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Modeling the weight gain of freshwater-reared rainbow trout (*Oncorhynchus mykiss*) during the grow-out phase

Peter Charrie Janampa-Sarmiento[1]* (iD), Rodrigo Takata[2] (iD), Thiago Mendes de Freitas[2] (iD), Licius de Sá Freire[2] (iD), Marcelo Menezes de Britto Pereira[2] (iD), Vincent Lugert[3,4] (iD), Guilherme Melgaço Heluy[1] (iD), Marcelo Maia Pereira[1,5] (iD)

[1] Universidade Federal Rural do Rio de Janeiro, Instituto de Zootecnia, Programa de Pós-Graduação em Zootecnia, Seropédica, RJ, Brasil.
[2] Fundação Instituto de Pesca do Estado do Rio de Janeiro, Escritório da Região Serrana, Nova Friburgo, RJ, Brasil.
[3] Alfred Wegener Institute, Helmholtz Centre for Polar and Marine Research, Bremerhaven, Germany.
[4] Thünen Institute of Fisheries Ecology, Bremerhaven, Germany.
[5] Fundação Instituto de Pesca do Estado do Rio de Janeiro, Centro de Treinamento em Aquicultura de Rio das Flores, Rio das Flores, RJ, Brasil.

ABSTRACT - We used five nonlinear models to calculate the weight gain of rainbow trout (122.11±15.6 g) during the final grow-out phase of 98 days under three different feed types (two commercials diets, A and B, and one experimental diet, C) in triplicate groups. We fitted the von Bertalanffy growth function with allometric and isometric scaling coefficient, Gompertz, Logistic, and Brody functions to weight (g) at age data of 900 fish, distributed in nine tanks. The equations were fitted to the data based on the least squares method using the Marquardt iterative algorithm. The accuracy of the fitted models was evaluated using a model performance metrics, combining mean squared residuals (MSR), mean absolute error (MAE), and Akaike's Information Criterion corrected for small sample sizes (AICc). All models converged in all cases tested. The evaluation criteria for the Logistic model indicated the best overall fit (0.704) under all different feed types, followed by the Gompertz model (0.148), and the von Bertalanffy-I and von Bertalanffy-A with 0.074 each. The obtained asymptotic values are in agreement with the biological attributes of the species, except for the Brody model, whose values were massively exceeding the biologic traits of rainbow trout in 0.556 of tested cases. Additionally, ΔAICc results identify the Brody model as the only model not substantially supported by the data in any case. All other models are capable of reflecting the effects of various feed types; these results are directly applicable in farm management decisions.

Keywords: aquaculture, logistic model, non-linear equations, *Oncorhynchus mykiss*

Introduction

Rainbow trout (*Oncorhynchus mykiss*) aquaculture is one of the most widespread aquaculture activities in the world. Its contribution to the worldwide aquaculture production (excluding aquatic plants) is 0.01 and 0.04 for global harvest and value, respectively. With a world production of 814.000 metric tons in 2016, rainbow trout aquaculture generated an income of 3.4 billion United States Dollars (USD) (FAO, 2018).

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The demand for rainbow trout is high, because it contains all the essential amino acids (Sabetian et al., 2012) and has a lower saturated fat content, which is recommended for the prevention of human cardiovascular diseases (Scherr et al., 2014). In addition, it has a wide acceptance in the consumer market because of its soft and delicate texture, white to pink color, and mild flavor (Singh et al., 2016).

In aquaculture production, the growth performance of the reared organisms is the most important factor regarding economic benefit (Baer et al., 2011). Fish growth is the positive result between anabolic and catabolic interaction, and when a more positive balance is desired, feed supply in terms of quality and quantity can be used as a strategy (Cho and Bureau, 2001).

For rainbow trout, like most carnivorous species, high quality and quantities of protein (45-50 g crude protein for 100 g of diet) and energy (around 4,500 kcal for kg of diet) in diets are recommended for optimal growth (Rodrigues et al., 2013). However, diets with this type of requirements increase production cost (Badillo et al., 2014). Therefore, improving the efficiency of fish production is always desired and can be achieved by studying growth curves, which offer an empirical support during the management of growth traits (Dumas et al., 2007; Lugert et al., 2019).

