

Large runs of homozigosity regions in *Arapaima gigas* (Pirarucu) suggest the existence of genomic regions in single-copy and a sex-related dosage-compensation mechanism.

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Abstract

Arapaima gigas, known as Pirarucu, is the largest freshwater bony fish in the world that dwells in the Amazon Basin. It is an Osteoglossiformes with great potential for aquaculture because of its large size, fast growing rate, and quality of flesh. Albeit these advantages, Pirarucu's reproductive management in captivity is limited, in particular, due to the lack of external sexual dimorphism, which makes sex identification difficult in this species. Here we used genomic data from Pirarucu to seek molecular markers which could assist in their sex identification and in unraveling the molecular mechanisms involved in sex differentiation. Previous studies on genome comparison of both sexes identified male specific regions, suggesting the XY system for Pirarucu. However, because of its small size, the topic is still in debate. In this study, we aimed to search for single-copy genomic regions in one sex of Pirarucu, which could be associated with the sex determination mechanism, by identifying sex-specific runs of homozygosity (ROH) regions. We used genomic data from six adults, three males and three females available at NCBI under the Bioproject IDs PRJEB22808 and PRJNA540910. BWA (v. 0.7.12) and Samtools (v. 1.7) were used for the genome indexing, mapping, and alignment steps of reads against the reference genome of Pirarucu ID GCA_900497675.1 deposited also in NCBI. Bedtools genomecov (v. 2.24) was used to analyze the total sample coverage. For calling variants, Varscan (v. 2.4.0) was used. The results were processed using R (v. 3.6.0) and the graphics were generated with ggplot2 library (v.3.2.1). To identify ROH regions, we verified the occurrence of heterozygous sites along the genome of each sample and selected those scaffolds that presented (1) the average of sites in heterozygosity = to 5 for one sex and (2) the size of the scaffold being = to 500.000 bp. We identified 22 scaffolds with large ROH in one sex and with the antagonistic scenario in the other one, suggesting that these regions are in single-copy in one sex and being affected by the dosage compensation mechanism in the opposite sex. These scaffolds are promissory candidates of a molecular marker for sex differentiation in Pirarucu, although analyses with more samples and molecular tests are needed. Furthermore, identifying ROH for comparative genomic analysis demonstrated to be an interesting strategy to assist us in the unraveling of the sex determination system in Pirarucu.

Funding:

Link to Video: