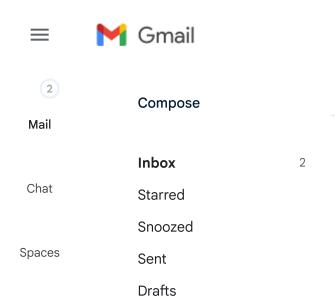


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	N	More		Our decision is: Revisions Required			
	Label	s					
				 Reviewer A:			
				Dear Authors,			
						pt for review. You have taken into account the feedback provided on the initial review of the nanuscript have resulted in a more robust paper overall. In light of the revisions, the pape	
				Recommendation: -			
				Reviewer B:			

Meet



Labels

More



Reviewer B:

Overall, this study would make an interesting addition to previously published studies. The study system is particularly interesting given their current dist make sense. As such, I had to stop reading before finishing the manuscript.

English needs improving throughout document as lots of spelling errors and sentences that don't make sense.

I don't think the Results and Discussion should be merged as it currently is and strongly recommend the authors to use separate headings for these two

There are statements as to why different sequence lengths show how diverse this population is and how it might have a big ecological effect, but I don't evidence and examples.

I stopped reading at line 187 as I feel the authors need to first go through their manuscript to ensure that the English makes sense and accurately reflect getting lost in translation. There are a lot of big statements that I do not think are justified nor appropriate for this study.

22-26: very broad introduction to phylogeography that is also quite repetitive and simplistic.

29-31: Not sure if the entire classification is needed here as the reader can determine this from its binomial nomenclature.

36: "megadiverse organisms' evolution" doesn't really make sense...perhaps consider changing to something along the lines of "...have all contributed to

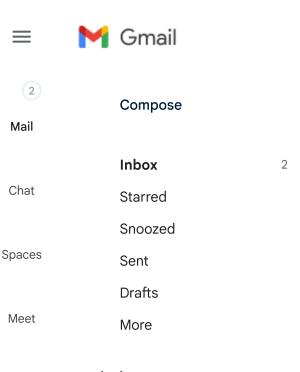
42: the previous study did not use the 'worlds' A. panchax, just a few populations distributed across SE Asia, but not all.

58-59: I'm not sure what the authors are trying to say here. Are they saying that all Indonesian waters are polluted?

63-66: would be good to have sample sizes for each station

Figure 1: quality needs to be improved as currently quite grainy

71: is that 20 samples for all sites together? Or each site? If it's all sites together, this sample size is quite small



Labels

K Biodiversitas X 3

100: what does 'it' refer to?

102: in line 96 the authors state that only 'some' sequences of a previous study was used. In line 102, it is not clear whether it is 'some' or all sequence of populations you included and why the authors did not include them all

Figure 2: again, the quality of the figure is poor and difficult to read.

Table 1: sample spelt wrong in table

114-130: quite extensive section on DNA quality and nanodrop results. I do not think that this adds to the study and recommend that it be removed and r

135-146: should be in the Discussion

Figure 3: is Figure description confused with Figure 4?

Figure 4: Figure 4 and 3 could be merged and quality improved so that it is readable

163-167: should be in Discussion

178: why is it essential to understand evolution?

182: Beck et al. did not say this

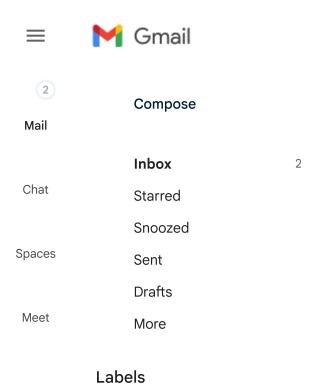
Recommendation: Resubmit for Review

Reviewer C:

Comments to the Author

This study contains novel data on the population genetics and phylogeography of *Aplocheilus panchax*. Given the restricted distribution in Southeast As from a relatively unsampled area. Moreover, the data set recover original mitochondrial sequence. Since this species does not occur outside of this regic globally, and this paper contributes substantially in this regard.

In my modest opinion, the manuscript is it is not well written and unclair in some sentences. There are a number of factors that currently detract from the



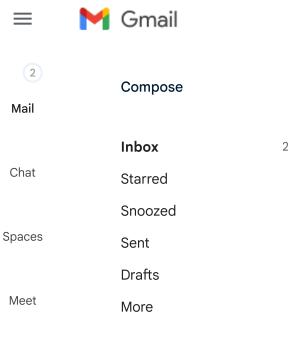
Riodiversitas X

Major concerns:

· Methodological considerations

The authors have minimized methodological features in relation to the molecular phylogenetic and genetic population analyses, being these methods fur in the methods section for the generation of genetic analysis, and some of the statistical additional analyses are required.

