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The decoupled nature of basal metabolic rate and body temperature in endotherm evolution

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Supplementary Information.

Robustness of results to covariates.

The decoupled pattern between *BMR* and T_b that we found in mammals was not because we accounted for each covariate across extant species in the variable rates regression models nor because we did not consider the scaling of *BMR* and T_b to vary across mammalian orders (Table S16 and S17). In fact, in 60.4% of mammalian branches, faster rates of *BMR* evolution were totally decoupled from T_b evolution (T_b has a single constant rate in those branches) when *branch-wise* rates were estimated from variable rates regression models that accounted only for *Mass*. Additionally, when rates were estimated from variable rates regressions that allowed the scaling of *BMR* and T_b to vary across orders, they were totally decoupled in 58% of branches, again, because *BMR* evolved at faster rates while T_b at a single constant rate in those branches. Finally, the remainder branches where *BMR* evolved at fast rates were best explained by the fast rates of T_a changes rather than by the fast rates of T_b evolution (Table S16 and S17).

Supplementary tables of phylogenetic regressions.

In regressions from **Table S1 to S3** we compared several regression models for mammalian *BMR* and T_b in order to estimate the *branch-wise* rates of evolution with the regression model that best represent the data. Specifically, we evaluated whether regressions models that allow the relationship between *BMR*-*Mass* (the scaling of *BMR*), *BMR*- T_b (the temperature dependence of *BMR*), and T_b -*Mass* (the scaling of T_b) to vary across orders of the mammalian tree have a better fit to the data. Phylogenetic regression analyses were conducted with the *constant-rate* and *variable-rates* models. We evaluate the relationship across 9 orders who had at least 10 data points. We compared and selected between the constant vs variable-rates regression models by means of Bayes Factor (BF), where $BF = 2^{*(\log \text{Marginal Likelihood Complex Model}) - (\log \text{Marginal Likelihood Simple Model})}$. $BF < 2$ indicates weak evidence for the Complex model (the variable-rates regression), $BF > 2$ indicates positive evidence for the Complex Model, BF 5-10 indicates strong support for the Complex Model, and $BF > 10$ indicates very strong support for the Complex Model¹. We found that the *variable-rates* regression fit the data better than the *constant-rate* regression in all comparisons. Then, we reached the simpler reduced *variable-rates* regression model based on strict criteria. First, when more than one clade had a non-significant slope (grey regression models coefficients in Table S1 to S3), we removed the single most non-significant slope from the regression that includes different slopes across all orders (the full model). Then we reiterated this procedure until we get the regression with significant covariates only. Second, when two orders had significant slopes, but the slopes were not statistically different between them we merged those two orders. Finally, to select between a simpler *variable-rates* regression (less significant covariates) and a complex *variable-rates* regression (more significant covariates) we compared their log Marginal-likelihoods by means of Bayes Factor.

Regressions from **Table S4 to S6** evaluate the relationship between *BMR*-*Mass*, *BMR* - T_b , and T_b -*Mass* across orders of the birds' tree in order to estimate the *branch-wise* rate of evolution with the regression model that fit the data better. We evaluated the relationship across orders that had at least 10 data points and included all orders with less than 10 data points in the reference group of the regression. We compared and selected between the constant vs *variable-rates* regression models by means of Bayes Factor, and we reach the simpler *variable-rates* regression model using the same criteria for mammals in **Table S1 to S3**.

Table S7 show the best-fitted phylogenetic regressions (on top of the table) for mammalian *BMR* and T_b that includes the covariates obtained after the model reduction in **Table S1 to**

S3. These regressions were compared with other several regressions that evaluated the effect of additional covariates on mammalian *BMR* and T_b . For instance, we evaluated the effect of ambient temperature (T_a) on *BMR* and T_b , the effect of a second-order polynomial term for *Mass* to predict *BMR*, and a differential effect of T_a on *BMR* in two size groups – one group of species smaller than 603g and another group of species bigger than 603g. This last regression evaluates the proposal of Naya et al.² who found a non-significant effect of T_a on *BMR* across species bigger than 603g using phylogenetic regressions that does not account for variation in the rate of evolution.

Inspection of parameter significance and regression models comparison, by mean of Bayes Factor, show that the inclusion of T_a had a significant effect on *BMR* with a single slope for all species, but this model did not improve the fit to the data over the regression including only *Mass* and T_b to predict *BMR*. On the other hand, the quadratic term for *Mass* to predict *BMR* was significant but it neither improve the fit to the data compared to the simpler regression including *Mass* only. Finally, we found that T_a had a significant effect on *BMR* across species smaller 603g but not in species bigger than 603g. However, this model had the worst fit to the data when compared to all the remainder regression models to predict *BMR*.

Table S8 show the phylogenetic regressions for birds *BMR* and T_b that includes the covariates obtained after the model reduction in **Table S4 to S6**. These regressions were compared with regression that include the effect of T_a on birds *BMR* and T_b . After inspection of parameter significance and phylogenetic regression model's comparison by means of Bayes Factor we found that *BMR* is predicted only by *Mass* with a single slope for all species, and T_b is predicted also by *Mass* but only in the clade of Columbiformes (regression on top of the Table).

