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Research Article

Morphometric relationships and growth models for the oyster *Crassostrea corteziensis* cultivated at the southeastern coast of the Gulf of California, Mexico

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ABSTRACT. This study aimed to determine weight-size relationships and to fit the best growth model of the Cortez oyster *Crassostrea corteziensis* from early juvenile to adult during one single culture cycle. The morphometric data (n = 50 oysters sampled each two weeks during January 2010 to March 2011) of shell height-shell length [SH-SL], shell height-shell width [SH-SW], shell width-shell length [SW-SL], body weight-shell length [BW-SL], body weight-shell height [BW-SH] and body weight-shell-width [BW-SW] (log-transformed) were determined by regression analysis. The SL and SH measurements (R^2 = 0.98) were consistently proportional to the BW, being the BW-SL and BW-SH morphometric relationships the more suitable for growth evaluation of *C. corteziensis* in culture. Four different equations of the Schnute model, as well as Special cases 1 and 2 (equivalent to the Von Bertalanffy growth model, VBGM, and Logistic models, respectively), were evaluated utilizing length-at-age data to estimate individual growth parameters. The parameters were obtained using the maximum likelihood algorithm and the Akaike information criterion was applied to rank the models examined. The growth curve displayed a rapid increase until the size of 41.68 ± 16.18 mm in length. In the present study, the symmetrical sigmoid curve was the best hypothesis that fit the data; however, it is assumed that the age data are sufficiently informative to describe the growth pattern of *C. corteziensis*, with either Schnute model Special case 2. Results from morphometry and growth model in this study represent useful tools to analyze growth performance of the Cortez oyster in culture better.

Keywords: *Crassostrea corteziensis*, Cortez oyster, biometrics, growth model, aquaculture, management.

INTRODUCTION

The world oyster industry produces around 16% of the total aquaculture production (FAO, 2015) and is represented by several *Saccostrea*, *Ostrea* and *Crassostrea* species. The Cortez oyster *Crassostrea corteziensis* (Hertlein, 1951) is distributed along the Pacific coast from the Gulf of California to Peru (Fisher *et al.*, 1995). Mainly due to overexploitation, its natural populations are remarkably reduced in northwestern Mexico, and since a few decades ago, the oyster industry was supported with the introduction of the exotic oyster *Crassostrea gigas* (Chávez-Villalba *et al.*, 2005). However, drastic mortality in juveniles and adults of farmed *C. gigas* caused by high temperatures in summer, massive die-offs in winter and the presence of pathogens, have been reported since 1997 (Cáceres-Martínez *et al.*, 2004).

After many attempts (Cáceres-Puig *et al.*, 2007; Pérez-Enríquez *et al.*, 2008; Hurtado *et al.*, 2009), production of larvae and spat of *C. corteziensis* improved and is now produced commercially. Thus, the culture of this oyster species is considered as an alternative to compensate the massive losses of *C. gigas*. Although some information on its growth performance is available (Chávez-Villalba *et al.*, 2005,

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2008, 2010; Castillo-Durán *et al.*, 2010), an analysis of the accuracy between growth parameters and models of this oyster is necessary to evaluate management and production under culture conditions better. The weight-length relationship is widely used in the analysis of fishery data since it enables the evaluation of wild and cultivated fish and shellfish populations when only length measurements exist (Froese, 2006; Grizzle *et al.*, 2017), delineate growth of stocks (Peixoto *et al.*, 2004) and allows life history and morphological comparisons of populations from different regions (Karakulak *et al.*, 2006). In aquaculture, morphometric relationships represent a simple alternative to estimate weight from length measurements by more exact and complete mathematical models (Hopkins, 1992), these precise growth-time measurements help to analyze growth models (Kovitvadhi *et al.*, 2008).

