# Electronic supplementary materials for: Developmental plasticity of growth, genetic variation and maternal effects in response to temperature

## 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).

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.* [Insert section from DArT here on complexity reduction methods, DArT tested four methods in Gambusia so it’s unclear what method was used for us].

Sequences from all lanes were then processed using DArT specific pipelines. The main pipeline filtered out poor quality sequences [Details needed from DArT]. For our samples, this filtering process by DArT resulted in a total of 185,963 SNPs.

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.

## Model fitting and selection of random effects structure

We fitted seven different models to investigate what random effects structure was best suited for our dataset. Only the intercept was included as fixed effects in these models and lizard identity was included twice to partition out permanent environmental effects (*PE*) given we had repeated measures of the same individuals (Wilson et al., 2010). Age was z-transformed. In model 1 we assume that additive genetic variance, maternal effect variance and permanent environmental variance was constant across age by fitting a random intercept for lizard identity (*G*), dam identity *(M*) and for permanent environmental effects (PE). In model 2, we assumed all variance components varied across age following a linear relationship and included random linear slopes for *G, M, PE*. In model 3, we assumed that all variance components changed with age in a quadratic fashion by including random quadratic slopes for *G, M, PE.* In model 4, we included random intercept for *G* and random linear slopes for *M* and *PE*. In model 5, we included random intercept for M and random linear slopes for *G, PE*. In model 6, we included random intercept for *PE* and random linear slopes for *G* and *PE*. Finally, in model 7, we included a random intercept for *PE* and random quadratic slopes for *G* and *M*. WAIC values are presented in Table S1. Model 1 has the highest WAIC value indicating that it is the least supported model. Model 2 was had the lowest WAIC value

Model 1 has the highest WAIC value indicating that it is the least supported model. Model 3 was had the lowest WAIC value indicating that it is the best supported model. Between model 5 -6, model 6 had the highest DIC, indicating that *PE* should be included as a random intercept only. Model 7 was the second best supported model and improvement in WAIC value was marginal by including a quadratic slope for PE. To avoid overfitting, To avoid overfitting, we selected the more parsimonious model (Model 7) and used this random effect structure for the remaining analysis unless stated otherwise.

**Table S1** WAIC of six intercept models with different combinations of random effects structures for additive genetic variance, maternal variance and permanent environmental variance. DIC was calculated by subtracting the DIC value of each model from the DIC value of model 1. *G M, PE* represents additive genetic variance, maternal variance and permanent environment variance, respectively.

|  |  |  |  |
| --- | --- | --- | --- |
| Model | WAIC |  | Std. Error |
| Model 3 - quadratic slopes for *G, M, PE* | -3258 | 0 | 0 |
| Model 7 - intercept for *PE*, quadratic slopes for *G, M* | -3261 | -1.122 | 3.245 |
| Model 4 - intercept for *G*, linear slopes for *M, PE* | -1382 | -939.4 | 38.91 |
| Model 2 - linear slopes for G, *M, PE* | -1381 | -939.5 | 39.03 |
| Model 6 - intercept for *PE*, linear slopes for *G, M* | -1382 | -940 | 38.94 |
| Model 5 - intercept for *M*, linear slopes for *G, PE* | -1370 | -945.4 | 40.3 |
| Model 1 - intercepts for *G*, *M, PE* | 4550 | -3905 | 49.91 |

## Does our data have heterogenous residual variance?

Residual variance may conflate with estimates of other variance components if it changes over time (heterogenous variance) and is not properly accounted for. We therefore explicitly modelled residual variance to verify if this was the case using WAIC values. We fitted two models, both of which had the same fixed and random effects structure as Model 7 described above. The first model had homogenous residual variance whereas in the second model we modelled residual variance with a linear slope thereby allowing it to vary with age. 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 |
| Model 7 with heterogenous variance | -3280 | 0 | 0 |
| Model 7 with homogenous variance | -3261 | -9.783 | 6.429 |

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

We fitted random intercepts for , , and to estimate the overall estimate across age. In other words, the average variance across all age classes. We found that additive genetic variance, permanent environmental variance and heritability of growth appears to be higher in the hot developmental temperature treatment however, there were no significant differences among treatment groups (Table S3).

