Supporting information I:

Model description

1. Overview

We developed a simulation model to study fish morphological evolution in size-structured resources (prey). We combined an individual-based model and difference equations to describe alewives, prey of the alewives, and their ecological interactions. The descriptions of fish survival, development, foraging, and reproduction are shown in the second section. Prey of alewives was modeled as multiple, different-sized clusters, and difference equations described it. Prey abundance was affected by the competition within a prey cluster, the foraging for smaller-bodied prey clusters, the predation by larger-bodied prey clusters, and the foraging by alewives. The descriptions of the
Figure SI.1.1: Flow diagram of a model for studying alewife morphological evolution. The equation numbers are in [ ]. The algorithm numbers are in ( ).

structure and dynamics of prey clusters are shown in the third section. The last section shows the initial conditions for simulations. Fig.SI.1.1 shows the processes in this model, and model symbols are shown in Table SI.2.1 in supporting information II.
2. Fish vital processes

An individual 1) survived at the current life stage, 2) survived and developed to the next life stage, or 3) died for each time step. We implemented Algorithm (SI.1) to simulate these vital processes. To facilitate the computation, individuals were sorted into 250 equal-width, body-length bins, which ranged from 0 to the maximum mean asymptotic body length, \( bMx \). The default value for \( bMx \) was 273.684 mm to set the average body length of 5-year-old females of the largest genotype to approximately the average total body length of adults from three anadromous alewife populations (= 260 mm) (Palkovacs et al., 2008).
Update the age of the individual \((\text{age}_i = \text{age}_i + \text{time step})\).

Calculate \(m_i\) by using Eq. (SI.14).

Calculate \(ddS_i(t)\) by using Eq. (SI.16).

Calculate \(sm_i(t)\) by using Eq. (SI.29).

\(u \sim \text{Uniform distribution } [0, 1]\)

if the individual is not reproductively matured then

\[\text{if } u < (P_{x,sg_i}ddS_i(t)) \text{ then} \]

The individual, \(i\), survives at the current life stage.

\(u \sim \text{Uniform distribution } [0, 1]\)

\[\text{if } u < sm_i(t) \text{ then} \]

\(sm_i = \text{true}\)

end

else if \(u < [(P_{x,sg_i} + G_{x,sg_i})ddS_i(t)]\) then

The individual, \(i\), survives and develops to the next life stage.

by setting \(sg_i = sg_i + 1\).

\(u \sim \text{Uniform distribution } [0, 1]\)

\[\text{if } u < sm_i(t) \text{ then} \]

\(sm_i = \text{true}\)

end

else

The individual, \(i\), dies.

end

else

[\(u < [(P_{x,sg_i} + G_{x,sg_i})ddS_i(t)]\) then

The individual, \(i\), survives at the current life stage.

else

the individual, \(i\), dies.

end

end

if the individual is alive then

Update the body length, \(b_i\), by using Eq. (SI.1).

end

Algorithm 1: Survival and development process for an individual. \(P\) was the probability of an individual surviving at the current life stage for a time step without density-dependent effects; \(G\) was the probability of an individual surviving and developing to the next life stage for a time step without density-dependent effects; \(sg\) was the index for a life stage; \(x\) was the index for a sex; \(i\) was the index for an individual; \(m\) was the metabolic rate; \(ddS\) was the density-dependent survival rate; \(sm\) was the probability that an individual sexually matured; \(sm\) was the status of sexual maturation.
We used density-dependent and density-independent rates for fish vital processes. The default values for the density-independent survival and growth rates of female alewives are shown in a form of a stage-classified matrix population model. The matrix does not contain fertility, which is described in the reproduction subsection, because fertility was not fixed.

\[
\begin{bmatrix}
P_{1,1}(=0) & 0 & 0 & 0 & 0 & 0 \\
G_{1,1}(=0.670) & P_{1,2}(=0) & 0 & 0 & 0 & 0 \\
0 & G_{1,2}(=0.670) & P_{1,3}(=0) & 0 & 0 & 0 \\
0 & 0 & G_{1,3}(=0.670) & P_{1,4}(=0) & 0 & 0 \\
0 & 0 & 0 & G_{1,4}(=0.670) & P_{1,5}(=0.6281) & 0 \\
\end{bmatrix}
\]

The growth rates, \(G\), for the first to the fifth life stages were derived from instantaneous juvenile natural mortality estimated by Gibson et al. (Gibson & Myers, 2004). The survival rate, \(P\), for the fifth life stage was derived from median instantaneous adult natural mortality estimated by Gibson et al. (Gibson & Myers, 2003).

Male alewives sexually mature earlier than the females (Mullen et al., 1986). For this reason, females had four immature life stages, and males had three immature life stages. The matrix below shows vital rates for male
2.1. Body growth

The body length of an individual increased for each time step by using Eq. (SI.1).

\[ b(t)_{i} = b(t - 1) + \Delta b(t)_{i} \]  

(SI.1)

where, \( b \) was total body length (mm). Body length at age 0 was 0. Body growth, \( \Delta b(t)_{i} \), was calculated by using Eq. (SI.2).

\[ \Delta b(t)_{i} = bB_{i}(t) + bD_{i}(t) \]  

(SI.2)

where, \( bB \) was the baseline growth; \( bD \) was the growth affected by genetics, environments, and individual variation. We used the von Bertalanffy growth function to calculate \( bB \) and \( bD \). The baseline growth was given by Eq. (SI.3).

\[ bB_{i}(t) = bMx(1 - bA)kV_{i}(t) \]  

(SI.3)

where, \( bMx \) was the maximum mean asymptotic body length; \( bA \) affected the minimum asymptotic body length (\( = bMx(1 - bA) \)). When there was
no environmental effect on growth \((ce = 0)\) (Eq. (SI.10)), \(bA\) determined only the effect size of the allele improving growth. The default value for \(bA\) was 0.25 to make the body length of the smallest genotype at age 2 shorter than the average total body length of adults from three landlocked alewife populations \(= 97mm\) (Palkovacs et al., 2008). \(kV\) was the degree of growth calculated from the von Bertalanffy growth function (Eq. (SI.4)).

\[
kV_i(t) = e^{ev \frac{age_i(t-1)}{tx}} - e^{ev \frac{age_i(t)}{tx}} \tag{SI.4}
\]

where, \(age\) was the age of an individual; \(x\) was the index for sex; \(tx\) was the age (year) of the largest genotype becoming sexually matured. During spawning, 3-to-4-year-old males are abundant, and females dominate among older fish (Mullen et al., 1986). To reflect this, the default value for \(tx\) was 5 for females and 4 for males. The default value for an exponent, \(ev\), was \(log_{e}0.05\) to complete 95% of growth at \(tx\) when \(ce\), which was the environmental effect on growth (Eq. (SI.13)), was constant over time.

