

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.

Anonymous Referee #2

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The premise of the paper is to provide the community with a comprehensive phylogenetic analysis of the Octocorallia, using specimens from the Atlantic. For a phylogenetic analysis to be comprehensive, specimens throughout the distributional range have to be included to avoid taxonomic bias. In the case of the Octocorallia, some species, genera, and even families are rare and / or geographically restricted to areas outside of the Atlantic. In addition, it is known that many geminate species are shared between the Pacific and the Atlantic. Because the phylogenetic reconstruction is based on mt-MutS and nd2, and a significant amount of the data comes from McFadden et al. 2006,

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this paper has therefore to overcome the limitations of McFadden et al 2006 to be a significant contribution. Some of the limitations of the McFadden et al study were that the genetic data employed were not sufficient to resolve deep nodes. In addition, taxon sampling was limited to a few genera for many families (and this had significant bearing on the proportion of octocoral families appearing as monophyletic). It is therefore unclear, for this paper by Morris et al, how knowledge on the phylogenetics of the Octocorallia will be significantly improved by using the same genes and artificially restricting taxon sampling by focusing solely on the Atlantic.

There are several patterns in the phylogenetic trees that make me doubt of the trustworthiness of the data. In the Calcaxonia alone, there are several patterns that are very odd, based on previously-published data, and based on data available on GenBank. For instance: Metallogorgia (Chrysogorgiidae) most closely related to one Narella (Primnoidae) ; one Isidella (Isididae) most closely related to Radicipes (Chrysogorgiidae) ; some Acanella (Isididae) clustering with sea pens. . . I have never seen patterns like these. Of course, it does not mean that they are not real, but the way the data is presented shows that little care was taken in the taxonomy, which makes me further doubt the results. For instance, in the list of specimens (table 1S), there are obvious taxonomic errors (e.g. Viminella is an ellisellid, not an isidid ; Gersemia is in the Nephtheidae ; Paragorgia54831 is, according to Herrera et al 2010, Sibogorgia cauliflora, etc. . .). There are also errors in the geolocation of specimens (e.g. Protopitulum from Nigeria, not matching coordinates). In the text, I found four different spellings of Isididae, three of them in the abstract (and more in table S1). In the phylogenetic tree, I found a "bamboo coral". Checking the results is very difficult, to impossible, because the trees do not include information on individual specimens. We can therefore not match a the phylogenetic placement of a particular taxon with its GenBank number ; we cannot determine which Paragorgia, on the tree, were sequenced for this study, or for the Herrera et al (2010) study. In addition, there are no museum voucher numbers to refer to. Because many branches are suspicious, I doubt that the structure of the tree is accurate, and I will therefore not comment further on the results and the

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interpretations by the authors.

Because of the severe problems outlined above (taxonomic bias due to limiting the study to the Atlantic and odd results probably due to human errors), I am not recommending this paper for publication. For this study to be a significant contribution to the field, I would recommend that the authors work on taxon sampling in a global perspective (and include the several new octocoral families that were recently described), contemplate using more markers, check their taxonomic identifications, their molecular data, and all clerical work, and present their data in a more comprehensive way, facilitating data check and reproducibility.

Other comments:

Phylogenetic analysis: First, it is important to use a robust DNA alignment program: Clustal is one of the least accurate alignment software available in the market for phylogenetics, based on benchmarks (see for example Loytynoja and Goldman, 2008). Given the complex indels present in the Octocorallia at mtMutS, the alignment is particularly important. Second, there is no indication in the text on how exactly the alignment was done. Even if the phylogeny is estimated based on nt, the alignment of protein-coding regions has to be done on amino acids ; nt have to be aligned based on the aa alignment (see for example Abascal et al 2010). Third, were the trees estimated from nt or aa or both? Are your models of molecular evolution for nt or aa? What were the chosen models? Concerning the phylogenetic estimation: (1) bayesian analysis: some important parameters are omitted (e.g. length burnin), (2) maximum parsimony parameters are omitted (type of search. . .), (3) for the ML analysis, why did you build the tree in GARLI and performed the bootstrap in RaxML? GARLI does support bootstrapping through the "-bootstrapreps" option. Concerning the results of the analyses: (1) "concatenated phylogenetic tree" : the alignments are concatenated, not the trees. You say that you built a consensus, but I don't see polytomies, even though there are few well supported branches. Did you really do a consensus? (2) "**** indicates branches with >90% Bayesian support and high MP support" : first, nodes are supported, not

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branches. second, why not provide information on nodes <90%? would you ignore a node with 80% support? Thirst, what is "high MP support"? Fourth, where is the ML information? Your trees are hard to read, pixellated, and the labels are heterogeneous and contain typos ; I would revise them.

The text needs to be thoroughly edited ; some sentences are ambiguous, and there are many typos. One sentence (page 16981) is duplicated (between lines 10 and 15). Terminology needs to be homogenized and corrected (e.g. Octocorallia, as well as all taxonomic categories about the genus level are not italicized ; you use nad2 and NAD2, etc. . .).

Table 2: the reference of CO3bam5657F should be Brugler and France 2008 ; the reference of Mutchry3458r should be Pante et al 2012

References: Hellberg 2006 was published in BMC, not MBC ; Herrera et al in press is now in print (Mol Ecol, 2012 Dec;21(24):6053-67. doi: 10.1111/mec.12074. Epub 2012 Oct 23) ; Pante et al, not Plante et al, and the correct citation is PLoS ONE 7(6): e38357. doi:10.1371/journal.pone.0038357 ; van der Ham et al, not Van de Ham

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