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Original Article

Estimation of genetic parameters for weight and length gains in tambaqui (*Colossoma macropomum*)

Estimativa de parâmetros genéticos para ganho de peso e comprimento em tambaqui (*Colossoma macropomum*)

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Abstract

The goal of this study was to determine the genetic parameters for growth traits in tambaqui (*Colossoma macropomum*) fish of similar age and weight. The data set included monthly measurements of body weight and length from120 fish for a year (1,440 measurements). The study found that weight gain had a heritability estimate of 0.01, while length gain had a heritability estimate of 0.27. There was a high positive correlation (0.84) between weight and length gains. The genetic variance and heritability of body weight decreased with age. This study suggests that breeding programs should select for body weight and weight gain to promote genetic gain in tambaqui. Selecting younger animals can also help reduce costs while still achieving genetic gains.

Keywords: genetic correlation, growth, heritability, fish, tambaqui, selection.

Resumo

O objetivo do presente estudo foi determinar os parâmetros genéticos para características de crescimento em indivíduos de tambaqui (*Colossoma macropomum*) de idade e peso semelhantes. Um conjunto de dados incluiu medições mensais de peso corporal e comprimento de 120 peixes durante 1 ano (1.440 medições). As estimativas de herdabilidade para ganho de peso foi de 0,01, enquanto o comprimento foi 0,27. Houve correlação genética alta, positiva e favorável (0,84) entre o ganho de peso e comprimento. A variância genética aditiva e a herdabilidade do peso corporal diminuíram com o aumento da idade. Estes resultados sugerem que os programas de melhoramento devem utilizar o peso corporal e o ganho de peso para promover ganho genético no tambaqui. Além disso, a seleção de animais mais jovens também pode ajudar na redução dos custos, e ao mesmo tempo, obter ganhos genéticos.

Palavras-chave: correlação genética, crescimento, herdabilidade, peixe, tambaqui, seleção.

1. Introduction

Genetic improvement programs have been carried out for terrestrial livestock since the 1940s. At least 30% of the increase in productivity of these terrestrial animals is attributed to the execution of such programs (Eknath et al., 1993). For fish farming, these applications were only described in the mid-1970s for common carp (Mondol et al., 2006; Ed-Idoko et al. 2021), salmon (Zhang et al., 2014; Christensen et al., 2018; Barria et al., 2019; Thodesen et al., 1999; Gjedrem, 2000; Rondeau et al., 2022) and tilapia (Eknath et al., 1993; Garcia et al., 2022). Nevertheless, there are numerous species with great potential for commercial exploitation.

The commercial exploitation of various species in aquaculture is a strategy to mitigate impacts generated by climate change, disease outbreaks, market fluctuations and other uncertainties. However, the stimulation for private companies to diversify species in production is rare, and investing in species with more advanced technological packages can generate more economic benefit while implying in lower risks (Cai et al., 2022). Species diversification in aquaculture combined with genetic improvement programs have great potential to respond to the growing demand for animal protein caused by the world population increase (Metian et al., 2020; Cai et al., 2022).

The tambaqui (*Colossoma macropomum*, Characiformes: Characidae) is a Neotropical species native to the Amazon basin, farmed in Brazil, Bolivia, Colombia, Paraguay, Venezuela (FishStatJ., 2021; Hilsdorf et al., 2022), Bangladesh, China, Indonesia and Vietnam (Woynárovich and Van Anrooy, 2019). In Brazil, tambaqui is the second most cultivated fish species. More than 154,990 tons of tambaqui and its hybrids were produced in 2022 (IBGE, 2023).

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Despite the economic importance of the species, there is a lack of precise data on aquaculture production of *Colossoma macropomum*. Moreover, few studies have reported components of variance and genetic parameters for weight and morphometric traits at adults and few articles on tambaqui genetics and breeding are available in the literature (Hilsdorf et al., 2022).