Based on the physiological concepts underlying the von Bertalanffy growth function, density-dependent growth mediated by resource competition is expected to affect the asymptotic size of fish, but not the growth rate at which this size is approached (Beverton & Holt, 1957; von Bertalanffy, 1960), and this was supported by theoretical and empirical studies (Walters & Post, 1993; Lorenzen, 1996; Shin & Rochet, 1998); for example, Lorenzen (Lorenzen, 1996, 2000) showed that a simple function with the asymptotic length de-
fined as a linear function of population biomass density described the density-dependent growth of fishes in various pond experiments ($L_{\infty B} = L_{\infty L} - gB$), where, $L_{\infty B}$, $L_{\infty L}$, $g$, and $B$ were the asymptotic body length, the limiting asymptotic body length, the decline in asymptotic body length per unit of biomass density, and biomass density, respectively). We used a stochastic, density-dependent extension of the von Bertalanffy growth function (Eq. (SI.5)) to describe fish growth in variable resources.

$$bD_i(t) \sim lnN(l_i, v_i) \quad (SI.5)$$

where, $bD_i(t)$, growth, was a random deviate drawn from the log-normal distribution ($lnN$) with the location, $l_i$, and the scale, $v_i$. To prevent biologically implausible growth, only uniform random deviates between $3.15 \times 10^{-5}$ and $1 - 3.15 \times 10^{-5}$, which were the quantiles within four standard deviations of the normal distribution, were used to draw random deviates from the log-normal distribution. $l$ and $v$ were calculated by using the mean, $\mu$, and the standard deviation, $\sigma$, of growth for a time step.

$$l_i = \log_e(\mu(t)_i) - \frac{1}{2}(v_i)^2 \quad (SI.6)$$

$$v_i = \log_e \left(1 + \frac{\sigma^2}{\mu(t)_i}\right) \quad (SI.7)$$

Standard deviation of growth, $\sigma$, was the product of mean growth, $\mu$, and
the coefficient variation of growth, $bcv$.

\[
\sigma = \mu(t)_{i}bcv \tag{SI.8}
\]

$bcv$ (default value = 0.01) determined the individual variation in growth. We used a local sensitivity analysis to study the effect of the individual variation in growth on fish morphological evolution. Mean growth, $\mu(t)_i$, was calculated by using Eq. (SI.9).

\[
\mu(t)_i = bMx \ cV_i(t)kV_i(t) \tag{SI.9}
\]

where, $bMx$ was the maximum mean asymptotic body length; $kV$ was the degree of growth calculated from the von Bertalanffy growth function. The asymptotic body length, $cV$ reflected the genetic and environmental effects on growth, and it was modeled as Eq. (SI.10).

\[
cV_i(t) = bA\{bR + (1 - bR)\[(1 - ce)A_i + ce \ ed_i(t)]\} \tag{SI.10}
\]

where, $bA$ controlled the minimum asymptotic body length ($0 \leq bA \leq 1$); $bR$ (default value = 0.1) was the minimum growth; $ed$ was the effect of resource mass on body length growth, and it is described in the following subsection; $ce$ determined the environmental effect on growth and sexual maturation. For this study, $ce$ was 0 (1) to focus on studying the default model behavior without the environmental effect on growth and sexual maturation and (2)
to limit the scope of this study. The genetic effect on growth, $A$, was given by Eq. (SI.11).

$$A_i = \frac{nmu_i}{nlu np} \quad (SI.11)$$

where, $nmu$ was the number of alleles improving growth; $nlu$ and $np$ were the number of loci affecting growth and the number of alleles per locus, respectively.

The minimum body length, $bMn$, was given by Eq. (SI.12).

$$bMn = bMx kV(1)[1 - (bA(1 - bR))] \quad (SI.12)$$

where, $bA$ determined the minimum body length; $bR$ was the minimum degree of growth; $kV(1)$ was the growth for 1-year-old fish calculated from the von Bertalanffy function.

### 2.2. Environmental effect

The effect of available prey mass on growth, $ed$, was calculated by using Eq. (SI.13).

$$ed_i(t) = e^{dg - \frac{ir_i(t)}{m_i(t)}} \quad (SI.13)$$

where, $dg$ was a scaling factor. The default value for $dg$ was $\log_e 0.75$ to set $ed$ to 0.75 when no density-dependent mortality occur ($\frac{ir_i(t)}{ed m_i(t)} = 1$). Density-dependent mortality is described in the following subsection. $ir$ was available prey mass for an individual.
The metabolic rate of an individual, $m$, was a function of body mass (Kleiber’s law (Kleiber, 1932)), and it was given by Eq. (SI.14).

\[
m_i(t) = \left[10^{-5.289}(bO_i(t))^{3.063}\right]^{3/4}
\]  

(SI.14)

where, $10^{-5.289}$ and $3.063$ were a scaling factor and an exponent for converting body length (mm) to body mass (g) for alewives, respectively (Schneider, 2000). $3/4$ was the exponent for converting body mass to metabolic rate. The body length (mm) under the optimum resources, $bO$, was calculated by using Eq. (SI.15).

\[
bO_i(t) = b(t - 1) + [(1 - bA) + bA[(1 - ce)A_i + ce)] kV_i(t)
\]  

(SI.15)

where, $b$ was body length (mm); $bA$ determined the minimum asymptotic body length; $ce$ determined the environmental effect on growth and sexual maturation; $A$ was the genetic effect on growth; $kV$ was the growth based on the von Bertalanffy growth function.

### 2.3. Density-dependent survival

A large body should be maintained by a sufficient food supply (Rosenzweig, 1968; Olalla-Trraga et al., 2006); accordingly, high metabolic rate of a large body can negatively affect survival if a food supply is limited. We reflected these relationships to describe the density-dependent survival of fishes. Density-dependent survival rate, $ddS$, was a function of a metabolic
rate, \( m \), and the prey mass accessible to an individual, \( ir \). The Beverton-Holt function was used to calculate \( ddS \) (Eq. (SI.16)).

\[
ddS_i(t) = \frac{1}{1 + cD \frac{m_i(t)}{ir_i(t)}} \tag{SI.16}
\]

where, \( cD \) was the scaling factor for density-dependent survival. The default value for \( cD \) was 10, which was an arbitrary value because of the lack of empirical data. \( m \) was a metabolic rate. The prey mass accessible to an individual, \( ir \), was affected by prey abundance, \( rsc \), prey body mass, \( rMu \), a functional response, \( frp \) (Eq. (SI.24)), and their foraging time for prey, \( ft \) (Eq. (SI.27)). We used Eq. (SI.17) to calculate \( ir \).

\[
ir_i(t) = \sum_r \sum_{rc} rsc_{r,rc}(t - 1)ru_{r,rc}frp_{i,r,rc}(t)ft_{i,r,rc}(t) \tag{SI.17}
\]

where, \( i \) was the index for an individual; \( r \) was the index for a prey cluster; \( rc \) was the index for a size class of a prey cluster; \( cp_{r,rc}(t) \) represented the resource competition among alewives.

\[
cp_{r,rc}(t) = \sum_i frp_{i,r,rc}(t)ft_{i,r,rc}(t) \tag{SI.18}
\]

We acknowledged that other density-dependent-survival functions can be used to describe the relationship between density-dependent survival and prey mass.
2.4. Fish’s Foraging

2.4.1. Body size and foraging for large prey. Body size and prey size are positively correlated for many fish species (Keast & Webb, 1966; Popova, 1967, 1978; Nielsen, 1980; Persson, 1990; Juanes et al., 1994). This trend is also found in alewifes (Kohler & Ney, 1980). To reflect this, for this model, fish body size limited the efficiency of their foraging for large prey. This was modeled as Eq. (SI.19).

\[ u_i(t) = 0.01[10^{-5.289}(bO_i(t)^{3.063})] \] (SI.19)

where, \( u \), a parameter for the sigmoid function for limiting the efficiency of their foraging for large prey; \( bO \) was the body length (mm) used for calculating the available prey mass for an individual (Eq. (SI.15)); \( 10^{-5.289} \) and 3.063 were a scaling factor and an exponent for converting fish body length (mm) to body mass (g), respectively (Schneider, 2000). The body mass was multiplied by 0.01 to allow one-year-old anadromous alewives to forage for fish eggs (0.1 – 0.2g). Fish gape size was assumed to be allometrically related to the body mass.

