

Appendix D from C. D. Muir and M. Thomas-Huebner, “Constraint around Quarter-Power Allometric Scaling in Wild Tomatoes (*Solanum sect. Lycopersicon*; Solanaceae)” (Am. Nat., vol. 186, no. 3, p. 000)

Clade-Wide Mass-Specific Allometric Scaling

We estimated the average clade-wide mass-specific allometric-scaling exponent ($\bar{\theta}_m$) as the average of the 17 accession-specific scaling exponents ($\theta_{m,j}$). We also estimated 95% confidence intervals around the average from the mixture distribution of accession-specific probability distributions of $\theta_{m,j}$. In these analyses, all accessions were given equal weight and treated as independent. In other words, we did not account for phylogenetic nonindependence, because we are not aware of methods to simultaneously estimate clade-wide mass-specific probability distributions and phylogenetic nonindependence. For technical reasons, we also used OLS rather than TLS parameter estimates to take advantage of analytical approximations for estimating confidence intervals from OLS fits. This choice most likely had a negligible affect on the results because OLS and TLS parameter estimates were very similar in this experiment (app. B). The R code to implement the calculations described here is available in the file “OnlineAppendixD_Code.R” in the Supporting Information directory.²

The best-fit model (table B1) was a cubic function with accession-specific intercepts ($b_{0,j}$) and quadratic coefficients ($b_{2,j}$):

$$\log A = b_{0,j} + b_1 \log M + b_{2,j} (\log M)^2 + b_3 (\log M)^3. \quad (\text{D1})$$

Exponentiating both sides yields a power function with the scaling exponent as a function of mass:

$$A = B_{0,j} M^{b_1 + b_{2,j} \log M + b_3 (\log M)^2}. \quad (\text{D2})$$

This can be more simply seen as

$$A = B_{0,j} M^{\theta_{m,j}}, \quad (\text{D3})$$

where

$$\theta_{m,j} = b_1 + b_{2,j} \log M + b_3 (\log M)^2. \quad (\text{D4})$$

We estimated the probability distribution for $\theta_{m,j}$ by using standard random variable algebra identities and approximations. The probability distribution of $\theta_{m,j}$ at a given $\log M$, which we index with m , for a given accession j under the assumptions of linear models is approximately normally

$$f(\theta_{m,j}) \sim \mathcal{N}(\mu_{m,j}, \sigma_{m,j}). \quad (\text{D5})$$

The normal approximation is close for large sample sizes, which our data satisfy because there are 251 degrees of freedom in the best-fit model. The mean of the distribution at a given mass ($\log M = m$) and estimated coefficients (\hat{b}_i) is

$$\mu_{m,j} = \hat{b}_1 + \hat{b}_{2,j} m + \hat{b}_3 m^2. \quad (\text{D6})$$

The standard deviation is

$$\sigma_{m,j} = \sqrt{x_j' \Sigma x_j}, \quad (\text{D7})$$

where Σ is the covariance matrix of model coefficients and x is a column of the design matrix that corresponds to the accession j with levels of the predictor variables $\log M$, $(\log M)^2$, and $(\log M)^3$. The right-hand side under the radical accounts for uncertainty in θ_m under the joint probability distribution of all terms in the model ($\hat{b}_1, \hat{b}_{2,j}, \hat{b}_3$) at a particular mass.

² Code that appears in the *American Naturalist* has not been peer-reviewed, nor does the journal provide support.

We calculated $\mu_{m,j}$ and $\sigma_{m,j}$ for all 17 accessions at 512 evenly spaced values of $\log M$ between $\min(\log M) = \log 0.073$ g and $\max(\log M) = \log 26.5$ g from this experiment. We calculated the clade-wide median (50% quantile) mass-specific scaling coefficient and 95% confidence intervals from the mixture density of the 17 accessions, treating each accession with equal statistical weight ($w_1 = w_2 = \dots = w_{17} = 1/17$):

$$f(\theta_m) = \sum_{j=1}^{17} w_j f(\theta_{m,j}). \quad (\text{D8})$$

We numerically calculated quantiles of the mixture distribution using the “UnivariateMixingDistribution” function in the `distr` package (ver. 2.5.3; Ruckdeschel et al. 2006) in R.

Literature Cited Only in Appendix D

Ruckdeschel, P., M. Kohl, T. Stabla, and F. Camphausen. 2006. S4 classes for distributions. R News 6:2–6.