

Genome-wide Assessment Elucidates Connectivity and the Evolutionary History of the Highly Dispersive Marine Invertebrate *Littoraria Flava* (Littorinidae:Gastropoda)

Thainá Cortez

USP: Universidade de São Paulo

Rafael Viana Amaral

USP: Universidade de São Paulo

Thadeu Sobral-Souza

Universidade Federal de Mato Grosso

Sonia Andrade (✉ soniacsandrade@ib.usp.br)

Departamento de Genética e Biologia Evolutiva, Universidade de São Paulo, SP, Brasil.

<https://orcid.org/0000-0002-1302-5261>

Research article

Keywords: marine connectivity, phylogeography, demographic history, population genomics, Littorinidae, ecological niche modeling

Posted Date: October 30th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-98868/v1>

License:  This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Abstract

Background: An important goal of population genetics studies in marine ecosystems is understanding how connectivity patterns, both spatial and temporal, are influenced by historical and evolutionary factors. When it comes to dispersion and connectivity in marine ecosystems, the role of historical and evolutionary factors over population dynamics and

structure still remains enigmatic. We evaluated the demographic history and population structure of *Littoraria flava*, a highly dispersive and widely distributed marine gastropod on the Brazilian intertidal zone, to predict the effects of such factors on intrapopulation divergence. To test the hypotheses that (1) the species has historically high levels of gene

flow on a macrogeographic spatial scale and (2) the species distribution in rocky shores consists of subpopulations due to high degrees of environmental heterogeneity, we collected specimens along the Brazilian coastline and combined different sets of genetic markers (mitochondrial DNA, nuclear internal transcribed spacer 2, and single nucleotide polymorphisms) with niche-based modeling to predict species paleodistribution.

Results: Low genetic structure was observed along the coastline, and all clustering and migration analyses supported the high gene flow over long distances hypothesis (> 3,000 km). Three genetic clusters were identified by the assignment test, each mostly composed of individuals from the three sampled regions. No fine-scale variation was observed for any location. The neutrality tests and the haplotype networks suggest that *L. flava* had experienced population bottleneck followed by population expansion. Both paleodistribution and coalescent simulations highlight that expansion events occurred in the Southeastern coastline during the Pleistocene interglacial cycles (21 kya).

Conclusions: This is the first study on the South American coast that highlights the demographic history on a marine gastropod based on genomic markers associated with niche modelling. We found that climatic changes since the interglacial periods are potentially relevant drivers for the species distribution in the past. Our findings could enhance the understanding of the population dynamics under an evolutionary view for widely distributed non-model marine organisms.

Full Text

This preprint is available for [download as a PDF](#).

