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RESEARCH ARTICLE

Why we cannot always expect life history strategies to directly inform on sensitivity to environmental change

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Abstract

- 1. Variation in life history traits in animals and plants can often be structured along major axes of life history strategies. The position of a species along these axes can inform on their sensitivity to environmental change. For example, species with slow life histories are found to be less sensitive in their long-term population responses to environmental change than species with fast life histories.
- 2. This provides a tantalizing link between sets of traits and population responses to change, contained in a highly generalizable theoretical framework.
- 3. Life history strategies are assumed to reflect the outcome of life history tradeoffs that, by their very nature, act at the individual level. Examples include the tradeoff between current and future reproductive success, and allocating energy into growth versus reproduction. But the importance of such tradeoffs in structuring population-level responses to environmental change remains understudied.
- 4. We aim to increase our understanding of the link between individual-level life history tradeoffs and the structuring of life history strategies across species, as well as the underlying links to population responses to environmental change.
- 5. We find that the classical association between lifehistory strategies and population responses to environmental change breaks down when accounting for individual-level tradeoffs and energy allocation.
- 6. Therefore, projecting population responses to environmental change should not be inferred based only on a limited set of species traits.
- 7. We summarize our perspective and a way forward in a conceptual framework.

KEYWORDS

dynamic energy budget, fast-slow continuum, functional traits, integral projection model, reproductive strategies

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1 | INTRODUCTION

The wide diversity in life history traits observed across plant and animal species can be summarised by two main axes reflecting different strategies in speed of life and reproduction (Capdevila et al., 2020; Gaillard et al., 1989; Salguero-Gómez, Jones, Jongejans, et al., 2016). This is typically reflected by the ranking of fast-growing, short-lived species with high fecundity at one extreme of the speed of life axis (also referred to as the fast-slow continuum) and slow-growing, longlived species with low fecundity at the other (in the next paragraph, we discuss in more detail the processes that shape these life history strategies). Similarly, highly semelparous species with a single reproductive event in their lifespan and high mortality are ranked at one extreme of the reproductive strategy axis, and iteroparous species with high spread in reproduction and low mortality on the other (Healy et al., 2019). When looking at only a particular group of living beings, the nature of the second axis might be variable depending on the traits considered, for example in mammals the second axis can relate to development rather than reproduction (Stearns, 1983). Early demographic modelling studies predicted that the long-term population responses of plant and animal species with slow life histories are buffered against increasing environmental variation (Morris et al., 2008) because the long-lasting adult stage typical of slower life histories allows these populations to better tolerate changes in the year-to-year variation expected under increasing environmental variation than faster ones. The degree of environmental variation is a useful proxy in demographic models to assess the potential impacts of climate change on populations (Stireman et al., 2005); where certain regions are expected to experience higher variability in climatic conditions, and others less (Lewis & King, 2017; van der Wiel & Bintanja, 2021). However, predictions from more recent demographic analyses regarding the sensitivity of faster versus slower populations to increasing environmental variation are inconclusive. When the vital rates of growth and reproduction are described more mechanistically using the trade-off between growth and reproduction, populations of species with fast life-histories are less sensitive in their long-term populations responses (Smallegange et al., 2020; Smallegange & Berg, 2019), and when vital rates are described phenomenologically, based on random variation of statistical averages, populations of species with slow life-histories are less sensitive in their long-term population responses to environmental variation (Paniw et al., 2018). Furthermore, the timescale considered matters. Populations of species with slow life histories have been found to be more sensitive in their short-term responses to disturbances than populations of species with fast life histories (Gamelon et al., 2014), and to be generally more sensitive to increases in mortality (Lebreton, 2006, 2011). These contrasting findings highlight the need to improve our mechanistic understanding of how the structuring of life history variation and population responses to environmental variation link together.

The historical foundation of the speed of life axis, also referred to as the fast-slow continuum, is based on the concept of life history trade-offs (Gaillard et al., 2016). Empirical studies using traits

measured at the population or species level find that there are general trade-offs underlying the structuring life history variation. A range of vertebrate-specific studies showed that underlying the speed of life axis is a trade-off in the value of traits related to reproduction and survival (reviewed in table 1 in Gaillard et al., 2016). Here, species range from high adult survival and low fecundity on one extreme of the speed of life axis, and low adult survival and high fecundity on the other. The existence of a speed of life axis was also found to depend on the selection of traits included and confounding factors accounted for (Jeschke & Kokko, 2009); with body size and phylogenetic relatedness considered the most important confounding factors. Many recent studies structured life history variation across vertebrates, invertebrates and plant species, in both terrestrial and aquatic systems. These studies still find speed of life as the primary axis of life history variation (Capdevila et al., 2020; Healy et al., 2019; Paniw et al., 2018). However, both fecundity and survival, important components of the speed of life axis in previous vertebrate-specific studies, are no longer consistently loaded on the main axis of life history variation. This means that the life history trade-offs inferred from the structuring of traits can also be slightly different. However, structuring population or species-level traits does not represent the only way to account for life history trade-offs.

Life history trade-offs reflected by species or population traits are shaped by limitations in energy allocation that fundamentally operate at the level of the individual organism (Cody, 1966; Stearns, 1989). Organisms have a limited amount of time or energy available and therefore allocating more energy to one biological function, such as growth, will leave less energy available to allocate to other functions (Gaillard et al., 2016). Primary examples are the life history trade-off in energy allocation between growth and reproduction (Gadgil & Bossert, 1970; Reznick, 1983), and between allocating energy to current versus future reproduction (Williams, 1966a, 1966b). Accounting for energy allocation processes at the individual organismal level is important as it allows for emergent differences in dynamics between populations or species even if they have similar traits. Such emergent differences, for example, might help explain the different life history strategies that may be observed between populations of the same species (Gamelon et al., 2021; Nilsen et al., 2009). It also ensures that the law of energy conservation is not violated, and therefore prevents the creation of 'free' biomass in model projections. This is important as it limits any extrapolation biases that might otherwise occur when projecting population responses based on life history strategies. Extending previous studies of life history variation by explicitly accounting for energy allocation at the individual organismal level might therefore lead to new insights on the links between life history trade-offs, traits, strategies, and population responses to environmental variation.

In this study, we aim to assess if life history trade-offs in energy allocation link to the structuring of life history strategies and how they inform on population responses to environmental change. To this end, we parameterised dynamic energy budget integral projections models (DEB-IPMs) (Smallegange et al., 2017)

for 34 species of ray-finned fish Actinopterygii. We choose rayfinned fish as our biological model system as they represent the most numerous group of vertebrates (Near et al., 2012) and display a particularly wide range of life history strategies also found in other species groups (Beukhof et al., 2019), that can also be found in other animal groups. In DEB-IPMs, the demographic rates of growth and reproduction are based on an individual-level trade-off between energy allocation into growth versus reproduction (Kooijman & Metz, 1984). Additionally, we extended these DEB-IPMs by incorporating skip and obligate breeding decisions at the individual level across semelparous and iteroparous species. These decisions represented the individual-level trade-off between allocating energy in current versus future reproduction. We used the parameterised DEB-IPMs to answer (i) how life history traits structure into life history strategies when applying a demographic modelling approach explicitly accounting for energy allocation trade-offs at the individual level, and (ii) if individuallevel life history trade-offs align with the patterning of traits along the life history strategy axes when using this approach. These two questions help elucidate the links between life history tradeoffs in energy allocation operating at the individual organismal level, population-level traits, and life history strategies across populations of different species. We then tested if (iii) population sensitivity to environmental variation covaries with either of the primary life history strategy axes, and also if (iv) population sensitivity to environmental variation covaries with individual life history traits. Finally, we used a perturbation analysis to assess (v) if trait importance might shift over the gradient of environmental variation. Together, these results help improve our understanding of how life history trade-offs, traits, and strategies, link together to shape population responses to environmental variation.

2 | MATERIALS AND METHODS

2.1 | Brief summary of the DEB-IPM

A DEB-IPM is a population model that tracks the survival, growth, and reproduction of cohorts of individuals in a population (Smallegange et al., 2017). The individuals in the population are exposed to environmental variation, affecting their feeding level, and, consequently, the energy available for individual growth and reproduction. Individuals within a certain cohort are exposed to the same sequence of environmental conditions over time, but do not necessarily experience the exact same feeding level at each time step; with some individuals being slightly more successful in gathering resources than others given a certain environment. This means that the life history trajectory of each individual in the model is unique. The individual-level life history functions used to model growth, reproduction and survival in the DEB-IPM are parametrised using a set of life history traits derived from demographic studies at the population level. The individual-level life history functions are then integrated over discrete time and a

continuous size distribution, to yield population-level outcomes, such as projections of population size and population growth rates. The population-level outcomes of the DEB-IPM are therefore an emergent property of individual-level processes and trade-offs. We use a selection of 34 ray-finned fish species as model organisms in the DEB-IPM. These species were selected because their life histories have been studied in particular detail and together they represent the full range of life history strategies observed in this species group (McBride et al., 2015). As many important life history processes such as growth, maturation, reproduction, and survival in ray-finned fish are dependent on body size, rather than age (Kozłowski, 1996; Peters, 1986; Stige et al., 2019), we express the individual level life history functions in our DEB-IPM as a function of individual body size.