Models are mathematical equations, meeting the specific attributes needed, to represent animal growth. Predominantly, non-linear equations are used to model population and/or individual growth of fish in their natural environment. However, research on modeling the growth of fish in aquaculture has proven great suitability and has presented relevant contributions within the last years (Santos et al., 2013; Lugert et al., 2017; Powel et al., 2019).

Therefore, the objective of this study was to evaluate the fit of five non-linear three-parametric growth models (von Bertalanffy with allometric and isometric scaling coefficients, Gompertz, Logistic, and Brody) to weight gain data of rainbow trout during the grow-out phase under aquaculture conditions and three different feed types.

Material and Methods

The data were collected on a commercial rainbow trout farm, which is located in the municipality of Nova Friburgo, a mountainous region of the state of Rio de Janeiro, Brazil (22°23'36" S, 42°29'12" W, 1.032 m altitude).

The fish, without distinction of sex, were acquired from the farms-own breeding program. Nine hundred fish with an age of 273 days post-hatch (dph), mean weight of 122.11±15.6 g, and mean length of 22.42±0.71 cm, were selected. They were randomly distributed into nine masonry tanks with a volume of 40 m^3 each. Table 1 shows the proximal composition profile of the three diets (two commercials diets, A and B, and one experimental diet, C), which were offered in three triplicate groups [(A/1, A/2, A/3) (B/1, B/2, B/3) (C/1, C/2, C/3)]. Rations were offered twice a day until apparent saturation during 98 days. Table 2 shows the weight and length at the beginning and the end of the trial for each feed type. Water quality was maintained within optimal rearing levels and monitored on a daily basis at: dissolved

Table 1 - Proximal composition of diets used in feeding of reared trout

	Diet A[1]	Diet B[2]	Diet C[3]
Crude protein (%)	42	42	40
Crude lipid (%)	9	9	11
Fiber (%)	5	4	1.7
Ash (%)	14	15	12
Gross energy (kcal/kg)	4555	4535.3	4600.8

[1] Diet supplied to tanks A1, A2, and A3.
[2] Diet supplied to tanks B1, B2, and B3.
[3] Diet supplied to tanks C1, C2, and C3.

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oxygen (7.7±0.6 mg.L^{-1}), oxygen saturation (89.9±5.4%), temperature (14.4±11 °C), pH (6.2±0.2), and dissolved ammonia (0.10±0.02 mg.L^{-1}).

The five nonlinear equations chosen were von Bertalanffy-A (with allometric scaling coefficient), von Bertalanffy-I (with isometric scaling coefficient), Gompertz, Brody, and Logistic (Table 3).

Models were fitted using the Marquardt algorithm (Marquardt, 1963) through the NLIN computational process of SAS (Statistical Analysis System, version 9.4). This process uses the nonlinear least squares (nls) method. The default convergence conditions used include measure of Bates and Watts (10^{-5}), inverse Hessian (1e-12), and number of iterations (100).

The accuracy of the fitted models was evaluated using a model performance metrics. The performance criteria to evaluate the goodness of fit are:

The mean squared residuals ($MSR = RSS * [n – p]^{-1}$), in which RSS is the residual sum of squares, n is the number of observations, and p is the number of parameters of the model (Rawlings et al., 1998).

The Akaike Information Criterion (AIC) corrected for small sample sizes (AICc),

$AIC = 2k – 2ln(\hat{L})$, in which k is the number of estimated parameters in the model, $\hat{L}$ is the maximum value of the likelihood function for the model, and ln is the natural logarithm (Akaike, 1973);

$AICc = AIC + \dfrac{2k^2 + 2k}{n – k – 1}$, in which n is the sample size and k is the number of parameters.

