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Appendix C from S. Tomiya, "Body Size and Extinction Risk in Terrestrial Mammals Above the Species Level"

(Am. Nat., vol. 182, no. 6, p. E196)

Comparative Analyses Using Expected Interbirth Interval Lengths

A preliminary assessment of the link between the tempos of life history and taxonomic durations was made by conducting regression analyses with expected interbirth interval lengths (in natural log scale) as the predictor variable. This variable represents the time between successive births given by the same female and has been shown to capture an important component of the multidimensional fast-slow continuum of life history in extant mammals (Bielby et al. 2007). With data from the PanTHERIA database (Jones et al. 2009), least squares regression equations describing the relationship between body mass and interbirth interval length were derived separately for a group of generally small mammals (rodents, lagomorphs, and lipotyphlans), ungulates (artiodactyls and perissodactyls), and carnivorans (fig. C1). These equations were then used to calculate the interbirth interval lengths of the fossil genera expected from their estimated body masses. The expected interbirth interval lengths are reported in the Generic Data file in the Dryad Digital Repository: http://dx.doi.org/10.5061/dryad.vr157 (Tomiya 2013).

The use of same predictive equation for lipotyphlans, lagomorphs, and rodents was perhaps not ideal but necessitated by the scarcity of data for lipotyphlans and lagomorphs. Note that if a single predictive equation were used to estimate the interbirth interval lengths of all fossil genera, the results of regression analyses would be identical to those of the analyses for masses and durations except for the linearly transformed predictor variable. Instead, by using separate predictive equations for different groups of mammals, some of the essential variations in the scaling of the tempo of life history across the body-size axis were taken into account (fig. C1). I acknowledge, however, that there are likely additional scaling variations at multiple biological levels, and these should be incorporated into future studies when more reproductive data for living mammals (those for lipotyphlans are especially scarce at present) and cladistic hypotheses explicitly relating living and extinct genera become available. The results of regression analyses are presented in figure C2 and are briefly discussed in the main text.

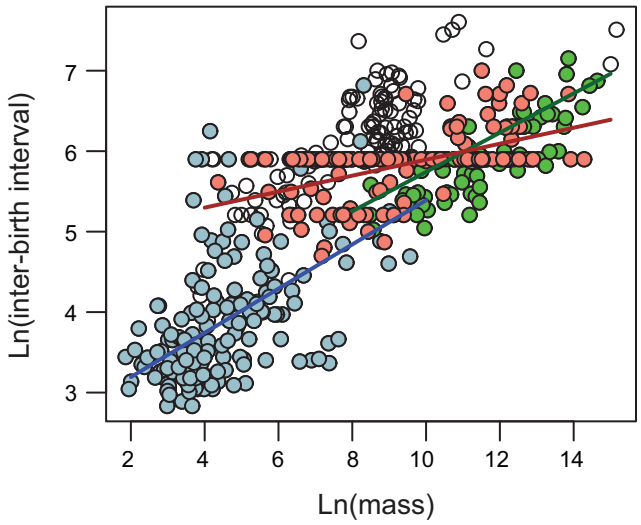

Figure C1: Least squares regression lines for prediction of interbirth interval lengths (L) from body masses (M). Rodents, lagomorphs, and lipotyphlans (blue, $N = 165$): $L = 0.275M + 2.643$, $R^2 = 0.307$. Artiodactyls and perissodactyls (green, $N = 94$): $L = 0.244M + 3.301$, $R^2 = 0.557$. Carnivorans (pink, $N = 145$): $L = 0.099M + 4.901$, $R^2 = 0.266$. Data from the PanTHERIA database (Jones et al. 2009). Original units for L and M are days and grams, respectively.