2.2 | Brief summary of environmental variation

We model environmental variation over time by exposing individuals in the population to a temporal sequence of good and bad environments. This translates into individuals experiencing high $E(Y)_{high}$ or low $E(Y)_{low}$ feeding levels, with individual variation in feeding level $\sigma(Y)$. Feeding level is a relative measure that captures the level of satiation of an organism from empty (feeding level = 0) to completely satiated (feeding level=1). The ordering of the temporal sequence of environments experienced by individuals is determined by the level of environmental autocorrelation (ρ). We use environmental autocorrelation to express environmental variability because realworld environmental variation often shows temporal autocorrelation (Garca-Carreras & Reuman, 2011; Inchausti & Halley, 2002; Ruokolainen et al., 2009). Specifically, ρ expresses the level of correlation between the environments experienced at subsequent time steps. Positive values $(0 > \rho > 1)$ mean environmental conditions at the next time step are likely to be similar to those experienced at the current time step. Negative values ($-1 < \rho < 0$) mean that environmental conditions at the next time step are more likely to be different from those experienced at the current time step. We examine population responses over the entire gradient of $-1 < \rho < 1$, thus exposing populations to a gradient from highly variable to highly invariable environments.

2.3 | Individual level life history functions

Individual life history trajectories are captured in the DEB-IPM by four fundamental functions: (1) The growth function G(L(t)) describes the probability that an individual grows from length L at time t to L' at t+1, conditional on survival. (2) The survival function S(L(t)) denotes the probability that an individual survives from time t to t+1 given that it is of length L. (3) The reproduction function R(L(t)) describes the number of offspring produced from time t to t+1 by a female of length L at time t. (4) The parent-offspring function D(L',L(t)) denotes the probability that a female of length

L at time t produces offspring of length L' at t+1, conditional on reproduction. We adjusted the reproduction and survival functions to approximate the individual-level trade-off of allocating energy into current versus future reproduction for the different types of breeders that occur in our dataset: Iteroparous obligate breeders, which have multiple reproductive events over their life cycle and reproduce every season irrespective of environmental conditions. Iteroparous skip breeders that also have multiple reproductive events over their life cycle, but pass up on the opportunity to breed in bad environments. Finally, semelparous skip breeders that have a single reproductive event in their life cycle followed by death, and pass up on the opportunity to breed in bad environments.

2.3.1 | Growth function

Body growth of fish is typically indeterminate and food supply driven (Sebens, 1987), following a von Bertalanffy growth curve:

$$G(L', L(t)) = \frac{1}{\sqrt{2\pi\sigma_L^2(L(t+1))}} e^{\frac{-(L'-E(L(t+1)))^2}{2\sigma_L^2(L(t+1))}}$$
(1)

where E(L(t + 1)) is the expected growth of individuals of length L:

$$E(L(t+1)) = \begin{cases} L(t)e^{-r_B} + (1 - e^{-r_B})L_m E(Y), & \text{if } L \le L_m E(Y), \\ 0, & \text{otherwise} \end{cases}$$
 (2)

with r_B as the von Bertalanffy growth coefficient (dimensionless), L_m as the maximum length, E(Y) as the expected feeding level, scaled between zero and one, and σ_L^2 the individual variance in length at t+1.

$$\sigma^{2}(L(t+1)) = \begin{cases} (1 - e^{-r_{B}}) L_{m} \sigma^{2}(Y), & \text{if } L \leq L_{m} E(Y), \\ 0, & \text{otherwise} \end{cases}$$
(3)

where $\sigma(Y)$ is the standard deviation of the expected feeding level between individuals.

2.3.2 | Survival function

The survival of individual fish is generally size-dependent, especially in the early life stages, with a decrease in predation mortality for increasing body sizes (Stige et al., 2019). Size-dependent survival is modelled using an exponential function. In iteroparous obligate and iteroparous skip breeders it takes the form:

$$S(L(t)) = \begin{cases} e^{-\left(\mu_{p} \frac{L_{m}}{L(t)}\right)}, & \text{if } L \leq \frac{L_{m}E(Y)}{k}, \\ 0, & \text{otherwise} \end{cases}$$
 (4)

where μ_p is the adult background mortality rate due to predation, and k denotes the fraction of assimilated energy allocated to metabolic maintenance and growth, following the Kooijman-Metz model (Kooijman & Metz, 1984). Semelparous skip breeders have two additional conditional statements on this survival function, which ensures they die after having reproduced.

$$S(L(t)) = \begin{cases} e^{-\left(\mu_{p}\frac{L_{m}}{L(t)}\right)}, & \text{if } L \leq L_{p} \& L \leq \frac{L_{m}E(Y)}{\kappa}, \\ e^{-\left(\mu_{p}\frac{L_{m}}{L(t)}\right)}, & \text{if } L > L_{p} \& L \leq \frac{L_{m}E(Y)}{\kappa} \& E(Y)_{t-1} = E(Y)_{low}, \\ 0, & \text{if } L > L_{p} \& L \leq \frac{L_{m}E(Y)}{\kappa} \& E(Y)_{t-1} = E(Y)_{high}, \\ 0, & \text{otherwise} \end{cases}$$
 (5)

with $E(Y)_{low}$ as the low expected feeding level, $E(Y)_{high}$ as the high expected feeding level, and L_n is the size at maturation.

2.3.3 | Reproduction function

Following the Kooijman-Metz model (Kooijman & Metz, 1984), we assume a quadratic scaling of reproductive output with female body size. In iteroparous obligate breeders, the reproduction function takes the form:

$$R(L(t)) = \begin{cases} 0, & \text{if } L_b < L < L_p, \\ \phi \left(E(Y) R_m \frac{L(t)^2}{L_m^2} \right), & \text{if } L_p < L < L_m E(Y), \\ \phi \left(\frac{R_m}{1 - k} \left[E(Y) L(t)^2 - \frac{k L(t)^3}{L_m} \right] \right), & \text{if } L_m < L \le \frac{L_m E(Y)}{k}, \end{cases}$$
(6)

where ϕ is the survival during the egg and larval phase, R_m is the maximum reproduction in number of eggs of an individual of maximum size L_m and L_b is the size at birth. Iteroparous and semelparous skip breeders pass up on the opportunity to breed in bad environments. This imposes an additional restriction on the fundamental reproductive function as compared to iteroparous obligate breeders:

$$R(L(t)) = \begin{cases} 0, & \text{if } L_b < L < L_p, \\ 0, & \text{if } L_p < L < L_m E(Y) \& E(Y) = E(Y)_{low}, \\ \phi \left(E(Y) R_m \frac{L(t)^2}{L_m^2} \right), & \text{if } L_p < L < L_m E(Y) \& E(Y) = E(Y)_{high}, \\ \phi \left(\frac{R_m}{1-k} \left[E(Y) L(t)^2 - \frac{kL(t)^3}{L_m} \right] \right), & \text{if } L_m < L \le \frac{L_m E(Y)}{k}, \end{cases}$$
 (7)

2.3.4 | Parent-offspring association function

The parent-offspring association function describes the probability that the offspring of an individual of length L is of length L' at t+1.

$$D(L', L(t)) = \begin{cases} 0, & \text{if } L_b < L < L_p, \\ \frac{1}{\sqrt{2\pi\sigma_{L_b}^2(L(t))}} e^{\frac{-(L' - E_{L_b}(L(t))}{2\sigma_{L_b}^2(L(t))}}, & \text{otherwise} \end{cases}$$
(8)

TABLE 1 Species life history trait table including references for the parametrization of the DEB-IPM models. Parameter values were obtained from published studies and the references are listed in parentheses behind the trait values. Units are listed in the top row. L_b = larval transformation length, $\sigma(L_b)$ = variation in transformation length, R_m = maximum number of eggs produced by adult of maximum $length \ L_m \ \phi = fraction \ egg \ and \ larval \ survival, \ r_B = von \ Bertalanffy \ growth \ coefficient \ (dimensionless), \ L_p = maturation \ length, \ L_m = maximum$ length and μ_n = Natural mortality rate.