Table S9 and S10 show results for the correlation between fast *branch-wise rates* of *BMR* and fast *branch-wise rates* of T_b in mammals (**Table S9**) and birds (**Table S10**). These rates were estimated according the best fitted *variable-rates* regression models showed in Table S7 and S8.

Table S11 show the phylogenetic regression models adjusted for the T_a of extant mammals and birds which includes latitude as the independent variable. In both cases the *variable-rates* regression model fit the data better than the *constant-rate* phylogenetic regression.

Table S12 show results for the correlation between *branch-wise rates* of *BMR* and *branch-wise rates* of T_a in mammals. **Table S13** show results for the correlation between fast *branch-wise rates* of *BMR* and fast *branch-wise rates* of T_a in birds.

Tables S14 and S15 show the results for the evaluation of evolutionary trends in *BMR*, T_b and T_a in mammals and birds. The path-wise rate of each variable was negative and significant only for T_b and T_a . This indicates that while *BMR* did not evolved with any trend (towards higher nor lower values), T_b and T_a evolved towards lower values across all mammals and birds.

Table S16 and S17 show results for the correlation between fast *branch-wise rates* of *BMR* and T_b evolution estimated with *variable-rates* regressions that accounted only for *Mass* (**Table S16**) and *variable-rates* regression models that allowed the scaling of *BMR* and T_b to vary across orders (**Table S17**). Despite the effect of fast *branch-wise rates* of T_b on fast *branch-wise rates* of *BMR* was significant, it explained a small amount of the variation in fast *BMR* rates (**Table S16 and S17**). Furthermore, the fast *branch-wise rates* of T_a change explained a bigger amount of variance in *BMR*, and the complex model that includes both

rates of T_b and T_a did not fit the data better than the simple regression model that includes only T_a rates ($BF = -10$ in mammals; $BF = -8$ in birds).

Table 1. Phylogenetic *variable-rates* regression models for BMR and $Mass$ in mammals, showing on top the best fitted-model selected by strict criteria. α = intercept, β = slope coefficient, ref = reference group (Carnivora), A = Marsupialia, B = Afrotheria, C = Xenarthra, D = Primates, E = Rodentia, F = Eulipotyphla, G = Chiroptera, and H = Artiodactyla. Black colours represent significant coefficient, grey colours represent non-significant coefficient at $p_{MCMC} = 5\%$. Sample size (n) = 483.

BMR Phylogenetic regression model	Marginal likelihood Constant-Rate	Marginal likelihood Var-Rates	Bayes Factor Var-Rates vs Constant-Rates	R ² Var-Rates Regression
BMR ~ $\alpha + \beta_1(Mass)$	-195.97	-116.6	158.74	0.926
BMR ~ (α ref) + $\beta_1(Mass*ref)$ + $\beta_2(ABE)$ + $\beta_3(CF)$ + $\beta_4(Mass*ABE)$ + $\beta_5(Mass*CF)$	-214.61	-136.05	157.12	0.929
BMR ~ (α ref) + $\beta_1(Mass*ref)$ + $\beta_2(A)$ + $\beta_3(BE)$ + $\beta_4(CF)$ + $\beta_5(Mass*A)$ + $\beta_6(Mass*BE)$ + $\beta_7(Mass*CF)$	-226.66	-146.56	160.2	0.929
BMR ~ (α ref) + $\beta_1(Mass*ref)$ + $\beta_2(A)$ + $\beta_3(BE)$ + $\beta_4(C)$ + $\beta_5(F)$ + $\beta_6(Mass*A)$ + $\beta_7(Mass*BE)$ + $\beta_8(Mass*C)$ + $\beta_9(Mass*F)$	-237.31	-160.02	154.58	0.929
BMR ~ (α ref) + $\beta_1(Mass*ref)$ + $\beta_2(A)$ + $\beta_3(B)$ + $\beta_4(C)$ + $\beta_5(E)$ + $\beta_6(F)$ + $\beta_7(Mass*A)$ + $\beta_8(Mass*B)$ + $\beta_9(Mass*C)$ + $\beta_{10}(Mass*E)$ + $\beta_{11}(Mass*F)$	-248.81	-171.37	154.88	0.928
BMR ~ (α ref) + $\beta_1(Mass*ref)$ + $\beta_2(A)$ + $\beta_3(B)$ + $\beta_4(C)$ + $\beta_5(E)$ + $\beta_6(F)$ + $\beta_7(H)$ + $\beta_8(Mass*A)$ + $\beta_9(Mass*B)$ + $\beta_{10}(Mass*C)$ + $\beta_{11}(Mass*E)$ + $\beta_{12}(Mass*F)$ + $\beta_{13}(Mass*H)$	-259.47	-183.28	152.38	0.928
BMR ~ (α ref) + $\beta_1(Mass*ref)$ + $\beta_2(A)$ + $\beta_3(B)$ + $\beta_4(C)$ + $\beta_5(D)$ + $\beta_6(E)$ + $\beta_7(F)$ + $\beta_8(H)$ + $\beta_9(Mass*A)$ + $\beta_{10}(Mass*B)$ + $\beta_{11}(Mass*C)$ + $\beta_{12}(Mass*D)$ + $\beta_{13}(Mass*E)$ + $\beta_{14}(Mass*F)$ + $\beta_{15}(Mass*H)$	-270.44	-195.26	150.36	0.928
BMR ~ (α ref) + $\beta_1(Mass*ref)$ + $\beta_2(A)$ + $\beta_3(B)$ + $\beta_4(C)$ + $\beta_5(D)$ + $\beta_6(E)$ + $\beta_7(F)$ + $\beta_8(G)$ + $\beta_9(H)$ + $\beta_{10}(Mass*A)$ + $\beta_{11}(Mass*B)$ + $\beta_{12}(Mass*C)$ + $\beta_{13}(Mass*D)$ + $\beta_{14}(Mass*E)$ + $\beta_{15}(Mass*F)$ + $\beta_{16}(Mass*G)$ + $\beta_{17}(Mass*H)$	-282.43	-209.76	145.34	0.929

