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Research Article

Improving von Bertalanffy growth parameters and natural mortality estimates in *Brama australis* (Valenciennes, 1838) using larval hatch size

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ABSTRACT. Accurate von Bertalanffy growth parameters (VBGP) are critical for fisheries assessment, but they are often biased by the absence of juvenile data, leading to errors in their estimation and derived variables such as natural mortality (M). This study re-estimates the VBGP and M in *Brama australis*, a commercially important fish resource in Chile. To correct this, a larval hatch size (L_0) was incorporated as a fixed "biological anchor point" (BAP) to constrain the von Bertalanffy growth function and mitigate extrapolation errors in theoretical age at zero length (t_0). We re-estimated growth parameters from three previous studies using a phylogenetic proxy for L_0 (*Brama japonica*, 0.48 cm). The method consistently produced revised parameters across all studies, converging to a pooled average of L_∞ = 56.17 cm, k = 0.32 yr^{-1}, and t_0 = -0.03 years, indicating faster growth and a biologically plausible t_0 compared to original estimates. This correction directly resulted in a higher and more precise estimate of M, which increased to a narrowed range of 0.48-0.50 yr^{-1} from an original 0.39-0.47 yr^{-1}. The revised parameters showed a markedly improved fit to Beverton and Holt's life-history invariants, reducing the total absolute mean difference from theoretical values from 64 to 3.4%. Our results demonstrate that the methodology used generated more realistic growth models and robust M estimates, providing essential corrections for stock assessment models and management of this fishery.

Keywords: *Brama australis*; von Bertalanffy growth parameters; natural mortality; life-history invariants; stock assessment; fishery management

INTRODUCTION

Growth parameters describe how fast fish grow and reach maturity, directly influencing stock productivity estimates and sustainable harvest levels (Pauly 1980, Campana 2001). Accurate growth data are essential for reliable stock assessments, as they underpin key outputs such as spawning stock biomass and recruitment predictions (Quinn & Deriso 1999). Traditionally, these parameters, particularly the von Bertalanffy growth coefficient (k) and asymptotic length (L_∞), are also used to estimate natural mortality (M), another critical input for stock assessment models (Gislason et al. 2010, Then et al. 2015). However, biases in growth curves (e.g. due to missing juvenile size classes) can propagate errors into M, current stock status and future prediction trends under different management scenarios, risking overexploitation (Chen et al. 2000, Girdler et al.

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2010). One of the most persistent challenges in fitting von Bertalanffy growth parameters (VBGP) for fish species lies in accurately estimating the t_0 parameter, which represents the theoretical age at zero length. This issue arises primarily from the lack of small-sized individuals in sampling, leading to extrapolation errors that distort the growth trajectory (Taylor et al. 2005, Then et al. 2015). For short-lived or fast-growing species, such biases can significantly affect the estimation of other critical parameters (k and L_∞), ultimately compromising M calculations (Chen et al. 2000, Perreault & Cadigan 2021). To address this, López-Veiga (1979) proposed incorporating larval hatch size (L_0) as a biological anchor point (BAP), enabling more accurate estimation of t_0, k, and L_∞ by aligning the growth curve with empirical early-life stage data. In formal literature, examples using this approach remain limited; nevertheless, Canales & Leal (2009) demonstrated its utility in improving growth parameters and, consequently, enhancing M estimates in *Engraulis ringens*, a small pelagic fish. *Brama australis* is an epi and mesopelagic fish, known as "reineta" in Chile or southern ray's bream internationally, and has attracted the attention of fish biologists, stakeholders, and fisheries managers in Chile. It has become the main artisanal fishing resource off central Chile. Annual average landings have remained at 35,000 t since 2014, although in 2024 and 2025 they declined to approximately 27,000 t. (SERNAPESCA 2025).