2.4.2. Gill-rakers and foraging for small resources. The role of a gill raker apparatus is related to prey retention efficiency (Drenner, 1977; Sanderson et al., 2001; Smith & Sanderson, 2008). An increasing number of gill rakers enhances cross-flow filtering, and closely spaced gill rakers limit
the escape possibility of small prey (Kahilainen et al., 2011); thus, a high number of long gill rakers is common in planktivorous fish species and morphs although benthic species and morphs usually display a low number of shorter gill rakers (Janssen, 1980; Gibson, 1988; Schluter & McPhail, 1992; Langeland & Nøst, 1995; Robinson & Parsons, 2002). For this model, gill-raker spacing, which determined the efficiency of their foraging for small prey, $l$, improved as the number of gill rakers increased (Kahilainen et al., 2011) and/or body size decreased (MacNeill & Brandt, 1990; Friedland et al., 2006; Palkovacs et al., 2008). These relationships were modeled as Eq. (SI.20).

$$ l_i(t) = lMn + (LMx - lMn)(1 - B) \left[ \frac{bO_i(t) - wMn}{wMx - wMn} \right]^{eb} \quad (SI.20) $$

where, $nml$ was the number of the alleles increasing a gill-raker number; $B$ ($= \frac{nml}{nll np}$) was the genetic effect on a gill-raker number; $nll$ was the number of the loci affecting a gill-raker number; $np$ was the number of alleles for a locus; $eb$ (default value = 0.125) determined the effect of fish body size on their foraging for small prey. Because $eb$ has not been empirically estimated, we used a sensitivity analysis to study the effect of $eb$ on fish morphological evolution. The maximum and minimum values for gill-raker spacing, $l$, were $LMx$ and $LMn$, respectively. The default value for $LMx$ was 0.02, which was twice the body mass of large zooplankton (= 0.01g). The default value for $LMn$ was 0.001, which was 10% of large zooplankton body mass. The maximum and minimum body masses were $wMx$ and $wMn$, respectively.
$wMx$ and $wMn$ were derived from the asymptotic body length, $bMx$, and the minimum body length, $bMn$, by using the alewife body-length-body-mass relationship (body mass (g) = $10^{-5.289}[\text{body length (mm)}]^{3.063}$) (Schneider, 2000).

2.4.3. Clogged gill rakers. Large particles are more likely to clog small inter-gill-raker spacing than small particles; accordingly, small gill-raker spacing can decrease the efficiency of their foraging for large prey. Eq. (SI.21) described a decrease in their foraging efficiency caused by small gill-raker spacing.

$$pf(k, l, lp) = \begin{cases} \left(\frac{1}{k}\right)^{lp} & \text{if } k > l \\ 1 & \text{if } k \leq tl \end{cases}$$

(SI.21)

where, $lp$ determined a decrease in the efficiency of their foraging for large prey. We used a local sensitivity analysis to study the effect of $lp$ on the morphological evolution of fish. The default value for $lp$ was 0.5, which was an arbitrary value chosen because of the lack of empirical data.
2.4.4. Foraging efficiency.

Body size and gill-raker spacing affected fishes’ foraging for different-sized prey for this model, and this was modeled as Eq. (SI.22) (Fig. 2).

\[
fe(k, u, l, fs, lp) = \begin{cases} 
 pf(k, l, lp)cF(u, l, fs) \left[ \frac{1}{1+e^{-fs(\log_{10} \frac{u}{l})}} \right] \left[ 1 - \frac{1}{1+e^{-fs(\log_{10} \frac{u}{l})}} \right] & \text{if } u > l \\
 0 & \text{if } u \leq l 
\end{cases}
\]

(SI.22)

where, \( fe \) was foraging efficiency; \( k \) was prey body mass; \( pf \) was the function describing a decrease in their foraging efficiency caused by small gill-raker spacing (See the clogged gill rakers subsection); \( fs \) determined a decrease in their foraging efficiency at around \( u \), which represented fish body size, and \( l \), which represented gill-raker spacing. The terms inside the first square bracket described the efficiency of their foraging for small prey. When \( u > l \), the foraging efficiency was 0.5 at \( l \). The terms inside the second square bracket described the efficiency of their foraging for large prey. When there is no decrease in the efficiency of foraging for large prey due to narrow gill-raker spacing (\( pf(k, l, 0) = 1 \)), \( cF \) set fish foraging efficiency to the maximum (=1) at \( \frac{\log_{10} u + \log_{10} l}{2} \) (Eq. (SI.23)).

\[
cF(u, l, fs) = \frac{2 + e^{-fs(\log_{10} \frac{u + \log_{10} l}{2} - \log_{10} l)} + e^{-fs(\log_{10} \frac{u + \log_{10} l}{2} - \log_{10} u)}}{e^{-fs(\log_{10} \frac{u + \log_{10} l}{2} - \log_{10} l)}}
\]

(SI.23)
Some large predators can demonstrate fast swimming speed and improved visual acuity (Keast & Webb, 1966; Webb, 1976; Beamish, 1978; Hubbs & Blaxter, 1986; Scharf et al., 2000); large preys may escape from predators better due to improved escape response, reaction distance, and swimming performance (Folkvord & Hunter, 1986; Blaxter & Fuiman, 1990; Scharf et al., 2000). These correlations were not modeled to limit the scope of this study.

2.4.5. Functional response. We assumed that fishes showed the type II functional response, which was given by Eq. (SI.24).

\[
frp_{i,r,rc}(t) = fnc(rsc_{r,rc}(t - 1), fe(rMu_{r,rc}, u_i, l_i), ht_r, bf_{r,rc})
\]  
(SI.24)

\[
fnc(x, af, ht, bf) = \frac{af \cdot x^{bf}}{1 + (af \cdot ht \cdot x^{bf})}
\]  
(SI.25)

where, \(frp\) was the efficiency of foraging with a functional response; \(fnc\) was a functional response; \(af\) was attack rate; \(bf\) was the exponent for prey density, whose default value was 1 because we assumed the type II functional response by fishes; \(ht\) was handling time, and it was given by Eq. (SI.36).

\[
ht_r = \frac{cH_r \cdot cn}{ra_r}
\]  
(SI.26)

where, \(cH\) was a parameter for handling time; \(cn\) was the number of size classes in a prey cluster. \(ra\) was the prey abundance predicted by a body-
mass-abundance relationship of ecological power laws (Marquet, 2002; Jennings & Mackinson, 2003) (Eq. (SI.36)).

2.4.6. Foraging time. Traditional foraging theories predict that a predator should choose a prey species providing a better net energy return rate (Schoener, 1971; Charnov, 1976; Stephens & Krebs, 1986; Scharf et al., 2000). Similarly, alewives interchangeably use filter-feeding and particulate-feeding modes as zooplankton size and density change (Janssen, 1976); therefore, for this model, alewives spent more time for foraging for prey with larger total mass (=abundance × body mass). We used Eq. (SI.27) to calculate the proportion of time that an individual foraging for different-sized prey, ft.

\[ ft_{i,r,rc}(t) = \frac{frp_{i,r,rc}(t)ru_{r,rc}}{\sum_r \sum_{rc} [frp_{i,r,rc}(t)ru_{r,rc}]} \] (SI.27)

where, ru was the per capita prey body mass.

2.5. Sexual maturation

Landlocked alewives display smaller adult body size and maturity at an earlier age than anadromous alewives (Palkovacs et al., 2008; Palkovacs & Post, 2008; Schielke et al., 2011). Landlocked alewives may spawn as early as 2 years old (Lackey, 1970) although 3-to-10-year-old adults of anadromous alewives dominate spawning grounds (Joseph & Davis, 1965; Marcy Jr, 1969; ONeill, 1980; Mullen et al., 1986). To reflect this correlation between body
size and sexual maturity, we assumed that the alleles increasing fishes' body size delayed their sexual maturation as a trade-off. Besides this pleiotrophic effect, an increase in resource availability generally accelerates fishes’ reproductive ontogeny and growth; therefore, fishes mature earlier at larger sizes when their resource is abundant (Trexler, 1989; Reznick et al., 1990). The genetic and environmental effects on sexual maturation, $sB$, were modeled as Eq. (SI.28).

$$sB_i(t) = (1 - ce)(1 - A_i) + ce \, ed_i(t) \quad \text{(SI.28)}$$

where, $ce$ was the parameter determining the environmental effect on fish growth and sexual maturation; $A$ was the genetic effect on fish growth and sexual maturation; $ed$ was the effect of prey mass on fish growth.

