Results, Tables, Figures

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# Results

*Energetic Costs of Sex-reversal* *Bassiana duperreyi* - A total of 760 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 1) that varied significantly by sex class (significant interaction between sex class × logmass – Fig. 2A). Sex-reversed male XX *B. duperreyi* had a scaling relationship that was most like their phenotypic counterparts (male XY - male XX; pMCMC = 0.33; Table 2) and lower than their genotypic counterparts (female XX - male XX; pMCMC = 0). For phenotypic males (male XX & male XX), this scaling relationship between logmass and metabolism changed similarly across differently sized individuals (Fig. 2B). Pairwise comparisons across sex class indicated no differences in body mass across our treatments (Fig. 2A; Table S1). The homogeneous variance model was the most parsimonious ([heteroscedastic model – homoscedastic model] loo: -5.5, SE = 6.87), accounting for 0.77% (95% CI:0.75 - 0.78) of the variation in metabolic rate.

*Pogona vitticeps* - A total of 1365 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 2) that varied significantly by sex class (significant interaction between sex class × logmass - Fig. 2C). 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), but lower than their phenotypic counterparts (female ZW - female ZZ; pMCMC = 0.04; Table 2). As female got larger, the mass scaling relationship of metabolism was between male ZZ and female ZW (Fig. 2D). Pairwise comparisons of body mass across sex class in *P. vitticeps* indicated no differences in body mass across treatments (Fig. 2C; Table S1). The heteroscedasticity variance model was the most parsimonious ([heteroscedastic model – homoscedastic model] loo: -189.8, SE = 33.96), accounting for 0.84% (95% CI:0.83 - 0.85) of the variation in metabolic rate.

*Effects of sex-reversal on growth and survival*

Growth rates for both SVL and mass supported the Null Hypothesis among *B. duperreyi*, where there were no detectable differences across sex class (Table 3; Table S3). Similarly, in *P. vitticeps* the Null Hypothesis was supported when comparing SVL and mass growth rates across sex class (Table 3; Table S3). Sex-reversed male *B. duperreyi* had the lowest rates of survival (77%; Table S4) in comparison to concordant females (87%) and concordant males (100%), but this relationship was non-significant (p = 0.29). Similarly, sex-reversed *P. vitticeps* individuals had the lowest rates of survival (75%; Table 3) in comparison to concordant females (83%) and concordant males (95%), but this relationship was also not significant (0.06).

# Tables & Figures

Table 1. Model coefficients for testing whether sex affects the slope of 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) | -4.56 | 0.18 | -4.90 | -4.20 |
| SexMaleSRXX | -0.15 | 0.09 | -0.32 | 0.02 |
| SexMaleXY | -0.12 | 0.09 | -0.29 | 0.06 |
| logMass | 1.34 | 0.24 | 0.87 | 1.81 |
| ztime | 0.01 | 0.02 | -0.02 | 0.05 |
| SexMaleSRXX:logMass | -0.56 | 0.17 | -0.90 | -0.23 |
| SexMaleXY:logMass | -0.74 | 0.17 | -1.07 | -0.41 |

Table 2. Model coefficients for testing whether sex affects the slope of metabolic rate for *Pogona vitticeps*, 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 (SexFemaleZW) | -1.86 | 0.09 | -2.04 | -1.67 |
| SexFemaleSRZZ | -0.13 | 0.08 | -0.28 | 0.03 |
| SexMaleZZ | -0.07 | 0.07 | -0.22 | 0.07 |
| logMass | 1.30 | 0.10 | 1.11 | 1.49 |
| ztime | 0.06 | 0.01 | 0.04 | 0.08 |
| SexFemaleSRZZ:logMass | -0.16 | 0.08 | -0.32 | -0.01 |
| SexMaleZZ:logMass | -0.37 | 0.09 | -0.55 | -0.21 |
| sigma\_Intercept | -1.60 | 0.02 | -1.64 | -1.56 |
| sigma\_logMass | -1.40 | 0.07 | -1.54 | -1.26 |
| sigma\_ztime | 0.22 | 0.02 | 0.18 | 0.27 |

Table 3. Posterior distributions for log metaboic rate (Log MR) and growth rate (SVL or mass) estimates when testing if sex-reversed individuals show support for Like Genotype or Like Phenotype hypothesis for *Bassiana duperreyi* and *Pogona vitticeps*.Estimates were comparisons from subtracting the model posterior distribution of the median for sex-reversed individuals by either their phenotypic or genotypic counterparts, depending on the hypothesis being tested.

| Species | Test | Contrast | Estimate | l-95% CI | u-95% CI | pMCMC Value |
| --- | --- | --- | --- | --- | --- | --- |
| *B. duperreyi* | Log MR | Male XY-MaleSR XX | 0.18 | -0.17 | 0.53 | 0.33 |
| **Female XX-MaleSR XX** | **-0.56** | **-0.90** | **-0.23** | **< 0.01** |
| SVL (mm/d) | Male XY-MaleSR XX | 0.01 | 0.00 | 0.02 | 0.29 |
| Female XX-MaleSR XX | 0.00 | -0.01 | 0.02 | 0.39 |
| Mass (cg/d) | Male XY-MaleSR XX | 0.00 | -0.02 | 0.01 | 0.73 |
| Female XX-MaleSR XX | -0.01 | -0.02 | 0.01 | 0.24 |
| *P. vitticeps* | Log MR | **Female ZW-FemaleSR ZZ** | **-0.16** | **-0.32** | **-0.01** | **0.04** |
| **Male ZZ-FemaleSR ZZ** | **0.21** | **0.09** | **0.32** | **< 0.01** |
| SVL (mm/d) | Female ZW-FemaleSR ZZ | 0.00 | -0.02 | 0.02 | 0.94 |
| Male ZZ-FemaleSRZZ | -0.01 | -0.02 | 0.01 | 0.48 |
| Mass (g/d) | Female ZW-FemaleSR ZZ | -0.03 | -0.12 | 0.05 | 0.40 |
| Male ZZ-FemaleSR ZZ | -0.08 | -0.18 | 0.00 | 0.06 |

![](data:application/pdf;base64,)

Figure 1. The Like Phenotype/Genotype Framework for testing the metabolic consequences of sex-reversal for ZZ/ZW and XX/XY genetic sex determination systems with different patterns of genetic sex determination. Colours indicate sex for *Bassiana duperreyi* (male XX - red: female XX - black: male XY - blue) and for *Pogona vitticeps* (female ZZ - red: female ZW - black: male ZZ - blue]. Body mass and metabolic rates have been log transformed to approximate linear relationships. Each pattern of genetic sex determination contains three competing hypotheses for the relationship between body mass and metabolic rates: Null hypothesis – no differences; Like phenotype hypothesis – similarities between reversed sex and concordant phenotype; Like genotype hypothesis – similarities between reversed sex and concordant genotype.

![](data:application/pdf;base64,)

Figure 2. Comparison of log 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.