Current unvalidated age estimates suggest that *B. australis* exhibits rapid growth and early maturation, with no significant differences in growth rates between sexes, and depending on the study, maximum ages in commercial catches between 8 and 12 years (Oyarzún et al. 2013, Arancibia et al. 2017, Moyano 2017). All these growth estimates are derived exclusively from studies conducted in Chilean waters and show marked variability across different studies. The primary operational challenge for researchers is that all historical samples are derived from commercial fisheries. Therefore, they lack small juvenile individuals under 20 cm due to gear selectivity or spatial segregation (Leal et al. *in press*). This data gap not only affects t_0 estimation but propagates uncertainty to other critical growth parameters k and L_∞ of species, as these values are interdependent in the von Bertalanffy model (Pilling et al. 2002). Thus, parameter uncertainty has challenged Chilean fisheries scientists in establishing reliable growth curves for *B. australis* stock assessment. Age estimates from the original studies (Oyarzún et al. 2013, Arancibia et al. 2017, Moyano 2017) were based on otolith readings and have not been formally validated through independent methods such as bomb radiocarbon or marginal increment analysis. The original authors acknowledged challenges in age determination for younger fish, which underscores the need for correction. Such compounded biases on VBGP values may lead to systematic errors in derived variables like M and stock productivity indices, ultimately undermining the reliability of management advice. The knowledge gap addressed by this study is twofold: first, previous growth models for *B. australis* have been developed without including of small-sized individuals (<20 cm), resulting in biased estimates of t_0 and potentially misleading values of M; second, the magnitude of this bias and its implications for life-history theory have not been systematically quantified. This study aims to re-estimate the VBGP (t_0, L_∞, k) for *B. australis* along the Chilean coast by incorporating larval hatch size (L_0) following the López-Veiga (1979) methodology. The goal is to mitigate biases caused by the underrepresentation of smaller individuals in sampling data and improve the estimation of M derived for stock assessment.

MATERIALS AND METHODS

von Bertalanffy growth parameters

To improve VBGP in *B. australis*, we compiled growth parameter estimates from different studies conducted in Chilean waters (Oyarzún et al. 2013, Arancibia et al. 2017, Moyano 2017). All original studies reported fork length (FL) in centimeters, and no conversions between length measurements were required. To address observed biases in t_0 estimation, we applied the methodology of López-Veiga (1979), which incorporates L_0 as a crucial BAP to improve growth curve fitting. Since empirical L_0 data for *B. australis* are currently unavailable, we utilized the reported hatch length of *Brama japonica*, L_0 = 0.48 cm (Moser 1996), as a phylogenetic proxy. *B. japonica* was selected as the proxy because it belongs to the same family (Bramidae) and shares a similar epi-mesopelagic ecology in the Pacific Ocean, with comparable adult size ranges and reproductive strategies (Mead 1972, Moser 1996, Leal et al. in press). While hatch size variability among Bramidae species has not been extensively documented, the close phylogenetic relationship and ecological similarity support its use as a reasonable first approximation. The standard von Bertalanffy growth function is expressed as:

$$L_t = L_\infty\left(1 - \mathrm{e}^{-k(t-t_0)}\right)$$

where L_t is the length at age t, L_∞ is the asymptotic length, k is the growth coefficient, and t_0 is the theoretical age at which the length is zero. To refine this model, three biologically meaningful points must be selected: L_0, the mean length at age from each study; L_1, the mean length at age t_1; and L_2, the mean length at age t_2. All re-estimation procedures were implemented in the R statistical computing environment (R Core Team 2023). The complete code is provided as supplementary material to ensure full reproducibility of the analysis. The re-estimation process followed these steps:

1) Calculation of anchor age points *(L_1* and *L_2):* for each original (orig) parameter set, we calculated the expected lengths at selected ages t_1 and t_2 using the original von Bertalanffy equation:

$$L_1 = L_{\infty\_orig} \times \left(e^{-k_{orig} \times (t_1 - t_{0\_orig})}\right)$$
$$L_2 = L_{\infty\_orig} \times \left(e^{-k_{orig} \times (t_2 - t_{0\_orig})}\right)$$

2) Definition of the objective function: the asymptotic length L_∞ re-estimated (L_{∞_reest}) is solved numerically using López-Veiga (1979) equation reformulated as an objective function to be minimized:

$$f\left(L_{\infty\_reest}\right) = \left[\left(\frac{L_{\infty\_reest} - L_0}{L_{\infty\_reest} - L_1}\right) - \left(\frac{L_{\infty\_reest} - L_0}{L_{\infty\_reest} - L_2}\right)^{\left(\frac{t_1}{n}\right)}\right]^2$$

where, n = t_2- t_1.