- 1. a) I don't see in the MS an implementation of the AMOVA analysis. The author must estimate the better grouping hypothesis for samples using different groups hypotheses to maximize the among group variance Φ
- 2. b) The authors do not include in the study, an indirect estimate of gene flow analyses for the different data sets, which represent important populations.
- 3. c) The range of the genetic distances presented here, are very large, and I suspect that there are any problem in the output of the MEGA progr
- 4. d) What are the bootstrap values to validate the node support in the tree topology?. I see bootstrap values very low in some of them.
- Content issues
- 1. a) I suggest to improve all the Figure quality because they are the results that must be well exposed in order to facilitate the comprehension of
- 2. c) It will be desirable a reorganization of the discussion contents and rewording any paragraphs to condense them, because they are very repe
- 3. d) A better integration of the killifish literature could help to develop the discussion further and increase readership. A large number of annual are for comparison.
- 3) Format consideration
 - 1. a) The authors must relocate the Fig. 2 in present version, from the Mat and Methods to the Results_Discussion section, because it constitutes



Labels

Q Biodiversitas X 3

Reviewer D:

This manuscript presents some interesting COI data and results on a previously unsampled (at least genetically) population of *Aplocheilus* fishes from B with the current version of the manuscript that need to be addressed before it is suitable for publication. First, the authors need to explain more about th sequences obtained by other aurhors. Is this the result of an indel, or did they simply sequence more of the gene? Second, they need to examine how the comparisons involving the Bangka samples appear anomalously large (as do some of the mutational distances in the haplotype network), and this content be checked for possible errors. Third, the authors adopt some of the recent taxonomic proposals by Katwate et al. (2018) but not others, and they do no study seem to support the taxonomic proposal that the authors reject (i.e., recognition of *A. armatus* as a separate species from *A. panchax*). Related to panchax. In fact, their data suggest that those specimens might represent yet another distinct species. In addition, the English grammar and logic are no manuscript file to improve some of these issues, but the manuscript would benefit from being reviewed for English style and grammar before it is resubm

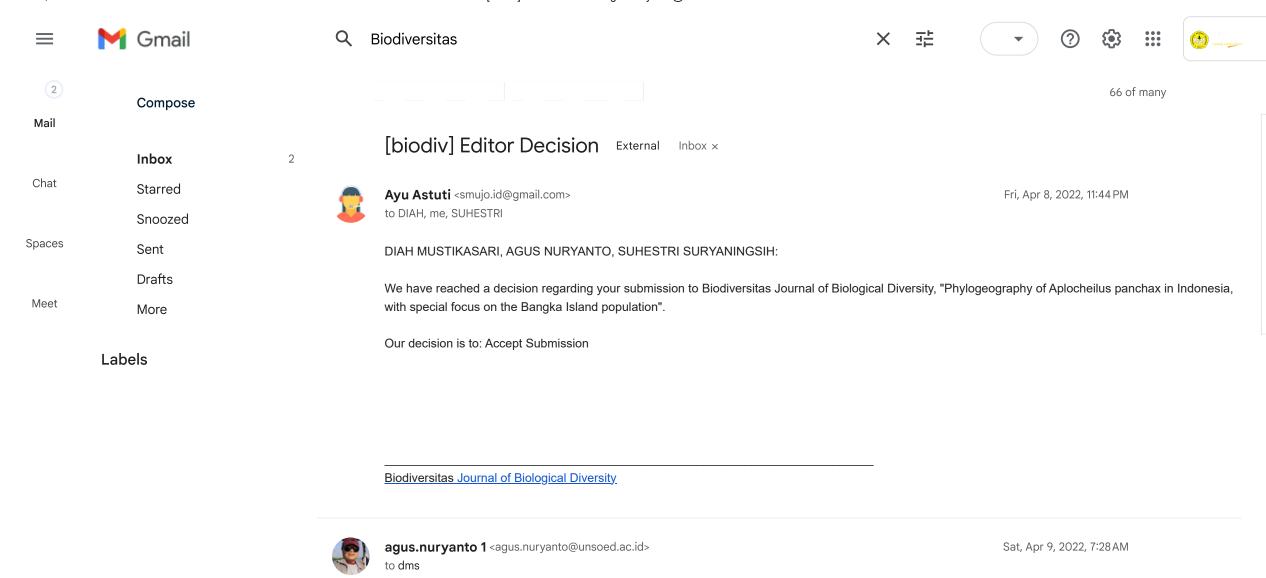
Recommendation: Resubmit for Review

Reviewer E:

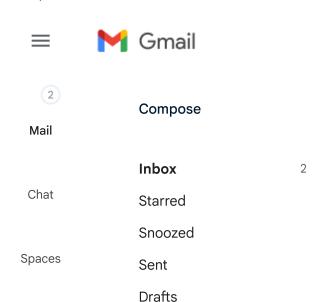
The authors provided an interesting study of the blue panchax (*Aplocheilus panchax*), in Indonesia. Specifically, the authors used a portion of the cytoch unstudied specimens from the pits of Bangka Island. I found the methods to be solid and results easy to interpret but feel that the paper can be shortene the overall quality of the paper. Specific comments are in returned ms.