Table 2 - Average weight (AW; g) and average length (AL; cm) of cultured rainbow trout with standard deviation (SD) at the beginning and the end of the fattening phase

Diet/Replicate	AW (g) ± SD	AL (cm) ± SD
Beginning		
All replicates	122.11±15.6 g	22.42±0.71 cm
Final		
A/1	417.12±59.12	32.31±1.62
A/2	355.15±76.15	29.80±1.88
A/3	426.15±51.57	32.06±1.45
B/1	491.78±67.88	33.09±1.41
B/2	487.95±68.71	33.00±1.66
B/3	501.03±69.62	33.42±1.69
C/1	497.25±71.56	33.07±1.78
C/2	531.68±75.11	33.45±1.72
C/3	498.30±76.15	33.01±1.84

Table 3 - The five models[1] fitted to the growth data of cultured rainbow trout

Model	Equation	Reference
Bertalanffy-I	$Y = A * (1 – exp (–B * (t – T_0)))^3$	von Bertalanffy, 1934
Bertalanffy-A	$Y = A * (1 – exp (–B * (t – T_0)))^b; b \neq 3$	
Gompertz	$Y = A * exp (–exp (–B * (t – T)))$	Tjørve and Tjørve, 2017
Logistic	$Y = A * (1 + exp (–B * (t – T)))^{-1}$	Pearl, 1930
Brody	$Y = A * (1 – K * exp (–B * t))$	Brody, 1945

[1] von Bertalanffy with isometric scaling coefficient (Bertalanffy-I) and von Bertalanffy with allometric scaling coefficient (Bertalanffy-A), Gompertz, Logistic, and Brody model.
Y = dependent variable; A = asymptote; B = exponential rate of approximation to the asymptote; T = location of the point of inflection (POI); K = integration constant without biological interpretation; T_0 = intercept on the x-axis; b = scaling coefficient for allometry.

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We calculated the difference in AICc (ΔAICc) values to test the support of inferior models by the data. ΔAICc is calculated as: AICc (AICc $_i$ – AICc $_{min}$) (Katsanevakis and Maravelias, 2008). Models with ΔAICc >10 have no support by the data, while models with ΔAICc <2 have substantial support (Burnham and Anderson, 2002). Models with ΔAICc between 4-7 are somewhat supported by the data and might be considered.

The Mean Absolute Error (MAE) is the average absolute difference between observed and predicted outcomes and is calculated as: *MAE = mean* (|*observed – predicted*|).

The MSR, AICc, and MAE were calculated using the SAS software.

Finally, the results from MSR, AICc, and MAE were analyzed using a scoring system in which each best fit accounted for one score. The model that had the best fit in most tested cases achieved the highest score.

In addition, we interpreted the estimated regression parameters of each model in regards to the biological attributes of the species.

Results

Values of parameter *b* (Table 4), the allometric constant of the length-weight relationship equation, ranged between 2.879 and 3.239 in all tested groups. As *b* never equaled 3.0, it indicates a strong allometric relationship between length and weight.

All models met convergence in all (nine out of nine evaluations) tested cases through Marquardt's iterative method and their parameters were obtained (Table 5). All models needed a comparably low number of iterations, and convergence was generally met within 17 and 95 iterations.

Parameter *A* values ranged between 563.14 and 31333.6. Within each group, the lowest value was always obtained by the Logistic model, while the highest value was always estimated by the Brody model. In contrast, parameter *B* values ranged between 0.0086 and 4.9661 with lowest values obtained by the Gompertz model, and highest by both Bertalanffy models.

Parameter *T* ranged between 303.2 and 372.3 in the Gompertz model and between 311.8 and 341.5 in the Logistic model.

All models, except Brody, displayed sigmoid curves (Figure 1). Bertalanffy-I and Brody are highlighted as they predicted negative weight prior to the data.

The lowest MSR values were produced by the Logistic model in 0.67 of tested cases, followed by the Gompertz (0.22) and the von Bertalanffy-A (0.11) models (Table 6). Von Bertalanffy-I and Brody did not perform the lowest MSR in any case. MAE was lowest in the Logistic model in seven out of nine tested groups, 0.78. The von Bertalanffy-I model produced the lowest MAE twice (0.22) (Table 6). The lowest

Table 4 - Scaling coefficient of allometry of rainbow trout derived via length-weight relationship

Diet/Replicate	b
A/1	2.879
A/2	3.239
A/3	3.115
B/1	3.103
B/2	3.090
B/3	2.883
C/1	3.157
C/2	3.210
C/3	3.104

Values obtained from weight-length equation $W = aL^b$.

