# Electronic supplementary materials for: Heritability and developmental plasticity of growth in an oviparous lizard

## Model fitting and selection of random effects structure

We fit different models to investigate what random effect structure was best suited for our dataset. Only the intercept was included as fixed effects in these models. We fit models that contained random intercepts and slopes (a linear and quadratic slope of age) at each of the three random effect levels. In all cases age was z-transformed. Our pedigree had lower levels of paternal half-sibs than we expected from our breeding design because of either sperm precedence or male mating monopolization that was outside our control (See Table S8). Decoupling genetic (G) and maternal effects (M) may therefore have been difficult. As such, we also fit the same models but excluding M to test if G and M were confounded. Given that we fit random slopes of age to estimate changes in variance across age, this meant decoupling G from PE effects might also be challenging. As such, we also fit models that only included G and M. The full list of models are provided in Table S1.

WAIC and LOO values are presented in Table S1. Model 1 and 10 has the highest WAIC/LOO values indicating that it is the least supported model. Model 3 was had the lowest WAIC/LOO value indicating that it is the best supported model, but it was equally supported when compared to Model 12 and 7. To avoid overfitting, we selected the more parsimonious model (Model 12) and used this random effect structure for the remaining analysis unless stated otherwise.

**Table S1** WAIC and LOO of six intercept-only models with different combinations of random effects structures for additive genetic variance, maternal variance and permanent environmental variance. ELPD was calculated by subtracting the WAIC or LOO value of each model from the top supported model (Model 3). *G M, PE* represents additive genetic variance, maternal variance and permanent environment variance, respectively.

| **Model** | **WAIC** |  | **Std. Error** | **LOO** |  | **Std. Error** |
| --- | --- | --- | --- | --- | --- | --- |
| Model 3 - quadratic slopes for G, M, PE | -3,259.965 | 0.0000000 | 0.000000 | -3,203.554 | 0.000000 | 0.000000 |
| Model 12 - quadratic slopes for G, M, no PE | -3,258.837 | -0.5641396 | 2.695904 | -3,200.844 | -1.354735 | 3.343870 |
| Model 7 - intercept for PE, quadratic slopes for G, M | -3,257.481 | -1.2421184 | 2.198210 | -3,198.953 | -2.300256 | 2.636267 |
| Model 15 - quadratic slope for G, no M, no PE | -3,160.411 | -49.7772232 | 12.578927 | -3,087.986 | -57.783897 | 13.113953 |
| Model 8 - intercept for PE, quadratic slopes for G, no M | -3,156.190 | -51.8875502 | 12.458543 | -3,081.839 | -60.857298 | 12.965812 |
| Model 9 - quadratic for G, PE, no M | -3,155.031 | -52.4669378 | 12.441781 | -3,071.752 | -65.900994 | 12.869740 |
| Model 2 - linear slopes for G, M, PE | -1,388.074 | -935.9455490 | 39.082022 | -1,366.237 | -918.658624 | 39.685522 |
| Model 11 - linear slopes for G, M, no PE | -1,385.250 | -937.3576158 | 39.096887 | -1,365.840 | -918.856813 | 39.684447 |
| Model 6 - intercept for PE, linear slopes for G, M | -1,385.153 | -937.4062000 | 39.079780 | -1,364.405 | -919.574474 | 39.663731 |
| Model 14 - quadratic slope for G, intercept for M, no PE | -1,384.591 | -937.6872905 | 39.997084 | -1,352.782 | -925.385957 | 40.651716 |
| Model 5 - intercept for M, linear slopes for G, PE | -1,382.770 | -938.5974803 | 39.997376 | -1,350.058 | -926.747853 | 40.634918 |
| Model 4 - intercept for G, linear slopes for M, PE | -1,381.457 | -939.2541392 | 39.065262 | -1,358.305 | -922.624242 | 39.686994 |
| Model 16 - linear slope for G, no M, no PE | -1,380.496 | -939.7346124 | 40.100532 | -1,353.143 | -925.205637 | 40.667781 |
| Model 13 - quadratic slope for M, intercept for G, no PE | -1,158.093 | -1,050.9362464 | 40.631958 | -1,150.479 | -1,026.537654 | 41.076650 |
| Model 1 - intercepts for G, M, PE | 4,550.295 | -3,905.1301304 | 49.985693 | 4,551.696 | -3,877.624811 | 50.352545 |
| Model 10 - intercept for G, M, no PE | 4,568.722 | -3,914.3435529 | 50.083175 | 4,569.741 | -3,886.647328 | 50.450121 |



## Does our data have heterogenous residual variance?

Residual variance may impact estimates of heritability if changes over time (heterogenous variance) are not properly accounted for. We therefore explicitly modelled residual variance to verify if this was the case comparing homogeneous and heterogenous models using LOO and WAIC values. We fitted two models, both of which had the same random effects structure as our top supported model described above (Table S1). The model with heterogenous variance was best supported (Table S2), we therefore modelled heterogenous variance in all subsequent models unless stated otherwise.