3) Numerical minimization: the one-dimensional minimization was performed using the "*optimize ()*" function in R. The search interval for L_{∞_reest} was defined as: interval = [max (L_1, L_2, L_0) × 1.01, 60 cm].

This lower bound ensures that L_{∞_reest} is greater than all observed lengths. In contrast, the upper bound of 60 cm was selected based on the maximum lengths reported in the original studies (56-60 cm), expanded by a reasonable margin to ensure the global optimum was captured.

4) Calculation of re-estimated parameters: once the optimal L_{∞_reest} was identified, the remaining parameters (k and t_0) were computed as:

$$k = \frac{1}{t_1} \ln\left(\frac{L_{\infty\_reest} - L_0}{L_{\infty\_reest} - L_1}\right)$$
$$t_0 = \frac{1}{k} \ln\left(1 - \frac{L_0}{L_{\infty\_reest}}\right)$$

5) Selection of age pairs***:*** the previous process should be repeated for each parameter set, with multiple age pairs (t_1 and t_2) to evaluate parameter robustness. The selection followed these criteria: t_1 varied from 1 to 6 years (representing early to intermediate ages), and t_2 varied from 7 to 12 years. A minimum separation of 4 years between the two selected ages was considered to capture sufficient growth information. Only age pairs that yielded numerical convergence of the objective function (i.e. where the objective function reached a minimum within the search interval) were retained for further evaluation. From the convergent solutions, the optimal age pair was selected based on the lowest global mean squared error (MSE).

6) Global MSE calculation: To compare the fit of different age pairs and ensure robustness, we calculated the global MSE between the original and re-estimated growth curves. This metric was computed by: generating a sequence of 100 ages from 0 to 15 years, calculating the predicted lengths from both the original and re-estimated equations at each age, and computing the MSE between the two curves.

The best re-estimated parameter sets derived from each original report were pooled to compute a single average value for L_∞, k, and t_0. To quantify the uncertainty of the re-estimated growth parameters, a nonparametric bootstrap approach was used (Efron & Tibshirani 1993). This method involved simulating 1,000 new datasets by resampling with replacement from the average re-estimated parameters, while adding a small amount (8%) of random noise to each replicate. A 95% confidence interval for the growth curve was then constructed from the resulting distribution of simulated curves.

Natural mortality (M)

M was estimated using the Natural Mortality Tool (Cope 2020), a web-based application that implements empirical estimators derived from meta-analyses of fish life-history traits. We applied the re-estimated growth parameters L_∞ and k as primary inputs, considering 12°C as the mean annual sea surface temperature for central Chile (SHOA 2024). To incorporate additional biological information to estimate M, the tool was configured to integrate other life history traits such as longevity and age at maturity ($t_{m50\%}$). Based on Chilean age reports, longevity was set at 12 years for *B. australis*. The $t_{m50\%}$ was derived by back-calculating from length at maturity ($L_{m50\%}$ = 37 cm) (Leal et al. 2017) using the original and re-estimated growth parameters in the inverse von Bertalanffy equation:

$$t_{m50\%} = t_0 - \frac{1}{k} \ln\left(1 - \frac{L_{m50\%}}{L_\infty}\right)$$

From the available methods within the tool, based on the foundational works of Pauly (1980), Jensen (1997), and Then et al. (2015), a subset of eight estimators was selected for final inference. The tool synthesizes the results from these individual estimators

to generate a weighted density distribution. The median of this composite distribution was adopted as the final robust estimate of M to mitigate the bias of any single method.