Growth traits are priorities for the establishment of breeding programs, mainly due to their easy measurement and estimation of medium to high heritability (Gjedrem, 2012; Oliveira et al., 2012; Marcos et al., 2016; Mello et al., 2016; Campos et al., 2020). Tambaqui growth can be evaluated in terms of body weight, length, width, weight gain and growth rate, among others (Marcos et al., 2016; Mello et al., 2016; Campos et al., 2020). However, there are few articles describing the genetic parameters for tambaqui older than 3 years. The objective of this study was to estimate the genetic parameters for growth traits in tambaqui individuals of similar age and weight as a reference for use in breeding programs.

2. Material and Methods

The dataset for this study was taken from 120 tambaquis from the Department of Fisheries and Aquaculture of the Brazilian Agricultural Research Corporation in Palmas, Tocantins, Brazil. These 120 animals, consisting of 66 males and 54 females, were half- sibs maternal; oocytes of one female were fertilized by the semen of two males due a large volume of oocytes produced by this species, during the reproductive season 2012/2013, from the satellite Center for Fish Breeding in the northern region of the state of Mato Grosso (Delicious Fish), Brazil (12° 51' 56.40" S; 55° 50' 03.30" W). Further, 5.50 mg of carp pituitary extract/kg live weight were employed in two applications for females and 2.50 mg of carp pituitary extract/kg live weight were applied in a single application for males, management similar to that described by Marcos et al., 2016. They were obtained from 14 females and 13 males from the Aquabrasil project, which was coordinated by Brazilian Agricultural Research Corporation (Embrapa) (Resende, 2009).

After fertilization, all animals were kept separately by maternal half-sib and their pedigree information was preserved until identification. Embryos remained in the incubator until the complete absorption of the yolk sac (4-6 days). Then, post-larvae were transferred to circular tanks, kept into laboratory and fed exclusively with artemia. From day 12-16 it was started the introduction of commercial feed (40% of crude protein) *ad libitum*, together with artemia, until the larvae are able to feed exclusively with commercial feed. After 40 days, animals were transferred to breeding units in the growth tank with 32% crude protein feed, while keeping half-sib maternal groups. All these procedures were described by Mello et al. (2016). When fish reached minimum 20.00 g, they were individually identified by transponder tags (PIT) implanted in the dorsal region released in growth tanks and fed *ad libitum*. The animals were transferred to Fazenda São Paulo in Brejinho de Nazaré, Tocantins, Brazil when they reached 2.5 years of age, and housed in two ponds (with 60 fish in each). Approval from an Animal Care and Use Committee was not necessary for this study, as the data were obtained from an existing database (Embrapa Fisheries and Aquaculture).

Body weight and length measurements were performed monthly from January to December 2016, in the first half of each month, totaling 12 data collections. The first evaluation was conducted when the fish were 1095 days (3 years) of age. The animals were collected by trawling and placed in individual plastic bags with holes to allow water to escape before weighing. Body weight was measured with a tripod scale and body length with a measuring tape resting on top of a table.

Heritability (Equation 1) and genetic correlations (Equation 2) were estimated for weight gain and length gain, calculated as the difference between final (at 4 years of age) and initial (at 3 years of age) body weights and lengths, respectively (Equation 3). Genetic parameters were also estimated for body weight and length at 3, 3.5, and 4 years of age.
where, WG= weight gain; BW4 = body weight at 4 years of age and BW3 = body weight at 3 years of age.

$$h^2 = \frac{\sigma_a^2}{\sigma_p^2} \tag{1}$$

where, h^2= heritability of weight gain and growth; σ_a^2 = additive genetic variation of the trait under study and σ_p^2 = phenotypic variation of the trait under study (Falconer and Mackay, 1996).

$$r_g\left(BW, LW\right) = \frac{cov_{BW,LW}}{\sigma_{BW} * \sigma_{LW}} \tag{2}$$

where, $r_g\left(BW, LW\right)$ = genetic correlation between body weight and length; $cov_{BW,LW}$ = covariance between body weight and length; σ_{BW} = standard deviation of body weight and σ_{LW} = standard deviation of body length (Falconer and Mackay, 1996).