Recommendation: -

Recommendation: Revisions Required



Meet



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More



[biodiv] Editor Decision External Inbox ×



Smujo Editors <smujo.id@gmail.com>

o me

AGUS NURYANTO:

We have reached a decision regarding your submission to Biodiversitas Journal of Biological Diversity, "Phylogeography of the blue panchax, Aplocheilu

Our decision is: Revisions Required

Reviewer U:

Dear Authors,

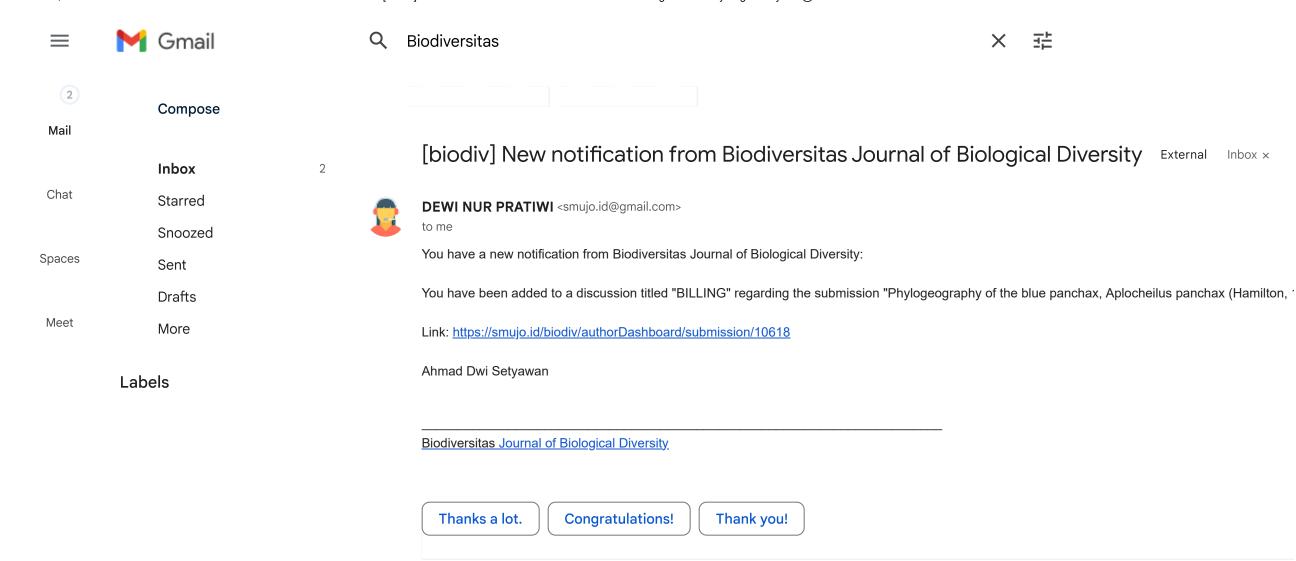
Thank you for preparing and submitting this interesting paper investigating the DOI gene in a novel population of the blue panchax. I found your paper to and the findings should add some value to the current literature in A. panchax.

There are some revisions required in order to consider this manuscript for publication. I have included specific feedback on the word document version c using highlighted text or tracked changes. Additionally, please consider the following key areas when making revisions:

- 1. Methods. Could you provide some more information on how you handled the fish samples. For example, how much tissue was taken? Where was it to
- 2. Dendrograms. You may want to make it a bit clearer as to which are your new samples, and which are from the existing databases of COI genes.

With these revisions the paper should be in a good position for consideration.

Recommendation: Revisions Required



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You have been added to a discussion titled "Uncorrected Proof" regarding the submission "Phylogeography of the blue panchax, Aplocheilus panchax (F

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Ahmad Dwi Setyawan

Biodiversitas Journal of Biological Diversity



agus.nuryanto 1 <agus.nuryanto@unsoed.ac.id>

to Ahmad

Dear Editor,

Thank you very much for the information. We would go through the manuscript and make corrections accordingly.

Best regards,

Agus Nuryanto