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Interactive comment on “Comprehensive phylogenetic reconstruction of relationships in *Octocorallia* (*Cnidaria: Anthozoa*) from the Atlantic ocean using *mtMutS* and *nad2* genes tree reconstructions” by K. J. Morris et al.

K. J. Morris et al.

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General comments

We gratefully acknowledge the helpful comments made by the reviewers that have provided additional insights and will allow us to improve the quality and readability of a revised paper. In this full revision we will address all major and minor issues as follows:

We will change the introduction and discussion to reflect the fact that the aim of this manuscript is not to challenge the findings of McFadden et al 2006. We used that pa-

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per as a foundation on which to construct our analysis, including the use of the same markers and integration of McFadden's Atlantic samples for our study. The intention here was that any results would be directly comparable. As part of this process McFadden very kindly provided the initial alignments of their sequences which we used as a guide. It is true that the majority of the new samples added to this alignment belonged to the families Paragorgiidae and Isididae, which were not previously represented.

We decided to limit the phylogenetic tree construction to Atlantic samples partly to be in keeping with the goals of EU FP7 Project HERMONIE (Hotspot Ecosystem Research and Man's Impact On European Seas), for which this special issue is dedicated. A major aim of HERMONIE is was to use the knowledge gained during the project to contribute to EU environmental policies and thus we did not feel the inclusion of Pacific samples would be directly relevant to the project. Admittedly, we accept this should have been explicitly clear within the manuscript, which in retrospect perhaps should be entitled 'A descriptive study of the phylogenetic diversity of octocorals from the Atlantic', rather than 'Comprehensive phylogenetic reconstruction of relationships in Octocorallia (Cnidaria: Anthozoa) from the Atlantic ocean using mtMutS and nad2 genes tree reconstructions'. We therefore suggest this as a new title, with the aim of describing the Octocorallia in Atlantic waters and their phylogenetic diversity. All necessary changes on the manuscript will reflect this revision.

Having taken on the reviewers concerns regarding identification of oddly placed specimens, we were able to re-examine all of the available data and change identifications as appropriate and listed below:

Ch35 was listed as Acanella, replaced by Distichoptilum gracile Ch233 was listed as Acanella, replaced by Distichoptilum gracile Ch17 was listed as Acanella, replaced by Chrysogorgia Ba1 was listed as Gryphyllum, replaced by Kertonisidae Ma11 is Metallogorgia melanotrichos, not Narella 15 is Acanthogorgia, not Villigorgia 13 is now removed due to problems with identification

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These appear to fit more naturally with the rest of the species within nodes and branches created by the tree.

We regret that these errors occurred in manuscript preparation and thank the reviewers for bringing them to our attention. It is believed these were transcription issues, which now have been corrected. These changes also fit more coherently with the tree produced with the exception of sample Az15 which maybe a result of degraded DNA or error (this sample was identified as *Acanthogorgia* by experts in the Azores before being given for inclusion in this study). Tables and trees have been updated with these results. Once accepted, we will make all sequences publicly available through GenBank with voucher specimens being held in the discovery collections at National Oceanography Centre, Southampton. We can also make the alignment available for review if requested. Figures and tables have been updated to reflect this information. Figures are also changed to increase resolution and make sample identification clearer.

We agree that this study strongly supports the presence of the previously reported clades in Octocorallia, as noted in the discussion. However, we dispute that it does not show a fourth clade composed of Pennatulacea. During the research project of the lead author, (K. Morris) from which this paper has mainly been produced, all available mtMutS and nad2 global samples at the time were used to construct a phylogenetic tree. With the increased inclusion of Bamboo corals (Isididae) in comparison to previous studies, there was a distinct separation of the seapens from 3rd reported clade leading to the production of a fourth clade (Fig 1.3) (see link below for tree image - full information available at http://eprints.soton.ac.uk/338892/1.hasCoversheetVersion/Morris_PhD_2011.pdf)

This is something we believe is shown in this study and may well be attributed to the large inset present within the Isididae, leading to their separation. Additional samples that have become available since the thesis work have also been included and support this separation. We chose to concentrate on the Atlantic samples rather than the worldwide distribution to be in keeping with the HERMONIE theme of this special issue.