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8. Dicentrarchus labrax 17.0 (Nunk & Nielsen, 2005) 0.225 id 520,228 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993 9. Engraulis engrasicolus 14.5 (Morote et al., 2010) 1.867 id 226,500 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993 10. Engraulis in produx 35.0 (Hunter, 1977; O'Connell, 1981) 0.536 id 21,006 (Froese & Pauly, 2002) 0.002 (Houde & Zastrow, 1993 13. Gadus morhua 20.0 (Fahay, 2007) 1.392 id 5,000,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993 14. Gasterosteus aculeatus 15.0 (Fahay, 2007) 2.000 id 470 (Froese & Pauly, 2002) 0.018 (Houde & Zastrow, 1993 15. Cillichtlys mirabilis 15.0 (Moser, 1996) 1.000 id 27,000 (Moser, 1996; Shanks & 0.013 (Brothers, 1975) Eckert, 2005) 16. Lepomis gibbosus 15.0 (Auer, 1982) 2.100 id 27,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993 17. Melanogrammus aeglefinus 20.0 (Fahay, 2007) 3.417 id 223 (Froese & Pauly, 2002) 0.113 (Glesson & Bengton, 1993 18. Menidia beryllina 24.0 (Fahay, 2007) 3.417 id 223 (Froese & Pauly, 2002) 0.113 (Glesson & Bengton, 1993 19. Micropterus salmoides 40.0 (Heidinger, 1976) 6.167 id 82,000 (Kelley, 1962) 0.016 (Houde & Zastrow, 1993 20. Oryzias latipes 15.5 (Iwamatsu, 2004) 1.950 id 141 (Leaf et al., 2011) 0.033 (Houde, 1994; Lee et al., 2014) 1.950 id 141 (Leaf et al., 2011) 0.033 (Houde, 1994; Lee et al., 2014) 1.950 id 141 (Leaf et al., 2017) 0.007 (Houde & Zastrow, 1993 22. Pleuronectes platessa 14.0 (Houde & Zastrow, 1993) 0.667 id 552,000 (Pecuchet et al., 2017) 0.007 (Houde & Zastrow, 1993 23. Pennoxis annularis 16.0 (Auer, 1982) 1.233 id 325,677 (Morgan, 1954) 0.002 (Houde & Zastrow, 1993 24. Pseudopleuronectes annularis 14.0 (Chauge, 1994; Pseudopleuronectes annularis 14.0 (Chauge, 1994; Pseudopleuronectes annularis 14.0 (Chauge, 1994; Pseudopleuronectes annularis 14.0 (Chauge, 1994) 1.950 id 190,000 (Lappalainen et al., 2001) 0.013 (Houde & Zastrow, 1993 25. Salmo trutta 28.0 (Réalis-Doyelle et al., 2016) 0.132 id 10,000 (Lappalainen et al., 2008) 0.013 (Houde & Zastrow, 199	6. Clupea harengus	41.0 (Munk & Nielsen, 2005)	0.600 id	141,075 (Froese & Pauly, 2002)	0.001 (Houde & Zastrow, 1993)				
9. Engraulis engrasicolus 14.5 (Morote et al., 2010) 1.867 id 226,500 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 10. Engraulis ipponicus 40.0 (Takahashi & Watanabe, 2004; 6.167 id 160,000 (Jung et al., 2008) 2. O.001 (Houde & Zastrow, 1993) 13. Gadus morhua 2. O.0 (Fahay, 2007) 1. 972 id 2. Sp00,000 (Froese & Pauly, 2002) 2. O.001 (Houde & Zastrow, 1993) 14. Gasterosteus aculeatus 15.0 (Fahay, 2007) 2. 0.001 id 470 (Froese & Pauly, 2002) 0. 0.139 (Kraak et al., 1997; Swarup, 1958) 15. Gillichthys mirabilis 15.0 (Moser, 1996) 16. Lepomis gibbosus 15.0 (Auer, 1982) 17. Melanogrammus aeglefinus 15.0 (Auer, 1982) 17. Melanogrammus aeglefinus 18. Menidia beryllina 19. Micropterus salmoides 19. O.00 (Fahay, 2007) 19. Micropterus salmoides 19. O.00 (Fahay, 2007) 19. Micropterus salmoides 19. O.00 (Houde & Zastrow, 1993) 19. Micropterus salmoides 10. O.00 (Heluet, 1962) 10. O.07 (Rolley, 1962) 10. O.07 (Houde & Zastrow, 1993) 10. Oryzios latipes 15. 5 (Iwamatsu, 2004) 19. 50 id 141 (Leaf et al., 2011) 10. O.03 (Houde & Zastrow, 1993) 10. Oryzios latipes 15. 5 (Iwamatsu, 2004) 10. 1950 id 157,594 (Brazo et al., 1975) 10. O.007 (Houde & Zastrow, 1993) 10. Oryzios latipus 10. Oloue & Zastrow, 1993) 10. Oryzios latipus 10. Oloue & Zastrow, 1993 10. Oryzios & Pauly, 2002) 10. Oloue & Zastrow, 199	7. Danio rerio	14.0 (Singleman & Holtzman, 2014)	1.667 id	500 (Riehl & Baensch, 1973)	0.033 (Houde, 1994; Wilson, 2012)				
10. Engraulis japonicus	8. Dicentrarchus labrax	17.0 (Munk & Nielsen, 2005)	0.225 id	520,228 (Froese & Pauly, 2002)	0.001 (Houde & Zastrow, 1993)				
11. Engraulis mordax 35.0 (Hunter, 1977, O'Connell, 1981) 0.536 id 21,006 (Froese & Pauly, 2002) 0.002 (Houde & Zastrow, 1993 13. Gadus morhua 20.0 (Fahay, 2007) 1.392 id 5,900,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993 Wiedmann et al., 2014) 14. Gasterosteus aculeatus 15.0 (Fahay, 2007) 2.000 id 470 (Froese & Pauly, 2002) 0.139 (Kraak et al., 1997; Swarup, 1958) 15. Gillichthys mirabilis 15.0 (Moser, 1996) 1.000 id 27,000 (Moser, 1996; Shanks & Carlos and Eckert, 2005) 16. Lepomis gibbosus 15.0 (Auer, 1982) 2.100 id 5000 (Carbine, 1939; Scott & Crossman, 1973) 17. Melanogrammus aeglefinus 20.0 (Fahay, 2007) 1.392 id 5000 (Carbine, 1939; Scott & Crossman, 1973) 18. Menidia beryllina 24.0 (Fahay, 2007) 3.417 id 223 (Froese & Pauly, 2002) 0.011 (Houde & Zastrow, 1993 18. Menidia beryllina 24.0 (Fahay, 2007) 3.417 id 223 (Froese & Pauly, 2002) 0.113 (Gleason & Bengtson, 1994; Lee et al., 2014) 1.950 id 141 (Leaf et al., 2011) 0.033 (Houde, 1994; Lee et al., 2014) 1.950 id 141 (Leaf et al., 2011) 0.033 (Houde, 1994; Lee et al., 2014) 1.950 id 15.5 (Houde & Zastrow, 1993 22. Pleuronectes platessa 14.0 (Houde & Zastrow, 1993) 0.667 id 552,000 (Pecuchet et al., 2017) 0.007 (Houde & Zastrow, 1993) 23. Pomoxis annularis 16.0 (Auer, 1982) 1.233 id 325,677 (Morgan, 1954) 0.002 (Houde & Zastrow, 1993) 24. Pseudopleuronectes 13.0 (Fahay, 2007) 0.177 id 648,836 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993) 25. Salmo trutta 28.0 (Réalis-Doyelle et al., 2016) 0.203 id 10.0794 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993) 29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.013 (Houde & Zastrow, 1993) 29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.013 (Houde & Zastrow, 1993) 29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.013 (Houde & Zastrow, 1993) 29. Sanderinus alpinus	9. Engraulis engrasicolus	14.5 (Morote et al., 2010)	1.867 id	226,500 (Froese & Pauly, 2002)	0.001 (Houde & Zastrow, 1993)				
13. Gadus morhua 20.0 (Fahay, 2007) 1.392 id 5,900,000 (Froese & Pauly, 2002; Wiedmann et al., 2014) 2.001 (Houde & Zastrow, 1993) 2.001 id 470 (Froese & Pauly, 2002) 2.0139 (Kraak et al., 1997; Swarup, 1958) 2.5 (Gillichthys mirabilis 2.5 (Moser, 1996) 1.000 id 27,000 (Moser, 1996; Shanks & Chekert, 2005) 2.000 (Houde & Zastrow, 1993) 2.5 (Gillichthys mirabilis 2.00 (Fahay, 2007) 2.100 id 5000 (Carbine, 1939; Scott & Crossman, 1973) 2.5 (Corosman, 1973) 2.5 (Corosma	10. Engraulis japonicus		6.167 id	160,000 (Jung et al., 2008)	0.001 (Houde & Zastrow, 1993)				
Wiedmann et al., 2014	11. Engraulis mordax	35.0 (Hunter, 1977; O'Connell, 1981)	0.536 id	21,006 (Froese & Pauly, 2002)	0.002 (Houde & Zastrow, 1993)				
Swarup, 1958 15.0 (Moser, 1996) 1.000 id 27,000 (Moser, 1996; Shanks & Col 13 (Brothers, 1975) 16. Lepomis gibbosus 15.0 (Auer, 1982) 2.100 id 5000 (Carbine, 1939; Scott & Crossman, 1973) 17. Melanogrammus aeglefinus 20.0 (Fahay, 2007) 1.392 id 969,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 18. Menidia beryllina 24.0 (Fahay, 2007) 3.417 id 223 (Froese & Pauly, 2002) 0.113 (Gleason & Bengtson, 1993) 19. Micropterus salmoides 40.0 (Heidinger, 1976) 6.167 id 82,000 (Kelley, 1962) 0.016 (Houde & Zastrow, 1993) 19. Micropterus salmoides 20.0 (Auer, 1982) 1.950 id 141 (Leaf et al., 2011) 0.033 (Houde, 1994; Lee et al., 2014) 21. Perca fluviatalis 20.0 (Auer, 1982) 0.255 id 157,594 (Brazo et al., 1975) 0.041 (Houde & Zastrow, 1993) 22. Pleuronectes platessa 14.0 (Houde & Zastrow, 1993) 0.667 id 552,000 (Pecuchet et al., 2017) 0.007 (Houde & Zastrow, 1993) 23. Pomoxis annularis 16.0 (Auer, 1982) 1.233 id 325,677 (Morgan, 1954) 0.002 (Houde & Zastrow, 1993) 24. Pseudopleuronectes 13.0 (Fahay, 2007) 0.177 id 648,836 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 25. Rutilus rutilus 14.9 (Copp, 1990) 0.132 id 190,000 (Lappalainen et al., 2008) 0.033 (Houde, 1994) 26. Salmo salar 26.7 (Kazakov, 1981; Pearlstein et al., 2016) 0.200 id 8616 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993) 29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.013 (Houde & Zastrow, 1993) 0.567 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 0.567 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 0.567 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 0.567 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 0.567 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 0.567 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 0.500,000 (Froese & Pauly, 2002) 0.001	13. Gadus morhua	20.0 (Fahay, 2007)	1.392 id		0.001 (Houde & Zastrow, 1993)				
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20. Oryzias latipes 15.5 (Iwamatsu, 2004) 1.950 id 141 (Leaf et al., 2011) 0.033 (Houde, 1994; Lee et al., 2014) 21. Perca fluviatalis 20.0 (Auer, 1982) 0.255 id 157,594 (Brazo et al., 1975) 0.041 (Houde & Zastrow, 1993) 22. Pleuronectes platessa 14.0 (Houde & Zastrow, 1993) 0.667 id 552,000 (Pecuchet et al., 2017) 0.007 (Houde & Zastrow, 1993) 23. Pomoxis annularis 16.0 (Auer, 1982) 1.233 id 325,677 (Morgan, 1954) 0.002 (Houde & Zastrow, 1993) 24. Pseudopleuronectes 13.0 (Fahay, 2007) 0.177 id 648,836 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 25. Rutilus rutilus 14.9 (Copp, 1990) 0.132 id 190,000 (Lappalainen et al., 2008) 0.033 (Houde, 1994) 26. Salmo salar 26.7 (Kazakov, 1981; Pearlstein et al., 2016) 0.145 id 10,794 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993) 27. Salmo trutta 28.0 (Réalis-Doyelle et al., 2016) 0.200 id 8616 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993) 28. Salvelinus alpinus 24.8 (Pavlov & Osinov, 2008) 0.165 id 5400 (Tallman et al., 1996) 0.013 (Houde & Zastrow, 1993) 29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.017 (Houde & Zastrow, 1993) 30. Sardina pilchardus 15.5 (Morote et al., 2010) 1.667 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 31. Scopthalmus maximus 38.4 (Al-Maghazachi & Gibson, 1984; Russell, 1976) 0.750 id 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 32. Solea solea 12.0 (Munk & Nielsen, 2005) 0.750 id 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993)	18. Menidia beryllina	24.0 (Fahay, 2007)	3.417 id	223 (Froese & Pauly, 2002)	0.113 (Gleason & Bengtson, 1996)				