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Table 5 - Estimated parameters of the analyses of all models

Diet/Replicate	Bertalanffy-A	Bertalanffy-I	Gompertz	Logistic	Brody
A/1					
A	1851.51	1787.79	1066.26	640.422	31333.6
B	1.5561	1.62004	0.0086	0.0212	1.0231
T_0	0.4332	0.4253	-	-	-
T	-	-	363.396	341.45	-
K	-	-		-	9.73E-05
A/2					
A	1691.66	1811.84	993.717	563.137	26172.3
B	1.4541	1.3498	0.0075	0.0196	1.0218
T_0	0.3484	0.3652	-	-	-
T	-	-	372.248	340.977	-
K	-	-	-	-	9.51E-05
A/3					
A	1300.12	1326.05	914.752	607.151	26848.5
B	2.1541	2.0965	0.0100	0.0230	1.0283
T_0	0.4568	0.46333	-	-	-
T	-	-	343.422	333.248	-
K	-	-	-	-	0.0001
B/1					
A	813.149	818.14	708.243	580.258	2309.69
B	4.3229	4.2631	0.0166	0.0319	1.6227
T_0	0.5694	0.5732	-	-	-
T	-	-	307.779	314.955	-
K	-	-	-	-	0.0019
B/2					
A	932.708	939.621	775.099	602.873	18651.6
B	3.5678	3.5171	0.0144	0.0291	1.0519
T_0	0.5446	0.5483	-	-	-
T	-	-	315.87	319.900	-
K	-	-	-	-	0.0002
B/3					
A	790.726	785.567	692.953	580.100	1702.4
B	4.5913	4.6656	0.0178	0.0335	2.0666
T_0	0.5890	0.5849	-	-	-
T	-	-	304.738	312.964	-
K	-	-	-	-	0.0029
C/1					
A	887.826	897.565	757.364	603.146	4545.94
B	3.8950	3.80767	0.0152	0.0300	1.2544
T_0	0.5532	0.5593	-	-	-
T	-	-	312.644	318.262	-
K	-	-	-	-	0.0009
C/2					
A	1423.25	1468.95	1042.95	714.11	42975.00
B	2.6598	2.5415	0.0119	0.0270	1.0247

Continues...

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Table 5 (Continued)

Diet/Replicate	Bertalanffy-A	Bertalanffy-I	Gompertz	Logistic	Brody
T_0	0.5134	0.5232	-	-	-
T	-	-	337.103	330.91	-
K	-	-	-	-	9.92E-05
C/3					
A	757.439	761.187	676.967	572.771	1510.02
B	4.9661	4.9036	0.0185	0.0346	2.3416
T_0	0.5880	0.5914	-	-	-
T	-	-	303.187	311.817	-
K	-	-	-	-	0.0034

A = asymptote; B = exponential rate of approximation to the asymptote; T = point of inflection (POI); T_0 = intercept on the x-axis; K = integration constant without biological interpretation.