Beverton and Holt's invariant ratios (BHIR)

Finally, the life history parameters for *B. australis* estimated in this study were analyzed against BHIR. These ratios, which include $M \times t_{m50\%}$, M / k and $L_{m50\%} / L_\infty$, represent a form of symmetry in life history traits that is consistent across different species and populations (Jensen 1996). This comparison allowed us to evaluate the biological plausibility of our derived parameter set and contextualize our findings within a broader theoretical framework of fish population dynamics.

RESULTS

Re-estimation of growth parameters

The application of the López-Veiga (1979) methodology is exemplified by its use on the VBGP from Moyano (2017): $L_t = 56.91\ (1 - e^{-0.18(t+3.20)})$. This process yielded a range of revised parameter sets depending on the selected age pairs (t_1, t_2). The pair $t_1 = 6$ and $t_2 = 12$ years produced the most robust fit, indicated by the lowest global MSE value. The resulting best-fit growth equation was $L_t = 54.56\ (1 - e^{-0.31(t+0.03)})$. This re-estimation resulted in a lower L_∞, a substantially higher k, and a theoretical age at t_0 closer to zero compared to the original parameters (Table 1, Fig. 1).

For the other parameter sets (Oyarzún et al. 2013, Arancibia et al. 2017), the optimal age pairs were identified as $t_1 = 3$, $t_2 = 12$ and $t_1 = 5$, $t_2 = 9$ years, respectively. The re-estimated parameters for these studies did not differ significantly from the trends observed in the Moyano (2017) example, consistently showing a decrease in L_∞, an increase in k, and a correction of t_0 to values near zero (Table 2). The pooled average of the re-estimated parameters across all three studies was $L_\infty = 56.17$ cm, $k = 0.32$ yr^{-1}, and $t_0 = -0.03$ years.

Visual analysis revealed a clear convergence in the growth trajectories predicted by the three sets of re-estimated parameters, forming a distinct cluster that diverged from the original models, particularly for younger age classes (Fig. 2). However, the magnitude of the correction from the original curves varied among studies. The adjustment was most substantial for the datasets from Moyano (2017) and Arancibia et al. (2017), whose re-estimated curves exhibited a significant shift. In contrast, the original growth curve from Oyarzún et al. (2013) exhibited the smallest deviation from the cluster of re-estimated models, indicating a lesser degree of correction was required. The curve generated from the average re-estimated parameters ($L_t = 56.17\ (1 - e^{-0.32(t+0.03)})$) is also presented, providing a synthesized growth model for *B. australis*.

Natural mortality

Re-estimation of the growth parameters directly impacted derived life-history traits, particularly $t_{m50\%}$ and consequently M estimates. The age at maturity ($t_{m50\%}$) increased when calculated using the re-estimated parameters. This change arises from the mathematical relationship between k, L_∞, and $L_{m50\%}$ in the inverse von Bertalanffy equation; higher k values and adjusted L_∞ result in a different point along the growth trajectory where $L_{m50\%}$ is reached. Consequently, the M estimates, which are positively correlated with k, also increased and exhibited a more constrained range (0.48-0.50 yr^{-1}) compared to the original estimates (0.39-0.47 yr^{-1}) (Table 3). The convergence of these values to a narrow interval supports the calculation of a mean M = 0.48 yr^{-1}.

Beverton and Holt's invariant ratios

The re-estimated parameters produced BHIR that were consistently closer to their expected theoretical values ($M \times t_{m50\%} \sim 1.65$; $M/k \sim 1.50$; $L_{m50\%}/L_\infty \sim 0.66$) than those derived from the original parameters (Table 4). The total absolute difference from the theoretical invariants decreased from an average of 64% across the original parameter sets to just 3.4% for the re-estimated sets. The magnitude of this improvement varied among studies, with the most substantial change occurring for the parameters from Arancibia et al. (2017) (from 82 to 2% difference) and the least pronounced for Oyarzún et al. (2013) (from 27 to 14% difference).