Figures

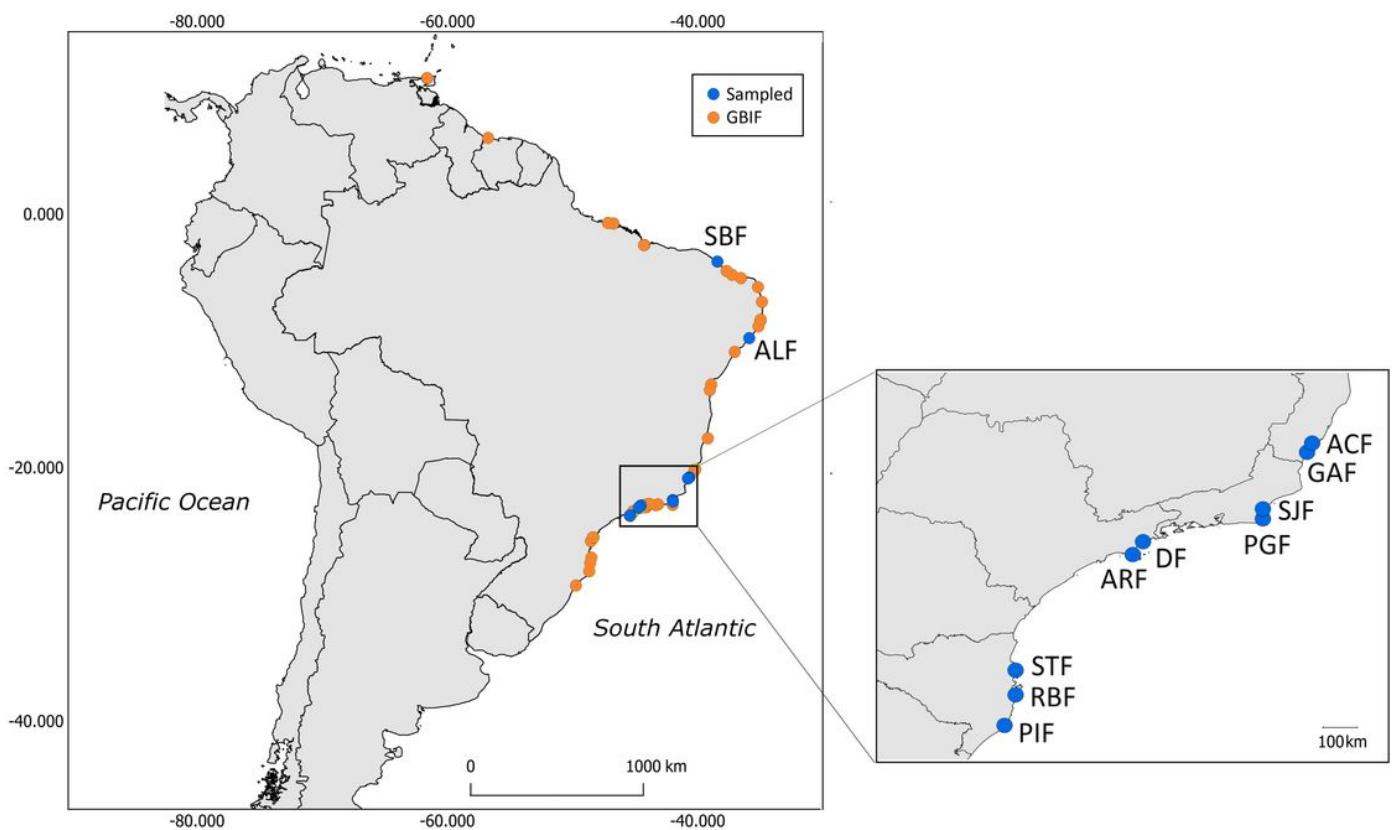


Figure 1

Distribution of sampling locations along the Brazilian coastline. The blue dots indicate sampling collection points, and the orange dots indicate the occurrence points of *Littoraria flava*, according to GBIF, used in the niche modeling analyses.

