Relationships between crayfish population genetic diversity, species richness, and abundance within impounded and unimpounded streams

Comments

Title

I suggested including the locality where this study was conducted in the title.

Abstract

There are no comments in this section.

Keywords

In this section, you've included some keywords mentioned in the abstract, such as AGDCs, SGDCs, and MIH. I suggest replacing these keywords with others, such as mtCOI, ISSR, metric diversity, etc.

Introduction

Broadly speaking, I suggest that the introduction not be divided into small subtitles. Instead, the information should be addressed in an interconnected manner, presenting all aspects upon which this study is based.

Line 55. I consider that there is a lack of reference before the second sentence.

Line 115-119. I consider the transition between lines 115 to 119 to be a little abrupt. I suggest connecting the ideas to help the reader obtain a better understanding of the diversity metrics used and their relationship with the assessed habitat characteristics.

Line 134. Given that in your study the comparative basis between connected and fragmented habitats relies on the impoundments and unimpoundments of streams, I propose a more detailed explanation of the characteristics of both types of streams, and how these characteristics could influence the dispersal process.

Line 139-140. Could you explain in the text how habitat fragmentation impacts the dispersal ability of species? I suggest including some examples.

Line 163-164. See previous comment in Line 134

Line 165. Please briefly explain why *Faxonius validus* and *F. erichsonianus* were chosen as focal species for this study.

Line 172. Please consider these habitat characteristics to complete the information requested in the comment on Line 134.

Material & Methods

Line 207-211. Please, could you clarify the timing of the sampling? I understand that the first sampling took place during the spring and fall of 2015, but there was no sampling during the spring of 2016 and fall of 2017. If this is the case, I suggest adjusting lines 207-208.

Line 239. I suggest including the accession number for mtCOI sequences in the Results section and deleted on this line.

Line 264 -265. Delete "As with other types of dominant markers (e.g., Amplified Fragment Length Polymorphisms; Vos et al. 1995)"

Line 296-303. I consider it unnecessary to include the description of haplotypic and nucleotide diversity. Simply referring to them should suffice.

Results

Line 388-391. Include in this paragraph the accession numbers for mtCOI sequences for *F. validus* and *F. erichsonianus.*

Line 411, 417, and 421. I suggest deleting these subtitles and integrating these results into a single section.

Discussion

Line 545-455. This sentence indicates that a high abundance of crayfish reflects low population genetic diversity. However, some studies have suggested that large populations allow for maintaining high genetic diversity (Frankham et al., 2010; Allendorf et al., 2013). How can we explain this discrepancy in their results?

Line 455-459. Delete the sentence 'but population genetic diversity was highest at downstream sites.' Instead, I suggest connecting the idea from lines 455 and 456 with the sentence in lines 457-459.

Line 460. I suggest starting the sentence with 'Population genetic diversity was highest at downstream sites' and later including the information presented in lines 460-463.

Line 541-542. The study by Sinn et al. (2022) addressed the use of ISSRseq as a genomic tool based on the ISSR methodology. However, ISSRseq requires Illumina library preparation and other analytic methodologies. Therefore, I suggest adjusting Lines 541-542 to clarify this point.

Line 561-562. Please, could you explain what efforts allow an increase in the dispersal and gene flow in these species?