**Table S2** Comparisons of expected log predictive density values for LOO and WAIC values to test the importance of heterogenous and homogenous residual variance. Note that difference in values are calculated by subtracting values from the model with lowest LOO and WAIC values i.e. the heterogenous variance model.

| **Model** | **WAIC** |  | **Std. Error** | **LOO** |  | **Std. Error** |
| --- | --- | --- | --- | --- | --- | --- |
| Heterogeneous | -3,278.496 | 0.000000 | 0.000000 | -3,216.530 | 0.000000 | 0.000000 |
| Homogeneous | -3,258.837 | -9.829498 | 6.724934 | -3,200.844 | -7.842624 | 6.994518 |



## The influence of developmental temperature on genetic and non-genetic variance across age



To test how variance components and heritability change with age in each treatment group, we fitted an intercept in our fixed effects and used the best supported random effect structure (Model 12) with heterogenous residual variance. There were no differences among treatment groups (Fig. 1 & 2). Heritability at an average age was moderate to low across the treatments (Table S3). The and matrices for each treatment group are presented in Table S4-S5.

**Table S3**. Treatment comparisons of additive genetic, maternal, and residual variance along with heritability (h2) at an average age. The lower and upper bounds of the 95% credible intervals are provided.

| **Treatment** | **Variable** | **Estimate** | **Lower** | **Upper** |
| --- | --- | --- | --- | --- |
| Hot | Vg | 0.015 | 0.009 | 0.024 |
|  | Vmaternal | 0.055 | 0.001 | 0.161 |
|  | Vresidual | 0.017 | 0.016 | 0.019 |
|  | h2 | 0.221 | 0.071 | 0.487 |
| Cold | Vg | 0.016 | 0.011 | 0.024 |
|  | Vmaternal | 0.146 | 0.042 | 0.299 |
|  | Vresidual | 0.014 | 0.012 | 0.015 |
|  | h2 | 0.107 | 0.046 | 0.229 |

**Table S4.** *G* and *M* variance-covariance / correlation matrices between growth trajectory parameters(intercept, linear slope, and quadratic slope) for lizards from the hot developmental temperature treatment group (nlizards = 125, nobs = 1,330). Variances are represented along the diagonal, covariances are represented in the upper triangle and correlations are represented in the lower triangle. Values in the brackets represent the 95% credible intervals. Note that residual variance slope is in on log scale (i.e., for every 1 SD unit increase in age we expect a decrease in log(SD)).

|  |  |  |  |
| --- | --- | --- | --- |
| *G* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | 0.015  (0.009 - 0.024) | 0.00201  (-0.00339 - 0.0087) | -0.00663  (-0.0125 - -0.0022) |
| Linear Slope | 0.122  (-0.241 - 0.465) | 0.016  (0.008 - 0.027) | 0.00438  (3.9e-07 - 0.0101) |
| Quadratic Slope | -0.557  (-0.774 - -0.275) | 0.372  (4.04e-05 - 0.695) | 0.009  (0.004 - 0.015) |
| *M* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | 0.055  (0.001 - 0.161) | 0.101  (0.00258 - 0.218) | -0.0309  (-0.0677 - -0.000631) |
| Linear Slope | 0.889  (0.206 - 0.995) | 0.253  (0.17 - 0.373) | -0.0722  (-0.108 - -0.0456) |
| Quadratic Slope | -0.88  (-0.995 - -0.21) | -0.932  (-0.994 - -0.793) | 0.024  (0.013 - 0.041) |
|  | | *Residual* | *Residual Slope* |
|  | |  | |
|  | | 0.0169  (0.0155 - 0.0185) | -0.135  (-0.188 - -0.0808) |

**Table S5.** *G* and *M* variance-covariance / correlation matrices between growth trajectory parameters (intercept, linear slope and quadratic slope) for lizards from the cold developmental temperature treatment group (nlizards = 136, nobs = 1596). Variances are represented along the diagonal, covariances are represented in the upper triangle and correlations are represented in the lower triangle. Values in the brackets represent the 95% credible intervals. Note that residual variance slope is in on log scale (i.e., for every 1 SD unit increase in age we expect a decrease in log(SD)).

