Reviewer Report

Title: Genome sequence of the barred knifejaw Oplegnathus fasciatus (Temminck & Schlegel, 1844): the first chromosome-level draft genome in the family Oplegnathidae

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Reviewer name: Alejandro Gutierrez

Reviewer Comments to Author:

In this manuscript Xiao et al. reports the genome assembly of the rock bream (O. fasciatus) a species of increasing economic importance in Asia. This species exhibits sex dimorphism in growth and also a sex determination system based on multiple sex chromosomes X1X1X2X2/X1X2Y, which makes it interesting species to study. The draft genome of the rock bream will be a valuable resource to facilitate future research aimed at improving relevant traits and understanding of determination systems.
The authors used an adequate amount of sequence data from three different sources (Illumina short reads, PacBio and Hi-C), which allowed them to generate a robust genome assembly. Furthermore, the authors annotated the genome using multiple strategies. Finally, they carried out some phylogenetic analyses including other fish species. The methods followed to obtain the assembly are good in general, and well described.
L33-L35 Please re-phrase, maybe say "sexual dimorphism in growth"
L37 ...basing -> based
L43 "…We assembled the O.fasciatus" <genome?>
L77 Again please re-phrase "the growth sexual dimorphism"
L99-L100 "A whole genome using Illumina DNA seq…" re-phrase
L115 Was the blood extracted from the same fish used for pacBio and Illumina?
L162 "the results showed <that> 99.8%.."
L172 Typo Repreatmasker
L252 Is not clear how you came up to those 812 orhtogroups, and the same for L256
L266 I don't think the authors should claim that the Notothenioidei should be elevated to the order level, but I would accept that their results suggest or show evidence of this.
General Comments:
There are many issues with the English throughout the manuscript and these must be addressed before considering for publication. I strongly encourage the authors to proof-read the manuscript before re-submitting.
I wonder why the authors chose to sequence a female fish, while the male fish could have had provided the full sequence of the Y chromosome which could've brought insights into sex determination, the identification of sex specific regions, etc. I mention this because you stress that the genome assembly is useful for the understanding of these mechanisms this but then there's no mention of this important topic in the discussion.

Level of Interest

Please indicate how interesting you found the manuscript: Choose an item.

Quality of Written English

Please indicate the quality of language in the manuscript: Choose an item.

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