Among the range of individual growth models used in fisheries, the Von Bertalanffy model (VBGM) is the most popular and commonly applied growth estimation. Nevertheless, Katsanevakis & Maravelias (2008) have demonstrated that the use of multi-model inference (MMI) is a better alternative than the *a priori* use of VBGM, and many authors have adopted this approach (Zhu *et al*., 2009; Alp *et al*., 2011; Baer *et al*., 2011; Mercier *et al.,* 2011). The literature provides alternatives to the VBGM, such as the Gompertz growth model, Logistic model (Ricker, 1975) and Schnute model (Schnute, 1981). When more than one model is used, its selection is usually based on the shape of the anticipated curve, biological assumptions, and fit of the data. Parametric inference and estimation, as well as the precision of these estimates, are based solely on the fitted model. Another approach is to fit more than one model and select the best one based on information theory. This approach has been recommended as a more robust alternative when compared with other traditional ones (Katsanevakis, 2006). The most common information-theory approach is to use the Akaike information criterion (AIC) (Katsanevakis, 2006; Wang & Liu, 2006; Katsanevakis & Maravelias, 2008; Zhu *et al*., 2009; Cerdenares-Ladrón de Guevara *et al*., 2011; Cruz-Vásquez *et al*., 2012).

Therefore, the aim of this work is threefold: first, to analyze the weight-shell biometrics (height, length and width) relationships; second, to determine the growth parameters using a multi-model approach; and finally, to figure out which model fits best the length-at-age raw data for the Cortez oyster, *C. corteziensis,* cultivated in a subtropical coastal lagoon from southeastern Gulf of California, Mexico.

MATERIALS AND METHODS

A total of 7,000 oyster seeds were obtained from the Centro de Reproducción de Especies Marinas del Estado de Sonora (CREMES), O.P.D., Kino Bay, Sonora, Mexico. *C. corteziensis* was cultured at the Macapule Bay, Guasave, Sinaloa, Mexico (25°20’-25°35’N, 109°00’-108°40’W), using racks suspended from a long-line system 0.15 m beneath the water surface.

Initial shell height and body weight were 4.31 ± 0.75 mm and 0.018 ± 0.009 g, respectively. Little oysters were acclimated as mentioned by Gallo-García *et al.* (2001), placed in plastic mesh bags (2 mm diameter) which were laid inside plastic trays. Then, five trays were overlapped to form a culture unit and finally, the culture units were tied to a long-line system (n = 500 oysters/bag in each tray).

When oysters reached 30 mm shell height, they were placed directly into the trays until reaching ≥65 mm. That is, cultivation operations consisted in reducing the density of oyster within the trays in the three first months (January to March 2010), from 500 at the beginning to 42 oysters at the end of the cultivation period. The study started in January 2010 and lasted until March 2011. Monthly, epibiotic organisms and mud accumulated in the ropes and trays of the suspended cultivation system were cleaned off with a soft brush and spatula.

Morphometric relationships

Shell measurements and body weight of 50 oysters were respectively obtained with a stainless steel caliper (0.01 mm) and a digital balance (0.01 g) every 15 days. Biometrics included: Shell height (SH, the maximum distance between the hinge to the furthermost edge), length (SL, the maximum distance between the anterior and posterior margins) and width (SW, the maximum distance at the thickest part of the two shell valves). Oysters were blotted dry in an absorbent paper before weighing to obtain the total body weight (BW). Growth relationship of BW and SH of the total oyster population sampled (n = 1,400) was estimated using the potential regression $W = aL^b$, where W is the BW (g), L is the SH (mm), a is the intercept and b is the slope. The goodness of fit was described using the correlation coefficient (Sokal & Rohlf, 1981). The coefficient of variation (CV) was calculated for all shell biometrics and weight.

The equation determined the morphometric relationships between variables (SH, SL, SW, and BW): $\log Y = \log a + b \log X$, where log Y and log X are the log shell size (SH and SW) or total body weight (BW) and Log shell size (SL, SH, and SW), respectively, while Log a is the intercept and b is the slope. The determination coefficient (R^2) was calculated to obtain the association degree between variables. The values of b obtained in a linear regression were significantly different from the isometric value ($b = 1$) or allometric range (negative allometry: $b < 1$ or positive allometry $b > 1$) when a *t*-test (Ho: $b = 1$) with a confidence level of 95% was applied, expressed by the following equation (Lleonart *et al.*, 2000): $t = (b-1)/Sb$, where t is the *t*-test value, b is the slope and Sb is the standard error of the slope b.