For this model, fishes reproduced once they were sexually matured, and the probability of sexual maturation, $sm$, was given by Eq. (SI.29).

$$sm_i(t) =
\begin{cases}
0 & \text{if } sB_i(t) = 0 \text{ or } age_i < (tx_x - eag_x) \\
(sB_i(t))^{\frac{1}{sg}} & \text{if } sB_{i,x}(t) > 0 \text{ and } (tx_x - eag_x) \leq age_i < tx_x \\
1 & \text{if } age_i \geq tx_x
\end{cases} \quad \text{(SI.29)}$$

where, $sg$ was life stage; $i$ was the index for an individual; $x$ was the index for sex; $tx$ was the oldest age for sexual maturation; $eag$ was the duration (years) that an individual had a chance of sexual maturation −1. When
\[ e_{ag} = 0, \text{ all individuals sexually matured at } t_x. \]

### 2.6. Reproduction

Fertility in many fish species increases with body size (Bagenal, 1967; Gross, 1987). We used Eq. (SI.30) to describe this relationship.

\[
F_i(t) = f_{mx} \left( \frac{w_i(t)}{w_{Mx}} \right)^{frb} \quad (SI.30)
\]

where, \( F \) was the mean number of newborn female offspring from a mated female for a time step; \( f_{mx}, w, \) and \( w_{Mx} \) were the maximum fertility, body mass, and the maximum body mass, respectively; \( f_{mx} \) for alewives was 121.27 to set the maximum annual reproductive rate for three-year-old females of the largest genotype to 85, which was the median of the maximum annual reproductive rate estimated in eight alewife populations with the two-parameter compensatory spawner-recruit Beverton-Holt model (Myers et al., 1999; Barrowman, 2000; Myers et al., 2001; Gibson & Myers, 2004); \( frb (= 0.893) \) was an exponent for the body-mass-fertility conversion, which was based on the body-mass-fertility relationship in whitefish and vendace (Sandlund et al., 2013). The body-mass-fertility relationship in alewives has not been estimated.

Alewives breed once a year at ponds, lakes, or slow-flowing portions of stream (Scott & Scott, 1988). Alewives show polygynandrous (promiscuous) mating system and iteroparity. Anadromous and landlocked alewives do not
typically co-exist in the same lake (Palkovacs et al., 2008). The polygynandrous mating, oviposition, and fertilization of alewives were simulated by using Algorithm (SI.2).
if an individual is a sexually-matured female then
   \( nf \sim \text{discrete normal distribution } (\mu = F_i(t)cX, \sigma^2 = (Fsd_i(t))^2) \)
   if \( nf > 0 \) then
      \( j = 1 \)
      while \( j < (nf + 1) \) do
         Draw one gamete from the chosen male and one gamete
         from the female individual, and then set the genotype for
         offspring.
         \( u \sim \text{Uniform distribution}[0,1] \)
         if \( u < fp \) then
            The newborn offspring is female.
         else
            The newborn offspring is male.
         end
         \( j = j + 1 \)
      end
   end
end

Algorithm 2: Algorithm for the polygynandrous mating, oviposition, and fertilization of alewives
where, $Fsd$ was the standard deviation of the number of female offspring from a mated female for a time step. $nf$ was the number of offspring from a mated female for a time step. To prevent biologically implausible fertility of fish, only uniform random deviates between $3.15 \times 10^{-5}$ and $1 - 3.15 \times 10^{-5}$, which were the quantiles within four standard deviations of the normal distribution, were used to draw random deviates from the normal distribution. Instead of the discrete normal distribution, Poisson distribution can be used to draw the number of newborn offspring if the mean and standard deviation are equal. $cX$ was a factor for converting the number of female offspring to the number of male and female offspring. $cX$ was given by Eq. (SI.31).

$$cX = \left[ 1.0 + \left( \frac{1.0 - fp}{fp} \right) \right] \quad \text{(SI.31)}$$

where, $fp$ was the proportion of newborn female offspring. The default value for $fp$ was 0.5 because the sex ratio of alewives is approximately $1:1$ (Mullen et al., 1986). For the gamete formation, one of two alleles was randomly chosen for each locus. Genetic mutation in alewives was implemented by switching alleles (0 or 1) with the genetic mutation rate ($= 10^{-5}$).

3. Size-structured prey clusters (prey of alewives)

We modeled the prey of alewives as multiple, discrete, size-structured clusters with different trophic positions. Instead of using conventional approaches with the assumption of the continuous body size distribution of species, we
took this food web modeling approach to study fish morphological evolution in food webs governed by mechanisms previously not investigated. Prey clusters were sorted by their representative body masses in ascending order. The representative body masses except the maximum \((r \mu_{r_{\text{rn}}})\) or minimum \((r \mu_{r_{1}})\) representative body masses was determined by Eq. (SI.32).

\[
r \mu_{r} = \left( \frac{r \mu_{r_{\text{rn}}}}{r \mu_{r_{1}}} \right)^{\frac{r-1}{r-1}}
\]

where, \(r\) was the index for a prey cluster; \(r_{n}\) was the number of prey clusters.

For this study, two or three prey clusters were simulated because one or more clusters went extinct when over three clusters were simulated under the default parameter setting. The default value for \(r \mu_{r_{\text{rn}}}\) was 5 when there were three prey clusters, and it was 0.224 when there were two prey clusters. The default for \(r \mu_{r_{1}}\) was 0.01. Under these settings, the representative body masses for three prey clusters were 0.01g, which represented the body mass of large zooplankton, 0.224g, which represented the body mass of a large fish egg, and 5g, which represented the body mass of small organisms foraging for zooplanktons and fish eggs. Only the smallest two prey clusters were simulated when there were two prey clusters.

The range of body mass of a prey cluster \([r \mu_{r} - 3wSD_{r}, r \mu_{r} + 3wSD_{r}]\) was defined by using the representative body mass, \(r \mu_{r}\), and the standard deviation of body mass in a prey cluster, \(wSD\). We used Eq. (SI.33) to
calculate $wSD$.

$$wSD_r = rCV \ rMu_r$$  \hspace{1cm} (SI.33)

where, $rCV$ (default value = 0.3) was the coefficient variation of the body mass.

The range of body mass in a prey cluster was divided into equal-width body size classes. For simplicity, we assumed that organisms in prey clusters were diploid and reproduced asexually. In addition, we assumed that unlinked-biallelic QTL determined the body mass of organisms in prey clusters. The default number of the loci affecting prey body mass was 10; therefore, the number of size classes in a prey cluster, $cn$, was 21 (the number of alleles at loci × the number of alleles for a locus +1), which described the prey size spectrum with the moderate increase in computation time.

### 3.1. Prey dynamics

Trophic interactions and within-trophic competitions affected prey abundance. Prey abundance was negatively influenced by (1) the competition within a prey cluster, (2) the predation by larger-bodied prey clusters, and (3) the predation by alewives; prey abundance was positively influenced by foraging for smaller-bodied prey clusters. We used the discrete Lotka-Volterra equation (Eq. (SI.34)) to describe prey dynamics (Leslie, 1958; Liu & Elaydi, 2001).

$$rt_{r,rc}(t) = \frac{1 + ri_{r,rc} + pI_{r,rc}(t)}{1 + sI_r(t) + nI_{r,rc}(t) + fI_{r,rc}(t)}$$  \hspace{1cm} (SI.34)
where, $r_t$ was prey abundance before the dynamics within a prey cluster was calculated by using Eq. (SI.44); $s_I$, $n_I$, $p_I$, and $f_I$ were the effect of the competition in a prey cluster, the effect of smaller-bodied prey clusters on larger-bodied prey, the effect of larger-bodied prey clusters on smaller-bodied prey, and the effect of fish’s foraging for prey, respectively. $s_I$, $n_I$, $p_I$, and $f_I$ were calculated by using allometric relationships derived from ecological power laws (Eq. (SI.35), Eq. (SI.38), Eq. (SI.42)), which are described in the following subsections. $r_i$ was the intrinsic growth rate of a size class of a prey cluster. $r_i$ was 1 for the size classes of the smallest-bodied prey cluster, but it was 0 for the size classes of other prey clusters.

