

Reviewer Report

Title: "Whole genome sequencing of Chinese clearhead icefish, *Protosalanx hyalocranius*"

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Reviewer name: Frederic Brunet

Reviewer Comments to Author:

I have not much to say about the quality of the work mastered here by the authors to generate the assembly of another fish genome, but among the Stomatii, a taxonomic location not yet been investigated.

Sentence line 185-186 is not well written. The phylogeny does not match the statement. Maybe the authors should rather name the taxonomic groups rather than naming two species that twisted their meaning.

Sentence line 204-206. This sentence shows that the authors have been misled. There was only one event of whole genome duplication at the base of the Teleost genome. The different average rate of evolution in the different species observed by gene comparison has a different meaning than the one stated here. In this case, it is more suitable to rephrase this sentence. See similar comparisons made in the trout genome paper by Berthelot et al. 2014. Therefore, fig.2 is just a glimpse of what can be done, and this interpretation is too scarce and misleading.

Besides, recently published genomes have a finer tuned gene descriptions as better annotated sequences and more genes are described. *Oreochromis niloticus*, the Nile tilapia is a good example. On the contrary, the medaka genome lacks several genes, found in several other fish species, and sometimes key genes.

One suggestion would be to find out the number of duplicates originating from the teleost fish duplications compared to what have been described in the other species.

What TRF stands for in Table 2?

Line 184 typo in the word "sequence".

several "&" instead of "and".

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