Supporting Information

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SI Modeling the Data

We required an appropriate model to apply across all species to the response of adult dry mass to temperature. Previous research has suggested a range of models as the best descriptor of the body mass thermal reaction norm. We therefore required a method to apply this range of equation forms (linear, exponential, Arrhenius, and power) to the full dataset intraspecifically to determine which best described the empirical data. Further, we had to be able to account for differences within each species, driven by sex and by the fact that different studies may have been carried out on the same species. This goal was achieved using a linear mixed-effects model. Applying this design allows models to be fitted to all mass data at the same time, as interspecific mass differences are accounted for by species-specific intercept terms. Furthermore, intraspecific differences between temperature-dependent slopes can be accounted for in species-specific slope terms:

$$\ln M = \beta 0ij + \beta 1ij(\ln T - \ln 20) + \varepsilon ij \quad \text{[S1A]}$$

$$\beta 0ij = \beta 0 + u0ij \quad \text{[S1B]}$$

$$\beta 1ij = \beta 1 + u1ij, \quad \text{[S1C]}$$

where M = dry mass (milligrams), T is temperature (degrees Celsius), i indexes the species (within which study and sex are nested), and j is the temperature. β_0 and β_1 are the intercept and slope fixed effects, respectively; u_{0i} and u_{1i} are species-specific random effects terms that allow for intraspecific differences in the intercepts and slopes, respectively, assumed to be normally distributed; and ε is the error, assumed to be normally distributed. Temperatures were centered to improve the interpretation of parameter terms and to reduce the correlation between slope and intercept terms. A centering temperature of 20 °C was applied, as this temperature is within the boundaries used in most studies in the database and therefore required minimal extrapolation. Subtracting this centering temperature from each of the model types allowed each rate to be examined in terms of changes from that at 20 °C. Within the species-specific intercept term u_{0i} the effects of sex (a) and study (b) can be nested, to account for differences within species driven by different studies and by different sexes:

$$\ln M = \beta 0ij + \beta 1ij(\ln T - \ln 20) + \varepsilon ij \quad \text{[S2A]}$$

$$\beta 0ij = \beta 0 + u0i(b/a)j \quad \text{[S2B]}$$

$$\beta 1ij = \beta 1 + u1ij, \quad \text{[S2C]}$$

where study is nested within species and sex is nested within study. In all cases, incorporating the random effects of sex (a) and study (b) improved the fit of the models and thus had to be included to account for the differences between these factors. These factors also may need incorporating within the species-specific slope terms; however, when these terms were incorporated into both intercept and slope parameter terms, they were highly correlated in all statistical models for growth and development rates (i.e., correlation between a_0 and a_1 >0.9, b_0 and b_1 >0.9). To avoid over-parameterization of these models, we allowed random variation in intercepts only for sex and study for all mixed-effects models.

To initially test for linearity, a power model was fitted to the data; then we wanted to see whether the fixed-effects parameter β_1 is significantly different from 1. The slope parameter β_1 represents the exponent of the power model; thus, if the best-fit model had a slope of 1, this would indicate a linear relationship between temperature and mass. We therefore do not include a species-specific slope term at this stage, as we wish to calculate the mean parameter β_1 across all species at once. Because the best-fit parameter β_1 was significantly different from 1 (−0.41 ± 0.03 [95% CI]), a simple linear model (as an alternative model type) could be rejected. Further, the data were distributed heteroscedastically on an arithmetic scale.

To determine the best-fit model for the data on mass response to temperature, power, exponential, and Arrhenius models subsequently were fitted to the data (Table S1). Average species masses varied greatly; therefore, in each model type intercepts were allowed to vary randomly to account for species-specific masses. These models initially were fit assuming a fixed slope, assuming similar relative changes in mass with temperature. However, these models also were fit to allow slopes to vary randomly, thus allowing species-specific changes in mass with temperature.

Initially, the best equation was chosen for each model type (power, exponential, or Arrhenius) using modified likelihood ratio tests to determine whether each model type required slopes with species-specific random effects to improve fit. Having selected the best equation, the model types were compared using Akaike Information Criteria (AIC). Akaike weights (ω_i) indicated that the evidence was largely in favor of an exponential model, suggesting this to be the best fit to the data, given the model applied here (Table S1).