$$WG = BW4 - BW3 \tag{3}$$

Analysis of variance was performed by the least-squares method using the GLM procedure of SAS version 9.4 (SAS Institute Inc., 2013) and ANOVA in MS Excel software (Office 365). Variance in weight gain, body weight at 3, 3.5, and 4 years of age, and body length at 3 and 3.5 years of age was calculated using Equation 4, whereas variance in length gain and body length at 4 years of age was calculated using Equation 5. Maternal and paternal effects were modeled as fixed effects but were excluded from the equations for lack of significance. The effect of age was not considered in the model as a fixed or covariable effect, as the animals had the same date of birth, as well as the same date of biometrics collection, being contemporary, with no significant effect.

$$Y_i = \mu + S_i + e_i \tag{4}$$

$$Y_{ij} = \mu + S_i + P_j + e_{ij} \tag{5}$$

where Y_{ij} is the dependent variable, μ is the overall mean of the population, S_i is the effect of sex, P_j is the effect of pond, and e_{ij} is the random error associated with each observation.

Genetic parameters were estimated by a multi-trait animal model (Equation 6) using the airemlf90 algorithm (Misztal et al., 2014).

$$y = X_{\beta} + Z_{\alpha} + \varepsilon \tag{6}$$

where y is the vector of observations, β is the vector of fixed effects, α is the vector of random effects, X and Z are the design matrices for fixed and random effects, respectively, and ε is the vector of random errors.

3. Results

Tables 1 and 2 show the phenotypic means and standard deviations of growth traits of males, females, and combined sexes, as well as weight and length gain between 3 and 4 years of age. Analysis of variance (ANOVA, with a confidence level greater than or equal to 95%) was performed to evaluate the existence of differences between the weights and lengths of the animals, including differences within sexes. The data show a significant difference at the 5% probability level, with older animals and females being heavier and longer. Table 3 presents the heritability estimates for weight and body length gain and their genetic correlation, as well as the estimates of (co) variances. The estimated heritability of weight gain was almost null (0.01), meaning that, the response to selection for weight gain would be low even if breeders with high values for weight were selected. On the other hand, length gain had heritability of 0.28, indicating a good genetic gain from direct selection for this trait. Selection for length may be an alternative to indirectly select animals for weight, as there was a positive favorable genetic correlation between traits (0.99).

The heritability value of body weight decreased with increasing age, ranging from 0.50 (high magnitude) at 3 years to 0.17 (low magnitude) at 4 years of age (Table 4). This result indicates that the selection of young animals for body weight is efficient, not requiring the animals to enter the adult stage to be selected as parents for the next generation. An early selection by animals directly impacts production costs, such as shorter animal feeding time, labor, space in the nurseries and sanitary management. The genetic correlations between body weight at different ages were high, positive, and favorable, indicating that selection for one of these traits, for example, body weight at 3 years of age, can result in an increase in body weight at 3.5 or 4 years of age, which is desirable.

The heritability value of length increased with increasing age (Table 5), different from those obtained for body weight, although the magnitude of heritability remained close (0.27, 0.33, and 0.33 at 3, 3.5, and 4 years of age, respectively). Standard errors were relatively high, this result can be attributed to the statistical nature of body length. There was a lower dispersion of values in relation to the mean, with about 4–5% of variation, whereas heritability values of weight had a coefficient of variation of 13–18%. Therefore, due to the pedigree (few animals in the effective number) and restricted number of animals analyzed in this study, it is more difficult to detect genetic differences in length than in body weight.

Individuals from the same family were kept together in the same nursery tank at the beginning of their development, waiting for the individual to reach the appropriate size to carry out individual identification (microchip). At younger stages, the environmental effect has a great influence on the estimates of genetic parameters, possibly impacting the decrease in heritability estimates for growth traits at younger ages in the present work. Furthermore, genetic correlations between body weights at different ages were greater than 0.60, suggesting that correlated responses in body weight at older ages (245 days) could be achieved by selecting fish at younger ages (106 days).

