Processes that drive the population structuring of Jenynsia lineata (Cyprinidontiformes, Anablepidae) in the La Plata Basin

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Abstract

1. Species are not genetically homogeneous, as the genetic structure among populations is related to the degree of isolation amongst them, such as isolation-by-distance, isolation-by-barrier and isolation-by-environment. 2. To decipher the isolation processes that drive population structuring in Jenynsia lineata we analyzed 221 sequences of the mitochondrial cytochrome c oxidase I gene (COI), which came from 19 localities. Jenynsia lineata is a small viviparous fish that inhabits a wide range of habitats in South America. Then, we examined the influence of the three most common types of isolation to explain the genetic variation found in this species. 3. Our results revealed a marked structuration, with three groups: i) La Plata/Desaguadero Rivers (sampling sites across Argentina, Uruguay, and Southern Brazil), ii) Central Argentina, and iii) Northern Argentina. A distance-based redundancy analysis including the explanatory variables geographical distances, altitude, latitude, basin, was able to explain up to 65% of the genetic structure. A variance partitioning analysis showed that the two most important variables underlying the structuration in J. lineata were altitude (isolation-by-environment) and type of basin (isolation-by-barrier). 4. Our results show that in this species, the processes of population diversification are complex and are not limited to a single mechanism. Population-structuring may lead to population reproductive isolation and ultimately to speciation. 5. This study demonstrated that the process of diversification of populations is complex and is not limited to a single mechanism. The processes that play a prominent role in this study could explain the high rate of diversity that characterizes freshwater fish species. And these processes in turn are the basis for possible speciation events.

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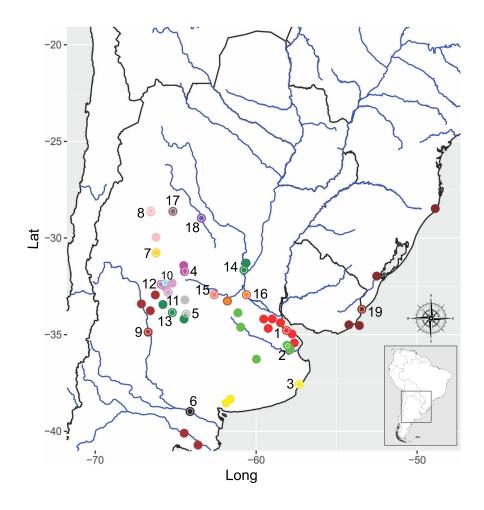
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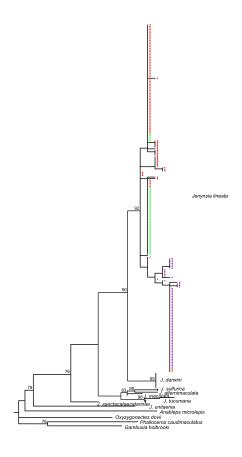
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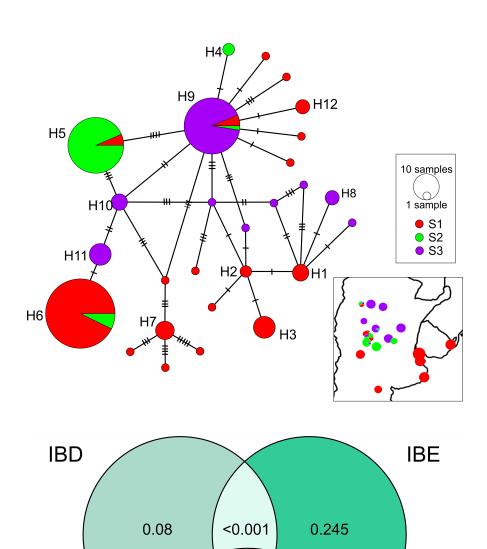
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