**Supplementary material**

**Text S1.** The Lower São Francisco River (LSFR) region.

The basin is utilized for various activities, including crop irrigation, electric power generation, and water supply for small and large urban centers. The river originates in Southeastern Brazil, at an altitude of 1,800 m, and flows into the Northeastern coast of Brazil [92].

The Lower São Francisco River (LSFR) region has a mean annual rainfall ranging from 400 to 1,300 mm [93]. The region is characterized by mostly intermittent or temporary tributaries, whose flow is regulated by three hydroelectric power plants (Paulo Afonso, Moxotó, and Xingó). The region includes counties such as Ilha das Flores, Brejo Grande (Sergipe State), and Piaçabuçú (Alagoas State) [94-96], where quilombola[[1]](#footnote-1) and artisanal fishing communities reside. In addition to subsistence farming and livestock activities [97], practices such as fish farming and white shrimp production also contribute to increasing the income of local populations [71, 98, Figure S2].

The beach in this LSFR region is bordered by a submerged reef bank, resulting in a cusp-shaped morphological feature [99]. Marine terraces are predominant from the Peba point to the northern limit of the study area [100]. The erosion is primarily caused by an imbalance in sediment balance, which has been influenced by human activities, particularly the construction of dams. This has impacted the flow of sediment in the lower part of the river. The construction of 33 dams in the SFR basin, including nine in the river's course, has been linked to this issue [101-103]. [104] observed a significant loss of emersed area, estimated at around 80,000 m² between 1971 and 1987. This led to the destruction of the village of Cabeço, situated on the bank of the river mouth in Brejo Grande, Sergipe. Human activities, such as fish ponds, shrimp farming, cattle breeding, and agricultural cultivation, continue to take place in the coastal region of the delta, despite the economic damage caused by erosion. These occupations extend into protected areas, such as the Santa Isabel Biological Reserve and the Piaçabuçu Environmental Protection Area (APA) [105-107]. Due to the impact of human activities on the coastal dynamics of the São Francisco delta, it is imperative to plan the use and occupation of this region properly. These measures are essential for reducing the risks associated with coastal erosion and ensuring the sustainability of human activities in this complex environment [103].

**Text S2.** Methodology

Fifty-six specimens were analysed using the phenol-chloroform protocol by [57], with adaptations. The mitochondrial gene *Cox*1 fragment was amplified using primers LCOCI1490: 5’-GGTCAACAAATCATAAAGATATTGG-3’ and HCOCI2198: 5’-TAAACTTCAGGGTGACCAAAAAATCA-3’ [58]. Polymerase Chain Reaction (PCR) was performed according to a protocol described by [49], consisting of an initial denaturation step at 95.0°C for 5 min, followed by 35 cycles at 92,0°C for 30s, 51,0°C for 30s and 72,0°C for 30s, and a final extension at 72,0°C for 2 min. PCR was performed in a final volume (50 µL) containing primers (100 ng/µL), MgCl2 (2 mM), dNTP (1.25 mM), amplification buffer (1 X), 1 U/μL Taq polymerase (Sinapse INC Biotech®), 30-40 ng total DNA - ultrapure water was used to complete the final volume [59]. The PCR product was purified using the *GFX™*PCR DNA and Gel Band kit according to the manufacturer's recommendations (*GE Healthcare©*) and visualised on a 1% agarose gel. Subsequently, amplified fragments (both strands) of all specimens were sequenced in the automatic *ABI PRISM TM 377 DNA Sequencer* by *Macrogen* ([www.Macrogen.com](http://www.macrogen.com)) After sequencing, all electropherograms were checked manually. Finally, consensus strings were generated in MEGA 10.2.2 software [108] and compared with reference *L. fortunei* sequences available in GenBank ([www.ncbi.nlm.nih.gov/nuccore/](http://www.ncbi.nlm.nih.gov/nuccore/)) - the BLASTn tool ([www.ncbi.nlm.nih.gov/BLAST/](http://www.ncbi.nlm.nih.gov/BLAST/)) was used to confirm the identity of haplotypes (Figure 2; Supplementary material - Table S2), according to [45,48]. Two sequences for *Lithophaga curta* were used as an outgroup (Genbank accession numbers: AB076944; MK727546).

Genetic distances were estimated using the Kimura 2-parameter evolutionary model (K2P) [109]. A Neighbour-Joining (NJ) tree [110] was constructed using this model for graphical representation. Clade support was assessed by 1000 bootstrap pseudoreplicates using MEGA 10.2.2 [108] following [111]. Given the criticism of using K2P as a surrogate model [112] proposed by [113], we used p-distance. The best molecular evolution model (HKY+G) with Akaike Information Criterion, corrected (AICc) using jModelTest software [114]. The Automated Barcode Gap Discovery (ABGD) method [115] was used to detect the potential gap in the barcodes and to separate the data into different groups for *Cox*1 sequences. This analysis was performed on a web interface (<https://bioinfo.mnhn.fr/abi/public/abgd/>) using the simple distance model (p-distance) with a gap of 1.5. The maximum intraspecific divergence (P) value was set between 0.001 and 0.1, and the number of recursive steps is the default (10). Mr Bayes v.3.2.6 [116] was used to construct the tree. As the differences between the models were minimal, both in terms of estimated genetic divergence and tree topology, we represented the HKI+5G molecular evolution model. Visualization and editing of clades were performed in FigTree v1.4.2 [117].

1. Quilombola communities are ethnic groups primarily composed of rural or urban black populations. Their members are descendants of former slaves and define themselves in terms of specific relationships with the land, kinship, territory, ancestry, and their own cultural traditions and practices. [↑](#footnote-ref-1)