|  |  |  |  |
| --- | --- | --- | --- |
| *G* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | 0.016  (0.011 - 0.024) | 0.00258  (-0.00186 - 0.00754) | -0.00583  (-0.0108 - -0.00177) |
| Linear Slope | 0.166  (-0.136 - 0.436) | 0.014  (0.009 - 0.021) | 0.00761  (0.00356 - 0.0128) |
| Quadratic Slope | -0.414  (-0.62 - -0.157) | 0.595  (0.332 - 0.799) | 0.012  (0.007 - 0.018) |
| *M* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | 0.146  (0.042 - 0.299) | 0.178  (0.0878 - 0.291) | -0.0773  (-0.13 - -0.0373) |
| Linear Slope | 0.978  (0.937 - 0.997) | 0.239  (0.159 - 0.339) | -0.0961  (-0.138 - -0.0638) |
| Quadratic Slope | -0.971  (-0.998 - -0.917) | -0.926  (-0.993 - -0.805) | 0.046  (0.027 - 0.071) |
|  | | *Residual* | *Residual Slope (SD)* |
|  | | 0.0136  (0.0125 - 0.0147) | 0.00119  (1.51e-06 - 0.00517) |

## Accounting for scale-effects using coefficients of variation

As the mean body mass increases over time, the variance may also increase concurrently due to scale effects and potentially bias estimates of quantitative genetics parameters (Wilson, Kruuk, et al., 2005). We therefore calculated coefficients of variation (CV) across age for each variance component using the following equation:

where is the CV for a given variance component e.g. is the CV of maternal effects. The CV of maternal effects () and showed similar changes across age as V with higher CV early and late in life for both M and G, although the shape of the relationship was different (Fig. S1-2). There were no treatment differences in , (Fig. S1 & S2).



**Figure. S1** Scatterplot showing the relationship of the how the coefficient of variance of additive genetic variance (*G*) and maternal effects (*M*) changed with age for the hot developmental treatment (n = 125, red) and the cold developmental treatment (n = 136, blue). Points represent posterior means, thin lines represent the 95% credible intervals, thick lines represent the mean for each treatment group.



**Figure. S2** Scatterplot showing the relationship of the how heritability (h2) and the proportion pf maternal effects (*M2*) changed with age for the hot developmental treatment (n = 125, red) and the cold developmental treatment (n = 136, blue). Points represent posterior means, thin lines represent the 95% credible intervals, thick lines represent the mean for each treatment group.

## Do growth trajectories differ among incubation treatments?

To test for treatment differences in growth trajectories, we fitted four models with different combinations of treatment interactions with the linear and quadratic age parameters and compared their WAIC/LOO values (Table 1 in main manuscript). Given that three models were nearly equally supported we present the parameter estimates and their uncertainty from the full model (Table S7).



|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Table S6. Estimates from the full model with interaction between treatment and age (linear and quadratic growth rate). Bolded estimates are significantly different from zero. \* indicates that value is above zero prior to rounding. nobs = 2926. Age measured in days was z-transformed (mean = 361.34, SD = 185.16) | | | | | | | |
| **Parameter** | | | | **Estimate** | | **Lower** | **Upper** |
| *Fixed effects* | | | |  | |  |  |
| Intercept | | | | **-1.00** | | **-1.04** | **-0.97** |
| Treatment | | | | **-0.09** | | **-0.12** | **-0.06** |
| Age | | | | **0.50** | | **0.46** | **0.53** |
| Age2 | | | | **-0.19** | | **-0.22** | **-0.16** |
| Treatment Age | | | | -0.01 | | -0.02 | 0.04 |
| Treatment Age2 | | | | 0.030 | | -0.010 | 0.060 |
|  |  |  |  |
| *Random effects* | | | |  | |  |  |
| ***M*** | | | |  | |  |  |
| Intercept (SD) | | | | 0.017 | | 0.001 | 0.049 |
| Slope (SD) | | | | 0.072 | | 0.046 | 0.100 |
| Quadratic (SD) | | | | 0.015 | | 0.000 | 0.042 |
| intercept – slope (COR) | | | | 0.05 | | -0.85 | 0.87 |
| intercept – quadratic (COR) | | | | 0.057 | | -0.91 | 0.84 |
| slope – quadratic (COR) | | | | 0.035 | | -0.86 | 0.87 |
| ***G*** | | | |  | |  |  |
| Intercept (SD) | | | | **0.13** | | **0.12** | **0.15** |
| Slope (SD) | | | | **0.12** | | **0.10** | **0.14** |
| Quadratic (SD) | | | | **0.12** | | **0.10** | **0.14** |
| intercept – slope (COR) | | | | -0.02 | | -0.17 | 0.21 |
| intercept – quadratic (COR) | | | | -0.47 | | -0.61 | -0.31 |
| slope – quadratic (COR) | | | | 0.67 | | 0.52 | 0.79 |
| **Residual (log SD)** | | | | **-2.09** | | **-2.12** | **-2.06** |
| Residual x Age (log SD) | | | | **-0.05** | | **-0.09** | **-0.01** |

## Egg mortality analysis

Egg mortality did not differ significantly between the two treatments (see, @egg\_mort\_tbl).