DISCUSION

Accurate estimations of VBGP are fundamental in fisheries management, as they provide direct inputs for stock assessments and serve as the basis for deriving other essential parameters, such as M (Quinn & Deriso 1999, Punt et al. 2016). One ongoing challenge in estimating VBGP is the limited availability of young or old fish (Isely & Grabowski 2007, Thorson & Minto 2015). Various methods have been proposed to correct these biases, including length-at-age back-calculation (Francis 1990), combining observed age-length data with

Table 1. Example of growth parameter re-estimation for *B. australis* using the López-Veiga (1979) method. Applied to the original parameters from Moyano (2017) (L_∞ = 56.91 cm, k = 0.18 yr^{-1}, t_o = -3.20 years). The best-fit solution (lowest global mean squared error (MSE)) is highlighted in bold.

t_1	t_2	L_∞	k	t_0	Global MSE
1	10	60.0	0.69	-0.01	112.85
2	12	60.0	0.43	-0.02	69.92
3	7	60.0	0.34	-0.02	56.32
6	**12**	**54.56**	**0.31**	**-0.03**	**43.43**
Originals parameters		56.91	0.18	-3.20	NA

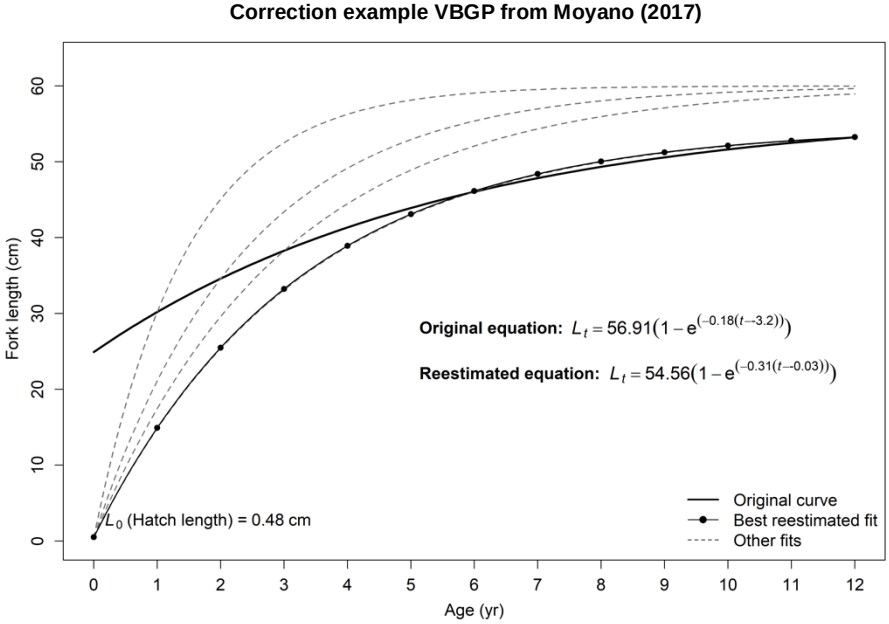

Figure 1. Re-estimation of von Bertalanffy growth parameters (VBGP) for *B. australis* from the original parameter set (Moyano 2017), using the López-Veiga (1979) method. The original curve (solid black line) shows a bias *to* = -3.20 years, while the best re-estimated fit (thin black line with closed dots; t_1 = 6, t_2 = 12 years) corrects t_o = -0.03 years. Grey dashed lines represent alternative age-pair combinations evaluated.

back-calculated lengths (Moyano et al. 2018), and constraining model fits by fixing L_∞ or t_0 parameters (Pardo et al. 2013). More recently, Bayesian approaches incorporating prior knowledge have been implemented to produce combined estimates from previous information and available data (Siegfried & Sansó 2006, Smart & Grammar 2021, Neves et al. 2022).