Lee et al., 2014 21. Perca fluviatalis 20.0 (Auer, 1982) 0.255 id 157,594 (Brazo et al., 1975) 0.041 (Houde & Zastrow, 1993) 22. Pleuronectes platessa 14.0 (Houde & Zastrow, 1993) 0.667 id 552,000 (Pecuchet et al., 2017) 0.007 (Houde & Zastrow, 1993) 23. Pomoxis annularis 16.0 (Auer, 1982) 1.233 id 325,677 (Morgan, 1954) 0.002 (Houde & Zastrow, 1993) 24. Pseudopleuronectes 13.0 (Fahay, 2007) 0.177 id 648,836 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 25. Rutilus rutilus 14.9 (Copp, 1990) 0.132 id 190,000 (Lappalainen et al., 2008) 0.033 (Houde, 1994) 26. Salmo salar 26.7 (Kazakov, 1981; Pearlstein et al., 2007) 0.145 id 10,794 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993) 27. Salmo trutta 28.0 (Réalis-Doyelle et al., 2016) 0.200 id 8616 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993) 28. Salvelinus alpinus 24.8 (Pavlov & Osinov, 2008) 0.165 id 5400 (Tallman et al., 1996) 0.013 (Houde & Zastrow, 1993) 29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.017 (Houde & Zastrow, 1993) 30. Sardina pilchardus 15.5 (Morote et al., 2010) 1.667 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 31. Scopthalmus maximus 38.4 (Al-Maghazachi & Gibson, 1984; Russell, 1976) 0.750 id 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 32. Solea solea 12.0 (Munk & Nielsen, 2005) 0.750 id 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zas	19. Micropterus salmoides	40.0 (Heidinger, 1976)	6.167 id	82,000 (Kelley, 1962)	0.016 (Houde & Zastrow, 1993)				
22. Pleuronectes platessa 14.0 (Houde & Zastrow, 1993) 0.667 id 552,000 (Pecuchet et al., 2017) 0.007 (Houde & Zastrow, 1993) 23. Pomoxis annularis 16.0 (Auer, 1982) 1.233 id 325,677 (Morgan, 1954) 0.002 (Houde & Zastrow, 1993) 24. Pseudopleuronectes americanus 13.0 (Fahay, 2007) 0.177 id 648,836 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 25. Rutilus rutilus 14.9 (Copp, 1990) 0.132 id 190,000 (Lappalainen et al., 2008) 0.033 (Houde, 1994) 26. Salmo salar 26.7 (Kazakov, 1981; Pearlstein et al., 2014) 0.145 id 10,794 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993) 27. Salmo trutta 28.0 (Réalis-Doyelle et al., 2016) 0.200 id 8616 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993) 28. Salvelinus alpinus 24.8 (Pavlov & Osinov, 2008) 0.165 id 5400 (Tallman et al., 1996) 0.013 (Houde & Zastrow, 1993) 29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.017 (Houde & Zastrow, 1993) 30. Sardina pilchardus 15.5 (Morote et al., 2010) 1.667 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 31. Scopthalmus maximus 38.4 (Al-Maghazachi & Gibson, 1984; Russell, 1976) 300,000 (Froese & Paul	20. Oryzias latipes	15.5 (Iwamatsu, 2004)	1.950 id	141 (Leaf et al., 2011)					
23. Pomoxis annularis 16.0 (Auer, 1982) 1.233 id 325,677 (Morgan, 1954) 0.002 (Houde & Zastrow, 1993 on 2002) 24. Pseudopleuronectes americanus 13.0 (Fahay, 2007) 0.177 id 648,836 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993 on 2003) 25. Rutilus rutilus 14.9 (Copp, 1990) 0.132 id 190,000 (Lappalainen et al., 2008) 0.033 (Houde, 1994) 26. Salmo salar 26.7 (Kazakov, 1981; Pearlstein et al., 2016) 0.145 id 10,794 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993 et al., 2007) 27. Salmo trutta 28.0 (Réalis-Doyelle et al., 2016) 0.200 id 8616 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993 et al., 2016) 28. Salvelinus alpinus 24.8 (Pavlov & Osinov, 2008) 0.165 id 5400 (Tallman et al., 1996) 0.013 (Houde & Zastrow, 1993 et al., 2016) 29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.017 (Houde & Zastrow, 1993 et al., 2016) 30. Sardina pilchardus 15.5 (Morote et al., 2010) 1.667 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993 et al., 2017) 31. Scopthalmus maximus 38.4 (Al-Maghazachi & Gibson, 1984; Russell, 1976) 3.002 id 5,000,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993 et al., 2017) 32. Solea so	21. Perca fluviatalis	20.0 (Auer, 1982)	0.255 id	157,594 (Brazo et al., 1975)	0.041 (Houde & Zastrow, 1993)				
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26. Salmo salar 26.7 (Kazakov, 1981; Pearlstein et al., 2007) 0.145 id 10,794 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993 et al., 2007) 27. Salmo trutta 28.0 (Réalis-Doyelle et al., 2016) 0.200 id 8616 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993 et al., 2010) 28. Salvelinus alpinus 24.8 (Pavlov & Osinov, 2008) 0.165 id 5400 (Tallman et al., 1996) 0.013 (Houde & Zastrow, 1993 et al., 2010) 29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.017 (Houde & Zastrow, 1993 et al., 2010) 30. Sardina pilchardus 15.5 (Morote et al., 2010) 1.667 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993 et al., 2017) 31. Scopthalmus maximus 38.4 (Al-Maghazachi & Gibson, 1984; Russell, 1976) 3.022 id 5,000,000 (Pecuchet et al., 2017) 0.001 (Houde & Zastrow, 1993 et al., 2017) 32. Solea solea 12.0 (Munk & Nielsen, 2005) 0.750 id 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993 et al., 2002)		13.0 (Fahay, 2007)	0.177 id	648,836 (Froese & Pauly, 2002)	0.001 (Houde & Zastrow, 1993)				
et al., 2007) 27. Salmo trutta 28.0 (Réalis-Doyelle et al., 2016) 0.200 id 8616 (Froese & Pauly, 2002) 0.013 (Houde & Zastrow, 1993) 28. Salvelinus alpinus 24.8 (Pavlov & Osinov, 2008) 0.165 id 5400 (Tallman et al., 1996) 0.013 (Houde & Zastrow, 1993) 29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.017 (Houde & Zastrow, 1993) 30. Sardina pilchardus 15.5 (Morote et al., 2010) 1.667 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 31. Scopthalmus maximus 38.4 (Al-Maghazachi & 3.022 id 5,000,000 (Pecuchet et al., 2017) Gibson, 1984; Russell, 1976) 32. Solea solea 12.0 (Munk & Nielsen, 2005) 0.750 id 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993)	25. Rutilus rutilus	14.9 (Copp, 1990)	0.132 id	190,000 (Lappalainen et al., 2008)	0.033 (Houde, 1994)				
28. Salvelinus alpinus 24.8 (Pavlov & Osinov, 2008) 0.165 id 5400 (Tallman et al., 1996) 0.013 (Houde & Zastrow, 1993) 29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.017 (Houde & Zastrow, 1993) 30. Sardina pilchardus 15.5 (Morote et al., 2010) 1.667 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 31. Scopthalmus maximus 38.4 (Al-Maghazachi & Gibson, 1984; Russell, 1976) 3.022 id 5,000,000 (Pecuchet et al., 2017) 0.001 (Houde & Zastrow, 1993) 32. Solea solea 12.0 (Munk & Nielsen, 2005) 0.750 id 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993)	26. Salmo salar		0.145 id	10,794 (Froese & Pauly, 2002)	0.013 (Houde & Zastrow, 1993)				
29. Sander vitreus 20.0 (Auer, 1982) 0.237 id 600,000 (Wolfert, 1969) 0.017 (Houde & Zastrow, 1993) 30. Sardina pilchardus 15.5 (Morote et al., 2010) 1.667 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 31. Scopthalmus maximus 38.4 (Al-Maghazachi & Gibson, 1984; Russell, 1976) 3.022 id 5,000,000 (Pecuchet et al., 2017) 0.001 (Houde & Zastrow, 1993) 32. Solea solea 12.0 (Munk & Nielsen, 2005) 0.750 id 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993)	27. Salmo trutta	28.0 (Réalis-Doyelle et al., 2016)	0.200 id	8616 (Froese & Pauly, 2002)	0.013 (Houde & Zastrow, 1993)				
30. Sardina pilchardus 15.5 (Morote et al., 2010) 1.667 id 169,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993) 31. Scopthalmus maximus 38.4 (Al-Maghazachi & 3.022 id Gibson, 1984; Russell, 1976) 5,000,000 (Pecuchet et al., 2017) 0.001 (Houde & Zastrow, 1993) 32. Solea solea 12.0 (Munk & Nielsen, 2005) 0.750 id 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993)	28. Salvelinus alpinus	24.8 (Pavlov & Osinov, 2008)	0.165 id	5400 (Tallman et al., 1996)	0.013 (Houde & Zastrow, 1993)				
31. Scopthalmus maximus 38.4 (Al-Maghazachi & 3.022 id 5,000,000 (Pecuchet et al., 2017) 0.001 (Houde & Zastrow, 1993 Gibson, 1984; Russell, 1976) 32. Solea solea 12.0 (Munk & Nielsen, 2005) 0.750 id 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993)	29. Sander vitreus	20.0 (Auer, 1982)	0.237 id	600,000 (Wolfert, 1969)	0.017 (Houde & Zastrow, 1993)				
Gibson, 1984; Russell, 1976) 32. Solea solea 12.0 (Munk & Nielsen, 2005) 0.750 id 300,000 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993)	30. Sardina pilchardus	15.5 (Morote et al., 2010)	1.667 id	169,000 (Froese & Pauly, 2002)	0.001 (Houde & Zastrow, 1993)				
	31. Scopthalmus maximus	, ,	3.022 id	5,000,000 (Pecuchet et al., 2017)	0.001 (Houde & Zastrow, 1993)				
33. Sprattus sprattus 25.0 (Munk & Nielsen, 2005) 3.583 id 14,630 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993)	32. Solea solea	12.0 (Munk & Nielsen, 2005)	0.750 id	300,000 (Froese & Pauly, 2002)	0.001 (Houde & Zastrow, 1993)				
	33. Sprattus sprattus	25.0 (Munk & Nielsen, 2005)	3.583 id	14,630 (Froese & Pauly, 2002)	0.001 (Houde & Zastrow, 1993)				
34. <i>Trisopterus luscus</i> 18.0 (Rodríguez et al., 2018; 2.500 id 521,738 (Froese & Pauly, 2002) 0.001 (Houde & Zastrow, 1993 Russell, 1976)	34. Trisopterus luscus	-	2.500 id	521,738 (Froese & Pauly, 2002)	0.001 (Houde & Zastrow, 1993)				