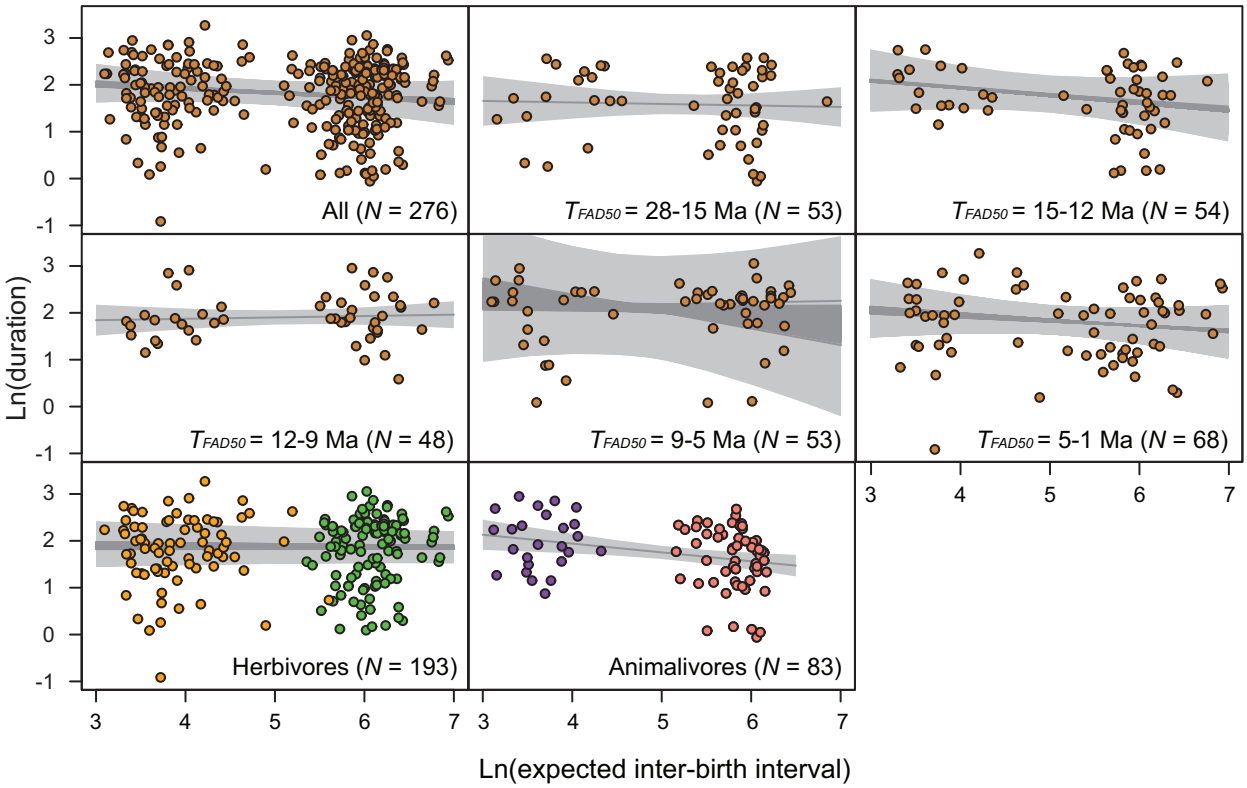

Figure C2: Relationships between expected interbirth interval lengths and sampling-adjusted durations. Results are presented as in figure 5 but only for the full data set and pertinent data subsets. Original interbirth interval lengths and masses in units of days and grams, respectively.

Table C1. Regression statistics for expected interbirth interval lengths

Included genera	λ_ε	Slope	R^2	Proportion $P < .05$
All	.160 (.141, .196)	−.090 (−.239, .059)	−.007 (−.013, −.004)	.000
$T_{\mathrm{LAD50}} = [28, 15)$	.000 (.000, .000)	−.032 (−.246, .181)[a]	.002[a]	NA (P = .763)[a]
$T_{\mathrm{LAD50}} = [15, 12)$	.050 (.000, .185)	−.158 (−.344, .027)	.067 (.062, .069)	.000
$T_{\mathrm{LAD50}} = [12, 9)$	.000 (.000, .000)	.029 (−.105, .164)[a]	.004[a]	NA (P = .659)[a]
$T_{\mathrm{LAD50}} = [9, 5)$	.570 (.425, 1.000)	−.094 (−.437, .248)	−.044 (−.273, −.016)	.000
$T_{\mathrm{LAD50}} = [5, 1)$	.155 (.125, .175)	−.111 (−.342, .119)	−.029 (−.040, −.019)	.000
Herbivores	.180 (.150, .225)	−.008 (−.067, .052)	−.009 (−.018, −.004)	.000
Animalivores	.000 (.000, .000)	−.188 (−.324, −.053)[a]	.086[a]	NA (P = .007)[a]

Note: Term λ_ε = phylogenetic signal in residual error. The mean values of generalized least squares (GLS) regression slopes and associated 95% confidence intervals (in parentheses) were calculated following the model averaging procedure of Burnham and Anderson (2002, p. 162, 164) with all 1,000 estimates given equal weights. Calculation of the coefficients of determination for GLS regression follows Judge (1985, eq. [2.3.12]), and the resulting values of R^2 are not confined to the interval [0, 1]. All other estimates are medians and their 95% confidence intervals (in parentheses) from 1,000 analyses for each data (sub)set, obtained by the bias-corrected percentile method of Efron (1981, eq. [4.4]).

[a]Parameter estimates and statistics from ordinary least squares regression.

Literature Cited Only in Appendix C

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