Comparing Adult and Progeny Mass Changes. We compiled data for progeny size in multicellular organisms using the search terms "(egg OR progeny OR hatchling) AND temperature AND (weight OR *mass OR size)." We assume progeny were acclimated if produced at the experimental temperature, i.e., the parental generation was introduced to temperatures before copulation and was maintained at these temperatures until egg laying. Similar to the adult data, progeny sizes were converted to dry masses (Dataset S1) and an exponential linear mixed-effects model was applied to the data following the methods applied to adults, but with only study nested within the species intercept term. The mean percentage changes in mass $°C^{-1}$ were plotted for aquatic and terrestrial species (Fig. S2*A*). These environments showed no significant difference in temperature-size response. Further, we compiled "paired" data, where temperature-size responses were available for both adult and progeny mass in a single species. By subtracting the % change in mass per °C in progeny from that of adult mass change for the paired data, we could further test whether differences in environment were driven by differences in progeny size response. We found the result was unchanged; aquatic species still showed a significantly stronger temperature-size response than terrestrial species (Fig. S2*B*).

Screening the Data. To ensure patterns associated with organism body mass were not driven by the fit of the model to different species, we screened the data further to exclude the species represented by only two data points, or those with R^2 values below 0.8 (Fig. S3). This showed that the patterns in terrestrial and aquatic species were not driven by the fit of the model to the data, as the same patterns of increasingly negative temperature-size response in aquatic and increasingly positive temperature-size response in terrestrial species were maintained (Fig. S4).

Alternative Hypotheses for Temperature-Size Changes

In contrast to the hypothesis of oxygen availability driving temperature-size differences in different environments, alternatives based on temperature- and size-dependent differences in aquatic and terrestrial environments between 0 and 30 °C cannot explain our observations. First, although oxygen solubility declines as water warms [Q_{10} ~0.81 in freshwater and 0.83 in seawater of salinity 35 (1)], when it is combined with the greater increase in oxygen diffusivity (Q_{10} ~1.3–1.4) it yields a slight net increase in oxygen availability with warming (Q_{10} ~1.05–1.16) (2), which does not differ from the increase in air (Q_{10} ~1.06) (2). Second, the viscosity of water but not air reduces with warming [Q_{10} ~0.77 for water (3, 4); Q_{10} ~1.06 for air (4)], but the effects of this are inconsistent with the cause of the observed size responses. Reduced water viscosity with warming will increase the energetic efficiency of locomotion and of the generation of feeding and ventilation currents, especially in small species that are heavily influenced by viscosity (5), but life history theory predicts that such energetic gains typically would favor larger, rather than the observed smaller, mature size at increased temperature (6). The other predicted consequence of these viscosity changes is that larger size would be selectively favored in cooler aquatic conditions to counter the effect of increased viscous forces (5). This, in fact, is consistent with the observed stronger TSR in aquatic vs. terrestrial species; however, its effect would decrease not increase, as observed over the size range of species in our dataset, with increasing species size, as the energetics of larger species with higher Reynolds numbers are less constrained by viscous forces (5). Finally, changes to density are minor in both air and water [Q_{10} ~0.967 for air and from 1 to 0.995 for water (4)]. We know of no other systematic differences in thermal sensitivities between terrestrial and aquatic environments that could explain the observed results.

1. Verberk WCEP, Bilton DT, Calosi P, Spicer JI (2011) Oxygen supply in aquatic ectotherms: Partial pressure and solubility together explain biodiversity and size patterns. *Ecology* 92(8):1565–1572.
2. Richard T (2012) Oxygen diffusion in air. Available at www.compost.css.cornell.edu/oxygen/oxygen.diff.air.html.
3. Sengers JV, Watson JTR (1986) Improved International formulation for the viscosity and thermal conductivity of water substance. *J Phys Chem Ref Data* 15(4):1291–1314.
4. The Engineering ToolBox (2011) Water–dynamic and kinematic viscosity. Available at www.engineeringtoolbox.com.
5. Vogel S (2003) *Comparative Biomechanics: Life's Physical World* (Princeton Univ Press, Princeton, NJ).
6. Roff DA (2002) *Life History Evolution* (Sinauer, Sunderland, MA).