### 3.1.1. Within-trophic competition and trophic interactions.

We used a body-mass-abundance relationship of ecological power laws (Marquet, 2002; Jennings & Mackinson, 2003) (Eq. (SI.36)) to calculate the effect of the competition within a prey cluster on prey abundance, $s_I$, which was given by Eq. (SI.35).

$$s_I(t) = \frac{1}{r_a} \sum_{r_c} r_{sc,rc}(t - 1)$$

(SI.35)

where, $r_{sc}$ was prey abundance after the dynamics within a prey cluster was calculated by using Eq. (SI.44). We used Eq. (SI.36) to describe the body-mass-abundance relationship, and the body-mass-abundance relationship was used to calculate the expected prey abundance, $r_a$.

$$r_a = cA(rMu_r)^{-\gamma A}$$

(SI.36)
where, $ra$, $cA$, $eA$, and $rMu$ were the expected prey cluster abundance, a constant for prey body mass, an exponent for prey body mass, and the representative body mass of a prey cluster, respectively. $eA$ estimated at Tuesday Lake in 1984 (Reuman et al., 2008), Tuesday Lake in 1986 (Jonsson et al., 2005; Reuman et al., 2008), and Ythan Estuary (Reuman et al., 2008) were 0.84, 0.75, and 1.1, respectively. We used a local sensitivity analysis to study the effect of $eA$ on fish morphological evolution. The default value for $eA$ was 0.75.

The strength of trophic interactions was a function of predator-prey body mass ratio (West et al., 1997; Brown & Gillooly, 2003; Emmerson & Raffaelli, 2004; O’Gorman et al., 2010). The effect of the predation by larger-bodied prey clusters on smaller-bodied prey, $nI$, was described by Eq. (SI.37).

$$ nI_{r,rc}(t) = \sum_{r \neq r} \left[ fnc(\sum_{rc} rsc_{r,rc}(t - 1)), in_{r,r}, \frac{cH_r}{ra_r}, bf_r \right] $$ (SI.37)

where, $fnc$ (Eq. (SI.25)) was a functional response; $cH$ and $bf$ were handling time and an exponent for prey abundance in a functional response, respectively. The default value for $cH$ was 0.1 to reduce the foraging efficiency by 50% when the abundance of prey was 10% of the abundance predicted by the body-mass-abundance relationship (Eq. (SI.36)). $in$ was a scaling factor for $nI$, and it was a function of predator-prey body mass ratio. We used
Eq. (SI.38) to calculate $in_r$.

$$in_{r_1,r_2} = \begin{cases} 
  c_i \left( \frac{rM_{u_1}}{rM_{u_2}} \right)^{eI} & \text{if } rM_{u_2} \geq rM_{u_1} \\
  0 & \text{if } rM_{u_2} < rM_{u_1}
\end{cases} \quad (SI.38)$$

where, $r1$ and $r2$ were the indices for a smaller-bodied prey cluster and a larger-bodied prey cluster, respectively; $c_i$ (default value = $2.5 \times 10^{-6}$) was a scaling factor for predator-prey body mass ratio; $eI$ was an exponent for predator-prey body mass ratio. The default value for $eI$ was 0.25, which was the theoretically predicted value based on an allometric scaling relationship to approximate basal metabolic rate per unit body mass (West et al., 1997; Brown & Gillooly, 2003; O’Gorman et al., 2010).

Eq. (SI.39) described the effect of smaller-bodied prey clusters on larger-bodied prey, $pI_r$.

$$pI_{r,rc}(t) = \sum_{r_k \neq r} \left[ i_p r_k \sum_{r_c} r_s c_{r_k,rc}(t-1) \right] \quad (SI.39)$$

where, $i_p$ was a scaling factor for the effect of foraging by a smaller-bodied cluster on larger-bodied prey. $i_p$ was given by Eq. (SI.38).

$$i_{p_{r_2,r_1}} = pc \frac{fnc(\sum_{rc} r_s c_{r_1,rc}(t-1), in_{r_1,r_2}, \frac{cH_{r_1}}{r_{r_1}}, b_{fr_1})}{\sum_{rc} r_s c_{r_1,rc}(t-1)} \quad (SI.40)$$

where, $r1$ and $r2$ were the indices for a smaller-bodied cluster and a larger-
bodied cluster, respectively; \( pc \) (default value = 0.01) was a scaling factor for predator-prey body mass ratio; \( fnc \) was a functional response (Eq. (SI.25)); \( cH \) was handling time; \( bf \) was an exponent for prey abundance; \( ra \) was the prey cluster abundance predicted by the body-mass-abundance relationship (Eq. (SI.36)).

### 3.1.2. Fish’s foraging effect on prey abundance.

The effect of alewives’s foraging on prey abundance, \( fI \), was given by Eq. (SI.41).

\[
fI_{r,rc}(t) = \sum [fc_{r,s}nc_{r,rc}(t)cn] \tag{SI.41}
\]

\[
f_c = cn ci(rMu_rwf)^cI \tag{SI.42}
\]

The number of size classes in a prey cluster, \( cn \), scaled \( fI \) to set the effect of foraging by an individual on a size class of a prey cluster to \( fc \) when an individual spent an equal proportion of the total foraging time for all size classes of a prey cluster with the maximum foraging efficiency (\( = 1 \)). The representative body mass for alewives (\( wf = 30.27g \)) was the mean body mass of female alewives of the largest genotype at the stable-stage distribution, which was calculated from a Leslie matrix shown in the fish vital processes section. \( nc \) was the number of alewives foraging for prey, and it was given by Eq. (SI.27).

\[
nc_{r,rc}(t) = \sum_i \left[ \frac{fr_p_{i,r,rc}(t)}{rsc_{r,rc}(t-1)} ft_{i,r,rc}(t) \right] \tag{SI.43}
\]
where, \( frp \) was the efficiency of foraging with a functional response (Eq. (SI.24));
\( ft \) was foraging time.

### 3.2. Dynamics within prey cluster

A fraction of prey in a size class of a prey cluster was assumed to move to neighbour size classes for each time step because of genetic mutation. Eq. (SI.44) described this process, and it was calculated after prey abundance, \( rt \), was calculated by using Eq. (SI.34).

\[
\begin{align*}
r_{sc_{r,rc}}(t) &= \begin{cases} 
(1 - m_r)rt_{r,rc}(t) + \left[\frac{r_c - 1}{tp_r}m_rrt_{r,rc-1}(t)\right] \\
(1 - m_r)rt_{r,rc}(t) + [(1 - \frac{r_c + 1}{tp_r})m_rrt_{r,rc+1}(t)] & \text{if } 1 < r_c < tp_r, \quad \text{(SI.44)} \\
[(1 - m_r)rt_{r,rc}(t)] + [(1 - \frac{r_c + 1}{tp_r})m_rrt_{r,rc+1}(t)] & \text{if } r_c = 1 \\
[(1 - m_r)rt_{r,rc}(t)] + \left[\frac{r_c - 1}{tp_r}m_rrt_{r,rc-1}(t)\right] & \text{if } r_c = tp_r
\end{cases}
\end{align*}
\]

\[
m_r = \left(\frac{tp_r}{1}\right)(mta_r)^1(1 - mta_r)^{tp_r - 1} \quad \text{(SI.45)}
\]

where, \( r_{sc} \) was prey abundance after the dynamics within a prey cluster was calculated by using Eq. (SI.44); \( rt \) was prey abundance before the dynamics within a prey cluster was calculated by using Eq. (SI.44); \( mta \) was the mutation rate for prey; \( tp \) was the number of alleles in the loci determining prey body size \(+1\); \( mt \) was the fraction of prey moving to neighbour size classes. For simplicity, we assumed that only one mutation occur for prey for each
time step.