Table 2. Phylogenetic *variable-rates* regression models for BMR and T_b in mammals, showing on top the best-fitted model selected by strict criteria. α = intercept, β = slope coefficient, ref = reference group (Carnivora), A = Marsupialia, B = Afrotheria, C = Xenarthra, D = Primates, E = Rodentia, F = Eulipotyphla, G = Chiroptera, and H = Artiodactyla. Black colours represent significant coefficient, grey colours represent non-significant coefficient at $p_{MCMC} = 5\%$. Sample size (n) = 483.

BMR Phylogenetic regression model	Marginal likelihood Constant-Rate	Marginal likelihood Var-Rates	Bayes Factor Var-rates vs Constant-Rates	R ² Var-Rates Regression
BMR ~ $\alpha + \beta_1(T_b)$	-655.06	-623.69	62.74	0.008
BMR ~ (α ref) + $\beta_1(T_b*ref)$ + $\beta_2(A)$ + $\beta_3(T_b*A)$	-663.6	-632.03	63.14	0.017
BMR ~ (α ref) + $\beta_1(T_b*ref)$ + $\beta_2(A)$ + $\beta_3(G)$ + $\beta_4(T_b*G)$ + $\beta_5(T_b*G)$	-670.79	-638.26	65.06	0.042
BMR ~ (α ref) + $\beta_1(T_b*ref)$ + $\beta_2(A)$ + $\beta_3(G)$ + $\beta_4(H)$ + $\beta_5(T_b*A)$ + $\beta_6(T_b*G)$ + $\beta_7(T_b*H)$	-674.68	-644.15	61.06	0.094
BMR ~ (α ref) + $\beta_1(T_b*ref)$ + $\beta_2(A)$ + $\beta_3(D)$ + $\beta_4(G)$ + $\beta_5(H)$ + $\beta_6(T_b*A)$ + $\beta_7(T_b*D)$ + $\beta_8(T_b*G)$ + $\beta_9(T_b*H)$	-683.88	-650.96	65.84	0.095
BMR ~ (α ref) + $\beta_1(T_b*ref)$ + $\beta_2(A)$ + $\beta_3(D)$ + $\beta_4(F)$ + $\beta_5(G)$ + $\beta_6(H)$ + $\beta_7(T_b*A)$ + $\beta_8(T_b*D)$ + $\beta_9(T_b*F)$ + $\beta_{10}(T_b*G)$ + $\beta_{11}(T_b*H)$	-693.69	-661.08	65.22	0.099
BMR ~ (α ref) + $\beta_1(T_b*ref)$ + $\beta_2(A)$ + $\beta_3(D)$ + $\beta_4(E)$ + $\beta_5(F)$ + $\beta_6(G)$ + $\beta_7(H)$ + $\beta_8(T_b*A)$ + $\beta_9(T_b*D)$ + $\beta_{10}(T_b*E)$ + $\beta_{11}(T_b*F)$ + $\beta_{12}(T_b*G)$ + $\beta_{13}(T_b*H)$	-702.87	-671.25	63.24	0.102
BMR ~ (α ref) + $\beta_1(T_b*ref)$ + $\beta_2(A)$ + $\beta_3(C)$ + $\beta_4(D)$ + $\beta_5(E)$ + $\beta_6(F)$ + $\beta_7(G)$ + $\beta_8(H)$ + $\beta_9(T_b*A)$ + $\beta_{10}(T_b*C)$ + $\beta_{11}(T_b*D)$ + $\beta_{12}(T_b*E)$ + $\beta_{13}(T_b*F)$ + $\beta_{14}(T_b*G)$ + $\beta_{15}(T_b*H)$	-711.72	-685.85	51.74	0.085
BMR ~ (α ref) + $\beta_1(T_b*ref)$ + $\beta_2(A)$ + $\beta_3(B)$ + $\beta_4(C)$ + $\beta_5(D)$ + $\beta_6(E)$ + $\beta_7(F)$ + $\beta_8(G)$ + $\beta_9(H)$ + $\beta_{10}(T_b*A)$ + $\beta_{11}(T_b*B)$ + $\beta_{12}(T_b*C)$ + $\beta_{13}(T_b*D)$ + $\beta_{14}(T_b*E)$ + $\beta_{15}(T_b*F)$ + $\beta_{16}(T_b*G)$ + $\beta_{17}(T_b*H)$	-721.57	-687.26	68.62	0.1

