Supplementary analysis (SMR), Tables and Figures

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# Results

*Supplementary Analysis*

Default priors for all Bayesian models were used. For all population-level (i.e. Fixed effects), the default prior for the intercept is a normal distribution with a mean 0 and standard deviation 10. The default prior for the shape parameter of the intercept was a Student-t distribution with mean 0, scale 2.5, and 3 degrees of freedom. The default prior for residuals (sigma) was a Student-t distribution with mean 0, scale 2.5, and 3 degrees of freedom. The Cholesky factor was used as the default prior for correlations between random effects

We defined standard metabolic rate (SMR) as the the lowest 10% of values of oxygen consumption rate during our overnight trials. Once these data were removed we had a total of 83 measurements for 40 individuals (male XX: *n = 13*, female XX: *n = 15*, male XY: *n = 12*) were recorded. There was a strong scaling relationship between log metabolic rate and log mass (Table S1). Sex-reversed male XX *B. duperreyi* had a scaling relationship that was most like their phenotypic counterparts (male XY - male XX; pMCMC = 0.26; Table S1) and lower than their genotypic counterparts (female XX - male XX; pMCMC = 0.07). For phenotypic males (male XX & male XX), this scaling relationship between logmass and metabolism changed similarly across differently sized individuals (Fig. S1). The homogeneous variance model was the most parsimonious ([heteroscedastic model – homoscedastic model] loo: -1.31, SE = 2), accounting for 0.73% (95% CI:0.63 - 0.8) of the variation in metabolic rate.

*Pogona vitticeps* - Once SMR data (lowest 10%) were filtered we had a total of total of 146 measurements for 96 individuals (female ZZ: *n = 28*, female ZW: *n = 30*, male ZZ: *n = 38*) were recorded. There was a strong scaling relationship between log metabolic rate and log mass (Table S2). Sex-reversed female *P. vitticeps* (female ZZ) had a scaling relationship that was overall higher than their genotypic counterparts (male ZZ - female ZZ; pMCMC = 0.61), but lower than their phenotypic counterparts (female ZW - female ZZ; pMCMC = 0.64; Table 2).The heteroscedasticity variance model was the most parsimonious ([heteroscedastic model – homoscedastic model] loo: -16.4, SE = 5.03), accounting for 0.86% (95% CI:0.79 - 0.92) of the variation in metabolic rate.

# Tables & Figures

![](data:application/pdf;base64,) Figure S1. # Tables & Figures ![](data:application/pdf;base64,) Figure S2. Comparison of log standard metabolic rate (V̇ mL min) across log body mass (g) by sex class for *Bassiana duperreyi* (A-B) and *Pogona vitticeps* (C-D). Sex-reversed individuals (male XX or female ZZ) are denoted by red colour, phenotypic females (female XX or female ZW) are denoted in black, phenotypic males (male XY or male ZZ) are denoted in blue. Fitted lines were obtained from predicted values from the brms model for each species and confidence bands were constructed from the SE of prediction values for each sex (A,C). Density plots above each regression plot denote the distribution in body mass (log mass) by sex for each species. To visualize how log metabolic rate changes across log body mass, panels (B and D) show the distribution of predicted metabolic rate at three areas of log body mass (mean, +1.5SD, and -1.5SD) denoted by the dash-dot line in panels A and C for each sex and species.

Table S1. Model coefficients for testing whether sex affects the slope of standard metabolic rate for *Bassiana duperreyi*, where the intercept is concordant females. Metabolic rate and mass were log transformed and time was z-transformed. Columns l-95% CI and u-95% CI, are the lower and upper bound of the 95% credible interval for each parameter, estimated from the posterior distribution..

| Covariate | Estimate | Est.Error | l-95% CI | u-95% CI |
| --- | --- | --- | --- | --- |
| Intercept (SexFemaleXX) | -4.78 | 0.12 | -5.02 | -4.52 |
| SexMaleSRXX | -0.06 | 0.08 | -0.22 | 0.10 |
| SexMaleXY | -0.12 | 0.09 | -0.28 | 0.05 |
| logMass | 1.70 | 0.39 | 0.93 | 2.52 |
| ztime | 0.01 | 0.04 | -0.06 | 0.08 |
| SexMaleSRXX:logMass | -0.70 | 0.40 | -1.52 | 0.08 |
| SexMaleXY:logMass | -0.14 | 0.48 | -1.09 | 0.85 |