4. Initial condition

Only prey had been simulated for the first 1000 years to form size-structured prey clusters without alewives. At the 1001th year, adult alewives (500 males and 500 females) were introduced into an ecosystem. Under the default parameter setting, when the default values for $ci$, $pc$, and $cA$ were used, the abundance of prey clusters converged to positive values when alewives were introduced into the ecosystem. The alleles for the alewives of the initial population were randomly drawn by using allele frequencies. The default value for the initial frequency of the allele improving growth ($P(A)_{t=0}$) was 0.99, and that for the frequency of the allele increasing a gill-raker number ($P(B)_{t=0}$) was 0.01; therefore, we attempted to describe anadromous alewives with standing genetic variation for the initial population. We used a local sensitivity analysis to study the effect of the initial allele frequencies on fish morphological evolution.

We used the body-mass-abundance relationship (Eq. (SI.36)) to set the abundance of organisms in a prey cluster for the initial time step. The initial size distribution for prey was given by Eq. (SI.46).

$$rsc_{r,rc}(0) = ra_r \left[ \text{cdfNorm}(bl_{r,rc} + \frac{6 \cdot wSD_r}{tpr_r}, rMu_r, wSD_r) - \text{cdfNorm}(bl_{r,rc}, rMu_r, wSD_r) \right]$$

(SI.46)
where, \( \text{cdfNorm} \) was the cumulative normal distribution function; \( tp \) was the number of alleles in the loci determining prey body size +1; \( rMu \) was the representative body mass of a prey cluster; \( wSD \) (default value = 0.3 \( \times \) \( rMu \)) was the standard deviation of body mass in a prey cluster; \( bl \) was the lower bound of a size class (bin).
References


Scott, W. B., & Scott, M. G. 1988. *In: Atlantic fishes of Canada.* Published by the University of Toronto Press in cooperation with the Minister of Fisheries and Oceans and the Canadian Government Publishing Centre, Supply and Services Canada.


Supporting information II:
Model input parameter settings

Table SI.2.1: List of symbols

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Equation([ ]) or algorithm(( ))</th>
<th>Default value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A$</td>
<td>[SI.11]</td>
<td>-</td>
<td>The genetic effect on growth</td>
</tr>
<tr>
<td>$af$</td>
<td>[SI.25]</td>
<td>-</td>
<td>Attack rate</td>
</tr>
<tr>
<td>$B$</td>
<td>[SI.20]</td>
<td>-</td>
<td>The genetic effect on a gill-raker number</td>
</tr>
<tr>
<td>$b$</td>
<td>[SI.1]</td>
<td>-</td>
<td>Body length (mm)</td>
</tr>
<tr>
<td>$bA$</td>
<td>[SI.3,SI.10,SI.12]</td>
<td>0.25</td>
<td>The parameter controlling the minimum asymptotic body length</td>
</tr>
<tr>
<td>$BB$</td>
<td>[SI.2,SI.3]</td>
<td>-</td>
<td>The baseline body length growth</td>
</tr>
<tr>
<td>$bcv$</td>
<td>[SI.8]</td>
<td>-</td>
<td>The coefficient variation of body length growth</td>
</tr>
<tr>
<td>$bf$</td>
<td>[SI.25]</td>
<td>-</td>
<td>An exponent for prey density in a functional response</td>
</tr>
<tr>
<td>$bl$</td>
<td>[SI.46]</td>
<td>-</td>
<td>The lower bound for a size class in a prey cluster</td>
</tr>
<tr>
<td>$bMx$</td>
<td>[SI.9,SI.12]</td>
<td>273.68mm</td>
<td>The maximum body length</td>
</tr>
<tr>
<td>Symbol</td>
<td>Description</td>
<td>Units</td>
<td>Notes</td>
</tr>
<tr>
<td>--------</td>
<td>-------------</td>
<td>-------</td>
<td>-------</td>
</tr>
<tr>
<td>$bMn$</td>
<td>The minimum body length</td>
<td>[SI.12]</td>
<td>-</td>
</tr>
<tr>
<td>$bO$</td>
<td>Body length (mm) used for calculating the available resource mass for an individual</td>
<td>[SI.19]</td>
<td>-</td>
</tr>
<tr>
<td>$bR$</td>
<td>The minimum degree of body length development</td>
<td>[SI.12,SI.10]</td>
<td>0.1</td>
</tr>
<tr>
<td>$cA$</td>
<td>A scaling factor for species body mass-abundance relationship</td>
<td>[SI.35]</td>
<td>$5.0 \times 10^6$</td>
</tr>
<tr>
<td>$cD$</td>
<td>A scaling factor for $\frac{m}{r}$ to calculate density-dependent-survival rate</td>
<td>[SI.16]</td>
<td>10</td>
</tr>
<tr>
<td>$ce$</td>
<td>The parameter controlling the environmental effect on growth and sexual maturation</td>
<td>[SI.10,SI.28]</td>
<td>0</td>
</tr>
<tr>
<td>$cF$</td>
<td>The function controlling the foraging efficiency at the midpoint between $\log_{10} tu$ and $\log_{10} tl$ to 1 when $lp = 0$</td>
<td>[SI.23]</td>
<td>-</td>
</tr>
<tr>
<td>$cH$</td>
<td>The parameter controlling handling time</td>
<td>[SI.37]</td>
<td>0.1</td>
</tr>
<tr>
<td>$ci$</td>
<td>A scaling factor for $in$</td>
<td>[SI.38,SI.42]</td>
<td>$2.5 \times 10^{-6}$</td>
</tr>
<tr>
<td>$cn$</td>
<td>The number of size classes for a prey cluster</td>
<td>[SI.41]</td>
<td>21</td>
</tr>
<tr>
<td>$cp$</td>
<td>The number of individuals competing</td>
<td>[SI.18]</td>
<td>-</td>
</tr>
</tbody>
</table>

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<table>
<thead>
<tr>
<th>Symbol</th>
<th>SI</th>
<th>Description</th>
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<tbody>
<tr>
<td>$cV$</td>
<td>[SI.9,SI.10]</td>
<td>The asymptotic body length for a resource</td>
</tr>
<tr>
<td>$cX$</td>
<td>[SI.31]</td>
<td>A scaling factor for converting the number of new female offspring to the number of new male and female offspring</td>
</tr>
<tr>
<td>$ddS$</td>
<td>[SI.16]</td>
<td>Density-dependent-survival rate</td>
</tr>
<tr>
<td>$dg$</td>
<td>[SI.13]</td>
<td>$\log,0.75$ A scaling factor for $ed$</td>
</tr>
<tr>
<td>$eA$</td>
<td>[SI.35]</td>
<td>0.75 An exponent for body-mass-abundance relationship</td>
</tr>
<tr>
<td>$eag$</td>
<td>[SI.29]</td>
<td>Male: 2, Female: 3 The duration (years) that an individual had a chance of sexual maturation $-1$</td>
</tr>
<tr>
<td>$eb$</td>
<td>[SI.20]</td>
<td>0.125 The effect of body size on fish’s foraging for small prey</td>
</tr>
<tr>
<td>$ed$</td>
<td>[SI.10,SI.13,SI.28]</td>
<td>- The effect of resource mass on body length growth</td>
</tr>
<tr>
<td>$eI$</td>
<td>[SI.38,SI.42]</td>
<td>0.25 An exponent for predator-prey body mass ratio</td>
</tr>
<tr>
<td>$F$</td>
<td>[SI.30]</td>
<td>- The number of female offspring from a mated female</td>
</tr>
<tr>
<td>$fc$</td>
<td>[SI.42]</td>
<td>- A scaling factor for the effect</td>
</tr>
</tbody>
</table>
of foraging by an individual fish on a size class of a prey cluster