Our research shows that sampling bias has significantly distorted previous growth models for *B. australis*. By introducing a fixed biological reference point, the L_0, and following the approach of López-Veiga (1979), we corrected these biases, yielding a more biologically coherent growth model and a robust estimate of M.

Throughout the re-estimation process, we consistently found a set of revised parameters that converged across all three original studies. The larger corrections were for the datasets of Moyano (2017) and Arancibia et al. (2017), who previously reported t_0 values of -3.20 and -2.50 years, respectively, suggesting a biased description of growth at the early stage of the curve. Updated estimates settled around a pooled average of L_∞ = 56.17 cm, k = 0.32 yr^{-1}, and t_0 = -0.03 years. The substantial standard deviation around t_0 (standard deviation = 0.45), however, indicates considerable uncertainty in estimating the theoretical age at zero length. This variability likely reflects either biological differences in early life growth or methodological challenges in age determination for the youngest

Table 2. Summary of original and re-estimated von Bertalanffy growth parameters for *B. australis* from three independent studies. The average of the re-estimated parameters is provided, with standard deviation (sd) values given in parentheses.

Study	Size range (cm)	L_∞ (cm)		k (yr^{-1})		t_0 (years)	
		Original	Re-estimated	Original	Re-estimated	Original	Re-estimated
Oyarzun et al. (2013)	20 - 58	58.95	58.40	0.28	0.32	-0.37	-0.03
Moyano (2017)	25 - 58	56.90	54.56	0.18	0.31	-3.19	-0.03
Arancibia et al. (2017)	25 - 55	59.55	55.56	0.19	0.33	-2.50	-0.03
Average (sd)	—	58.47	56.17 (3.82)	0.22	0.32 (0.089)	-2.02	-0.03 (0.45)