Regression analysis determined the morphometric data for SH-SL, SH-SW, SW-SL, BW-SL, BW-SH, and BW-SW (log-transformed). Scatter diagrams with the linear model (Dobson, 2008) was used to analyze the SH and BW relationship.

Growth model selection and parameter inference

Multimodel approach allows testing each model as a different hypothesis of growth pattern, thus, six different equations of Schnute model were evaluated utilizing length-at-age data to determine which growth pattern best represent the data, as well as to estimate individual growth parameters (Schnute & Groot, 1992; Katsanevakis, 2006; Katsanevakis & Maravelias, 2008). As stated by Aragón-Noriega (2016) the theory behind this statement is that the Schnute model has four solution cases, but it is only one model (Schnute, 1981). Special cases 1 and 2 of the Schnute model were the same as the VBGM and Logistic models, respectively. Actually, case 2 represents Gompertz, where $a > 0$ and $b = 0$.

The Schnute growth model (Schnute, 1981) is a general four-parameter growth model that takes four mathematical forms depending on the values of a and b about 0. In this study, we will describe Schnute case 1 when $a \neq 0$, $b \neq 0$, as follows:

$$L_t = \left\{ Y_1^b + \left(Y_2^b - Y_1^b\right)\left[\frac{1 - e^{-a(t-\tau_1)}}{1 - e^{-a(\tau_2-\tau_1)}}\right]\right\}^{\frac{1}{b}}$$

Schnute case 2 when $a \neq 0$, $b = 0$, as follows:

$$L_t = Y_1 exp\left[ln\left(\frac{Y_2}{Y_1}\right)\frac{1 - e^{-a(t-\tau_1)}}{1 - e^{-a(\tau_2-\tau_1)}}\right]$$

Schnute case 3 when $a = 0$, $b \neq 0$, as follows:

$$L_t = \left\{ Y_1^b + \left(Y_2^b - Y_1^b\right)\left[\frac{t - \tau_1}{\tau_2 - \tau_1}\right]\right\}^{\frac{1}{b}}$$

Schnute case 4 when $a = 0$, $b = 0$, as follows:

$$L_t = Y_1 exp\left[ln\left(\frac{Y_2}{Y_1}\right)\frac{t - \tau_1}{\tau_2 - \tau_1}\right]$$

Special Case 1 is the same equation than Schnute case 1 but with $a > 0$ and $b = 1$; Special Case 2 is the same equation than Schnute case 1 but with $a > 0$ and $b = -1$. In these two special cases, parameter b is fixed, and no search is necessary because these two cases become one three-parameter model. The following parameters are used in these models:

τ_1: is the lowest age in the data set.

τ_2: is the highest age in the data set.

a: is the relative growth rate parameter.

b: is the incremental relative growth rate (incremental time constant).

Y_1: is the size at age $\boldsymbol{\tau_1}$.

Y_2: is the size at age $\boldsymbol{\tau_2}$.

To compute L_∞ using the Schnute model in the four cases and the two Special cases (for cases 3 and 4 it was not possible to calculate this parameter), the following equations were used:

when $a \neq 0$, $b \neq 0$

$$L_\infty = \left[\frac{e^{a\tau_2}Y_2^b - e^{a\tau_1}Y_1^b}{e^{a\tau_2} - e^{a\tau_1}}\right]^{\frac{1}{b}}$$

when $a \neq 0$, $b = 0$

$$L_\infty = exp\left[\frac{e^{at2}lnY2 - e^{at1}lnY1}{e^{at2} - e^{at1}}\right]$$

To compute t_0 when $a \neq 0$, $b \neq 0$

$$t_0 = t_1 + t_2 - \frac{1}{a}ln\left[\frac{e^{at_2}Y_2^b - e^{at_1}Y_1^b}{Y_2^b - Y_1^b}\right]$$

To compute t^* when $a \neq 0$, $b \neq 0$

$$t^* = t_1 + t_2 - \frac{1}{a}ln\left[\frac{b\left(e^{at_2}Y_2^b - e^{at_1}Y_1^b\right)}{Y_2^b - Y_1^b}\right]$$

when $a \neq 0$, $b = 0$

$$t^* = t_1 + t_2 - \frac{1}{a}ln\left[\frac{e^{at_2} - e^{at_1}}{ln\left(\frac{Y_2}{Y_1}\right)}\right]$$

