Reviewer 1

This is a detailed description of the phylogenetics of a little-known group, using 20 transcriptomes (12,674 orthologs) to build a backbone phylogeny, then 2 mtDNA genes and 3 nuclear genes across 121 species to flesh this tree out. The combination of molecular phylogenetics and thorough knowledge of morphology are a strength.

We thank the reviewer for their careful assessment of our manuscript and their constructive remarks. We have improved and clarified the manuscript according to the suggestions. Please find below a detailed point-by-point response to all comments (reviewers' comments in black, our replies in blue).

Personally, I would not use the 90 morphological characters in the phylogenetic analysis though. The paper essentially tests the taxonomy of the group using independent molecular characters. The current taxonomy is a direct reflection of morphological characters already, so there is a degree of circularity here, especially when you then map morphological characters onto the tree (or are characters in Figs. 3-4 excluded from the phylogenetic analysis?). Having said that, the molecular characters (98%?) probably swamp the morphological characters, but it very much depends on how many are phylogenetically informative, and the distribution of their character states.

We respectfully disagree that there is circularity in using transformations of morphological characters where they have been used in phylogenetic inference. This issue has been discussed extensively in the literature and we provide here a few quotes that used a 'total evidence' approach:

de Queiroz (1996) states "one practice that can be discouraged is excluding entire sets of characters for the simple reason that they include the characters of interest as one or a few of their members."

Lucknow and Brunei (1997) state that "characters for a cladistic analysis should be evaluated as homology statements rather than functional ones. As with any partitioning of data, character exclusion may lead to weaker phylogenetic hypotheses, and the practice of mapping characters onto a tree, rather than including them in the analysis, should be avoided."

Harlin (1999) states: "It is commonly argued (e.g. Coddington, 1988; Brooks & McLennan, 1991) that it is circular to include characters in a phylogenetic analysis if the evolution of the same characters later will be studied or if they are to be included in a statistical test. … Since characters themselves do not have anything to do with the choice of phylogenetic hypothesis it is illogical to argue that it is circular to test characters that was used in the primary phylogenetic analysis."

We agree with the Reviewer that these 90 morphological characters likely have little influence on the phylogenetic inference given the amount of DNA data. In fact, the analysis of the molecular partition alone and of the molecular partition plus the morphological partition produced a generally very similar topology except in the position of *Terebellides* and some small rearrangements (Supplementary Figures S8 and S10). However, one of the authors on the currently accepted hypothesis of Terebelliformia relationships, Kirk Fitzhugh, is proponent of 'total evidence' and we included such an analysis to preclude criticism from him based on that approach being lacking.

To allow readers to assess the phylogenetic hypotheses reconstructed based on the morphological partition alone, the current version of the manuscript now also includes an analysis of the molecular partition constrained by the transcriptome backbone as Supplementary Figure S11 (in addition to the unconstrained analyses of the different partitions, and the constrained 'total evidence' matrix which were already part of the original submission).

References

de Queiroz K. 1996. Including the characters of interest during tree reconstruction and the problems of circularity and bias in studied of character evolution. American Naturalist 148: 700-708.
Luckow M, Bruneau A. 1997. Circularity and independence in phylogenetic tests of ecological hypotheses. Cladistics 13: 145-151.
Harlin M. 1999. The logical priority of the tree over characters and some of its consequences for taxonomy. Biol J Linn Soc 68:497-503.

The writing does get a bit dense and descriptive, particularly as it relates to taxonomy. It would help if some of this could be reduced, or perhaps structured with subheadings to make it more accessible? Some of the writing is a bit casual or careless, but only in a minor way: taxa are always singular, and taxa need to be distinguished from their members. I make some suggestions below, but it could benefit from a read through by a systematist to formalize some of the language.

Thank you for highlighting these issues, which have been corrected in the current version.

Specifics:

20 Suggest saying actual rank, rather than "group within" (e.g. "subfamily of")

Changed as suggested.

36 "OF annelid"?

Fixed.

37 Taxa are always singular, so say "members of" for example.

Changed as suggested throughout the text. This specific instance was changed to "Members can be recognized…".

39 As above- reword to distinguish between talking about a taxon and its members.

Changed to "and its species range...".

41 "continually" might be better.

Changed as suggested.

58 Delete: "on"

Changed as suggested.

73 Colon break or new sentence needed at "other data", or re-word.

Changed as suggested into two sentences.

102 "total evidence approach" may be a bit misleading here, as it might suggest using morphological data (and maybe others) to create the phylogeny, whereas I don't think you mean that.

Removed "total evidence" to read "We used this approach, …"

113 The transcriptome approach is a little light on replicate taxa. It is hard to make reliable generalisations and re-classification of Melinninae with just the one taxon, as we don't know whether it represents an anomaly at the level of the entire subfamily, or just one particular species. The finer mtDNA analysis ameliorates this problem.

We fully agree on this point. As the reviewer mentions, there were 5 additional Melinnidae terminals in the molecular five gene partition and morphological dataset that show that *Melinna oculata* is not an outlier in Melinnidae.

132 "positions were"?

We reworded to: "had only 4.6-7.2 million reads but the samples were kept because their phylogenetic position was resolved with high confidence"

153 "NUMBER of loci"

Changed as suggested.

155 Might be a good idea to check that the phylogeny favoured is the same for a consistent dataset. Looks like this is robust from the Results section. Need to give some values for the amount of missing data.

The phylogenetic hypothesis in Figure 1 was supported in most concatenation and coalescent-based analyses. Coalescent-based species tree approaches perform well irrespective of the amount of missing taxa in the gene trees as has been cited in the text. To give a sense of the number of taxa in each gene tree, we added mean and standard deviation of the number of species in each alignment: "We therefore used all 12,674 loci for estimation of gene trees (mean number of sequences per alignment = 9.4, standard deviation = 4.8)."

172 "excluded"?

Corrected.

263 Looking at the tree, would it not be better to say that Ampharetidae, as currently described, is POLYphyletic? That is, you have not labelled ancestral taxa leading to Melinninae in orange.

Thank you. Corrected as suggested.

322 Better to say: "placed in the Ampharetinae".

Corrected as suggested.