Table 3. Phylogenetic *variable-rates* regression models for T_b and *Mass* in mammals, showing on top the best-fitted model selected by strict criteria. α = intercept, β = slope coefficient, ref = reference group (Carnivora), A = Marsupialia, B = Afrotheria, C = Xenarthra, D = Primates, E = Rodentia, F = Eulipotyphla, G = Chiroptera, and H = Artiodactyla. Black colours represent significant coefficient, grey colours represent non-significant coefficient at $p_{\text{MCMC}} = 5\%$. Black colours represent significant coefficient, grey colours represent non-significant coefficient at $p_{\text{MCMC}} = 5\%$. Sample size (n) = 483.

T_b Phylogenetic regression model	Marginal likelihood Constant-Rate	Marginal likelihood Var-Rates	Bayes Factor Var-rates vs Constant-Rates	R ² Var-Rates Regression
$T_b \sim \alpha + \beta_1(\text{Mass})$	-890.72	-811.34	158.76	0.0078
$T_b \sim (\alpha \text{ ref}) + \beta_1(\text{Mass*ref}) + \beta_2(\text{G}) + \beta_3(\text{Mass*G})$	-899.07	-819.14	159.86	0.0171
$T_b \sim (\alpha \text{ ref}) + \beta_1(\text{Mass ref}) + \beta_2(\text{F}) + \beta_3(\text{G}) + \beta_4(\text{Mass*F}) + \beta_5(\text{Mass*G})$	-906.31	-827.7	157.22	0.025
$T_b \sim (\alpha \text{ ref}) + \beta_1(\text{Mass*ref}) + \beta_2(\text{A}) + \beta_3(\text{F}) + \beta_4(\text{G}) + \beta_5(\text{Mass*A}) + \beta_6(\text{Mass*F}) + \beta_7(\text{Mass*G})$	-915.74	-837.82	155.84	0.024
$T_b \sim (\alpha \text{ ref}) + \beta_1(\text{Mass*ref}) + \beta_2(\text{A}) + \beta_3(\text{E}) + \beta_4(\text{F}) + \beta_5(\text{G}) + \beta_6(\text{Mass*A}) + \beta_7(\text{Mass*E}) + \beta_8(\text{Mass*F}) + \beta_9(\text{Mass*G})$	-924.63	-847.99	153.28	0.023
$T_b \sim (\alpha \text{ ref}) + \beta_1(\text{Mass*ref}) + \beta_2(\text{A}) + \beta_3(\text{E}) + \beta_4(\text{F}) + \beta_5(\text{G}) + \beta_6(\text{H}) + \beta_7(\text{Mass*A}) + \beta_8(\text{Mass*E}) + \beta_9(\text{Mass*F}) + \beta_{10}(\text{Mass*G}) + \beta_{11}(\text{Mass*H})$	-933.08	-856.62	152.92	0.024
$T_b \sim (\alpha \text{ ref}) + \beta_1(\text{Mass*ref}) + \beta_2(\text{A}) + \beta_3(\text{B}) + \beta_4(\text{E}) + \beta_5(\text{F}) + \beta_6(\text{G}) + \beta_7(\text{H}) + \beta_8(\text{Mass*A}) + \beta_9(\text{Mass*B}) + \beta_{10}(\text{Mass*E}) + \beta_{11}(\text{Mass*F}) + \beta_{12}(\text{Mass*G}) + \beta_{13}(\text{Mass*H})$	-942.95	-866.34	153.22	0.022
$T_b \sim (\alpha \text{ ref}) + \beta_1(\text{Mass*ref}) + \beta_2(\text{A}) + \beta_3(\text{B}) + \beta_4(\text{C}) + \beta_5(\text{E}) + \beta_6(\text{F}) + \beta_7(\text{G}) + \beta_8(\text{H}) + \beta_9(\text{Mass*A}) + \beta_{10}(\text{Mass*B}) + \beta_{11}(\text{Mass*C}) + \beta_{12}(\text{Mass*E}) + \beta_{13}(\text{Mass*F}) + \beta_{14}(\text{Mass*G}) + \beta_{15}(\text{Mass*H})$	-949.91	-871.13	157.56	0.029
$T_b \sim (\alpha \text{ ref}) + \beta_1(\text{Mass*ref}) + \beta_2(\text{A}) + \beta_3(\text{B}) + \beta_4(\text{C}) + \beta_5(\text{D}) + \beta_6(\text{E}) + \beta_7(\text{F}) + \beta_8(\text{G}) + \beta_9(\text{H}) + \beta_{10}(\text{Mass*A}) + \beta_{11}(\text{Mass*B}) + \beta_{12}(\text{Mass*C}) + \beta_{13}(\text{Mass*D}) + \beta_{14}(\text{Mass*E}) + \beta_{15}(\text{Mass*F}) + \beta_{16}(\text{Mass*G}) + \beta_{17}(\text{Mass*H})$	-957.59	-880.55	154.08	0.027