The models were fitted using maximum likelihood. A multiplicative error structure was considered. The maximum likelihood fitting algorithm was based on the equation:

$$(\Phi|data) = -\left(\frac{n}{2}\right)(ln(2\pi) + 2 * ln(\sigma) + 1)$$

where Φ represents the parameters of the models and σ represents the standard deviations of the errors calculated using the following equation:

$$\sigma = \sqrt{\frac{1}{n}\sum(lnLt_{observed} - lnLt_{estimated})^2}$$

The model selection approach was used to select the best candidate growth model (Katsanevakis, 2006) based on the AIC approach, defined as $AIC = -2LL + 2\theta_i$, where LL is the maximum log-likelihood and θ_i is the number of parameters in each model tested. The AIC is a goodness of fit test that provides a quantitative value for each equation to select the hypothesis that best fit the data. Differences in AIC ($\Delta_i = AIC_i - AIC_{\min}$) values were estimated among all the models used in this study. The model with the lowest AIC value was chosen as the best model. A criterion proposed by Burnham & Anderson (2002To statistically decide the model fitness of the data,) was evaluated, in which $\Delta_i < 2$ is evidence of substantial support, $4 < \Delta_i < 7$ has some support, and $\Delta_i > 10$ shows essentially no support from data.

The plausibility of each model was estimated using the following formula for the Akaike weight:

$$w_i = \frac{\exp(-0.5\Delta_i)}{\sum_{i=1}^{6}\exp(-0.5\Delta_i)}$$

Following the multi-model inference approach, the model-averaged asymptotic length $\bar{L}_\infty$ was estimated as a weighted average using the six models, with the prediction of each model weighed by W_i. Thus, the model-averaged asymptotic length was estimated as follows:

$$\bar{L}_\infty = \sum_{i=1}^{6} W_i \hat{L}_{\infty,j}$$

The 95% confidence interval of growth model parameters (ϕ) were estimated after Venzon & Moolgavkar (1988) using the likelihood profile method. These estimations are based on a chi-square distribution with d degrees of freedom. The confidence interval was defined as all values of (ϕ) that satisfy the inequality:

$$2((Y \mid \theta)\text{-}(Y \mid \theta_{best})) < \chi^2_{1,1\text{-}\alpha}$$

where $L(Y \mid \theta_{best})$ is the negative log-likelihood of the fitted value of θ and $\chi^2_{1,1\text{-}\alpha}$ are the values of the chi-square distribution with $d = 1$ (3.84).

RESULTS

The scatter diagram of BW-SH for all oyster sampled (Fig. 1) exhibited a curvilinear relationship with the equation $y = 0.0002(x^{2.9447})$ ($R^2 = 0.97$).

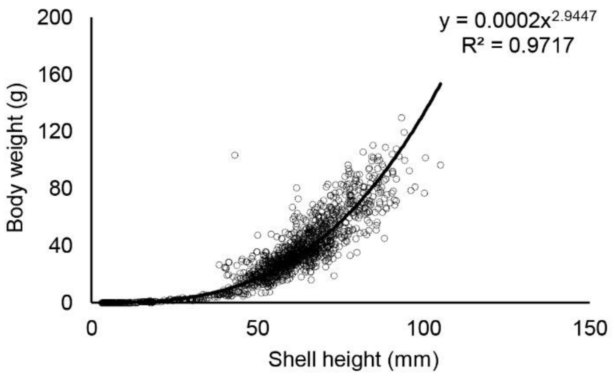

Figure 1. Morphometric relationship between shell height (SH) and body weight (BW) of the Cortez oyster (*Crassostrea corteziensis*) for all culture dataset (during January 2010 to March 2011). The best-fit power regression model is shown.

Table 1. Descriptive statistic parameters for *Crassostrea corteziensis* cultivated for 420 days. SD: standard deviation, CV: coefficient of variation.