$r_B(-)$	$L_p(cm)$	$L_m(cm)$	$\mu_p(t^{-1})$
1.392 (Kingsford et al., 2019)	9.07 (Kavanagh, 2000)	15.3 (Kavanagh, 1996)	0.477 (Kingsford et al., 2019)
0.490 (Froese & Pauly, 2002)	14.0 (Bergstad et al., 2001)	21.0 (Froese & Pauly, 2002)	0.600 (Cook, 2004; ICES, 1998)
0.480 (Froese & Pauly, 2002)	3.69 (Luo, 1991)	11.0 (Hildebrand, 1963)	2.360 (Newberger & Houde, 1995)
0.140 (Froese & Pauly, 2002)	54.00 (Tesch, 1977)	145.0 (Froese & Pauly, 2002)	0.230 (Svedäng, 1999)
1.330 (Tricas, 1986)	7.10 (Tricas, 1986)	9.5 (Tricas, 1986)	0.518 (Goatley & Bellwood, 2016)
0.320 (Froese & Pauly, 2002)	16.70 (Froese & Pauly, 2002)	51.0 (Froese & Pauly, 2002)	0.168 (Beverton, 1963; Cushing, 1959)
1.200 (Froese & Pauly, 2002)	2.50 (Froese & Pauly, 2002)	3.8 (Froese & Pauly, 2002)	1.515 (Weyl & Booth, 1999)
0.120 (Froese & Pauly, 2002)	42.00 (Spitz et al., 2013)	103.0 (Froese & Pauly, 2002)	0.240 (ICES, 2018)
0.470 (Froese & Pauly, 2002)	11.50 (ICES, 2016)	21.0 (Froese & Pauly, 2002)	0.900 (Brandhorst, 1974; Iversen et al., 1993; Schaefer, 1967)
1.700 (Froese & Pauly, 2002)	8.18 (Funamoto et al., 2004)	18.0 (Froese & Pauly, 2002)	0.630 (Iversen et al., 1993)
0.380 (Froese & Pauly, 2002)	13.50 (Richardson, 1980)	24.0 (Froese & Pauly, 2002)	0.970 (Hanan, 1981)
0.160 (Froese & Pauly, 2002)	68.30 (Froese & Pauly, 2002)	123.0 (Froese & Pauly, 2002)	0.216 (Dickie, 1963; Jones, 1966; Pinhom, 1975; Sinclair, 2001)
2.237 (Froese & Pauly, 2002)	5.50 (Froese & Pauly, 2002)	10.0 (Froese & Pauly, 2002)	1.060 (Jones & Hynes, 1950)
0.790 (McGourthy et al., 2009)	10.00 (Barlow, 1963)	21.0 (Eschmeyer & Herald, 1999)	4.761 (Fonds, 1973; Hernaman & Munday, 2005)
0.395 (Copp et al., 2004)	7.00 (van Kleef & Jongejans, 2014)	20.0 (Holtan, 1998)	0.540 (Goedde & Coble, 1981)
0.220 (Froese & Pauly, 2002)	34.90 (Froese & Pauly, 2002)	110.0 (Froese & Pauly, 2002)	0.430 (Jones & Shanks, 1990)
1.140 (Froese & Pauly, 2002)	4.50 (Gleason & Bengtson, 1996)	15.0 (Page & Burr, 1991)	0.993 (Hubbs, 1982)
0.245 (Jackson et al., 2008)	25.00 (Heidinger, 1976)	70.0 (Lee, 1980)	0.450 (Mueller et al., 2005)
3.650 (Leaf et al., 2011)	2.20 (Dhillon & Fox, 2004)	4.5 (Leaf et al., 2011)	1.515 (Weyl & Booth, 1999)
0.332 (Jackson et al., 2008)	19.20 (Froese & Pauly, 2002)	40.0 (Page & Burr, 1991)	1.170 (Goedde & Coble, 1981)
0.130 (Froese & Pauly, 2002)	30.80 (Froese & Pauly, 2002)	100.0 (Nielsen, 1986)	0.140 (Beverton, 1964; Siddeek, 1989)
0.246 (Jackson & Hurley, 2005)	20.50 (Edwards, 1982)	51.0 (Carlander, 1997)	0.84 (Allen et al., 1998)
0.310 (Froese & Pauly, 2002)	27.40 (Froese & Pauly, 2002)	64.0 (Robins & Ray, 1986)	0.300 (Dickie & McCracken, 1955)
0.107 (Sandlund et al., 2013)	10.27 (Paull et al., 2008)	50.2 (Verreycken et al., 2011)	0.400 (Britton, 2007)
0.270 (Froese & Pauly, 2002)	73.10 (Froese & Pauly, 2002)	150.0 (Froese & Pauly, 2002)	0.740 (Chaput, 2012)
0.240 (Froese & Pauly, 2002)	20.20 (Taube, 1976)	94.0 (Froese & Pauly, 2002)	0.670 (Carline, 2006)
0.075 (Loewen et al., 2010)	38.98 (Loewen et al., 2010)	107.0 (Froese & Pauly, 2002)	0.170 (Moore, 1975)
0.266 (Quist et al., 2003)	42.90 (Froese & Pauly, 2002)	107.0 (Scott & Crossman, 1973)	0.440 (Kocovsky & Carline, 2001)
0.360 (Froese & Pauly, 2002)	14.30 (Silva et al., 2013)	27.0 (Froese & Pauly, 2002)	0.667 (Bedairia & Djebar, 2009; Erdoğan et al., 2010)
0.250 (Froese & Pauly, 2002)	34.70 (Froese & Pauly, 2002)	100.0 (Nielsen, 1986)	0.246 (Chen & Xiao, 2006; Pitt, 1973; Wilderbuer & Turnock, 2009)
0.320 (Froese & Pauly, 2002)	24.60 (Mollet et al., 2007)	70.0 (Froese & Pauly, 2002)	0.100 (Lorenzen, 2005)
0.600 (Froese & Pauly, 2002)	10.00 (Glover et al., 2011; Peck et al., 2012)	16.0 (Whitehead, 1988)	0.377 (Bentley et al., 2019)
0.430 (Froese & Pauly, 2002)	19.20 (Alonso-Fernández et al., 2008)	46.0 (Froese & Pauly, 2002)	1.330 (Bauey & Kunzlik, 1984; Menon, 1950)