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glm(formula = PCM ~ log(DM):Environment + Environment, data = Ectotherms)


Deviance Residuals:

     Min        1Q    Median        3Q       Max

-4.60055  -1.00561  -0.04846   0.89595   4.57985


Coefficients:

                             Estimate   Std. Error  t value  Pr(>|t|)

(Intercept)                  -3.89856   0.24957     -15.621  <2e-16 ***

EnvironmentTerrestrial        2.18257   0.35868       6.085  1.97e-08 ***

log(DM):EnvironmentAquatic   -0.23210   0.07457     -3.112   0.00240 **

log(DM):EnvironmentTerrestrial  0.23282   0.08152      2.856   0.00518 **

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Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


(Dispersion parameter for gaussian family taken to be 3.015163)


Null deviance: 501.13  on 107  degrees of freedom

Residual deviance: 313.58  on 104  degrees of freedom

AIC: 431.61
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Fig. S1. Output for the best-fit general linear model (GLM) used to describe the percentage change in mass (*PCM*) in ectotherms per °C. The best-fit GLM included parameters for environment (aquatic vs. terrestrial) and the interaction between environment and natural-logged dry mass.

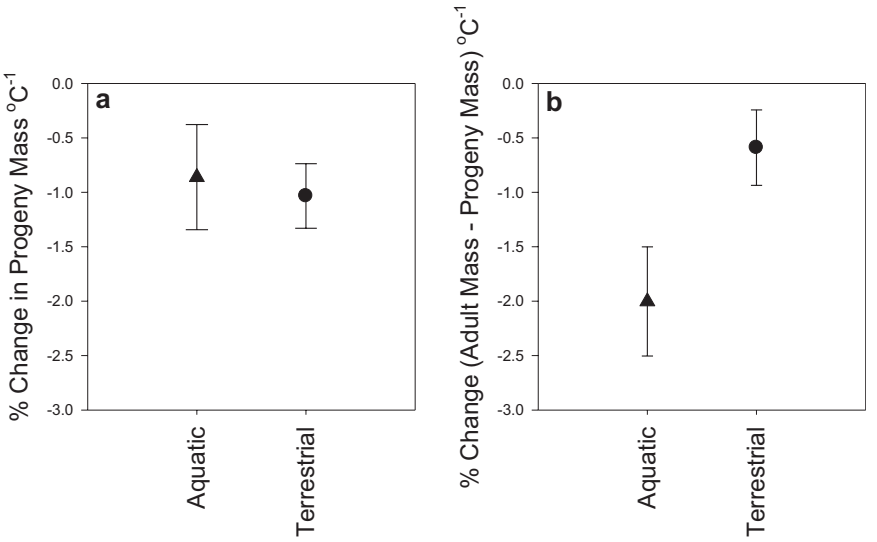

Fig. S2. (*A*) Mean ±95% CI for the percentage change in progeny mass per °C in aquatic and terrestrial species. There was no significant difference between the two environments (two-sample *t* test, t = 0.61, df =31, $P > 0.05$). (*B*) Mean ±95% CI for the percentage change in adult mass minus the percentage change in progeny mass per °C for paired data (i.e., for species for which both adult and progeny mass data existed). Subtracting progeny mass did not change the general result: aquatic adults still show a significantly stronger temperature-size response than terrestrial adults (two-sample *t* test, t = 2.38, df =20, $P < 0.05$).