**Table** **S7**. Analysis of egg mortality between treatmemnts. We fit a Bournoulli generalised linear mixed model with a logit link function to test whether egg mortality differed between treatments. We controlled for clutch ID as a random effect in our analysis**.**

| **Parameter** | **Estimate** | **Q2.5** | **Q97.5** |
| --- | --- | --- | --- |
| Intercept | 1.561 | 0.658 | 2.753 |
| Treatment | 0.804 | -0.041 | 1.729 |
| Clutch ID (SD) | 4.266 | 2.719 | 6.395 |











## Pedigree and Genomic Relatedness

We submitted a total of 437 tissues samples, five samples experienced problems during extraction and sequencing and were therefore excluded from the final dataset (n = 432). One individual was excluded from the dataset and may be related to contamination as this individual appeared to be unrelated to any other samples in the dataset.

DNA was extracted from tissue samples using a Qiagen DNeasy Blood and Tissue Kits following the manufacturer’s instructions. Diversity Arrays Technology (DArT) combines next generation sequencing platforms and genome complexity reduction methods (Kilian et al., 2012) to select the most appropriate method for *L.delicata.* Sequences were processed using DArT specific pipelines. The main pipeline filtered out poor quality sequences which resulted in a total of 185,963 SNPs for our final analysis.

Of the 121 females in the dataset 89.27% (108 of 121) had been sired by a single male. The average number of sires per dam was 1.12 (SD = 0.35). The range of sires per dam was 1 to 3. Of the 111 females in the dataset 80.187% (0 of 111) had been sired by a single male. The average number of sires per dam was 1.22 (SD = 0.46). The range of sires per dam was 1 to 3.

**Table S8.** Pedigree statistics for each treatment. The number of offspring and sires per dam (clutch) are provided for 23 and 29 C treatments. 'w' indicates a male not present within the breeding design resulting from mating or stored sperm from wild interactions.

