Abstract

Tambaqui (Colossoma macropomum) is the fish species most commonly raised in the Brazilian fish farms. The species is highly adaptable to captive conditions, and is both fast-growing and relatively fecund. In recent years, artificial breeding has produced hybrids with Characiform species, known as “Tambacu” and “Tambatinga”. Identifying hybrids is a difficult process, given their morphological similarities with the parent species. This study presents an innovative molecular approach to the identification of hybrids based primarily on Multiplex PCR of a nuclear gene (α-Tropomyosin), which was tested on 93 specimens obtained from fish farms in northern Brazil. The sequencing of a 505-bp fragment of the Control Region (CR) permitted the identification of the maternal lineage of the specimen, all of which corresponded to C. macropomum. Unexpectedly, only two CR haplotype were found in 93 samples, a very low genetic diversity for the pisciculture of Tambaqui. Multiplex PCR identified 42 hybrids, in contrast with 23 identified by the supplier on the basis of external morphology. This innovative tool has considerable potential for the development of the Brazilian aquaculture, given the possibility of the systematic identification of the genetic traits of both fry-producing stocks, and the fry and juveniles raised in farms.

Keywords

pisciculture, Multiplex PCR, mitochondrial DNA, genetic bottleneck