AICc values were most often obtained by the Logistic model (six out of nine cases). The Gompertz model produced the lowest AICc in two out of nine cases, and the von Bertalanffy-A model achieved the lowest AICc values in one of nine cases. The von Bertalanffy-I and the Brody models never achieved the lowest AICc.
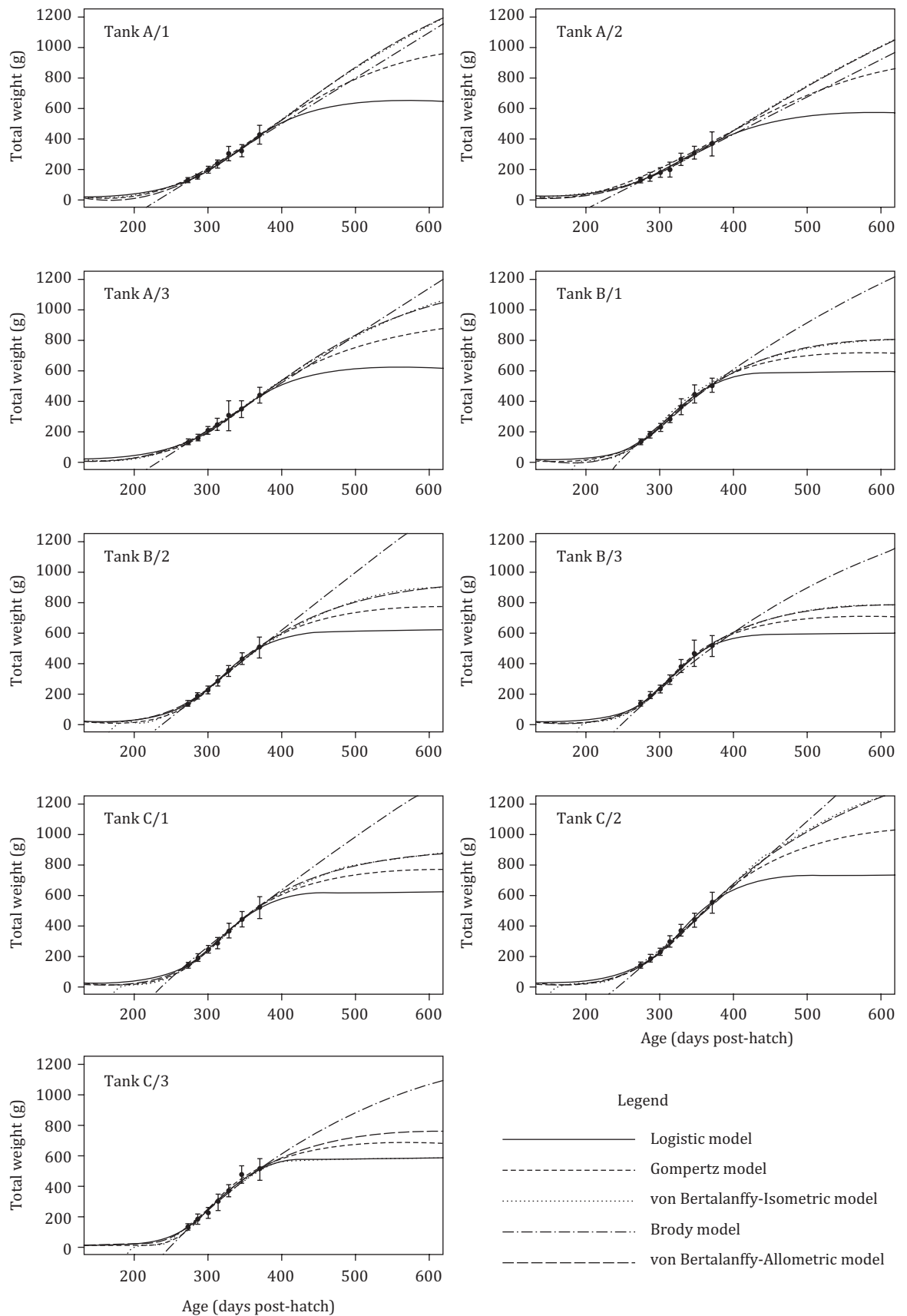
Undisputedly, the Logistic model achieved the best overall scoring with 19 out of 27 best fits (0.704) (Table 6). The Gompertz model achieved the best overall fit in 4 of 27 cases. The von Bertalanffy-I and von Bertalanffy-A models scored only 2 out of 27, and the Brody model did not archive the best fit in any tested cases and criteria. ΔAICc values ranged between 0.004 as the lowest and 14.9 as the highest. The Logistic model had substantial support by the data in all cases (Table 6); the Gompertz model, in six cases; and the von Bertalanffy-A and von Bertanlanffy-I, in five cases each. The ΔAICc values of the Brody model ranged between 2.2 and 14.9. Accordingly, the model was never substantially supported by the data.

Discussion

Convergence is met when the iterative process successfully estimates parameters for the function within the given maximum number of iterations set in the fitting algorithm (Rodrigues et al., 2010). In this study, all models met convergence in all tested cases using the Marquardt algorithm. This algorithm is described as more robust than others offered in statistical software (Elzhov et al., 2013; Lugert et al., 2017). This is especially important, as non-convergence situations of models for aquaculture data are described by several authors (Costa et al., 2009; Mansano et al., 2012; Allaman et al., 2013; Sousa Júnior et al., 2014).