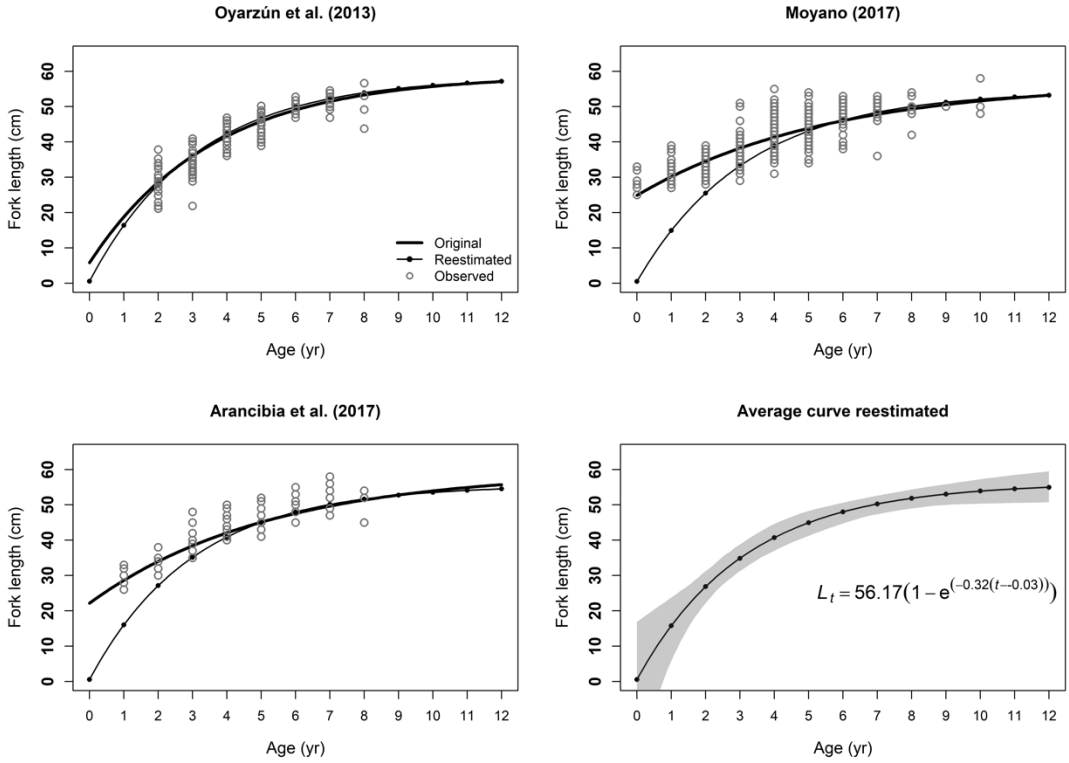

Figure 2. Comparison of original (solid black line) and best re-estimated (thin black line with closed dots) von Bertalanffy growth curves for *B. australis* from three studies: Oyarzún et al. (2013), Moyano (2017), and Arancibia et al. (2017). Observed data from the original studies are shown as grey open circles. The bottom-right panel displays the average re-estimated curve, with the shaded grey area representing the 95% confidence interval.

fish, suggesting this parameter should be interpreted with some caution.

Nevertheless, the adjustment to a t_0 value close to zero not only makes biological sense, aligning with the known hatch size (Moser 1996), but also adheres to the principle of parsimony in model fitting, steering clear of unnecessary extrapolation (Pilling et al. 2002). The increase in k indicates a quicker growth rate towards L_∞, which is a typical correction when early-life growth is accurately considered (Allen & Hightower 2010, Then et al. 2015). The slight adjustment needed for the Oyarzún et al. (2013) parameters, which already had a less biased t_0, further supports the method, showing that the López-Veiga (1979) approach effectively tailors the degree of correction to the initial level of bias.

The correction of VBGP had a direct and substantial impact on derived life-history traits such as $t_{m50\%}$ and consequently on M estimations. This recalculation is critical for estimating spawning stock biomass and understanding a stock's reproductive resilience (Hordyk et al. 2015a). M increased from an original wider range of 0.39-0.47 yr^{-1} to a narrowed range of 0.48-0.50 yr^{-1}. This higher and more precise M estimate suggests a faster biomass replacement rate for *B. australis* than

Table 3. Comparison of original and re-estimated age at maturity ($t_{m50\%}$) and natural mortality (M) for *B. australis* across three independent studies off Chile, including the relative changes (%). The average values for the re-estimated parameters are provided. Change (%) represents the relative shifting percentage after applying the López-Veiga (1979) methodology to re-estimate von Bertalanffy growth parameters.

Study	Age at maturity ($t_{m50\%}$)			Natural mortality (M yr^{-1})		
	Original	Re-estimated	Change (%)	Original	Re-estimated	Change (%)
Oyarzun et al. (2013)	3.16	3.14	-0.6	0.47	0.5	6.4
Moyano (2017)	2.65	3.66	38.1	0.39	0.48	23.1
Arancibia et al. (2017)	2.66	3.28	23.3	0.4	0.5	25
Average	2.82	3.34	18.4	0.42	0.48	14.3

Table 4. Beverton and Holt life-history invariant ratios calculated from original and re-estimated parameters. Theoretical expected values are $M \times t_{m50\%} = 1.65$, $M/k = 1.50$, and $L_{m50\%}/L_\infty = 0.66$. The percentage difference from the theoretical value for each ratio is shown in parentheses. The total absolute difference summarizes the overall improvement.

Study		Beverton and Holt's invariant ratios			Total difference
		$M \times t_{m50\%}$	M/k	$L_{m50\%}/L_\infty$	
Oyarzún et al. (2013)	Originals	1.48 (-10%)	1.68 (12%)	0.63 (-5%)	27%
	Re-estimated	1.57 (-5%)	1.58 (5%)	0.63 (-4%)	14%
Moyano (2017)	Originals	1.03 (-37%)	2.17 (44%)	0.65 (-1%)	83%
	Re-estimated	1.76 (6%)	1.56 (4%)	0.68 (3%)	13%
Arancibia et al. (2017)	Originals	1.06 (-35%)	2.11 (40%)	0.62 (-6%)	82%
	Re-estimated	1.64 (-0.7%)	1.51 (0.4%)	0.67 (0.9%)	2%
Average	Originals	1.19 (-28%)	1.99 (32%)	0.63 (-4%)	64%
	Re-estimated	1.66 (0.4%)	1.55 (3%)	0.66 (0%)	3.4%