Table 4. Phylogenetic *variable-rates* regression models for *BMR* and *Mass* in birds, showing on top the best-fitted model selected by strict criteria. α = intercept, β = slope coefficient, ref = reference group (Accipitriformes + Anseriformes + Apodiformes + Bucerotiformes + Caprimulgiformes + Charadriiformes + Coliiformes + Coraciiformes + Cuculiformes + Falconiformes + Galliformes + Gruiformes + Pelecaniformes + Piciformes + Podicipediformes + Procellariiformes + Psittaciformes + Strigiformes + Suliformes), A = Columbiformes, B = Passeriformes. Black colours represent significant coefficient, grey colours represent non-significant coefficient at $p_{\text{MCMC}} = 5\%$. Sample size (n) = 164.

BMR Phylogenetic Regression Model	Marginal likelihood Constant-Rate	Marginal likelihood Var-Rates	Bayes Factor Var-Rates vs Constant-Rate	R ² Var-Rates Regression
$\text{BMR} \sim \alpha + \beta_1(\text{Mass})$	-40.05	-26.18	27.74	0.878
$\text{BMR} \sim (\alpha \text{ ref}) + \beta_1(\text{Mass*ref}) + \beta_2(\text{B}) + \beta_3(\text{Mass*B})$	-51.72	-37.73	27.98	0.879
$\text{BMR} \sim (\alpha \text{ ref}) + \beta_1(\text{Mass*ref}) + \beta_2(\text{A}) + \beta_3(\text{B}) + \beta_4(\text{Mass*A}) + \beta_5(\text{Mass*B})$	-63.6	-49.75	27.7	0.878

Table 5. Phylogenetic *variable-rates* regression models for *BMR* and T_b in birds, showing on top the best-fitted model selected by strict criteria. α = intercept, β = slope coefficient, ref = reference group (Accipitriformes + Anseriformes + Apodiformes + Bucerotiformes + Caprimulgiformes + Charadriiformes + Coliiformes + Coraciiformes + Cuculiformes + Falconiformes + Galliformes + Gruiformes + Pelecaniformes + Piciformes + Podicipediformes + Procellariiformes + Psittaciformes + Strigiformes + Suliformes), A = Columbiformes, B = Passeriformes. Black colours represent significant coefficient, grey colours represent non-significant coefficient at $p_{\text{MCMC}} = 5\%$. Sample size (n) = 164.

BMR Phylogenetic Regression Model	Marginal likelihood Constant-Rate	Marginal likelihood Var-Rates	Bayes Factor Var-Rates vs Constant-Rate	R ² Var-Rates Regression
BMR ~ (α ref) + $\beta_1(T_b \cdot \text{ref})$ + $\beta_2(A)$ + $\beta_3(T_b \cdot A)$	-184.01	-181.19	5.64	0.048
BMR ~ (α ref) + $\beta_1(T_b \cdot \text{ref})$ + $\beta_2(A)$ + $\beta_3(B)$ + $\beta_4(T_b \cdot A)$ + $\beta_5(T_b \cdot B)$	-193.41	-191.3	4.22	0.062
BMR ~ α + $\beta_1(T_b)$	-177.92	-174.98	5.88	NA

Table 6. Phylogenetic *variable-rates* regression models for T_b and *Mass* in birds, showing on top the best-fitted model selected by strict criteria. α = intercept, β = slope coefficient, ref = reference group (Accipitriformes + Anseriformes + Apodiformes + Bucerotiformes + Caprimulgiformes + Charadriiformes + Coliiformes + Coraciiformes + Cuculiformes + Falconiformes + Galliformes + Gruiformes + Pelecaniformes + Piciformes + Podicipediformes + Procellariiformes + Psittaciformes + Strigiformes + Suliformes), A = Columbiformes, B = Passeriformes. Black colours represent significant coefficient, grey colours represent non-significant coefficient at $p_{\text{MCMC}} = 5\%$. Sample size (n) = 164.