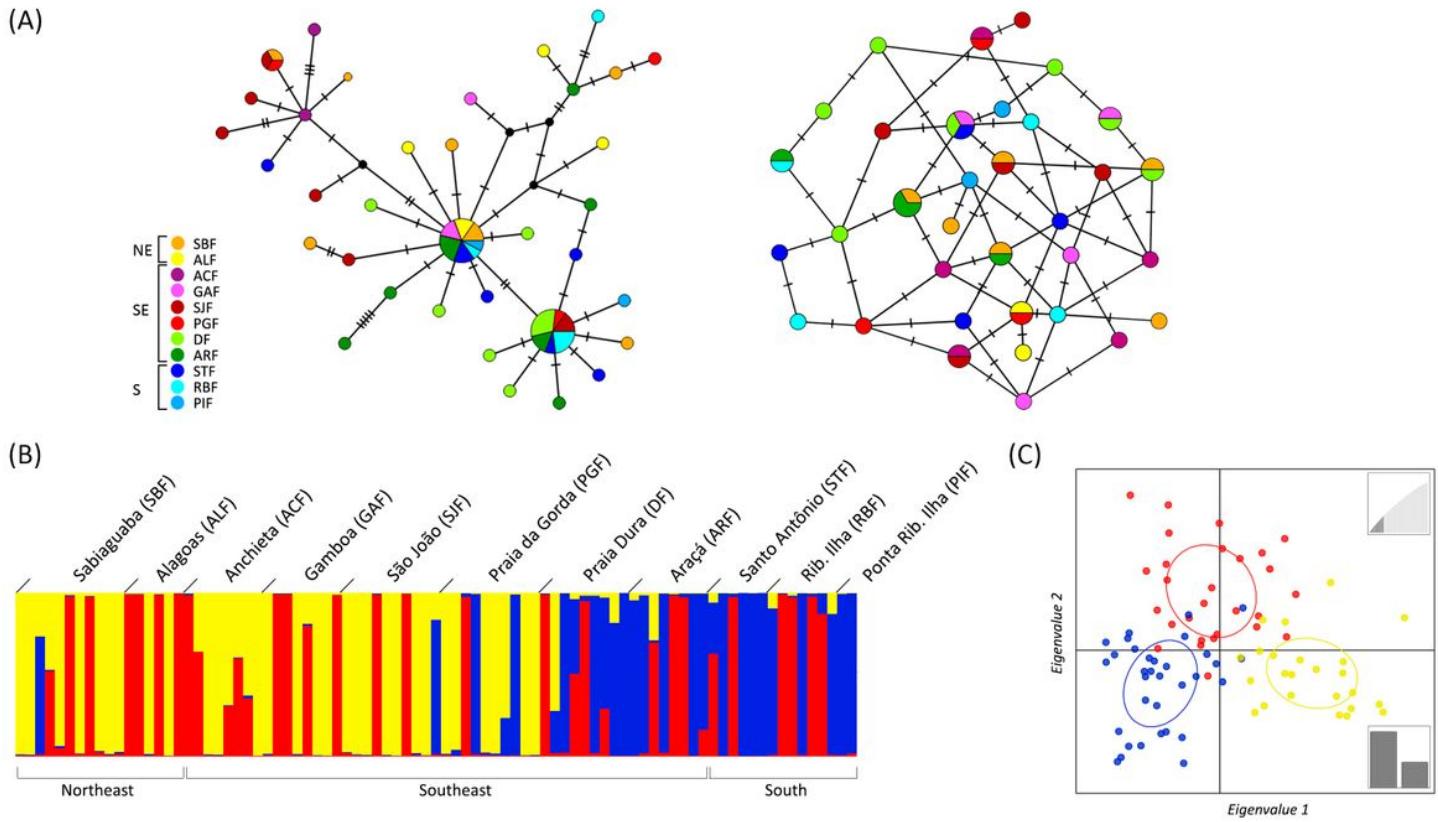


Figure 2

Haplotype networks and clustering analysis of *Littoraria flava*. (A) Minimum spanning network (MSN) of mtDNA, to the left, and ITS-2 data, to the right. Each node represents a haplotype, its size corresponds to the haplotypes' frequency, and its colors indicates the locality. Black nodes represent inferred ancestral nodes. (B) Assignment plot based on STRUCTURE analyses with 6,094 SNPs and K = 3. Each vertical bar corresponds to one individual, and the color indicates the proportion of membership in each genetic cluster. (C) Discriminant Analysis of Principal Components (DAPC) density plot for 85 *L. flava* individuals. Dots represent individuals with colors denoting the genetic groups identified by STRUCTURE. Abbreviations as in Table 1.