Table S2. Model coefficients form hetero testing whether sex affects the slope of metabolic rate for *Pogona vitticeps*, which heteroscedasticity was accounted for within the data. The intercept is concordant females. Metabolic rate and mass were log transformed and time was z-transformed. Columns l-95% CI and u-95% CI, are the lower and upper bound of the 95% credible interval for each parameter, estimated from the posterior distribution.

| Covariate | Estimate | Est.Error | l-95% CI | u-95% CI |
| --- | --- | --- | --- | --- |
| Intercept (SexFemaleZW) | -2.05 | 0.08 | -2.22 | -1.89 |
| SexFemaleSRZZ | -0.17 | 0.08 | -0.34 | -0.02 |
| SexMaleZZ | -0.08 | 0.07 | -0.22 | 0.06 |
| logMass | 1.41 | 0.18 | 1.08 | 1.76 |
| ztime | 0.00 | 0.03 | -0.07 | 0.07 |
| SexFemaleSRZZ:logMass | -0.08 | 0.19 | -0.42 | 0.31 |
| SexMaleZZ:logMass | -0.17 | 0.18 | -0.53 | 0.19 |
| sigma\_Intercept | -1.67 | 0.16 | -2.01 | -1.39 |
| sigma\_logMass | -1.51 | 0.47 | -2.35 | -0.53 |
| sigma\_ztime | -0.11 | 0.14 | -0.39 | 0.15 |

Table S2. Model coefficients form hetero testing whether sex affects the slope of metabolic rate for *Pogona vitticeps*, which heteroscedasticity was accounted for within the data. The intercept is concordant females. Metabolic rate and mass were log transformed and time was z-transformed. Columns l-95% CI and u-95% CI, are the lower and upper bound of the 95% credible interval for each parameter, estimated from the posterior distribution.

| Species | Hypothesis | Estimate | Estimate error | Estimate pMCMC |
| --- | --- | --- | --- | --- |
| *Bassiana duperreyi* | Like Phenotype -1.5 | -0.08 | (-0.29 - 0.13) | 0.45 |
| Like Phenotype mean | -0.03 | (-0.21 - 0.15) | 0.74 |
| Like Phenotype +1.5 | 0.02 | (-0.19 - 0.23) | 0.89 |
| Like Genotype -1.5 | 0.01 | (-0.19 - 0.21) | 0.89 |
| Like Genotype mean | -0.15 | (-0.32 - 0.02) | 0.10 |
| Like Genotype +1.5 | -0.30 | (-0.50 - -0.11) | 0.01 |
| *Pogona vitticeps* | Like Phenotype -1.5 | -0.06 | (-0.23 - 0.11) | 0.48 |
| Like Phenotype mean | -0.13 | (-0.28 - 0.03) | 0.10 |
| Like Phenotype +1.5 | -0.20 | (-0.37 - -0.03) | 0.03 |
| Like Genotype -1.5 | -0.15 | (-0.31 - 0.00) | 0.05 |
| Like Genotype mean | -0.06 | (-0.20 - 0.09) | 0.44 |
| Like Genotype +1.5 | 0.04 | (-0.12 - 0.19) | 0.64 |

Table S4. BBRMS model coefficients for each respective species when testing mass differences across sex class for animals used in respirometry experiments. Mass was log-transformed and lower and upper bounds were derived from the 95% credible interval for each parameter, estimated from the posterior samples.

| Species | Sex | Sample Size | Estimate | l-95% CI | u-95% CI | Contrast | pMCMC Value |
| --- | --- | --- | --- | --- | --- | --- | --- |
| *B. duperryii* | Female XX | 15 | 0.04 | -0.02 | 0.11 | Female XX-MaleSR XX | 0.45 |
| MaleSR XX | 13 | -0.02 | -0.10 | 0.05 | MaleSR XX-Male XY | 0.91 |
| Male XY | 12 | 0.02 | -0.06 | 0.09 | Male XY-Female XX | 0.70 |
| *P. vitticeps* | Female ZW | 30 | 0.01 | -0.10 | 0.11 | Female ZW-FemaleSR ZZ | 0.48 |
| FemaleSR ZZ | 28 | 0.06 | -0.04 | 0.16 | FemaleSR ZZ-Male ZZ | 0.44 |
| Male ZZ | 38 | 0.01 | -0.08 | 0.10 | Male ZZ-Female ZW | 0.96 |

