Appendix 1

Temperature Profiles

The study sites used in this analysis were selected to cover a gradient of abiotic conditions, including temperature. Figure A.1 shows the distribution of temperatures in time and space from the approximate hatch date through the first summer for 2011 (an example year).

Figure A.1. Temperature profiles for the study sites in the Lapwai Creek watershed from May 1 to October 31, 2011.
Appendix 2

Model derivation

The variance partitioning revealed substantial clustering by sampling visit, which means that observations made within a sampling visit were more similar than when compared with observations from all sampling visits. We hence modeled the growth rate variation under a hierarchical framework, that is, with both individual- and visit-level effects (Raudenbush and Bryk 2002). We investigated the effects of individual mass, mass relative to conspecifics (relative mass), population density, and temperature on individual growth rate. The models considered in this article are presented in Table 1 in the main text. Here we explain how these models were derived.

Individual mass and relative mass are at the same hierarchical level as the response variable growth. To introduce population density and temperature we had to account for the multilevel structure in the data as these variables are not independent among the individuals in a site (Raudenbush and Bryk 2002). An individual-level model of growth as a function of the individual-level variables mass and relative mass can be written as

\[
growth_{ij} = \beta_0 + \beta_1 \text{mass}_{ij} + \beta_2 \text{relative}_{ij} + r_{ij} \quad (\text{eq. A1})
\]

To allow for visit-specific intercepts and slopes, we can write

\[
\beta_0 = \gamma_{00} + u_{0j}, \quad \beta_1 = \gamma_{10}, \quad \text{and} \quad \beta_2 = \gamma_{20} + u_{2j}
\]

Combining into eq. A1, this model structure becomes a random intercept and slope model

\[
growth_{ij} = \gamma_{00} + \gamma_{10} \text{mass}_{ij} + \gamma_{20} \text{relative}_{ij} + \gamma_{11} \text{mass}_{ij} × \text{temp}_{ij} + \gamma_{21} \text{relative}_{ij} × \text{temp}_{ij} + u_{0j} + u_{2j} \text{relative}_{ij} + r_{ij} \quad (\text{eq. A2})
\]

We then added density and temperature to Eq. A2 by allowing the random intercept and slope to vary as functions of these visit-level variables. This means that the effects of individual mass and relative mass on its growth rate also depend on characteristics of the sampling visit to a study site. The size of the effect of the individual-level predictors hence depends on the visit-level predictor. For example, adding the visit-level covariate temperature, this becomes

\[
\beta_0 = \gamma_{00} + \gamma_{01} \text{temp}_{ij} + u_{0j}, \quad \beta_1 = \gamma_{10} + \gamma_{11} \text{temp}_{ij}, \quad \text{and} \quad \beta_2 = \gamma_{20} + \gamma_{21} \text{temp}_{ij} + u_{2j}
\]

Combining into Eq. A2, this becomes a hierarchical linear model with cross-level interactions

\[
growth_{ij} = \gamma_{00} + \gamma_{01} \text{temp}_{ij} + \gamma_{10} \text{mass}_{ij} + \gamma_{20} \text{relative}_{ij} + \gamma_{11} \text{mass}_{ij} × \text{temp}_{ij} + \gamma_{21} \text{relative}_{ij} × \text{temp}_{ij} + \gamma_{11} \text{mass}_{ij} × \text{temp}_{ij} + u_{0j} + u_{2j} \text{relative}_{ij} + r_{ij} \quad (\text{eq. A3})
\]

This model tests the effects of individual mass, its mass relative to PIT-tagged conspecifics, and the effects of temperature alone and in interaction with individual specific mass, on an individual’s growth rate. We performed the same analysis with population density as the visit-level predictor variable

\[
growth_{ij} = \gamma_{00} + \gamma_{01} \text{density}_{ij} + \gamma_{10} \text{mass}_{ij} + \gamma_{20} \text{relative}_{ij} + \gamma_{11} \text{mass}_{ij} × \text{density}_{ij} + \gamma_{21} \text{relative}_{ij} × \text{density}_{ij} + u_{0j} + u_{2j} \text{relative}_{ij} + r_{ij}
\]

We used SAS 9.2 Proc MIXED (SAS Institute, Cary, North Carolina, USA) specified with the Kenward and Roger (1997) approximation of denominator degrees of freedom, and maximum likelihood as the estimator in all the analyses. Models were ranked using Akaike’s Information Criterion (Akaike 1973);
the model with the lowest AIC value is the best approximating model of the data (Burnham and Anderson 2002).

**Literature cited**