Parameter		Suspended culture (420 days of cultivation)
Number of oysters		1400
Shell length (mm)	Mean ± SD	41.68 ± 16.18
	Min-Max	3.13-73.17
	CV	0.38
Shell height (mm)	Mean ± SD	54.29 ± 22.31
	Min-Max	4.31-105.06
	CV	0.41
Shell width (mm)	Mean ± SD	16.90 ± 8.05
	Min-Max	0.52-43.08
	CV	0.47
Body weight (g)	Mean ± SD	32.50 ± 24.55
	Min-Max	0.01-129.80
	CV	0.75

The CV obtained for all biometric parameters displayed high dispersion of *C. corteziensis* (Table 1) and varied from 0.38 (SL) to 0.75 (BW). The coefficient of determination (R^2) for all morphometric relationships fluctuated from 0.95 for the SH-SW relationship, to 0.98 found for the SH-SL, BW-SL and BW-SH relationships (Table 2). Except for the SH-SW interaction, the rest of the biometric relationships showed b values above 1 (positive allometry), ranging from 1.07 found for SH-SL, to 3.2 obtained for BW-SL (Table 2).

The growth parameters for *C. corteziensis* from each of the equations tested are shown in (Fig. 2, Table 3). The higher values of LL maximization determine the order of the models. For each particular model (hypotheses of growth pattern), Table 4 shows the corresponding AIC, Δi, W_i, L_∞, and the averaged L_∞.

The special case 2 (equivalent to the Logistic model, Fig. 2c) showed the lowest AIC value in the dataset. Another significant result shown in Table 4 is the Delta value (Δi) for each model; the Δi values were higher than 10 for the Case 2 (equivalent to Gompertz model) and special case 1 (equivalent to VBGM model) models, that is, there were not supported by the data. Special case 1 had the highest asymptotic length value

Table 2. Morphometric relationship of the Cortez oyster *Crassostrea corteziensis* cultured during 420 days. R^2: Determination coefficient, SH: shell height (mm), SL: shell length (mm), SW: shell width (mm), BW: body weight (g), SE: standard error, CI: confidence intervals; *$P < 0.05$.

Parameters	Allometric equation	R^2	SE of *b* (95% CI of *b*)	Relationship (*t*-test)
SH-SL	log SH = -0.0067+1.0720 log SL	0.98*	0.0049 (0.0047-0.0145)	+ allometry
SH-SW	log SH = 0.6539+0.8855 log SW	0.95*	0.0070 (0.0067-0.0207)	- allometry
SW-SL	log SW = -0.6262+1.1332 log SL	0.96*	0.0084 (0.008-0.0248)	+ allometry
BW-SL	log BW = -3.8585+3.2023 log SL	0.98*	0.1476 (0.1416-0.4368)	+ allometry
BW-SH	log BW = -3.7686+2.9456 log SH	0.98*	0.0134 (0.0128-0.0396)	+ allometry
BW-SW	log BW = -1.9331+2.6888 log SW	0.97*	0.0168 (0.0161-0.0497)	+ allometry