Table 1. Body weight traits of tambaqui (*Colossoma macropomum*) analyzed in the study.

Trait	General		Males		Females	
	n	**Mean ± SD**	***n***	**Mean ± SD**	***n***	**Mean ± SD**
BW3 (kg)	117	2.26* ± 0.38	65	2.16* ± 0.35	52	2.37* ± 0.39
BW3.5 (kg)	103	4.28* ± 0.57	58	4.05* ± 0.52	45	4.58* ± 0.50
BW4 (kg)	113	4.53* ± 0.82	64	4.19* ± 0.75	49	4.97* ± 0.69
WG (kg)	110	2.27 ± 0.76	63	2.03 ± 0.77	47	2.60 ± 0.63

BW3: body weight at 3 years of age; BW3.5: body weight at 3.5 years of age; BW4: body weight at 4 years of age; WG: one-year weight gain; SD: standard deviation. *P>0.05.

Table 2. Body length traits of tambaqui (*Colossoma macropomum*) analyzed in the study.

Trait	General		Males		Females	
	n	**Mean ± SD**	***n***	**Mean ± SD**	***n***	**Mean ± SD**
BL3 (cm)	117	48.85* ± 2.01	65	48.46* ± 1.91	52	49.33* ± 2.04
BL3.5 (cm)	103	56.56* ± 2.10	58	55.90* ± 1.92	45	57.42* ± 2.03
BL4 (cm)	112	59.47* ± 2.69	62	58.58* ± 2.65	50	60.58* ± 2.33
LG (cm)	109	10.62 ± 0.76	61	10.12 ± 2.83	48	11.25 ± 2.29

BL3: body length at 3 years of age; BL3.5: body length at 3.5 years of age; BL4: body length at 4 years of age; LG: one-year length gain; SD: standard deviation. *P>0.05.

4. Discussion

The market size of tambaqui can differ based on the regional demand in Brazil. For instance, the states of Rondonia and Amazonas prefer tambaqui weighing between 2 and 3 kg, whereas in Tocantins, the desired weight is 1.5 kg. Animals at these slaughter weights are up to 18 months of age, and have not yet reached sexual maturity, which happens between 3 and 4 years (Gomes et al., 2013; Morais and O'Sullivan, 2017). Body weight and length increased rapidly from the age of 3 to 4 years, varying from 2.26 to 4.53 kg and from 48.85 to 59.47 cm, respectively, a gain from 2.27 kg to 10.62 cm in a year. Females reached significantly greater weights and lengths compared to males at the ages evaluated (Table 1 and 2), corroborating Campos et al., 2020. As per the studies conducted by Vieira et al. (1999) and Mello et al. (2015), it has been observed that females tend to increase in size after attaining sexual maturity, which usually occurs when they are between 2.5 to 3 years old (Gomes et al., 2013). However, other studies show that females had a higher mean body weight than males even before reaching puberty, from the weight of 1.1kg (Almeida et al., 2016; Ariede et al., 2023).

Table 3. Estimates of (co)variances, heritability and genetic correlation for one-year weight and length gains in tambaqui (*Colossoma macropomum*).

Trait	Parameters	Mean
Weight gain	h^2	0.01 ± 0.01
	σ_p^2	0.50469
	σ_a^2	0.719E-03
	σ_e^2	0.50397
Length gain	h^2	0.28 ± 0.19
	σ_p^2	5.748
	σ_a^2	1.6282
	σ_e^2	4.1198
WG - LG	cov_a	0.034223
	cov_e	0.93224
	r_g	0.99 ± 0.65

WG: one-year weight gain; LG: one-year length gain.