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
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</thead>
<tbody>
<tr>
<td>$fe$</td>
<td>[SI.22] Fish foraging efficiency</td>
</tr>
<tr>
<td>$fI$</td>
<td>[SI.41] Fish foraging effect on a resource</td>
</tr>
<tr>
<td>$fmx$</td>
<td>[SI.30] 121.27 The maximum fertility</td>
</tr>
<tr>
<td>$fnc$</td>
<td>[SI.25] Functional response</td>
</tr>
<tr>
<td>$fp$</td>
<td>[SI.31] The proportion of new female offspring</td>
</tr>
<tr>
<td>$frb$</td>
<td>[SI.30] 0.893 An exponent for body mass-fertility conversion</td>
</tr>
<tr>
<td>$frp$</td>
<td>[SI.24] The efficiency of foraging with a functional response</td>
</tr>
<tr>
<td>$fs$</td>
<td>[SI.22] 10 The parameter controlling the difference between the efficiency of foraging on small (or the large) resources and that on medium-sized resources</td>
</tr>
<tr>
<td>$Fsd$</td>
<td>Algorithm 2 0.25$F$ The standard deviation of the number of female offspring from a mated female</td>
</tr>
<tr>
<td>$ft$</td>
<td>[SI.27] - The proportion of time an individual foraging a resource</td>
</tr>
<tr>
<td>$G$</td>
<td>algorithm 1</td>
</tr>
<tr>
<td>-----</td>
<td>-------------</td>
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<tr>
<td>$ht$</td>
<td>[SI.25]</td>
</tr>
<tr>
<td>$i$</td>
<td>Index</td>
</tr>
<tr>
<td>$in$</td>
<td>[SI.38]</td>
</tr>
<tr>
<td>$ip$</td>
<td>[SI.40]</td>
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<tr>
<td>$ir$</td>
<td>[SI.17]</td>
</tr>
<tr>
<td>$it$</td>
<td>[SI.35]</td>
</tr>
<tr>
<td>$kV$</td>
<td>[SI.4,SI.9]</td>
</tr>
<tr>
<td></td>
<td>SI.15,SI.12</td>
</tr>
<tr>
<td>$l$</td>
<td>[SI.20]</td>
</tr>
<tr>
<td>$lp$</td>
<td>[SI.21]</td>
</tr>
<tr>
<td>$lMx$</td>
<td>[SI.19]</td>
</tr>
<tr>
<td>$lMn$</td>
<td>[SI.19]</td>
</tr>
<tr>
<td>$m$</td>
<td>[SI.14]</td>
</tr>
<tr>
<td>Symbol</td>
<td>Description</td>
</tr>
<tr>
<td>--------</td>
<td>-------------</td>
</tr>
<tr>
<td>$mt$</td>
<td>The proportion of the resource changing body mass</td>
</tr>
<tr>
<td>$m_{ta}$</td>
<td>Mutation rate for resource organisms</td>
</tr>
<tr>
<td>$\mu$</td>
<td>Mean growth</td>
</tr>
<tr>
<td>$nc$</td>
<td>The number of individuals foraging for a resource</td>
</tr>
<tr>
<td>$nI$</td>
<td>The effect of predators on prey</td>
</tr>
<tr>
<td>$nll$</td>
<td>The number of loci controlling the lower-foraging bound</td>
</tr>
<tr>
<td>$nlu$</td>
<td>The number of loci controlling the upper-foraging bound</td>
</tr>
<tr>
<td>$nml$</td>
<td>The number of alleles lowering the lower-foraging bound</td>
</tr>
<tr>
<td>$nmu$</td>
<td>The number of alleles raising the upper-foraging-size bound</td>
</tr>
<tr>
<td>$np$</td>
<td>The number of alleles for a locus</td>
</tr>
<tr>
<td>$P$</td>
<td>The probability an individual surviving at the current life stage</td>
</tr>
<tr>
<td>$P(A)_{t=0}$</td>
<td>The initial frequency of the allele increasing body size</td>
</tr>
<tr>
<td>$P(B)_{t=0}$</td>
<td>The initial frequency of the allele</td>
</tr>
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</table>
decreasing gill-raker spacing

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>$pc$</td>
<td>1.0 × 10^{-2} A scaling factor for $ip$</td>
</tr>
<tr>
<td>$pf$</td>
<td>- A decrease in the foraging efficacy caused by small gill raker spacing</td>
</tr>
<tr>
<td>$pl$</td>
<td>- The effect of prey on predators</td>
</tr>
<tr>
<td>$r$</td>
<td>Index - Prey cluster</td>
</tr>
<tr>
<td>$rl$</td>
<td>[SI.38,SI.40] Index A prey cluster</td>
</tr>
<tr>
<td>$r2$</td>
<td>[SI.38,SI.40] Index A prey cluster</td>
</tr>
<tr>
<td>$ra$</td>
<td>[SI.36] - The expected abundance of a prey cluster</td>
</tr>
<tr>
<td>$rc$</td>
<td>[SI.45] Index A size class in a prey cluster</td>
</tr>
<tr>
<td>$rCV$</td>
<td>[SI.33] 0.3 The coefficient variation for the body mass of a prey cluster</td>
</tr>
<tr>
<td>$ri$</td>
<td>[SI.34] 1 for $r = 1$ The intrinsic growth rate for $a$ prey cluster</td>
</tr>
<tr>
<td>$rMu$</td>
<td>- The representative body mass of a prey cluster</td>
</tr>
<tr>
<td>$rMu_1$</td>
<td>[SI.32] 0.01g The mean body mass of the prey cluster with the minimum representative body mass</td>
</tr>
<tr>
<td>$rMu_{rn}$</td>
<td>[SI.32] 5g The mean body mass of</td>
</tr>
</tbody>
</table>
the prey cluster with the maximum representative body mass

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Definition</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>( r_n )</td>
<td>The number of prey clusters</td>
<td>[SI.32] 3</td>
</tr>
<tr>
<td>( r_{sc} )</td>
<td>The abundance of prey in a size class of a prey cluster after the genetic mutation of prey</td>
<td>[SI.44,SI.46]</td>
</tr>
<tr>
<td>( r_t )</td>
<td>The abundance of a resource before mutation</td>
<td>[SI.34]</td>
</tr>
<tr>
<td>( s_B )</td>
<td>The genetic and environmental effects on sexual maturation</td>
<td>[SI.28]</td>
</tr>
<tr>
<td>( \sigma )</td>
<td>Standard deviation of growth</td>
<td>[SI.7,SI.8]</td>
</tr>
<tr>
<td>( s_g )</td>
<td>Life stage</td>
<td>Index</td>
</tr>
<tr>
<td>( s_m )</td>
<td>The probability of sexual maturation</td>
<td>[SI.29]</td>
</tr>
<tr>
<td>( t )</td>
<td>Time</td>
<td>Index</td>
</tr>
<tr>
<td>( t_p )</td>
<td>The total number of alleles in the loci determining the body mass +1</td>
<td>[SI.45] 20</td>
</tr>
<tr>
<td>( t_x )</td>
<td>The age (year) of the largest morph becoming sexually matured</td>
<td>[SI.4,SI.29] Male: 4 Female: 5</td>
</tr>
<tr>
<td>( u )</td>
<td>Gape size</td>
<td>[SI.19]</td>
</tr>
<tr>
<td>( w )</td>
<td>The body mass (g) of an individual</td>
<td>[SI.30]</td>
</tr>
</tbody>
</table>

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<table>
<thead>
<tr>
<th>$wf$</th>
<th>[SI.41]</th>
<th>30.27g</th>
<th>The representative body mass for alewives</th>
</tr>
</thead>
<tbody>
<tr>
<td>$wSD$</td>
<td>[SI.33]</td>
<td>-</td>
<td>The standard deviation of the body mass of a prey cluster</td>
</tr>
<tr>
<td>$x$</td>
<td>Index</td>
<td>-</td>
<td>Sex</td>
</tr>
</tbody>
</table>
Table SI.2.2: Parameter values for a local sensitivity analysis about $eA$, $eI$, $lp$, and $eb$. $eA$ determined with-trophic competitions. $eI$ affected trophic interactions. $lp$ affected the effect of gill-raker spacing on the efficiency of alewives’ foraging for large prey. $eb$ determined the effect of fish body size on the efficiency of their foraging for small prey. The number of prey clusters was two or three.