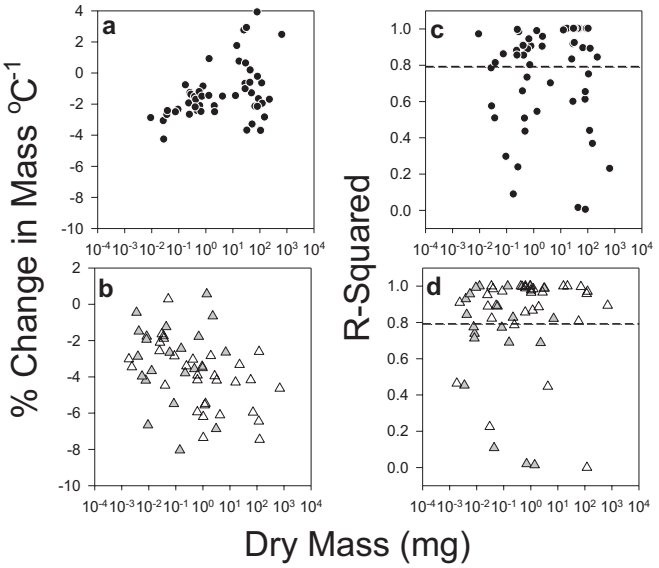

Fig. S3. Species-specific temperature-size responses (% change in mass per °C) expressed as a function of the organism size (dry mass) in (*A*) terrestrial and (*B*) aquatic (marine and freshwater) environments. Species-specific R-squared values expressed as a function of organism dry mass for (*C*) terrestrial and (*D*) aquatic species. Dashed lines represent an R^2 of 0.8, used to screen data used in Fig. S4. Filled circles are terrestrial metazoa, open triangles freshwater metazoa, and gray triangles marine metazoa.

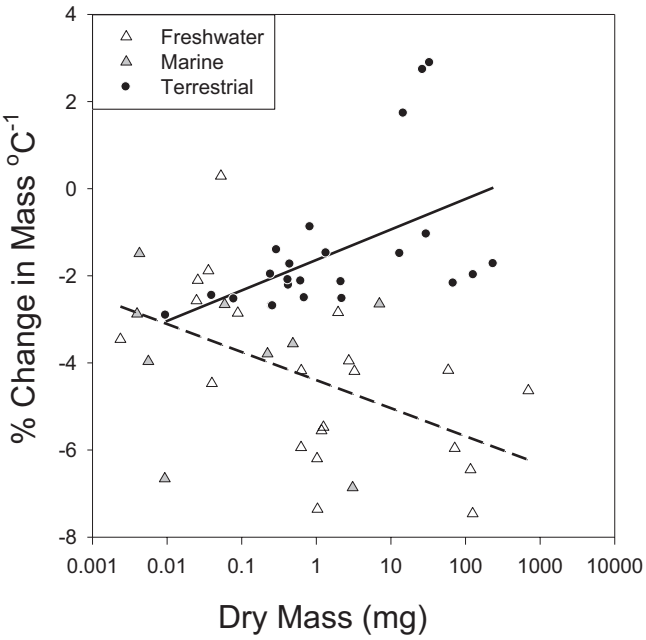

Fig. S4. Species-specific temperature-size responses (% change in mass per °C) expressed as a function of the organism size (dry mass) in aquatic (marine and freshwater) and terrestrial environments. Data are screened, such that R^2 for each species was >0.8 (Fig. S3). Terrestrial species have a significant positive regression ($PCM = -1.63 + 0.30*\log_{10}DM$, $R^2 = 0.25$, df = 23, $P < 0.05$); aquatic species have a significant negative regression ($PCM = -4.40 - 0.28*\log_{10}DM$, $R^2 = 0.25$, df = 29, $P < 0.01$).

Table S1. Models applied to mass (*M*), including centering temperature (20 °C)

Model	Equation	Multilevel centered model	AIC	Δ_i	ω_i	Best model
Power	$M = cT^d + \varepsilon$	$\ln M = \beta_0 + \beta_1(\ln T - \ln 20) + \varepsilon$	−9.50	77.2	0	
Exponential	$M = ce^{dT} + \varepsilon$	$\ln M = \beta_0 + \beta_1(T - 20) + \varepsilon$	−86.7	0.00	0.92	•
Arrhenius	$M = ce^{-E_a/kT_{(K)}} + \varepsilon$	$\ln M = \beta_0 - \beta_1\left(\frac{1}{kT_{(K)}} - \frac{1}{293k}\right)$	−81.7	5.00	0.08	

c and *d* are constants, *T* is temperature (°C), *T* (K) is temperature (degrees Kelvin), *k* is Boltzmann's constant (8.617×10^{-5} eV K^{-1}), and E_a is average activation energy for the rate-limiting enzyme-catalyzed biochemical reactions of metabolism. In the multilevel model, β_0 is the intercept term, β_1 is the slope term, and ε is the residual error. Δ_i is the AIC difference, and ω_i is the Akaike weight. All multilevel model parameter values (β_0 and β_1) required the inclusion of species-specific terms, along with values for sex (*a*) and study (*b*) nested within the species intercept parameter (β_0). The overall best-fit model is shown in the rightmost column ("Best model") and is defined as that with the highest Akaike weight.

Other Supporting Information Files

Dataset S1 (XLS)