Reviewer Report

Title: The genomic basis for colonizing the freezing Southern Ocean revealed by Antarctic toothfish and Patagonia robalo genomes

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Reviewer name: Ole K TÃ¸rresen

Reviewer Comments to Author:

Reviewer report.
Title: Genomic bases for colonizing the freezing Southern Ocean revealed by the genomes of Antarctic toothfish and Patagonia robalo
General comments
The authors have sequenced and assembled the genomes of two notothenioids, and have done extensive comparisons with regards to expansions of gene families and differential expression of genes. They show that several genes in the D. mawsoni has undergone positive selection, highlighting the evolution of the genes of that species.
Specific comments
Abstract: An extant species is not necessary a proxy for an extinct species.
Introduction:
Line 89-90: You specify "whole genome sequence analysis" as the criteria for mentioning the Antarctic rockcod as the only notothenioid reported so far, but MalmstrÃ¸m et al 2016 (https://www.nature.com/articles/ng.3645) did publish genomic sequences and the assembly of Chaenocephalus aceratus. However, they did not report any genomic/biological features of that particular species, so your phrasing is entirely correct.
Line 107-8: As you no doubt are aware of, size do not necessary have any bearing on buoyancy, only average density. It is not apparent to me that smaller size would mean easier to achieve neutral buoyancy.â€¨
â€¨
Results:
Line 138: Why was two different genome assemblers used? Also, in the header for Table S2b it is stated that E. maclovinus was assembled with both SOAPdenovo and Platanus.
Line 140 and other places across the manuscript: "Kb", that is, kilo base pairs, should be abbreviated "kb(p)". See: https://en.wikipedia.org/wiki/Metric_prefix
Line 164: The number of common genes is a bit strange. The vast majority of genes should be common between these species. I think you have written this wrong. In the referred figure, S3, it is specified that the number 8,825 is the amount of common gene clusters, and not just genes. One cluster might contain multiple genes.â€¨
Lines 182-192: You stated earlier "842 Mb for D. mawsoni and 727 Mb for E. maclovinus". You could say that quite a bit of that difference in genome size could be due to differences in repeat content, and not just percentage. 161.8 Mbp TEs in D. mawsoni and 74.6 Mbp in E. maclovinus, with a difference of 86.2

Mbp. It is not apparent that the percentages differences in repeat content actually translates to those large differences in repeats, because these repeat annotations can be quite different (many repeats are not annotated properly in different genomes).
Line 613: It is InterProScan, and not InterproScan.

Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

Conclusions

Are the conclusions adequately supported by the data shown? Choose an item.

Reporting Standards

Does the manuscript adhere to the journal's guidelines on minimum standards of reporting? Choose an item.

Choose an item.

Statistics

Are you able to assess all statistics in the manuscript, including the appropriateness of statistical tests used? Choose an item.

Quality of Written English

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

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