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>$eA$</td>
<td>0.75, 1, 1.25</td>
</tr>
<tr>
<td>$eI$</td>
<td>0.25, 0.4, 0.55</td>
</tr>
<tr>
<td>$eb$</td>
<td>0, 0.125, 0.25, 0.5, 0.75, 1</td>
</tr>
<tr>
<td>$lp$</td>
<td>0, 0.5, 1</td>
</tr>
</tbody>
</table>

Table SI.2.3: Parameter values for a local sensitivity analysis about the effect size of the alleles for fish growth ($bA$). $eA$ determined with-trophic competitions. $eI$ affected trophic interactions. $eb$ affected the effect of fish body size on the efficiency of alewives’ foraging for small prey. The number of prey clusters was two or three.

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>$eA$</td>
<td>0.75, 1, 1.25</td>
</tr>
<tr>
<td>$eI$</td>
<td>0.25, 0.4, 0.55</td>
</tr>
<tr>
<td>$bA$</td>
<td>0.125, 0.25, 0.375, 0.5</td>
</tr>
<tr>
<td>$eb$</td>
<td>0, 0.125, 0.25, 0.5</td>
</tr>
</tbody>
</table>
Table SI.2.4: Parameter values for a local sensitivity analysis about the effect of a decrease in the efficiency of their foraging for very large or very small prey ($fs$). $eA$ determined with-trophic competitions. $eI$ affected trophic interactions. $eb$ affected the effect of fish body size on the efficiency of their foraging for small prey. $lp$ affected the effect of gill-raker spacing on the efficiency of alewives’ foraging for large prey. The number of prey clusters was two or three.

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>$eA$</td>
<td>0.75, 1, 1.25</td>
</tr>
<tr>
<td>$eI$</td>
<td>0.25, 0.4, 0.55</td>
</tr>
<tr>
<td>$eb$</td>
<td>0, 0.125, 0.25, 0.5</td>
</tr>
<tr>
<td>$fs$</td>
<td>2.5, 5, 10, 20</td>
</tr>
</tbody>
</table>

Table SI.2.5: Parameter values for a local sensitivity analysis about handling time ($cH$) in the type II functional response. $eA$ determined with-trophic competitions. $eI$ affected trophic interactions. $eb$ affected the effect of fish body size on the efficiency of alewives’ foraging for small prey. The number of prey clusters was two or three.

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>$eA$</td>
<td>0.75, 1, 1.25</td>
</tr>
<tr>
<td>$eI$</td>
<td>0.25, 0.4, 0.55</td>
</tr>
<tr>
<td>$cH$</td>
<td>0, 0.05, 0.1, 0.25, 0.5</td>
</tr>
<tr>
<td>$eb$</td>
<td>0, 0.125, 0.25, 0.5</td>
</tr>
</tbody>
</table>
Table SI.2.6: Parameter values for a local sensitivity analysis about the individual stochasticity of fish growth (bcv). $e_A$ determined with-trophic competitions. $e_I$ affected trophic interactions. $eb$ affected the effect of fish body size on the efficiency of alewives’ foraging for small prey. The number of prey clusters was two or three.

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>$e_A$</td>
<td>$0.75, 1, 1.25$</td>
</tr>
<tr>
<td>$e_I$</td>
<td>$0.25, 0.4, 0.55$</td>
</tr>
<tr>
<td>$bcv$</td>
<td>$0.001, 0.01, 0.1, 0.2$</td>
</tr>
<tr>
<td>$eb$</td>
<td>$0, 0.125, 0.25, 0.5$</td>
</tr>
</tbody>
</table>

Table SI.2.7: Parameter values for a local sensitivity analysis about the initial allele frequencies ($P(A)_{t=0}, P(B)_{t=0}$). $P(A)_{t=0}$ was the initial frequency of the allele improving fish growth. $P(B)_{t=0}$ was the initial frequency of the allele increasing a gill-raker number. $e_A$ determined with-trophic competitions. $e_I$ affected trophic interactions. The number of prey clusters was two or three.

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>$e_A$</td>
<td>$0.75, 1, 1.25$</td>
</tr>
<tr>
<td>$e_I$</td>
<td>$0.25, 0.4, 0.55$</td>
</tr>
<tr>
<td>$P(A)_{t=0}$</td>
<td>$1, 0.9999, 0.999, 0.99, 0.5, 0.01, 0.001, 0.0001, 0$</td>
</tr>
<tr>
<td>$P(B)_{t=0}$</td>
<td>$0, 0.0001, 0.001, 0.01, 0.5, 0.99, 0.999, 0.9999, 1$</td>
</tr>
</tbody>
</table>

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Supporting information III:

Figures
Figure SI.3.1: The effect of a decrease in the efficiency of alewives’ foraging for very large or very small prey ($f_s$) on alewife morphological evolution. A low $f_s$ value indicated a slow decrease in the efficiency of their foraging for very large or very small prey. \( P(A) \) was the mean frequency of the allele improving their growth. \( P(B) \) was the mean frequency of the allele increasing their gill-raker number. There were three prey clusters. The intensity of within-trophic competitions was low ($e_A = 0.75$). Trophic interaction were strong ($e_I = 0.25$). A decrease in alewives’ body size substantially improved the efficiency of their foraging for small prey ($e_b = 0.125$). Alewives’ small gill-raker spacing moderately undermine the efficiency of their foraging for large prey ($l_p = 0.5$). Allele frequencies were recorded every 150 years in this figure.
Figure SI.3.2: The effect of handling time ($ht$) in the type II functional response on alewife morphological evolution. A high $ht$ value indicated long handling time. $P(A)$ was the mean frequency of the allele improving their growth. $P(B)$ was the mean frequency of the allele increasing their gill-raker number. There were three prey clusters. The intensity of within-trophic competitions was low ($eA = 0.75$). Trophic interactions were strong ($eI = 0.25$). Body size decrease in alewives substantially improved the efficiency of their foraging for small prey ($eb = 0.125$). Alewives’ small gill-raker spacing moderately undermined the efficiency of their foraging for large prey ($lp = 0.5$). Allele frequencies were recorded every 150 years in this figure.
Figure SI.3.3: The effect of the individual stochasticity of alewives’ growth ($bcv$) on alewife morphological evolution. A high $bcv$ value indicated the high individual stochasticity of their growth. $P(A)$ was the mean frequency of the allele improving their growth. $P(B)$ was the mean frequency of the allele increasing their gill-raker number. There were three prey clusters. The intensity of within-trophic competitions was low ($eA = 0.75$). Trophic interactions were strong ($eI = 0.25$). A decrease in alewives’ body size substantially improved the efficiency of their foraging for small prey ($eb = 0.125$). Alewives’ small gill-raker spacing moderately undermined the efficiency of their foraging for large prey ($lp = 0.5$). Allele frequencies were recorded every 150 years in this figure.