T_b Phylogenetic Regression Model	Marginal likelihood Constant-Rate	Marginal likelihood Var-Rates	Bayes Factor Constant vs Var-Rates	R ² Var-Rates Regression
$T_b \sim (\alpha \text{ ref}) + \beta_1(\text{Mass} \cdot \text{ref}) + \beta_2(A) + \beta_3(\text{Mass} \cdot A)$	-302.99	-262.77	80.44	0.016
$T_b \sim (\alpha \text{ ref}) + \beta_1(\text{Mass} \cdot \text{ref}) + \beta_2(A) + \beta_3(B) + \beta_4(\text{Mass} \cdot A) + \beta_5(\text{Mass} \cdot B)$	-312	-272.67	78.66	0.01
$T_b \sim \alpha + \beta_1(\text{Mass})$	-295.91	-255.92	79.98	NA

Table 7. Phylogenetic *variable-rates* regression models for *BMR* and T_b in mammals obtained after model reduction in Table S1 to S3. These regressions were compared with other several regressions that include additional covariates. α = intercept, β = slope coefficient. Black colours represent significant coefficient, grey colours represent non-significant coefficient at $p_{\text{MCMC}} = 5\%$. Sample size (n) = 461.

BMR Phylogenetic regression model	Marginal likelihood Constant-Rate	Marginal likelihood Var-Rates	Bayes Factor Var-rates vs Constant-Rates	R ² Var-Rates Regression
BMR ~ α + $\beta_1(\text{Mass})$ + $\beta_2(T_b)$	-192.25	-112.26	159.78	0.935
BMR ~ α + $\beta_1(\text{Mass})$ + $\beta_2(T_b)$ + $\beta_3(T_a)$	-197.38	-112.82	169.12	0.937
BMR ~ α + $\beta_1(\text{Mass})$	-197.76	-119.89	155.74	0.928
BMR ~ α + $\beta_1(\text{Mass})$ + $\beta_2(\text{Mass})^2$	-203.69	-126.80	153.78	0.927
BMR ~ α + $\beta_1(\text{Mass})$ + $\beta_2(\text{SmallerThan603})$ + $\beta_3(T_a \cdot \text{SmallerThan603})$ + $\beta_4(T_a \cdot \text{BiggerThan603})$	-201.19	-130.37	141.64	0.928
T_b Phylogenetic regression model	Marginal likelihood Constant-Rate	Marginal likelihood Var-Rates	Bayes Factor Var-Rates vs Constant-Rates	R ² Var-Rates Regression
$T_b \sim \alpha + \beta_1(\text{Mass}) + \beta_2(\text{BMR})$	-825.84	-764.72	122.24	0.143
$T_b \sim \alpha + \beta_1(\text{BMR})$	-827.19	-775.35	103.68	0.037
$T_b \sim \alpha + \beta_1(\text{Mass})$	-833.95	-781.08	105.74	0.006
$T_b \sim \alpha + \beta_1(\text{Mass}) + \beta_2(\text{BMR}) + \beta_3(T_a)$	-834.59	-773.97	121.24	0.142

Table 8. Phylogenetic *variable-rates* regression models for *BMR* and *T_b* in birds obtained after model reduction in Table S4 to S6. These regressions were compared with other several regressions that include additional covariates. α = intercept, β = slope coefficient, ref = reference group (Accipitriformes + Anseriformes + Apodiformes + Bucerotiformes + Caprimulgiformes + Charadriiformes + Coliiformes + Coraciiformes + Cuculiformes + Falconiformes + Galliformes + Gruiformes + Passeriformes + Pelecaniformes + Piciformes + Podicipediformes + Procellariiformes + Psittaciformes + Strigiformes + Suliformes), A = Columbiformes. Black colours represent significant coefficient, grey colours represent non-significant coefficient at $p_{\text{MCMC}} = 5\%$. Sample size (n) = 164.

BMR Phylogenetic Regression Model	Marginal likelihood Constant-Rate	Marginal likelihood Var-Rates	Bayes Factor Var-Rates vs Constant-Rate	R ² Var-Rates Regression
BMR ~ $\alpha + \beta_1(\text{Mass})$	-40.05	-26.18	27.74	0.878
BMR ~ $\alpha + \beta_1(\text{Mass}) + \beta_2(T_a)$	-49.14	-34.2	29.88	0.885
BMR ~ $\alpha + \beta_1(\text{Mass}) + \beta_2(T_b) + \beta_3(T_a)$	-57.49	-42.37	30.24	0.886
BMR ~ (α ref) + $\beta_1(T_b \cdot \text{ref}) + \beta_2(A) + \beta_3(T_b \cdot A)$	-184.01	-181.19	5.64	0.048
BMR ~ $\alpha + \beta_1(\text{Mass}) + \beta_2(T_b)$	-48.32	-33.91	28.82	0.878
T _b Phylogenetic Regression Model	Marginal likelihood Constant-Rate	Marginal likelihood Var-Rates	Bayes Factor Constant vs Var-Rates	R ² Var-Rates Regression
T _b ~ (α ref) + $\beta_1(\text{Mass} \cdot \text{ref}) + \beta_2(A) + \beta_3(\text{Mass} \cdot A)$	-302.99	-262.77	80.44	0.016
T _b ~ $\alpha + \beta_1(\text{Mass})$	-295.91	-255.92	79.98	NA
T _b ~ $\alpha + \beta_1(T_a)$	-298.45	-257.92	81.06	NA
T _b ~ $\alpha + \beta_1(\text{Mass}) + \beta_2(\text{BMR})$	-301.08	-259.64	82.88	NA
T _b ~ $\alpha + \beta_1(\text{Mass}) + \beta_2(T_a)$	-304.46	-264.24	80.44	NA

Table 9. Bayesian GLS regression between fast *branch-wise rates* ($r > 1$) of *BMR* and *T_b* in mammals. r values were estimated given the following *var-rates* phylogenetic regressions: *BMR* ~ *Mass* + *T_b*, and *T_b* ~ *Mass* + *BMR* (502 species had data for all variables). α = intercept, β = slope coefficient. CI = confidence interval. Sample size (n) = 254 branches with fast rates in both traits.

