

PRELIMINARY DATA ON THE SEX RATIO IN FULL-SIB FAMILIES OF TAMBAQUI *Colossoma macropomum*.

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Introduction

Techniques to control sex ratio in fish farming are essential in many instances such as to develop breeding programs or to produce monosex populations when differential growth or timing of puberty exists between the sexes. Despite of recent data showing that females of Tambaqui *Colossoma macropomum* have higher growth rates, the sex determination system and sex ratio in the species are still unknown. This preliminary study aimed to investigate the sex ratio in full sib families of *C. macropomum* to gain insight into the sex determination system and differential growth related to sex.

Methods

Four families of *C. macropomum* were obtained through artificial fertilization and reared in closed indoor systems while fed *ad libitum* until reaching gonadal differentiation to allow gender confirmation. These families were produced in Tocantins (F1, n = 160; F2, n = 80) and Amazonas (F3, n = 53; F4, n = 51). At the approximate bodyweight of 260.6 ± 74.8 g, fish were anesthetized and sacrificed, a piece of gonad collected and fixed in 10% formaldehyde for routine histological analysis aiming at sex identification.

Results and Discussion

Three studied families had balanced sex ratio (F1-F3; χ -square; $P > 0.05$) while one from an Amazonas hatchery had a significant higher number of males (F4; χ -square; $P < 0.05$). Though an apparent pattern of chromosomal sex determination system appears, the deviation in sex ratio found in one family indicates that the regulation of sex in Tambaqui could involve other factors (such as temperature) like in other teleosts. Males and females had similar growth performance in all families when considering body weight (F test; $P > 0.05$) and total length (F test; $P > 0.05$) during the early period considered in this study, also observed in recent studies on Tambaqui.

Conclusion

This preliminary study indicate *C. macropomum* has a balanced sex ratio with possible influence of environmental factors to be investigated. Future work should use these families to better investigate sex determination system in Tambaqui using next-generation sequencing (*i.e.* RADseq for QTL mapping) and epigenetic approaches.