previously assumed. Underestimating M is a known shortcoming in stock assessment that creates a risk of cryptic depletion, where a stock can be overfished without a corresponding sharp decline in catch rates due to high, unaccounted mortality (Hordyk et al. 2015b, Perreault & Cadigan 2021). The use of a multi-model estimator tool (Cope 2020) synthesizes information from various empirical relationships, providing a robust estimate that is less vulnerable to the limitations of any single method.

The most compelling validation of our re-estimated parameters is their strong alignment with BHIR (Beverton & Holt 1959, Jensen 1996). These BHIR represent evolutionary trade-offs that are conserved across diverse teleost taxa. The original parameters for some studies deviated sharply from these theoretical values, indicating biologically implausible life-history traits. When parameters were recalculated, they produced invariant ratios that were consistently closer to their expected values, reducing the total average difference from 64% to just 3.4%. This improvement demonstrates that incorporating L_0 rectifies the internal inconsistencies in the growth model, yielding a parameter set that describes coherent life-history attributes for *B. australis*. This finding aligns with Pilling et al. (2002) and Batts et al. (2019), who demonstrated that models incorporating early-life data produce more reliable and theoretically consistent parameter estimates, particularly when late-life data are limited or biased.

However, it is important to distinguish that while the revised parameters are demonstrably more internally consistent with selected evolutionary life-history relationships, this consistency does not automatically guarantee absolute accuracy in empirical biological reality. Moreover, several limitations of this study should be acknowledged. First, using L_0 from *B. japonica* as a proxy for *B. australis*, while justified by phylogenetic and ecological similarity, introduces uncertainty. Hatch size can vary within families due to maternal effects, temperature, and other environmental factors (Moser 1996). Direct measurement of *B. australis* larvae would provide the most accurate anchor point and should be a priority for future research. Second, our approach relies on previously published growth parameters rather than raw length-at-age data; this introduces dependence on the original authors' age determinations and sample representativeness. Third, the validation of the revised

parameters is indirect, based on conformity with theoretical life-history invariants rather than independent growth data (e.g. mark-recapture or controlled rearing). While the BHIR approach is widely accepted for evaluating biological plausibility, it does not constitute absolute validation. Finally, the bootstrap confidence intervals assume that the original parameter estimates are independent and identically distributed, which may not fully capture the underlying uncertainty structure.

Despite the methodological limitations inherent in our approach, the López-Veiga (1979) method effectively mitigates biases in growth models derived from length-at-age data lacking small juveniles, a common issue in fisheries-dependent sampling (Thorson & Minto 2015). We provide a robust, revised set of VBGP for *B. australis* that is biologically consistent with life-history theory and critical for accurate stock assessment. The subsequent increase in the M estimate underscores the profound implications of growth model misspecification. Future assessments for this important Chilean fishery resource should consider these revised parameters and evaluate their performance in stock assessment models, potentially using management strategy evaluation to test their robustness.

Credit author contribution

E. Leal: conceptualization, validation, methodology, R code development, formal analysis and writing-original draft; G. Moyano: writing, review and editing; C. Gatica: R code development, review and editing; P. Gálvez: review and editing. All authors have read and accepted the published version of the manuscript.

Conflict of interest

The authors declare that they have no known conflict of interest or personal relationships that could have influenced the work reported in this manuscript.

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Data availability

The data supporting this study are not publicly available due to the absence of a dedicated repository at the time of research conducted. However, the data and complete code could be provided as supplementary material to ensure full reproducibility of the analysis from the corresponding author upon reasonable request.

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