The allometric scaling coefficient *b* values obtained by weight-length relationship equation is similar to values described by Dumas et al. (2007) on 20 to 500 g size rainbow trout. This is in agreement with the assumption that isometric-growing fish can grow more allometrically in terms of weight-length relationship under aquaculture conditions (Jobling, 2003). Furthermore, cultured rainbow trout are known to have a largely varying parameter *b*, ranging from as low as 1.3 to as high as 6.6 (Dumas et al., 2007); in contrast to values of 2.88 to 3.39 for wild rainbow trout (Cilbiz and Yalim, 2017).

Parameter *A* describes the infinite size of an organism (in this case, weight), and can be interpreted as the possibility of the model to reflect the biological properties of the species. *O. mykiss* is known to exceed 120 cm in length (Eaton et al., 1995) and weight of 25 kg (Robins and Ray, 1986). Despite these massive documented maximal sizes, the species commonly does not exceed 60 cm in length (Bristow, 1992) and a responding weight of 5 kg (Davidson et al., 2014). Accordingly, all models tested in this study, except for the Brody model, estimated *A* within the biological range of the species. Besides, the obtained values are in accordance with observed values from other aquaculture studies of this species (Dumas et al., 2007; Davidson et al., 2014). It is important to note that the obtained

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Average weight in grams (○) ± standard deviation observed on rainbow trout.

Figure 1 - Growth simulations of rainbow trout from 1 until 700 age-days obtained by Logistic, Gompertz, Bertalanffy-Isometric, Brody, and Bertalanffy-Alometric models.

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Table 6 - Goodness of fit criteria of the von Bertalanffy-A, von Bertalnaffy-I, Gompterz, Logistic, and Brody equations fitted to weight gain data of rainbow trout

Diet/Replicate	Criteria	Bertalanffy-A	Bertalanffy-I	Gompertz	Logistic	Brody
A/1	MSR	1360.447*	1360.471	1361.333	1366.891	1395.461
	MAE	7.842723	7.846975	7.718985	7.519974*	11.34891
	AICc	1985.714*	1985.718	1985.842	1986.645	1990.72
	ΔAICc	0	0.004	0.128	0.931	5.006
A/2	MSR	2013.628	2013.834	2011.078	2003.461*	2046.022
	MAE	7.48467	7.493464	7.228328	6.423474*	8.803215
	AICc	2031.629	2031.649	2031.383	2030.647*	2034.725
	ΔAICc	0.982	1.002	0.736	0	4.078
A/3	MSR	2076.227	2076.248	2075.992*	2078.747	2098.83
	MAE	3.777341	3.775807*	3.847837	4.364751	6.487342
	AICc	2068.994	2068.996	2068.971*	2069.233	2071.127
	ΔAICc	0.023	0.025	0	0.262	2.156
B/1	MSR	1275.218	1275.780	1259.748	1223.763*	1313.151
	MAE	8.389967	8.427507	7.614307	5.389659*	10.62074
	AICc	1952.993	1953.079	1950.613	1944.962*	1958.709
	ΔAICc	8.031	8.117	5.651	0	13.747
B/2	MSR	1506.406	1506.629	1499.67	1487.210*	1524.561
	MAE	4.97224	4.991651	4.517254	3.346032*	6.054685
	AICc	1995.637	1995.666	1994.758	1993.123*	1997.985
	ΔAICc	2.514	2.543	1.635	0	4.862
B/3	MSR	2260.14	2259.234	2237.972	2187.720*	2307.357
	MAE	11.81514	11.83862	11.10749	8.670518*	13.09195
	AICc	2064.594	2064.516	2062.672	2058.243*	2068.626
	ΔAICc	6.351	6.273	4.429	0	10.383
C/1	MSR	1838.049	1838.397	1832.216	1823.449*	1855.811
	MAE	4.651593	4.672688	4.295837	3.788446*	6.677206
	AICc	2034.636	2034.673	2034.013	2033.073*	2036.521
	ΔAICc	1.563	1.600	0.940	0	3.448
C/2	MSR	1820.38	1820.517	1819.256*	1825.385	1867.426
	MAE	4.531407	4.525795*	4.691465	5.60685	7.425679
	AICc	2032.743	2032.758	2032.622*	2033.281	2037.744
	ΔAICc	0.121	0.136	0	0.659	5.122
C/3	MSR	2206.280	2207.290	2178.196	2106.247*	2271.289
	MAE	12.37772	12.38536	12.10744	10.7329*	14.4342
	AICc	2080.962	2081.053	2078.439	2071.822*	2086.683
	ΔAICc	9.14	9.231	6.617	0	14.861
Score**		2	2	4	19	0