BMR Fast Rates	Posterior mean	Lower 95% CI	Upper 95% CI	pMCMC
α	1.41	1.26	1.57	0*
$\beta_1(T_b \text{ Fast Rates})$	0.05	-0.02	0.12	0.09

Table 10. Bayesian GLS regression between fast *branch-wise rates* ($r > 1$) of *BMR* and *T_b* in birds. r values were estimated given the following *var-rates* phylogenetic regressions: *BMR* ~ *Mass*, and *T_b* ~ *Reference* + (*Mass* * *Reference*) + *Columbiformes* + (*Mass* * *Columbiformes*). α = intercept, β = slope coefficient. CI = confidence interval. Sample size (n) = 14 branches with fast rates in both traits.

BMR Fast Rates	Posterior mean	Lower 95% CI	Upper 95% CI	pMCMC
α	2.003	1.52	2.48	0*
$\beta_1(T_b \text{ Fast Rates})$	-0.12	-0.38	0.13	0.169

Table 11. Phylogenetic regressions applied to the extant *T_a* in mammals and birds. We included latitude and a second-order polynomial term for latitude as independent variables. α = intercept, β = slope coefficient. All coefficients were significant at $p_{\text{MCMC}} = 5\%$. Sample size (n) = 2922 mammalian species; 6142 avian species.

Phylogenetic Regression Model	Marginal likelihood Constant-Rate	Marginal likelihood Var-Rates	Bayes Factor Var-Rates vs Constant-rate	R ² Var-Rates Regression
Birds $T_a \sim \alpha + \beta_1(\text{Latitude}) + \beta_2((\text{Latitude})^2)$	-21088.4	-16894.5	8387.8	0.71
Mammals $T_a \sim \alpha + \beta_1(\text{Latitude}) + \beta_2((\text{Latitude})^2)$	-8793.1	-7922.5	1741.2	0.58

Table 12. Bayesian GLS regression between *branch-wise rates* ($r > 1$) of *BMR* and T_a in mammals. r values for T_a were estimated given the *var-rates* regression in Table 11. α = intercept, β = slope coefficient. CI = confidence interval. Sample size (n) = 602 branches with rate heterogeneity in both traits.

BMR Rates	Posterior mean	Lower 95% CI	Upper 95% CI	pMCMC
α (Intercept)	1.27	1.18	1.35	0*
$\beta_1(T_a \text{ Rates})$	0.36	0.31	0.41	0*

Table 13. Bayesian GLS regression between fast *branch-wise rates* ($r > 1$) of *BMR* and T_a in birds. r values for T_a were estimated given the *var-rates* regression in Table 11. α = intercept, β = slope coefficient. CI = confidence interval. Sample size (n) = 31 branches with fast rates in both traits.

BMR Fast Rates	Posterior mean	Lower 95% CI	Upper 95% CI	pMCMC
α	0.96	-0.35	2.26	0*
$\beta_1(T_a \text{ Fast Rates})$	0.16	-0.28	0.62	0.22

Table 14. Assessing the evolutionary trend in mammalian T_a , *BMR*, and T_b . We achieved this by conducting Bayesian PGLS regressions that includes the effect of path-wise rates of T_a , *BMR*, and T_b . The tree used for each PGLS was the consensus branch-scaled tree, and we used the Brownian motion model of trait evolution. α = intercept, β = slope coefficient. CI = confidence interval. Sample size (n) = 2922 species for T_a ; 502 species for *BMR* and T_b .

T_a	Posterior mean	Lower 95% CI	Upper 95% CI	pMCMC
α	26.95	26.4	27.41	0*
$\beta_1(\text{Latitude})$	0.034	0.028	0.04	0*
$\beta_2(\text{Latitude})^2$	-0.0065	-0.0067	-0.0063	0*
$\beta_3(\text{Path wise rate } T_a)$	-0.018	-0.021	-0.015	0*
BMR				
α	-6.41	-6.94	-5.92	0*
$\beta_1(\text{Mass})$	0.717	0.701	0.733	0*
$\beta_2(T_b)$	0.0608	0.046	0.075	0*
$\beta_2(\text{Path wise rate BMR})$	0.00025	-0.00013	0.00059	0.088
T_b				
α	39.39	37.91	40.74	0*
$\beta_1(\text{Mass})$	-0.734	-0.93	-0.53	0*
$\beta_2(\text{BMR})$	1.11	0.87	1.37	0*
$\beta_3(\text{Path wise rate } T_b)$	-0.0042	-0.0087	5.40E-04	0.046*