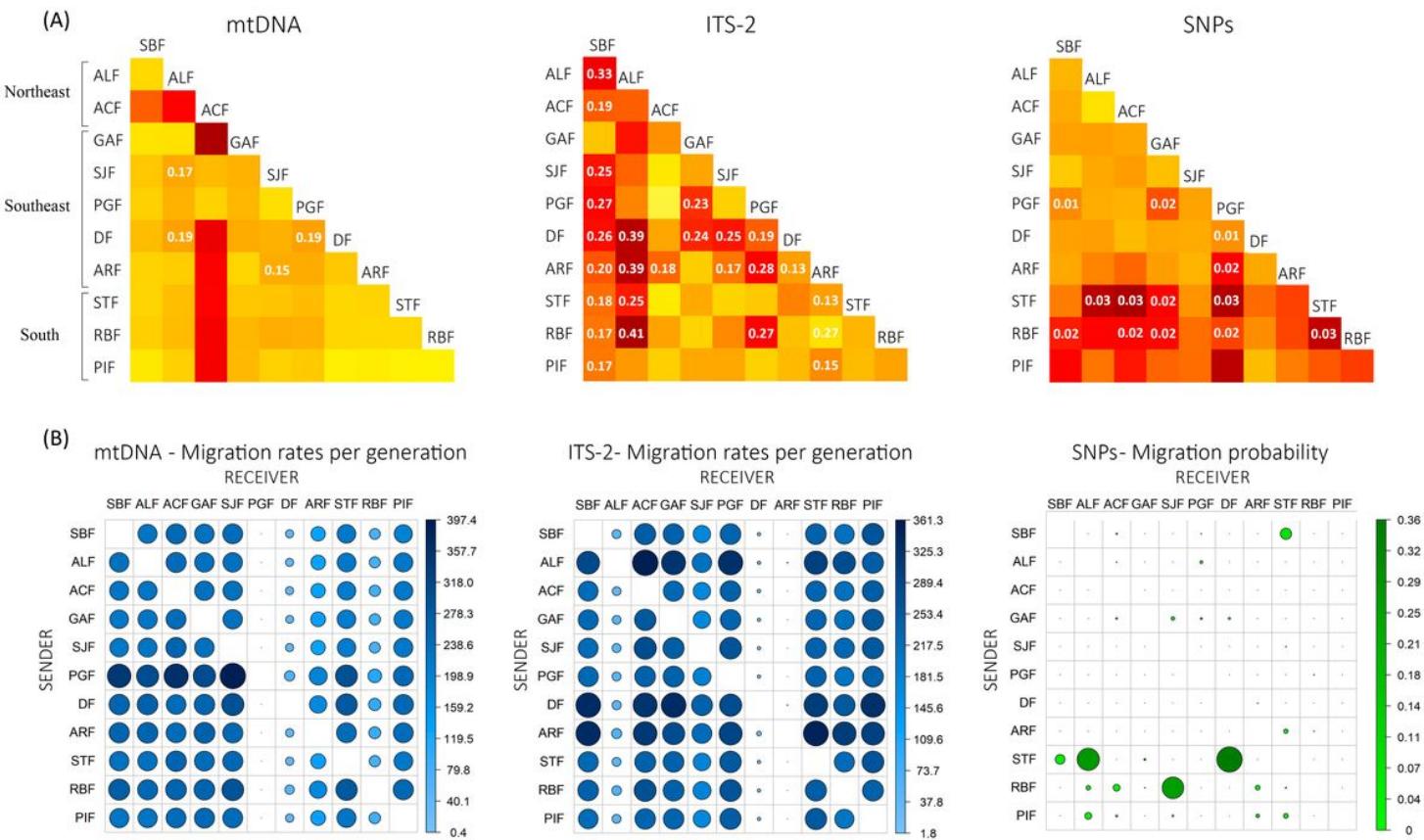


Figure 3

Population differentiation and migration results for mtDNA, ITS-2, and SNP markers from 11 sampled locations. (A) Heatmaps of the pairwise FST for each genetic marker. The color coding illustrates the observed FST value. Only the significant indices are shown ($p\text{value} < 0.05$). On the left, the localities are grouped according to the coastline regions. (B) Migration rates per generation according to Migrate-n analysis for both mtDNA and ITS-2. On the right, migration probabilities according Fastsimcoal for SNPs. The circle sizes and colors represent the rates of migrants from the source locality (rows) toward the receiver locality (columns). Abbreviations as in Table 1.