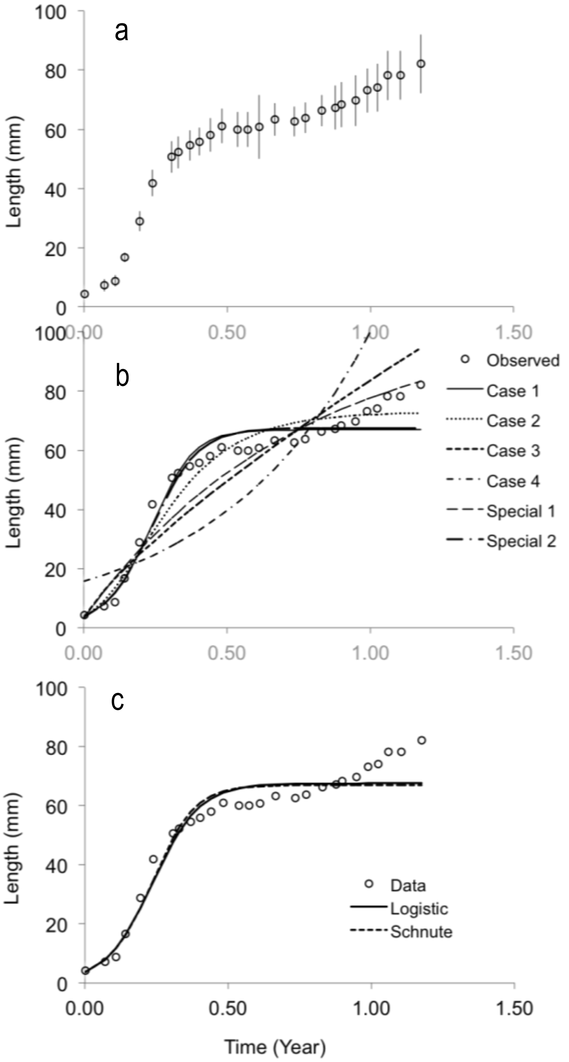

Figure 2. a) Observed data ± standard deviation and b) growth curves generated for *Crassostrea corteziensis* by Schnute cases model, and c) best models after AIC and W (%).

with L_∞= 104.4 mm, which seems an overestimation of the total length.

The anticipated growth curves should be different for each model (Fig. 2b), however the two growth curves displayed in Fig. 2c have very similar trajectories that in fact is the expected growth curves of the symmetric sigmoid curve. This figure includes the growth model fitted to the data, but the likelihood parameters are in Table 3.

DISCUSSION

Size-weight relationships are used for growth assessment (Andreu-Soler *et al.*, 2006), estimation of stock biomass (Gaspar *et al.*, 2012), and help to indicate fish condition (Karakulak *et al.*, 2006) of wild populations, among others applications. A complete growth assessment of cultivated bivalves includes shell size (length, height, and width) and body weight throughout the study of morphometric relationships (Syda-Rao, 2007; Grizzle *et al.*, 2017). The *b* (2.9447) and R^2 (0.97) values given by the potential regression for all sampled population of *C. corteziensis* were different in this study to those respectively obtained by Chávez-Villalba *et al.* (2005: $b = 2.8389$, $R^2 = 0.98$ and 2008: $b = 3.0953$, $R^2 = 0.84$) for the same oyster species cultured at around 450 km north of our cultivation location. The differences in these results can be explained by variations in some factors such as environmental conditions, the number of oyster sampled, density, final BW, survival, and culture time. Grizzle *et al.* (2017) found that water temperature, chlorophyll-*a* concentration, deployment and culture methods of the eastern oyster *C. virginica* influenced SH-BW relationship.

In the present study, the *b* value of the SH-SL, SH-SW and SW-SL relationships (log-transformed data) were between 0.8855 and 1.1332, similarly to that reported by Syda-Rao (2007) for the Indian oyster Pearl, after three culture years (0.13 to 1.61). However, it differs with Hanson *et al.* (1988) working with the clam *Anodonta grandis simpsoniana*, and Kovitvadhi

Table 3. Estimated growth parameters of cultivated *Crassostrea corteziensis* for each model. Parameter *a* is similar to *k* in the specialized models. *Fixed value (no search was necessary).

Model	Y_1	Y_2	a	B	LL
Special case 2	3.69	67.57	12.23	-1*	19.580
Special case 1	3.60	83.30	1.33	1*	2.918
Schnute case 1	3.76	66.94	14.20	-1.26	19.711
Schnute case 2	3.38	72.57	5.61	0*	14.367
Schnute case 3	3.80	94.49	0*	1.30	-0.462
Schnute case 4	15.75	138.29	0*	0*	-19.867

Table 4. Akaike information criterion (AIC), Akaike differences (Δ_i), Akaike weights (W_i), estimated asymptotic length (L_∞) and 95% conditional confidence limits (CL) for each candidate model for *Crassostrea corteziensis*.

Model					Asymptotic length (mm)		
	θ_i	AIC	Δ_i	W_i (%)	Point estimation	95%CL lower	95% CL upper
Special case 2	3	-32.12	0.00	77.51	67.6	65.0	70.5
Schnute 2	3	-21.69	10.43	0.42	72.9	69.0	77.0
Special case 1	3	1.21	33.32	0.00	104.4	96.0	113.5
Schnute 1	4	-29.60	2.51	22.07	66.9	63.5	70.5
L_∞ averaged					67.5	65.4	69.5

et al. (2008) culturing the freshwater mussel *Hyriopsis myersiana,* who obtained *b* values above 2.649 for the shell size morphometric equations. The different *b* values among the works can be attributed to factors such as species, shell shape (SH, SL, SW), and production conditions (Alunno-Bruscia *et al.*, 2001; Lajtner *et al.*, 2004; Díaz & Campos, 2014).