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As above, we conceded that the emphasis of the initial submission was wrong and we will be happy to constrain the scope of the manuscript in the subsequent revision.

Specific comments to the individual Referees.

All of Referee #1 Specific comments and Technical corrections have been addressed above and are now found in the corrected manuscript with the exception of changing the reference to “New species Ma33”. Advice has been sought from both Les Watling (Isididae expert, University of Hawaii) and Phil Alderslade (taxonomic expert, CSIRO, Australia) regarding its taxonomic placement – although this remains unresolved. This is considered a result of its unique sclerite and skeletal structure.

Referee #2 As previously noted, problematic samples, which were erroneously transcribed in manuscript preparation, have been revised. We would like to thank careful attention of the 2nd referee for bringing this to our attention. In the revised manuscript many branches that were previously identified as suspicious now no longer raise concern. We are happy to make genetic alignment available for review as supplementary data in the revised manuscript and will submit sequences if and when the manuscript is accepted.

Other comments:

In response to referee’s #2 comments regarding that there was no indication on how the alignment was performed, we would make reference to the Material and Methods (lines 145-157), where we believe we have stated how the alignments were produced and corrected by eye, according to published approaches. The alignment was in fact primarily done on nucleic acids followed by a final correction based on the on the amino acid sequences to ensure the identification of any stop codons and confirm the placement of gaps. This was also compared to the McFadden et al. (2006) alignment to allow a direct comparison of results, and was found to match well.

Further information regarding phylogenetic estimations have been included in the re-

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vised manuscript.

The reason why we used Garli and then RAxML is that Garli allowed us to specify the nucleotide substitution model, unlike RAxML (only allows GTR). Bootstrapping in Garli for such a big dataset requires a lot of computational resources and time, thus is faster to do it in RAxML.

We have changed the concatenated tree to concatenated alignment.

The consensus tree was produced by comparing all trees produced by the same alignment, i.e. the Bayesian, ML and MP trees, and comparing nodal and branch structures. They were then manipulated by rotating branches within nodes to form an agreed tree using the software FigTree. Where no agreement could be identified, differences in topologies were highlighted on the tree.

Financial and technical constraints prevent us from including more specimens and markers beyond the current analysis. Nonetheless, we maintain that using the two markers presented not only represents a valuable addition to the overall characterization of global octocoral diversity, but will also increase knowledge of the species present within the Atlantic.

Final comments

Overall, in our revised submission we have taken the focus of the paper away from a 'comprehensive phylogeny' to a descriptive study of the phylogenetic diversity of corals in the Atlantic. Specifically: we have double-checked the correspondence of taxonomic identifications and sequences and addressed transcription errors we have changed and thoroughly curated the tables and figures to add as much detail as possible regarding the samples and their identifications. all typing errors and suggestions from both Referees have been addressed in the revised manuscript.

Finally, we believe that this study contains valuable information, showing the species reported from the Atlantic to date, as well as their relative locations and distributions

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and their phylogenetic relationships to one another. It has also shown that there is a clear separation between the samples above 50 m and in deeper waters, within the Atlantic.

We also note that a large number of deep-water specimens of below 50 m from a range of areas have been included in this study. This indicates a wide spread distribution of Octocorallia throughout the Atlantic Basin, something which should be considered in EU environmental policies. We have changed the discussion to reflect this important conclusion and changed the discussion to focus on the descriptive study of the Atlantic Ocean, rather than comprehensive phylogenetic reconstruction. We believe that this manuscript presents a significant contribution to the scientific literature on octocorals and deep-sea organisms.

We are grateful to the reviewers and the editor for their time and consideration into improving upon the first submission.

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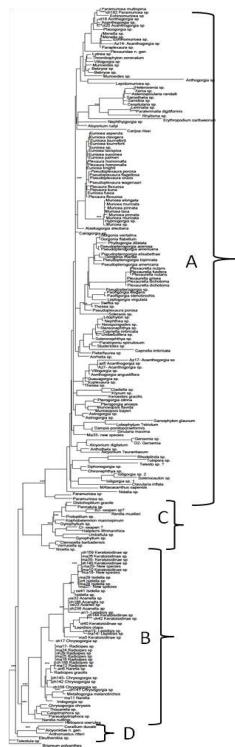


Fig. 1.

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