MSR - mean square residual; MAE - mean absolute error; AICc - Akaike Information Criterion corrected for small sample sizes.
ΔAICc values indicate support of the model by the data.
* Best adjustment criterion achieved among all models.
** Each best fit accounts for one score for the regarding model.

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A values are generally higher than harvest weights required by the average Brazilian market (350 to 400 g). Accordingly, parameter *A* can be considered a useful attribute in growth prediction for farming management purposes. Similar conclusions about parameter *A* are indicated by Gomiero et al. (2009) for *Brycon orbignyanus*, Mansano et al. (2012) for *Lithobates catesbeianus*, and Lugert et al. (2017) for *Scophthalmus maximus*, with all of the above in aquaculture grown species.

Parameter *B* denotes the precocity index. This means that the larger the numeric value, the quicker the fish will reach the asymptotic or infinite weight (Malhado et al., 2009). Estimated *B* values in this study (between 0.008 to 4.9661) have the tendency to be greater than those values (between 0.061 to 1.76) obtained from wild rainbow trout (Blair et al., 2013; Sloat and Reeves, 2014; Cilbiz and Yalim, 2017). Similarly, Lugert et al. (2016) found similar differences in parameter *B* between cultured and wild *Scophthalmus maximus*, relating these differences to the positive effect of controlled environmental conditions in recirculation production systems. Significant differences in parameter *B* are observed between the different models, with von Bertalanffy-A, von Bertalanffy-I, and Brody having the highest values between 1.02 and 4.97, while the Gompertz and Logistic models generally have the lowest (0.007 to 0.03). Our results are in agreement with results of Santos et al. (2013) on length growth modeling of *Oreochromis niloticus*, Yun et al. (2015) on weight growth modeling of *Carassius auratus gibelio*, and Lugert et al. (2016) on weight growth modeling of *Scophthalmus maximus*. Aversely to our findings, Gomiero et al. (2009) showed lower *B* estimates for Brody (0.003) and von Bertalanffy (0.00042) models on length growth of cultured *Brycon orbignyanus*.

The POI (parameter *T*) of the growth curve is only parameterized in the Gompertz and the Logistic models but can mathematically be calculated for each model via the first derivative of the function. At the POI, the growth rate reaches the maximum value, then decreases asymptotically towards zero, without reaching it. On this study, *T* values obtained by the Gompertz model (303.2 to 372.2 days) are similar to those values (274.5 to 343.5 days) estimated by Sloat and Reeves (2014) for wild rainbow trout. However, our estimated weights at the POI (between 203.2 g and 372.2 g) were higher compared with wild rainbow trout (91.06 to 117.28 g) (Sloat and Reeves, 2014), being evidence of genetic improvement of breeding strains, optimal feed supply, and good rearing conditions. Furthermore, in aquaculture operations, parameter *T* can be useful in the empiric adjustment of management strategies, as it is proven to correlate with other husbandry information. For instance, parameter *T* has significant meaning on cultured *Carassius auratus gibelio* because it positively correlates with dietary protein level (Yun et al., 2015). Likewise, *Oreochromis niloticus* shows significant influence of water temperature on weight gain and on the age at the inflexion point (Santos et al., 2013).