The allometric growth values obtained in this work indicate a higher dispersion of shell data within the cultivated oyster population, as confirmed with the estimated CV values. It suggests that internal and external factors such as genetic of seed and stocking density could partially explain the results. Haley & Newkirk (1977) concluded that the largest oysters from a specific genetic class continued to be faster growing and their shell biometrics were highly correlated to each other, meanwhile, Cigarría & Fernández (1998) tested different stocking densities culturing Manila clam *Ruditapes philippinarum* in oyster bags and concluded that shell biometric relationships of clam were affected by density.

On another hand, most of the *b* values of the shell biometrics-BW relationships of *C. corteziensis* were higher than 1 ($P < 0.05$). The *b* values of the BW with the three shell biometrics were above 2.13 coinciding with findings of Kovitvadhi *et al.* (2008) with the mussel *H. myersiana* cultured at different conditions. As well as oyster density (Cigarría & Fernández, 1998) and culture method (Roncarati *et al.*, 2010), the differences in morphometrics among culture phases may reflect the effect of reproductive activity. Chávez-Villalba *et al.* (2008) reported all reproductive phases of the Cortez oyster within one culture year period, which could partially explain the fluctuation in the obtained *b* values among the relationships. Gaspar *et al.* (2012) concluded that shell-BW relationships change with maturity, coinciding with the high variation we found in the CV and *b* values.

Model selection was performed using the AIC. The advantage of this approach is that the models are hierarchically ordered based on their fit to the data, and the parameters of the candidate models can be averaged. For this procedure, it is necessary to estimate the Akaike weight (Burnham & Anderson, 2002). In the present study, the W_i value, in favor of special case 2 (Logistic like model) was 77.5%, and the W_i value, in favor of Schnute case 1 model was 22.07%. The observation of Burnham & Anderson (2002), which stated that it is better to declare the best model only if the W_i value is higher than 80%, must be considered.

The advantage of the Schnute model is that shows a differential equation forming six different curve patterns depending on the parameter values. The Schnute model is a general four-parameter growth model with possible sub-models that includes not only asymptotic growth (such as Von Bertalanffy, Richards, Gompertz or logistic growth) but also linear, quadratic or exponential growth. Rather than modeling the instantaneous rate of change, Schnute model concentrates on the relative rate of change. Additionally, Schnute model shows a parameterization approach that is statistically stable (Schnute, 1981).

In the present study, the symmetrical sigmoid curve was the best hypothesis that fit the data; however, it is assumed that the age data are sufficiently informative to describe the growth pattern of *C. corteziensis*, with either Schnute model Special case 2.

The -*LL* were 19.580 and 19.711 for Special case 2 and Schnute case 1, respectively, but the AIC penalize the latter with more parameter resulting in AIC of -32.12 and -29.6 and consequently, and Δ_i value of 0 and 2.51. Thus, Special case 2 (Logistic like) become in the model best fit the data with the Akaike weight of 77.51%.

All shell measurements were consistently proportional to the BW during the culture. Therefore, BW-SL, BW-SH, and BW-SW morphometric relationships were suitable for growth evaluation of *C. corteziensis* cultivated in the Macapule Bay, Sinaloa. As clearly shown by Aragón-Noriega (2016), the best growth model should be applied to describe the growth performance of any specific species. Thus, the multi-model approach should replace the default use of a single model, and when possible, only the raw data should be used for modeling the individual growth of cultivated *C. corteziensis*. The advantage of this approach is that it allows contrasting different hypothesis of oyster growth providing a robust tool to define growth trajectory of the lifespan of *C. corteziensis*. Results from both evaluation techniques (morphometric and growth model) represent useful tools to analyze better the growth performance of the Cortez oyster in culture.

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