Table 15. Assessing the evolutionary trend in avian T_a , BMR , and T_b . We achieved this by conducting Bayesian PGLS regressions that includes the effect of path-wise rates of T_a , BMR , and T_b . The tree used for each PGLS was the consensus branch-scaled tree, and we used the Brownian motion model of trait evolution. α = intercept, β = slope coefficient. CI = confidence interval. The T_b database was obtained from Clarke & Rothery³ and we evaluated the effect of $Mass$ across order with at least 10 data points. After model reduction we found that $Mass$ had a significant effect only in Charadriiformes and Procellariiformes. Reference = Accipitriformes, Anseriformes, Apodiformes, Apterygiformes, Caprimulgiformes, Casuariiformes, Ciconiiformes, Columbiformes, Coraciiformes, Cuculiformes, Galliformes, Gaviiformes, Gruiformes, Passeriformes, Passeriformes, Pelecaniformes, Phoenicopteriformes, Podicipediformes, Sphenisciformes, Strigiformes, Struthioniformes, Tinamiformes. Sample size (n) = 6142 species for T_a ; 164 species for BMR ; 367 species for T_b .

T_a	Posterior mean	Lower 95% CI	Upper 95% CI	pMCMC
α	26.4	26.1	26.8	0*
$\beta_1(\text{Latitude})$	0.036	0.034	0.039	0*
$\beta_2(\text{Latitude})^2$	-0.006	-0.0061	-0.0059	0*
$\beta_3(\text{Path wise rate } T_a)$	-0.014	-0.016	-0.012	0*
BMR				
α	1.9	1.49	2.33	0*
$\beta_1(\text{Mass})$	0.68	0.64	0.72	0*
$\beta_2(\text{Path wise rate BMR})$	-0.0028	-0.006	9.00E-04	0.061
T_b				
$\alpha(\text{Reference})$	41.96	40.7	43.3	0*
$\beta_1(\text{Mass reference})$	-0.13	-0.25	-0.0081	0.013*
$\beta_2(\text{Procellariiformes})$	37.05	33.7	40.6	0.002*
$\beta_3(\text{Charadriiformes})$	44.5	41.72	47.3	0.033*
$\beta_4(\text{Procellariiformes*Mass})$	0.46	0.07	0.88	0.011*
$\beta_5(\text{Charadriiformes*Mass})$	-0.66	-1.02	-0.31	0*
$\beta_6(\text{Path wise rate } T_b)$	-0.0067	-0.013	9.40E-04	0.037*

Table 16. Bayesian GLS regressions which evaluate the effect of fast ($r > 1$) *branch-wise* rates of T_b and T_a on fast *branch-wise* rates of mammalian BMR . r values for BMR were estimated from *variable-rates* regression that accounted only for $Mass$. α = intercept, β = slope coefficient. All coefficients were significant at $p_{\text{MCMC}} = 5\%$. However, the regression that includes only fast rates of T_a have the best fit to the data, as indicated by its marginal likelihood (5 log-units higher than the model including fast rates of T_a and T_b - Bayes factor = 10 in support of the simplest model). Sample size (n) = 149 branches with fast rates in all traits.

Bayesian GLS regression	Marginal likelihood	R ²
Fast BMR rates ~ $\alpha + \beta_1(\text{Fast } T_a \text{ rates})$	-172	0.45
Fast BMR rates ~ $\alpha + \beta_1(\text{Fast } T_b \text{ rates}) + \beta_2(\text{Fast } T_a \text{ rates})$	-177	0.46
Fast BMR rates ~ $\alpha + \beta_1(\text{Fast } T_b \text{ rates})$	-213	0.04

Table 17. Bayesian GLS regressions which evaluate the effect of fast ($r > 1$) *branch-wise* rates of T_b and T_a on fast *branch-wise* rates of mammalian BMR . r values for BMR were estimated from *variable-rates* regression that allowed the scaling BMR and T_b to vary across orders. α = intercept, β = slope coefficient. All coefficients were significant at $p_{\text{MCMC}} = 5\%$. However, the regression that includes only fast rates of T_a have the best fit to the data, as indicated by its marginal likelihood (4 log-units higher than the model including fast rates of T_a and T_b - Bayes factor = 8 in support of the simplest model). Sample size (n) = 154 branches with fast rates in all traits.

Bayesian GLS regression	Marginal likelihood	R ²
Fast BMR rates ~ $\alpha + \beta_1(\text{Fast } T_a \text{ rates})$	-167	0.47
Fast BMR rates ~ $\alpha + \beta_1(\text{Fast } T_b \text{ rates}) + \beta_2(\text{Fast } T_a \text{ rates})$	-171	0.49
Fast BMR rates ~ $\alpha + \beta_1(\text{Fast } T_b \text{ rates})$	-210	0.07

References supplementary information.

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