

Resumo 102

Genotype-by-sequencing and conservation genetics of the critically endangered catfish jaú (*Zungaro jahu*, Ihering 1898) from the lower Paranaíba River, Brazil

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Genetic knowledge should always be considered when planning actions for the conservation of endangered species. Advances in genomic techniques over the last decade have led to the ability to generate huge amounts of genetic markers, making it easier to answer many important conservation questions for almost any organism. The jaú, *Zungaro jahu*, is a migratory catfish endemic to the La Plata River basin. It is an important sport and commercial fish, but endangered in most of its range due to overfishing and habitat loss, mostly by dams. The largest known population of jaú in the state of Minas Gerais, Brazil, is in the lower Paranaíba River (LPR). Our goals were to determine the genetic status of jaú in the LPR and define actions necessary for its conservation. We collected tissues from LPR jaú just downstream of the São Simão Dam (19° 1' S 50° 29' W), and used the standard procedure of the DNeasy Blood and Tissue Kit (Qiagen) to extract total genomic DNA. We constructed a genotyping-by-sequencing (GBS) library and sequenced it with 46 samples in one lane of an Illumina HiSeq2500. We used the PyRAD pipeline for SNP calling. We used the programs Lositan and BayeScan to infer loci under selection, which were annotated using the Basic Local Alignment and Search Tool (BLAST) algorithm. We used the program Structure to estimate genetic structure, and provided visual evaluation applying discriminant analysis of principal components (DAPC) using the Adegenet package in the R environment. We assessed Nei's pairwise F_{ST} values, estimated the fixation index coefficient (F_{IS}), and tested for departures from Hardy-Weinberg expectations per loci using the hierfstat package in the R environment. We used Arlequin package to calculate genetic diversity indices and the program N_e Estimator to assess the effective population size (N_e). We determined the genetic conservation status of LPR jaú using a novel approach based on the predicted amount of heterozygosity in the population after t generations (H_t) estimated by $H_t = H_o (1 - 0.5 * N_e)^t$. We identified 1,016 SNPs present in $\geq 80\%$ of the samples. Outlier tests recovered 285 candidate loci for natural selection that can be used to enhance high-resolution panels for other genetic studies on jaú. Two main clusters were recovered by DAPC analysis suggesting two sympatric populations. This result was also indicated by a significant F_{ST} value (= 0.061). The F_{IS} index (= 0.133) and the 295 loci displayed significant departure from Hardy-Weinberg equilibrium expectations indicated heterozygote deficiency and agrees with the low value of genetic diversity indices ($H = 0.08$), which are likely consequences of small N_e (= 24.1). Based on the rate of heterozygosity loss and N_e , the genetic conservation status of LPR jaú was classified as "critically endangered". Habitat management and/or restoration may increase the population size, but limitations hinder their implementation in the near future. Reestablishment of gene flow is necessary for genetic restoration of LPR jaú. Fish passage, translocation, and/or stocking are known ways for reestablishing gene flow in fish populations (Peixe Vivo, Cemig).

Keywords: Neotropical fish, conservation genetics, population genomics, gene flow restoration, fish management.