where $E_{(L_b)}$ is the expected length at birth of the offspring, and $\sigma^2_{(L_b)}$ is the expected variation in offspring size, as measured at the next population census in the model at t+1.

2.4 | Parametrisation of individual-level life history functions

A set of eight traits are used to parameterise the individual level life history functions in the DEB-IPM: Larval transformation length (L_b), variation in transformation length (σ_{l_s}), von Bertalanffy growth coefficient (r_B) , maturation length (L_p) , maximum adult length (L_m) , maximum number of eggs produced by adult of maximum length (R_m) , egg and larval stage survival rate (ϕ), and natural mortality rate (μ_p). We collected the values of these traits from scientific literature (values and references in Table 1). Where multiple studies were available, for example from studies of different populations, an average was taken. The trait values in Table 1, therefore, represent a generalised life history of a species based on combining information from multiple populations where available. We were able to collect speciesspecific values for six of these DEB-IPM parameter traits directly from scientific literature. We calculated two of the traits, survival during the egg and larval phase, ϕ , and variation in offspring size, σ_L^2 , manually:

$$\phi = 1 - e^{(-M \cdot n)} \tag{9}$$

where M is the instantaneous mortality coefficient of the species during the egg and larval phase, and n is the duration of the egg and larval phase, both in unit days. M and n values were collected from scientific literature (values and references in Table 1).

$$\sigma_{L_b}^2 = \left(c_i \cdot \| \frac{\min_{L_b} - \mu_{L_b}}{3} \| \right)^2 \tag{10}$$

in which \min_{L_b} represents the minimal larval or hatching size, collected from scientific literature, μ_{L_b} is the mean of the distribution of larval size, assumed to follow a normal distribution, and c_i is a multiplier constant set to 0.1, 0.5 or 1.0 for species with low, medium and high spread in spawning, respectively. The rationale being that species releasing all eggs in a single event will have a lower variation in offspring size measured at the next population census compared to species that release eggs daily over an extended period of time. The equation itself is an adaptation of the z-score formula to calculate the standard deviation of a normal distribution (Abdi, 2007).

2.5 | Population level integration and outcome variables

The individual-level growth, survival, reproduction, and parent-offspring association functions in the DEB-IPM are integrated over the length domain Ω to describe the dynamics of the total number of

female individuals in a population N, from time t to t+1 (Easterling et al., 2000).

$$N(L',L(t+1)) = \int_{\Omega} \left[D(L',L(t))R(L(t)) + G(L',L(t))S(L(t)) \right] N(L,t)dL$$
 (11)

Given a simulation of τ steps, the log of the stochastic growth rate of the population, $log(\lambda_s)$ can then be calculated

$$\log(\lambda_s) = \frac{1}{\tau} \sum_{\tau=0}^{\tau-1} \log \frac{\mathbf{p}(t+1)}{\mathbf{p}(t)}$$
 (12)

We define the sensitivity of the population to variation in the environment as the difference between maximum and minimum $log(\lambda_s)$ across simulated environments.

$$\Delta \log(\lambda_s) = \log(\lambda_{s_{\text{Min}}}) - \log(\lambda_{s_{\text{Min}}})$$
(13)

The population-level outcome variables of growth rates and sensitivity to environmental variation are therefore an emergent property of individual-level processes and trade-offs included in the DEB-IPM.

2.6 | DEB-IPM implementation and simulations

2.6.1 | Stochastic demographic model simulations

We implemented the parametrised DEB-IPMs into a stochastic demographic model using *Matlab* (version R2021a) to calculate stochastic population growth rates ($\log(\lambda_s)$) and sensitivity to environmental variation ($\Delta\log(\lambda_s)$). We ran simulations for each of the 34 model species, across an environmental autocorrelation range of $\rho=-1:1$, with a step size of 0.001. Each simulation consisted of 50,000 time steps, with an initial transient of 400 time steps, a starting population of one individual in each size bin, and a randomly chosen initial environmental state (see also Smallegange et al., 2014; Tuljapurkar et al., 2003).

2.6.2 | Stochastic demographic model details

The stochastic demographic model was defined as $\mathbf{p}(t+1) = \mathbf{A}(t) \cdot \mathbf{p}(t)$. The vector $\mathbf{p}(t)$ is the population vector at time t, and $\mathbf{A}(t)$ is a DEB-IPM at time t, defined by a two-state Markov chain habitat transition matrix \mathbf{H} (Caswell, 2001).

$$H = \begin{bmatrix} 1-p & q \\ p & 1-q \end{bmatrix} \tag{14}$$

In the habitat transition matrix, p equals the probability of switching from a good to a bad environment, and q equals the probability of switching from a bad to a good environment. The autocorrelation level in the model equals p = 1 - p - q (Caswell, 2001).

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TABLE 2 Phylogenetically informed principal component analysis (pPCA) loadings of life history traits and sensitivity to shifts in environmental variation on the first three principal components for three different models: Full model (FM) with all traits and phylogeny, FM without phylogeny, and model with phylogeny and body size corrected traits. Bold values indicate the principal component with which each trait is most strongly associated. Definitions of the descriptions of the PCA axes on the bottom bar: fast-slow fast slow continuum, reprod., reproductive strategy axes; sens., sensitivity to shifts in environmental variation.

pPCA	FM			FM-phylogeny			FM-body size residuals		
Eigenvalue >1	PC1	PC2	PC3	PC1	PC2	PC3	PC1	PC2	PC3
Cum. variance explained	0.486	0.658	0.775	0.486	0.658	0.775	0.285	0.480	0.615
$\Delta log(\lambda_s)$	0.289	-0.025	-0.690	-0.090	-0.042	-0.604	0.065	0.699	-0.135
r _B	-0.868	0.178	-0.183	-0.426	0.006	-0.149	-0.093	0.529	-0.624
ϕ	-0.182	0.918	-0.052	-0.005	0.729	-0.123	-0.922	0.033	0.023
R_m	0.591	-0.736	-0.066	0.250	-0.504	-0.013	0.901	0.106	0.081
μ_{p}	-0.709	0.176	0.055	0.364	0.022	0.058	-0.145	0.001	-0.299
L_p	0.905	-0.279	-0.057	0.458	-0.073	-0.058	0.442	-0.011	-0.769
$\sigma(L_b)$	-0.653	-0.413	-0.422	-0.344	-0.435	-0.316	0.446	0.678	0.296
L _b	0.294	0.047	-0.766	0.232	0.121	-0.699	-0.072	0.626	-0.050
L _m	0.941	-0.213	-0.016	-0.480	-0.014	-0.028	-	-	-
	fast-slow	reprod.	sens.	fast-slow	reprod.	sens.	reprod.	sens.	fast-slow

We used a fixed frequency of good environments of f = 0.5 for all levels of environmental autocorrelation examined. The feeding levels of individuals in good and bad environments are associated with positive $(\log(\lambda_s) > 1)$, and negative $(\log(\lambda_s) < 1)$, population growth rates, respectively. We set the feeding levels associated with good and bad environmental states at $E(Y)_{high} = 1.0$, and $E(Y)_{low} = 0.7$, for all species, and the variation in experienced feeding levels between individuals $\sigma(Y)$ at an intermediate level of $\sigma(Y) = 0.3$ (Smallegange et al., 2017). Summarising, at each time step in the stochastic demographic model, the DEB-IPM at time t, A(t) is calculated based on the experienced feeding level E(Y)at time t, determined by the habitat transition matrix, and subsequently stored.

PCA analysis

We used a varimax rotated, phylogenetically informed PCA (pPCA; Revell, 2009) to structure species life history traits into life history strategies, following the procedure outlined in (Capdevila et al., 2020; Paniw et al., 2018; Salguero-Gómez, Jones, Jongejans, et al., 2016), implemented using R (version 4.2.1). The life history traits included in this analysis were the eight DEB-IPM parameters and sensitivity to environmental variation $\Delta \log(\lambda_s)$. Trait values were log-transformed and scaled with a mean of one and a standard deviation of zero to meet pPCA assumptions. We constructed a species-level phylogenetic tree prior to performing the pPCA using data from the Open Tree of Life (https://tree.opentreeoflife. org, Hinchliff et al., 2015), and the R package ROTL (Michonneau et al., 2016). We used branch lengths as the measure of phylogenetic relatedness between species. Branch lengths were computed using the compute.brlen function, and polytomies resolved using the multi2di function, from the R package ape (Paradis et al., 2004).

We then checked that the constructed tree was rooted and there were no branches with zero length before implementing the pPCA. We implemented the pPCA using the phyl.pca function from the R package phytools (Revell, 2012). The pPCA linked the phylogeny to the life history traits using a modified covariance matrix, and simultaneously estimated Pagel's λ with maximum likelihood methods (Capdevila et al., 2020; Revell, 2009). Pagel's λ expresses the phylogenetic signal strength in trait evolution under a Brownian motion model (Blomberg & Garland Jr, 2002). A Pagel's λ value of zero indicates that the correlation in traits observed between species are independent of their shared evolutionary history, whereas a value of one indicates the correlation in traits is fully determined by it (Meireles et al., 2020; Revell, 2010). We applied the Kaiser's criterion to select the number of PCA-axes to keep, retaining only those axes with an eigenvalue > 1 (Kaiser, 1960). One species with outlier values for sensitivity and mortality, as determined based on z-scores (Gillichthys mirabilis; $\Delta log(\lambda_s) = 1.77$, $z_{\Delta log(\lambda_s)} = 4.18$; $\mu_p = 4.76$, $z_{\mu_p} = 4.65$) was excluded from the pPCA-analysis. Finally, we checked for the influence of phylogeny and body size on the final structuring of life history strategies (see Jeschke & Kokko for a detailed discussion; Jeschke & Kokko, 2009), by running pPCA analyses with and without phylogeny, and with and without a correction for body size. Body size was corrected for by using the residuals of linear regressions of log₁₀-transformed values of traits versus log₁₀-transformed adult body mass (Bielby et al., 2007; Gaillard et al., 1989). The resulting pPCA analyses allowed us to examine if the observed life history strategies differ when explicitly accounting for individual-level life history trade-offs (research question i), whether life history trade-offs align with the patterning of traits into life history strategies (research question ii), and if sensitivity to environmental variation covaries with either of the primary life history strategy axes (research question iii), or individual life history traits (research question iv).