Heritability estimates and genetic correlations for growth traits vary according to fish species and development stage (Rutten et al., 2005; Turra et al., 2012). The results of the present study showed that it is more difficult to identify genetic differences between individuals at older ages. The increase in heritability estimates for weight with increasing age was reported by Campos et al. (2020). The same authors found that age has a significant effect on the statistical model for predicting genetic parameters for estimated weights at 6 months, 1 year and age at slaughter of tambaqui.

In a study with 198 tambaqui, Mello et al. (2016) reported heritability estimates of 0.44 and 0.42 for weight at 12 and 24 months, respectively, and 0.31 and 0.46 for length at 12 and 24 months, respectively. Perazza et al. (2019) estimated heritability values of 0.26 and 0.49 for the body weight and 0.37 e 0.19 for standard length of tambaquis with less than one year old (221 days) and almost two years old (623 days), respectively.

According to the Mello et al. (2016), the values indicate that a large proportion of variance in growth characteristics is due to genetic factors. The animals used in these studies above were younger than those assessed in the current study. In the present work were observed estimates for weight decreased with increasing age, whereas estimates for length increased with increasing age corroborate with described Mello et al. (2016).

Rutten et al. (2005) in a study with 2,483 Nile tilapia (*Oreochromis niloticus*) aged 100 to 326 days, found heritability estimates for body weight of 0.16 to 0.26 (low to moderate magnitude) and genetic correlations above 0.90.

Table 4. Estimates of heritability (on diagonal), genetic correlation (above diagonal) and phenotypic correlation (below diagonal) for body weight traits in tambaqui (*Colossoma macropomum*).

	BW3	BW3.5	BW4
BW3	0.50 ± 0.04	0.99 ± 0.01	0.69 ± 0.04
BW3.5	0.54 ± 0.01	0.37 ± 0.03	0.68 ± 0.05
BW4	-0.15 ± 0.04	0.88 ± 0.05	0.17 ± 0.02

BW3: body weight at 3 years of age; BW3.5: body weight at 3.5 years of age; BW4: body weight at 4 years of age.

Table 5. Estimates of heritability (on diagonal), genetic correlation (above diagonal) and phenotypic correlation (below diagonal) for body length traits in tambaqui (*Colossoma macropomum*).

	BL3	BL3.5	BL4
BL3	0.27 ± 0.23	0.59 ± 2.98	0.58 ± 1.81
BL3.5	0.52 ± 0.20	0.33 ± 0.27	0.99 ± 1.1
BL4	0.21 ± 0.16	0.32 ± 0.30	0.33 ± 0.26

BL3: body length at 3 years of age; BL3.5: body length at 3.5 years of age; BL4: body length at 4 years of age.

The authors reported that correlations were more stable at higher ages, for example, genetic correlations were greater than 0.90 between age 100 and 115 days and all ages up to 115 days and between age 223 days and all ages up to 326 days of age. For instance, heritability estimates remained at about 0.20 after 150 days of age. Turra et al. (2012) evaluated 2,042 Nile tilapia aged 106–245 days and found heritability estimates for body weight ranged from 0.02 to 0.52 (low to high magnitude), increasing with age. The authors explain that the low heritability obtained at the beginning of the growth period may be a result of the inclusion of the family effect in the model, which resulted in lower estimation of additive genetic variance.

Despite differences in fish species and age, the heritability estimates and genetic correlations for body weight in the referred studies were similar to those found here for tambaqui. These results indicate that genetic parameters for growth traits in tambaqui should be determined in young animals (before sexual maturity) for correct quantification of family effects and efficient selection of breeders.

5. Conclusions

The tambaqui has the potential to become a significant export for aquaculture production in Brazil. In order to achieve this goal, breeding programs are essential to improve their performance and increase their carcass yields. Genetic studies play a crucial role in planning these breeding programs more efficiently. This study shows that selecting tambaqui based on their body weight and weight gain can significantly improve their performance in both intensive and semi-intensive farming. Furthermore, selecting younger tambaqui for these same traits can speed up the genetic gains, thus helping to achieve better results in a shorter time frame.

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