| **Treatment** | **Dam** | **Sire** | **Number of Offspring** |
| --- | --- | --- | --- |
| **23** | ld0005 | ld0095 | 2 |
|  | - | ld0442 | 1 |
|  | ld0015 | ld0095 | 1 |
|  | ld0016 | ld0051 | 1 |
|  | ld0019 | ld0137 | 1 |
|  | ld0025 | ld0018 | 2 |
|  | ld0033 | ld0069 | 2 |
|  | ld0035 | ld0049 | 2 |
|  | ld0039 | ld0150 | 2 |
|  | ld0057 | ld0104 | 4 |
|  | ld0062 | ld0011 | 4 |
|  | - | ld0137 | 1 |
|  | ld0067 | ld0095 | 2 |
|  | - | ld0442 | 4 |
|  | ld0068 | ld0006 | 2 |
|  | ld0069 | ld0102 | 1 |
|  | ld0081 | ld0111 | 2 |
|  | ld0085 | ld0076 | 3 |
|  | - | ld0137 | 1 |
|  | ld0090 | ld0027 | 4 |
|  | ld0091 | ld0043 | 1 |
|  | ld0093 | ld0140 | 3 |
|  | ld0101 | ld0077 | 1 |
|  | ld0103 | ld0150 | 3 |
|  | ld0106 | ld0175 | 6 |
|  | ld0116 | ld0143 | 4 |
|  | ld0122 | ld0076 | 5 |
|  | ld0125 | ld0107 | 2 |
|  | ld0126 | ld0115 | 3 |
|  | ld0132 | ld0042 | 1 |
|  | ld0136 | ld0077 | 2 |
|  | ld0139 | ld0006 | 3 |
|  | ld0144 | ld0013 | 2 |
|  | ld0147 | ld0018 | 2 |
|  | ld0152 | ld0140 | 3 |
|  | ld0156 | w0001 | 2 |
|  | ld0157 | w0002 | 2 |
|  | ld0161 | w0004 | 2 |
|  | ld0163 | w0005 | 1 |
|  | ld0164 | w0006 | 1 |
|  | ld0165 | w0008 | 1 |
|  | ld0166 | w0009 | 2 |
|  | ld0168 | w0036 | 1 |
|  | ld0173 | w0011 | 2 |
|  | ld0182 | w0013 | 1 |
|  | ld0185 | w0014 | 1 |
|  | ld0186 | w0015 | 1 |
|  | ld0189 | w0016 | 2 |
|  | ld0190 | w0017 | 1 |
|  | ld0191 | w0018 | 3 |
|  | ld0193 | ld0020 | 1 |
|  | ld0194 | w0019 | 1 |
|  | ld0195 | w0020 | 1 |
|  | ld0198 | w0022 | 1 |
|  | ld0202 | w0023 | 1 |
|  | ld0203 | w0024 | 2 |
|  | ld0204 | w0025 | 1 |
|  | ld0207 | w0026 | 2 |
|  | ld0208 | w0028 | 2 |
|  | ld0209 | w0029 | 2 |
|  | ld0210 | w0030 | 2 |
|  | ld0215 | w0031 | 2 |
|  | ld0390 | w0032 | 1 |
|  | ld0402 | ld0138 | 1 |
|  | – | w0033 | 2 |
|  | ld0403 | w0034 | 1 |
|  | ld2015 | ld0049 | 2 |
|  | – | ld0075 | 3 |
|  | – | ld0104 | 1 |
| **29** | ld0005 | ld0095 | 1 |
|  | – | ld0442 | 5 |
|  | ld0015 | ld0069 | 1 |
|  | ld0016 | ld0051 | 1 |
|  | ld0025 | ld0018 | 2 |
|  | ld0033 | ld0069 | 1 |
|  | ld0035 | ld0049 | 3 |
|  | ld0039 | ld0150 | 2 |
|  | ld0057 | ld0075 | 1 |
|  | – | ld0104 | 1 |
|  | ld0062 | ld0011 | 4 |
|  | – | ld0137 | 2 |
|  | ld0067 | ld0095 | 1 |
|  | – | ld0442 | 3 |
|  | ld0068 | ld0006 | 4 |
|  | ld0069 | ld0102 | 2 |
|  | ld0072 | ld0119 | 1 |
|  | ld0081 | ld0111 | 2 |
|  | ld0085 | ld0076 | 3 |
|  | – | ld0137 | 1 |
|  | ld0090 | ld0027 | 4 |
|  | ld0091 | ld0043 | 2 |
|  | ld0093 | ld0140 | 3 |
|  | ld0103 | ld0150 | 2 |
|  | ld0106 | ld0175 | 3 |
|  | ld0116 | ld0143 | 5 |
|  | ld0121 | ld0146 | 2 |
|  | ld0122 | ld0076 | 4 |
|  | ld0125 | ld0107 | 2 |
|  | ld0126 | ld0115 | 2 |
|  | ld0132 | ld0042 | 1 |
|  | ld0136 | ld0077 | 2 |
|  | ld0139 | ld0006 | 3 |
|  | ld0144 | ld0013 | 2 |
|  | ld0147 | ld0018 | 1 |
|  | ld0152 | ld0140 | 3 |
|  | ld0156 | w0001 | 2 |
|  | ld0157 | w0002 | 1 |
|  | ld0160 | w0003 | 2 |
|  | ld0161 | w0004 | 2 |
|  | ld0163 | w0005 | 1 |
|  | ld0164 | w0006 | 1 |
|  | ld0169 | w0010 | 2 |
|  | ld0173 | w0011 | 1 |
|  | ld0181 | w0012 | 1 |
|  | ld0182 | w0013 | 2 |
|  | ld0185 | w0014 | 2 |
|  | ld0186 | w0015 | 2 |
|  | ld0189 | w0016 | 1 |
|  | ld0190 | w0017 | 1 |
|  | ld0191 | w0018 | 2 |
|  | ld0193 | ld0020 | 2 |
|  | ld0194 | w0019 | 1 |
|  | ld0195 | w0020 | 1 |
|  | ld0197 | w0021 | 1 |
|  | ld0198 | w0022 | 1 |
|  | ld0202 | w0023 | 2 |
|  | ld0203 | w0024 | 1 |
|  | ld0204 | w0025 | 1 |
|  | ld0208 | w0028 | 1 |
|  | ld0210 | w0030 | 2 |
|  | ld0402 | ld0138 | 2 |
|  | – | w0033 | 2 |
|  | ld0403 | w0034 | 1 |
|  | ld2015 | ld0049 | 1 |
|  | – | ld0075 | 2 |