2.8 | Perturbation analysis

We used a perturbation analysis to examine which of the eight life history traits listed in Table 1 most strongly affected $\log(\lambda_s)$, and how trait importance might shift over the gradient of environmental autocorrelation (research question v). Each trait parameter i was perturbed by 1% and the elasticity of $\log(\lambda_s)$ calculated.

$$e_i^{(\log(\lambda_s))} = \frac{\log(\lambda_{\gamma_i}) - \log(\lambda_s)}{\gamma_i},$$
(15)

where the elasticity of $\log(\lambda_s)$ to perturbation of trait i by fraction γ_i , equals the difference in population growth rate with and without perturbation, divided by the fraction perturbed. This approach adds detailed insights into the sensitivity to environmental variation at the individual species level.

3 | RESULTS

3.1 | Life history strategies sensitivity to environmental variation

We find that species life history traits in ray-finned fish structure along three separate pPCA axes that cumulatively explain 78% of the total variation in life histories (Table 2: Full Model [FM], pPC1: 48.6%, pPC2: 17.2%, pPC3: 11.7%). Phylogenetic relatedness has little effect on species trait values in this analysis (Pagel's $\lambda = 6.7 \cdot 10^{-5} \pm 3.5 \cdot 10^{-7}$). Trait loadings indicate pPC1 and pPC2 are

analogous to the fast-slow and reproductive strategy axes observed in previous studies (Figure 1). Specifically, pPC1 shows the coupling of traits relating to growth and survival, with the highest positive loadings for maximum length (L_m) , maturation size (L_p) , and negative loadings for mortality rate (μ_p) , variation in offspring size $(\sigma(L_b))$, and growth rate (r_B) . This reflects a trade-off between growth and survival, i.e. larger, slow-growing species with high survival, versus smaller, fast-growing species with lower survival. Trait patterning on pPC2 shows a negative coupling between egg-and larval survival rate (ϕ) , and the maximum number of offspring produced (R_m) . This reflects a trade-off between allocating energy in many offspring with lowered survival versus fewer offspring with increased survival.

Sensitivity to environmental variation, $(\Delta log(\lambda_s))$, was only very weakly correlated with pPC1 and pPC2, and instead most strongly loaded onto pPC3 (Table 1: FM). Checking for the effect of phylogeny and body size does not alter this result (Table 1: FM—phylogeny; FM—body size residuals). When phylogeny is excluded, the loading of $\Delta(log(\lambda_s))$ is further reduced on pPC1, while remaining similarly weak on pPC2, and strongly loaded on pPC3. Correcting for body size changes the ordering of the principal components, but $\Delta(log(\lambda_s))$ remains strongly loaded on a separate axis with offspring size, and weakly loaded on the fast-slow and reproductive axes. Therefore, across our three pPCA models, we find no evidence of $\Delta(log(\lambda_s))$, i.e. sensitivity covarying with either the fast-slow axis or the reproductive strategy axis.

Next, we examined a potential interaction effect between the fast-slow and reproductive strategy axes on sensitivity, by excluding $\Delta(\log(\lambda_s))$ from the pPCA and modelling it as a function of pPCA scores using multiple linear regression (Table 3), pPC1, pPC2, pPC3,

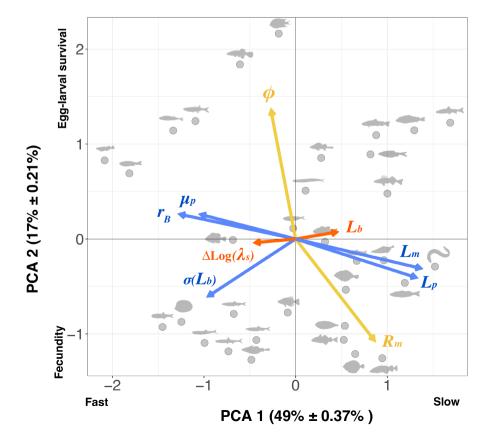


FIGURE 1 Biplot of phylogenetically corrected principal component analysis (pPCA), with the percentage of variance explained in brackets (±SE) for the 8 life history traits included as parameters in the dynamic energy budget integral projections models (DEB-IPMs), and the DEB-IPM derived trait of sensitivity $(\Delta \log(\lambda_s))$. Arrow lengths indicate mean loading of each trait, and arrow colour indicates to which pPCA axis it is most strongly associated (blue: pPC1, yellow: pPC2, and orange: pPC3). pPC1 is most strongly associated with growth and mortality traits, pPC2 most strongly with reproductive traits, and pPC3 with sensitivity and size at birth. Points represent the pPCA scores of the sample species on this two-dimensional space, which can be further identified by their silhouettes.

and pPC1×pPC2 scores only explained 7.5% of the variation observed in sensitivity across species. The model's F-statistic and associated p-value indicate there is no relationship between any of the predictors and sensitivity, and that it does not perform better than an intercept-only model. Finally, the residual standard error almost equals the intercept effect size, and is much larger than the other estimated effects, further indicating the poor predictive power of the PCA scores in terms of predicting $\Delta(\log(\lambda_s))$. Visually examining sensitivity values across the pPC1-pPC2 gradient also does not indicate a clear PC1-PC2 interaction pattern to be present (Figure S1). Therefore, we find no evidence of $\Delta(\log(\lambda_s))$ covarying with the interaction between the fast-slow and reproductive strategy axis in our study. Examples of species with similar life history strategies and contrasting responses to environmental variation are provided in Figure 2.

3.2 | Life history traits and sensitivity to environmental variation

In the pPCA analysis, $\Delta \log(\lambda_s)$ consistently negatively loaded on a separate axis together with offspring size L_b ; indicating that species

with smaller offspring sizes also tended to have lower sensitivity to environmental variation. However, when examined individually, the relationship between L_b and $\Delta \log(\lambda_s)$ was found to be highly nonsignificant (Table S1). This indicates that rather than being strongly associated to each other, L_h and $\Delta \log(\lambda_s)$ have in common that they are strongly dissociated from the patterns in trait loadings on pPC1 and pPC2. Additional testing confirmed no statistically significant relationship between $\Delta \log(\lambda_s)$ and any of the eight life history traits included in the study (Table S1). Although we did not find a clear relationship between sensitivity and traits across species, our perturbation analysis did show differences in trait importance in driving the population growth rates of individual species (Figure 3). Furthermore, there was a clear influence of reproductive decisions on these results. In 70% of iteroparous obligate breeders, maturation length L_p is the most important trait driving population growth rate, and there is generally no shift in trait importance depending on the degree of environmental autocorrelation. In iteroparous skip breeders, however, maximum length L_m (72%), and von Bertalanffy growth rates r_B (55%), are more important than L_p in driving population growth rates. Finally, in semelparous species, egg-larval survival rate ϕ is the most important trait driving population growth

TABLE 3 Main and interaction effects of phylogenetically informed principal component analysis (pPCA) scores on sensitivity to environmental change $\Delta \log(\lambda_s)$. For this analysis $\Delta \log(\lambda_s)$ was excluded from the pPCA analysis and subsequently modelled as a function of the pPCA scores using Multiple Linear Regression. The model terms explained little of the observed variation in sensitivity (R_{adj}^2). The insignificant and low-valued *F*-statistic indicates no predictor has a significant relationship with sensitivity and adds value to an intercept-only model. Finally, the Residual standard error almost equals the intercept effect size, and is much larger than the other estimated effects, indicating poor model fit.

Model terms	Coefficients	SE	p-Value	t-Value	F-statistic	p-Value	df	Residual SE	R ² adj
Intercept	0.23773	0.04065	<0.001	5.849	1.645	0.1895	28	0.2335	0.075
pPC (fast-slow)	-0.02073	0.04251	0.6279	-0.490					
pPC2 (repr. strategy)	-0.012368	0.04171	0.7634	0.304					
pPC3 (offspring size)	-0.02388	0.04138	0.5685	-0.577					
pPC1×pPC2	-0.10097	0.04550	0.0348*	-2.219					

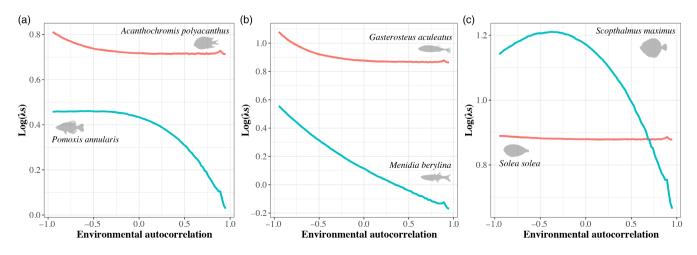


FIGURE 2 Examples of species with similar life history strategies and contrasting population growth rates $(Log(\lambda_s))$ in response to environmental autocorrelation. (a) Species with similar position on PC-1 only and dissimilar responses. (b) Species with similar low PC1 and high PC2 scores (top-left Figure 1) and dissimilar responses. (c) Species with similar high PC1 and low PC2 scores (bottom-left) and dissimilar responses.

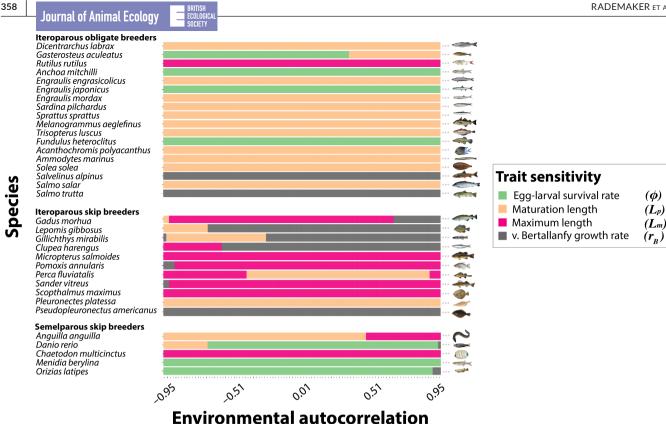


FIGURE 3 Species level perturbation plot highlighting the life history traits most strongly affecting population growth rate $\log(\lambda_{\epsilon})$ across the gradient of environmental autocorrelation. In the underlying perturbation analysis each trait was perturbed by 1% and the elasticity of $\log(\lambda_s)$ calculated. Model species are grouped depending on the reproductive decisions included in the dynamic energy budget integral projections model: (top) iteroparous obligate breeders (centre), iteroparous skip breeders and (bottom) semelparous skip breeders, respectively.

rates (60%), followed by r_B and L_p (both found in 40% of species). The variation in trait importance across the gradient of autocorrelation is generally inconsistent, that is specific traits can be important drivers of population growth rates both when environments are highly variable, or highly invariable. Notably, there is a pattern in the importance of egg-larval survival, which was only observed in species with relatively small adult body sizes (Gasterosteus aculeatus, Anchoa mitchilli, Engraulis engrasicolus, Engraulis japonicus, Fundulus heteroclitus, Danio rerio, Menidia beryllina, Oryzias latipes).

