of the foraminiferal fossil record. However, as far as the calibration of phylogenetic trees is concerned, it is our opinion that some taxonomic groups of planktonic forams provide very accurate stratigraphic data. Our answer to the first question asked by Smith is not an unqualified "yes", as suggested by [Forey](#), but a cautious "yes", indicating the potential of the fossil record to reveal evolutionary processes in some groups of microfossils.

[Forey](#) seems surprised that we question the reliability of our molecular data despite their good fit with the fossil record. Our comments, however, were mostly dealing with the inference of time from molecular data, the aspect that [Forey](#) himself considers not worthy of attention.

He proposes to leave time as arbiter of phylogenetic analyses. What sort of arbiter? One that gives a red card to molecular phylogeneticists if they propose that a given species appeared later than its fossil remnants? Or one that sends palaeontologists off the field if the molecular data suggest a gap in the fossil record? As [Paul](#) says, the fossil record is the only reliable source of information about the history of life on Earth. The dates provided by a good fossil record are necessary for understanding the evolutionary processes.

Erroneous interpretations

Concerning [MacLeod's](#) remarks on the accuracy of foraminiferal fossil record, we agree that foraminiferal phylogeny should be more extensively studied using cladistic principles. We can only hope that the interpretation of this phylogeny will be more accurate than that presented in his e-mail contribution.

[MacLeod](#) claimed that a strict consensus analysis of the molecular and fossil data presented in our paper¹ does not support the statement of their general agreement. However, his interpretation of our data is very frivolous.

He imposes a branching order to the fossil record tree of globigerinid clade that does not exist in stratigraphic data, as explained in our paper. The molecular data confirmed most of the globigerinid lineages inferred from the fossil record but, like the fossil data, they fail to resolve the relationships between these lineages.

Also, he does not refer to our remarks concerning the artificial attraction of two fast clock species in the globorotalid clade, which causes incongruence between the molecular and fossil phylogenies. As we explain in our paper, if we remove one of the fast clock species we can reconstruct the topology of the fossil tree.

This second example shows how a "total evidence" approach can be very tricky if not enough attention is paid to the biases in different data sets. It leads us to think that considering the various types of data separately, as proposed by [Pearson](#), may still be the best approach to phylogenetics.

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References

1. de Vargas, C., Zaninetti, L., Hilbrecht, H. & Pawlowski, J. Phylogeny and rates of molecular evolution of planktonic foraminifera: SSU rDNA sequences compared to the fossil record. *J. Molec. Evol.* **45**, 285-294 (1997).