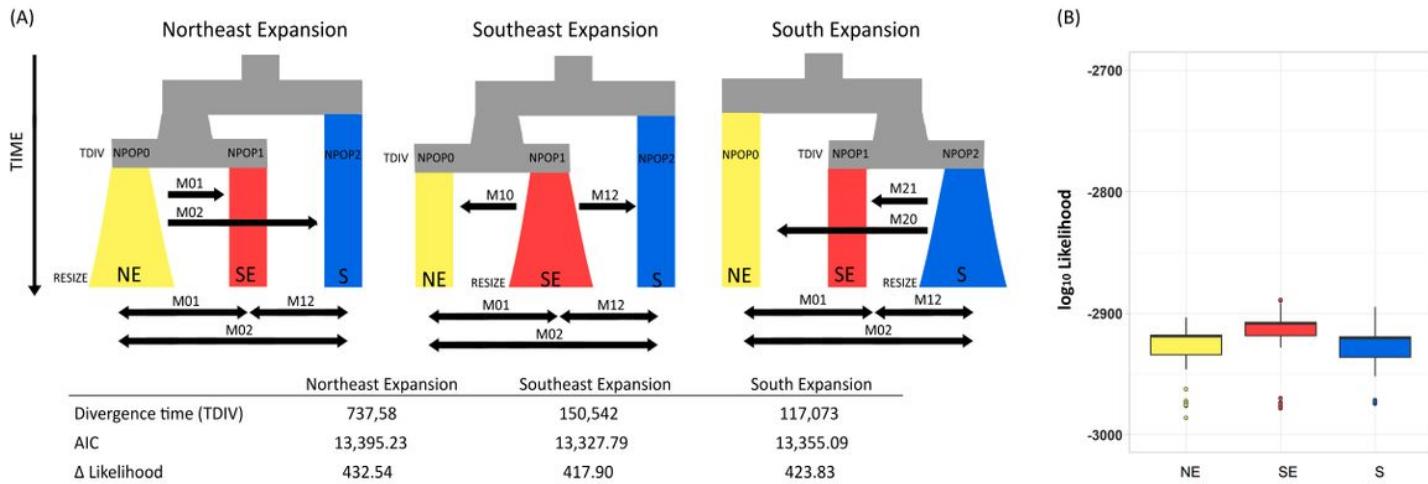


Figure 4

Comparisons among all demographic models, where the best-fitting scenario assumes the divergence of *Littoraria flava* populations originating in the Southeast region around 150,000 generations backward in time. (A) Illustrations of demographic models tested using Fastsimcoal with topologies showing the origins of divergence from the Northeast, Southeast, and South regions. Numbers below the models are divergence time, the Akaike Information Criterion, and the delta likelihood (difference between maximum possible and maximum obtained model likelihood in log₁₀ units) of each model. (B) Boxplots showing the log₁₀ Likelihood distributions based on the observed SFS, replicated using 200,000 coalescent simulations under each model.

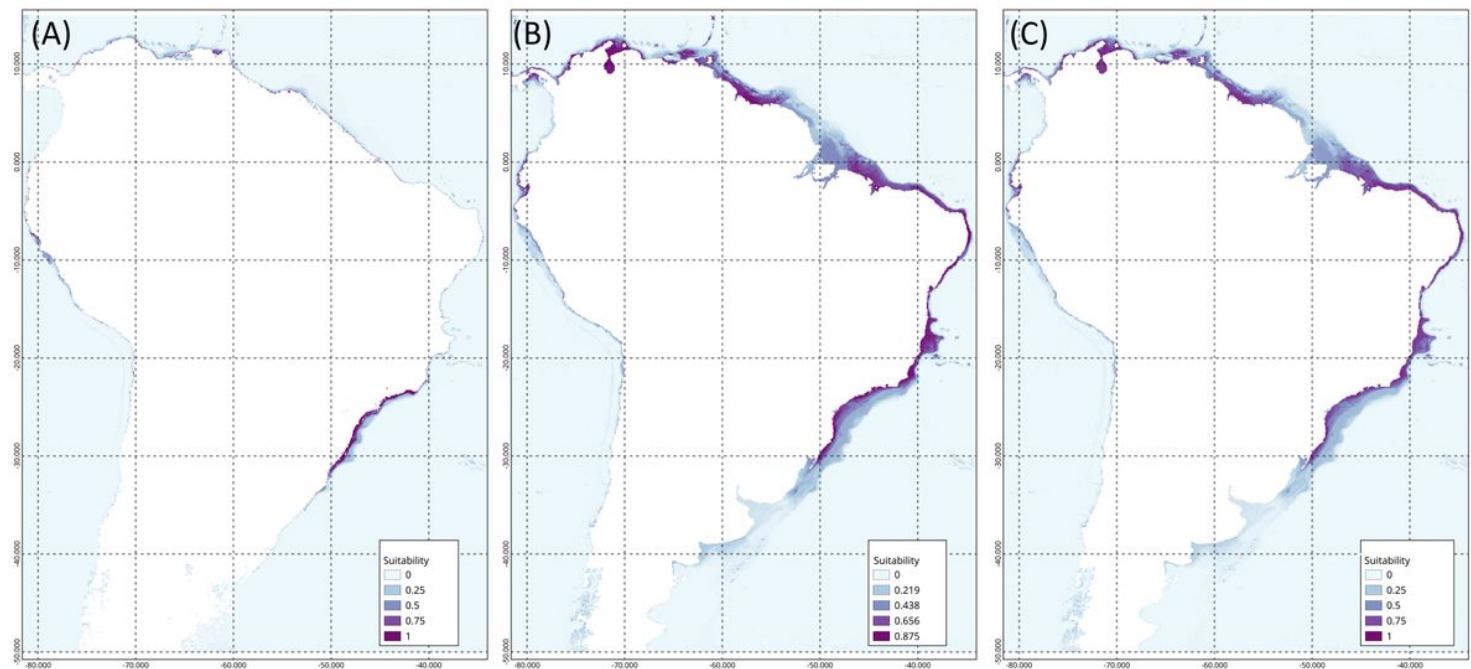


Figure 5

Modelled distributions of *Littoraria flava* for (A) Last Glacial Maximum (21 ka), (B) Middle Holocene (6 ka) and (C) present (0 ka) scenarios. The suitability value predicts how adequate the environment is for the species occurrence.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [Additionalfile1.pdf](#)
- [Additionalfile2.pdf](#)