When analyzing growth, model selection is a proven and reliable method to find the best suitable model for a given data set. The von Bertalanffy-I as the most widely, and *a priori*, used model has widely been disputed (Katsanevakis and Maravaelias, 2008), and Burnham and Anderson (2002) pointed out that the chances of *a priori* choosing the best suitable model for a given dataset are minor. Accordingly, model selection studies, as the current one, are of great importance in understanding the underlying biological properties of a reared species, by evaluating the most suitable model. Our results indicate that the von Bertalnaffy-I model is, besides the Brody model, the least suitable one to use on aquaculture data of *O. mykiss* during the grow-out phase.

In model selection, the goodness of fit should generally not be based on a single criterion. Correspondingly, it has become common practice to evaluate the most suitable model based on an evaluation metrics of mostly three statistical parameters of different properties (e.g., Yun et al., 2015; Lugert et al., 2017; Powell et al., 2019). The first parameter should be based on the residuals from fitting the model. The second parameter is often based on information theory, either AIC, AICc, or BIC. A third parameter is mostly somehow based on the deviation between estimated and sampled data. For these three categories of evaluation parameters, several different statistical parameters are available. The author needs to decide which parameter is most suitable for the study.

In our study, we used MSR, AICc, and MAE. The non-linear least squares method aims to achieve non-linear equation parameter by minimizing the Residual Sum of Squares (RSS). The smaller RSS, the smaller the MSR and the better the fit (Rawlings et al., 1998). In this study, the Logistic, von Bertalanffy-A, and Gompertz models achieved the smallest RMS values. Similar results were obtained by Mansano et al. (2012) and Costa et al. (2009) in growth studies of *Lithobates catesbeianus* and *Orechormis niloticus* under aquaculture conditions.

We used ΔAICc to identify whether our datasets were supported by more than one model. This was necessary, as the outcome from the analysis revealed very close numeric results between different models within tested groups. ΔAICc <2 indicates substantial support of a model by the data (Burnham and Anderson, 2002). Indeed, in five out of nine analyses, four out of five tested models were supported by the data, namely von Bertalanffy-A, von Bertalanffy-I, Gompertz, and Logistic. This might be due to the specific pattern of our recorded data (grow-out phase), which are distributed around the POI of the growth curve. Accordingly, several models of sigmoidal behavior can reflect this segment of the curve.

Primarily, we observed that the different non-linear models adjusted their fit individually to the various growth trajectories expressed by rainbow trout caused by different diet treatments. Araneda et al. (2013) observed similar results when fitting models on various growth data of *Penaeus vannamei*. This specific application has huge potential in predicting the effects of new feed formulations, harvest size, and production period in all aquaculture species. However, it is necessary to verify and validate this potential through studies with rigorous control of diet quality and quantity as recorded in carp (Yun et al., 2015).

Conclusions

The Logistic, Gompertz, and both versions of the von Bertalanffy models show capacity to fit the weight-at-age data of cultured rainbow trout during the grow-out phase. However, in the current study, the Logistic model achieved the highest accuracy in fit. Therefore, the Logistic model is the best model to represent growth of cultured rainbow trout during growth-out phase and is useful to predict long-term growth and harvest size in fish aquaculture management.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Conceptualization: P.C. Janampa-Sarmiento and M.M. Pereira. Data curation: L.S. Freire and M.M.B. Pereira. Formal analysis: V. Lugert. Funding acquisition: R. Takata, T.M. Freitas and M.M. Pereira. Investigation: P.C. Janampa-Sarmiento. Methodology: P.C. Janampa-Sarmiento, R. Takata, L.S. Freire, M.M.B. Pereira, V. Lugert, G.M. Heluy and M.M. Pereira. Project administration: R. Takata and T.M. Freitas. Resources: R. Takata and T.M. Freitas. Software: P.C. Janampa-Sarmiento and V. Lugert. Supervision: M.M. Pereira. Validation: M.M. Pereira. Visualization: P.C. Janampa-Sarmiento. Writing-original draft: P.C. Janampa-Sarmiento. Writing-review & editing: P.C. Janampa-Sarmiento, R. Takata, T.M. Freitas, L.S. Freire, M.M.B. Pereira, V. Lugert, G.M. Heluy and M.M. Pereira.

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