Table S5. BRMS Model coefficients for SVL and mass growth rate estimates across sex class *Bassiana duperreyi*. Growth rate was calculated by dividing the change in growth (SVL or mass) between the initial measurement and subsequent remeasurement by the total number of days elapsed. Due to the small size and rate of change in grams, mass was converted to centigrams (cg). Animals were remeasured between 3 and 6 months post hatch.

| Growth rate | Covariate | Estimate | l-95% CI | u-95% CI |
| --- | --- | --- | --- | --- |
| *SVL(mm/d)* | Intercept (O2\_SexFemaleXX) | -4.62 | -5.02 | -4.21 |
| Growth Rate (SVLmm) | 6.20 | -2.26 | 14.35 |
| O2\_SexMaleSRXX | -0.14 | -0.73 | 0.42 |
| O2\_SexMaleXY | 0.10 | -0.44 | 0.64 |
| Growth Rate (SVLmm):O2\_SexMaleSRXX | -4.07 | -16.08 | 7.37 |
| Growth Rate (SVLmm):O2\_SexMaleXY | -7.84 | -19.83 | 4.18 |
| *mass(cg/d)* | Intercept (O2\_SexFemaleXX) | -4.61 | -4.97 | -4.24 |
| Growth Rate (mass cg/d) | 1.06 | -0.98 | 3.04 |
| O2\_SexMaleSRXX | 0.20 | -0.47 | 0.87 |
| O2\_SexMaleXY | 0.18 | -0.45 | 0.82 |
| Growth Rate (mass cg/d):O2\_SexMaleSRXX | -2.59 | -6.49 | 1.25 |
| Growth Rate (mass cg/d):O2\_SexMaleXY | -2.13 | -5.89 | 1.73 |

Table S6. BRMS Model coefficients for SVL and mass growth rate estimates across sex class for *Pogona vitticeps*. Growth rate was calculated by dividing the change in growth (SVL or mass) between the initial measurement and subsequent remeasurement by the total number of days elapsed. Animals were remeasured between 3 and 6 months post hatch.

| Growth rate | Covariate | Estimate | l-95% CI | u-95% CI |
| --- | --- | --- | --- | --- |
| *SVL(mm/d)* | Intercept (O2\_SexFemaleZW) | -2.17 | -2.77 | -1.57 |
| Growth Rate (SVLmm) | 1.47 | -0.84 | 3.79 |
| O2\_SexFemaleSRZZ | 0.17 | -0.63 | 0.95 |
| O2\_SexMaleZZ | 0.01 | -0.73 | 0.74 |
| Growth Rate (SVLmm):O2\_SexFemaleSRZZ | -1.51 | -4.74 | 1.66 |
| Growth Rate (SVLmm):O2\_SexMaleZZ | -0.35 | -3.11 | 2.45 |
| *mass(g/d)* | Intercept (O2\_SexFemaleZW) | -1.79 | -2.30 | -1.27 |
| Growth Rate (mass g/d) | -0.07 | -2.55 | 2.41 |
| O2\_SexFemaleSRZZ | 0.00 | -0.77 | 0.75 |
| O2\_SexMaleZZ | -0.27 | -0.91 | 0.37 |
| Growth Rate (mass g/d):O2\_SexFemaleSRZZ | -0.90 | -4.48 | 2.78 |
| Growth Rate (mass g/d):O2\_SexMaleZZ | 0.92 | -2.08 | 3.83 |

Table S7. Frequency of mortality across sex class for *Bassiana duperryii* and *Pogona vitticeps*. These measurements were recorded from initial hatch date to 6 months post-hatch date.

| Species | Sex | Alive | Dead |
| --- | --- | --- | --- |
| *B. duperryii* | Female XX | 13 | 2 |
| MaleSR XX | 10 | 3 |
| Male XY | 12 | 0 |
| *P. vitticeps* | Female ZW | 25 | 5 |
| FemaleSR ZZ | 21 | 7 |
| Male ZZ | 36 | 2 |