DISCUSSION

4.1 Life history trade-offs, traits and strategies

We find three primary life history strategy axes when explicitly accounting for energy allocation trade-offs at the individual level (research question i). This includes the classical fast-slow axis and the often-reported secondary reproductive strategy axis (Capdevila et al., 2020; Healy et al., 2019; Morris et al., 2008; Paniw et al., 2018; Stearns, 1992), and a third axis for population sensitivity to environmental variation. Our results show differences between the life history trade-offs in energy allocation that we incorporated at the individual level (growth vs. reproduction, future vs. current

reproduction) and the life history trade-offs reflected by the patterning of species traits along our fast-slow and reproductive strategy axes (research question ii). This indicates that individual-level life history trade-offs do not necessarily apply to the population and species level. The assumption that the structure of individual differences in life history traits resembles in important ways the structure of variation across species underpins the pace of life syndrome (POLS), in which behavioural and physiological differences between individuals are postulated to covary with the slow-fast life-history continuum (Réale et al., 2010). Our results provide one explanation for why we lack robust empirical support for the predictions of the POLS framework (Laskowski et al., 2021). We argue we do not find an alignment because the general trade-offs in energy allocation faced by all individual organisms do not necessarily reflect the potential selective pressures and opportunities posed by the environment in which populations occur. For example, in marine systems, species can realise relatively high fecundity through a combination of oviparity and external fertilisation (Benun Sutton & Wilson, 2019; Gross & Shine, 1981). This strategy is not available to terrestrial species and comes at a cost of increased mortality when depositing undeveloped eggs in the external environment. This can for example explain why many marine species groups such as large ray-finned fish can combine the slow growth, longevity and low adult mortality rates typical of slow life histories with the high fecundity and

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FIGURE 4 Conceptual framework highlighting the characteristics of different kinds of demographic modelling approaches in life history research. The framework can be used to identify the most appropriate approach based on research specifics. The columns list three different modelling approaches (pattern, hybrid and process based models, respectively). The rows describe important modelling assumptions. The text in the row cells explains the limitation of each of the three modelling approaches in relation to these assumptions. This explanation is combined with both a 5-valued colour scale that indicates how the different modelling approaches perform in relation to each assumption (Red: poor, Orange: bad, Yellow: average, Light green: good, Dark green: very good). Finally, the bottom row lists an example research question that each modelling approach is suited to address. DEB-IPM, dynamic energy budget integral projections model.

high offspring mortality rates typical of fast life histories (Beukhof et al., 2019). Differences in selective pressures and opportunities between environments might also explain why populations of the same species can exhibit very different life history strategies in different areas (Gamelon et al., 2021). It is still important to account for the individual-level trade-offs in energy allocation when examining life history variation even if they don't reflect the trade-offs in traits at the population or species level. This is because they impose critical energetic constraints on individual development and reproduction that translate through in population dynamics (Karjalainen et al., 2016). Without such energetic constraints, the law of conservation of energy would be violated and biomass freely created in demographic model studies, affecting projected population production, structure and responses to the environment. Although demographic vital rates in our study are dependent on the energy.

4.2 | Responses to environmental variation

We failed to find a significant link between life history traits and strategies in ray-finned fish, and their sensitivity to environmental variation (research questions iii, iv). The implications of these results extend beyond the immediate species modelled. The large range of environmental conditions that were simulated (~50,000 scenarios

per species), in combination with the range in trait combinations across species, and the reproductive decisions incorporated in our models, provide broad insights into the idiosyncrasy of population responses to environmental variation. Part of the wide range of environmental variation that was simulated, e.g. extremely negative autocorrelation, might not generally be expected to occur in nature. However, recent studies show, for example, how terrestrial arctic species are already facing increasingly high interannual variability in environmental conditions (Schmidt et al., 2023), leading to very unpredictable feeding environments between years. The absence of a general link between population responses and species life history strategies also aligns with other demographic studies in terrestrial systems that have shown different populations of the same species can display highly different life history strategies and therefore different population responses (Gamelon et al., 2021; Nevoux et al., 2010; Nilsen et al., 2009). This intraspecific variation in life history strategies also highlights a potential limitation concerning the comprehensiveness of our current study. For example, different populations of Salmo salar can display different life history strategies, where some populations migrate to sea and others remain fully resident (Fleming, 1996; MacCrimmon & Gots, 1979). Both types even exist sympatrically in some populations (Verspoor & Cole, 1989). Because our study used life history trait values averaged across multiple populations, we therefore overlook this potentially important

RADEMAKER ET AL. when accounting for individual-level complexity comes at the cost of being able to examine fewer species when we wish to examine population responses to environmental variation. This leaves the question of how to best move forward in the future. We summarise our perspective in a conceptual framework (Figure 4), listing the strengths and weaknesses of varying demographic modelling approaches using functional traits to model population responses. We find that this framework actually points towards the potential of combining different methods to address large and complex questions, such as which species are most vulnerable to environmental change. For example, we can use (1) pattern based models to characterise the different life history strategies that have evolved across species, (2) a hybrid model, which combines patterns in traits in combination with a limited set of life history trade-offs and or processes, to identify which of these strategies and individual species show the highest sensitivity when exposed to environmental variation, and (3) a process model to study the responses of the most sensitive species to environmental change in a fuller ecological context, including feedbacks and accounting for trophic interactions. In this way, each approach acts as a focusing lens for the next one, and adds to their overall utility in addressing urgent conservation issues by combining their individual powers. We hope that this perspective can help pave the way towards a more integrative approach utilising functional traits to understand complex demographic processes in an era of change (Salguero-Gómez et al., 2018). **AUTHOR CONTRIBUTIONS** Isabel M. Smallegange conceived the idea; Isabel M. Smallegange and Mark Rademaker designed methodology; Mark Rademaker collected the data; Mark Rademaker analysed the data; Mark Rademaker led

source of intraspecific variation in life histories between populations. However, we believe that this does not negate, but rather strengthens and adds to the general message of our results: a need to study and account for individual-level life history complexity in order to examine complex population responses. If included, population responses might have been reasonably expected to be more idiosyncratic rather than more general. This strongly aligns with other recent findings. For example, Van de Walle et al. (2023) show that although across species a slow-fast continuum could be identified as the main axis of life history variation, there is no alignment to this pattern when examining the populations of a species individually. The authors therefore conclude that individual life-history variation is likely idiosyncratic across species. The importance of accounting for individual-level life history complexity to understand population level outcomes is also not an altogether new perspective. For example, a long line of ecological research shows that populations accounting for size-structure and individual growth have very different dynamics than those in which individuals are all assumed to be identical (de Roos & Persson, 2013). However, added complexity comes at a cost. Studies accounting for successively more individual-level complexity typically can examine fewer species, lowering sample size (34 in our study), and the outcomes are more system specific. This contrasts with the statistical power of broad cross-taxonomical approaches to use big functional-trait datasets to derive general inferences across large groups of species and systems (Kissling et al., 2018; Salguero-Gómez et al., 2015; Salguero-Gómez, Jones, Archer, et al., 2016), that in turn come at the cost of reduced mechanistic insight.

4.3 **Perspective**

Our results show that the classical association between life history strategies and responses to environmental variation breaks down when explicitly accounting for individual-level life history trade-offs. Contributing factors are that (i) trade-offs can differ between levels of organisation, and (ii) we must account for individual-level trade-offs in order to have a link between individual processes and population-level responses that is based on first principles, such as the conservation of energy. We postulated that the assumed alignment between individual, population, and species-level trade-offs depends on the specific selective pressures and opportunities posed by the environment. This alludes to another important level of organisation that is not always included in demographic models, including our own: feedback with the environment. Population modelling approaches accounting for both individual life-history mechanisms and environmental feedbacks show complex population dynamics, including alternative stable states (de Roos & Persson, 2013; Persson et al., 1998). Crucially, such complex dynamics are usually directly dependent on individual-level processes, such as size-dependent differences in mortality rates or feeding efficiency. We already highlighted how the gains from additional mechanistic insight

the writing; Anieke van Leeuwen and Isabel M. Smallegange contributed critically to the drafts and gave final approval for publication.

CONFLICT OF INTEREST STATEMENT

The authors have no conflicts of interest to declare.

DATA AVAILABILITY STATEMENT

Data available from the Dryad Digital Repository https://doi.org/10. 5061/dryad.2ngf1vhsh (Rademaker et al., 2023).

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

Figure S1. Histogram showing the distribution of sensitivity values across species.

Figure S2. Distribution of log-transformed trait values between species classified as sensitive or insensitive to shifts in environmental autocorrelation used for Kolmogorov–Smirnov test.

Table S1. Linear and non-linear test statistics of the relationship between $\Delta \log(\lambda_s)$ and log transformed life history traits.

Appendix S1. Sensitivity and individual traits.

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