**Table S3** Treatment comparisons of additive genetic variance, maternal variance, permanent environmental variance, residual variance and heritability. These are estimated from a model where random intercepts were fitted for all variance components. Bolded estimates are significantly different from zero. Hot treatment group nobs = 1892, cold treatment group nobs = 2036. Values with \* indicate very small values that were above zero.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Hot developmental temperature  (nlizards = 125) | | | Cold developmental temperature  (nlizards = 136) | | |
|  | Estimate | Lower | Upper | Estimate | Lower | Upper |
| Vadditive genetic | **0.028** | **0.001** | **0.056** | **0.01** | **0\*** | **0.025** |
| Vmaternal | **0.006** | **0\*** | **0.024** | **0.005** | **0\*** | **0.016** |
| Vpermanent environment | **0.015** | **0\*** | **0.053** | **0.008** | **0\*** | **0.025** |
| Vresidual | **0.25** | **0.23** | **0.271** | **0.274** | **0.254** | **0.294** |
| Heritability (h2) | **0.041** | **0.002** | **0.083** | **0.013** | **0\*** | **0.033** |

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 7) with heterogenous residual variance. There were no differences among treatment groups (Fig. 3). The and matrices for each treatment group are presented in Table S3-S4.

**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 = 1330). PE variance is also presented. Variances are represented along the diagonal, covariances are represented in the upper triangle and correlations are represented in the lower triangle. Bolded estimates are significantly different from zero. Values in the brackets represent the 95% credible intervals. Note that residual variance slope is in SD units.

|  |  |  |  |
| --- | --- | --- | --- |
| *G* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | **0.008  (0.002 to 0.018)** | 0.00163  (-0.0023 to 0.00611) | **-0.0817  (-0.134 to -0.0447)** |
| Linear Slope | 0.151  (-0.287 to 0.534) | **0.013  (0.008 to 0.02)** | **-0.101**  **(-0.146 to -0.07)** |
| Quadratic Slope | **-0.516  (-0.815 to -0.141)** | **0.636  (0.356 to 0.819)** | **0.011  (0.007 to 0.017)** |
| *M* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | **0.156  (0.052 to 0.306)** | **0.19  (0.102 to 0.305)** | **-0.00738  (-0.0185 to -0.00205)** |
| Linear Slope | **0.976  (0.932 to 0.997)** | **0.252  (0.179 to 0.362)** | **-0.0113  (-0.0225 to -0.00545)** |
| Quadratic Slope | **-0.973  (-0.997 to -0.924)** | **-0.927  (-0.992 to -0.818)** | **0.047  (0.031 to 0.071)** |
| *PE* | | *Residual* | *Residual Slope (SD)* |
|  | |  | |
| **0.00463 (0.000792 to 0.00796)** | | **4.64 (4.48 to 0.021)** | **-0.0237 (-0.06676 to -0.021)** |

**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). PE variance is also presented. Variances are represented along the diagonal, covariances are represented in the upper triangle and correlations are represented in the lower triangle. Bolded estimates are significantly different from zero. Values in the brackets represent the 95% credible intervals. Note that residual variance slope is in SD units.

|  |  |  |  |
| --- | --- | --- | --- |
| *G* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | **0.008  (0.001 to 0.018)** | **0.00132  (-0.00331 to 0.00704)** | **-0.00488  (-0.0104 to -0.000589)** |
| Linear Slope | **0.123  (-0.454 to 0.62)** | **0.014  (0.008 to 0.023)** | **0.00422  (0.000231 to 0.00917)** |
| Quadratic Slope | **-0.646  (-0.931 to -0.193)** | **0.411  (0.0231 to 0.731)** | **0.008  (0.004 to 0.013)** |
| *M* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | **0.032  (0 to 0.12)** | 0.0718  (-0.00275 **to** 0.183) | **-0.0227  (-0.0585 to 0.000568)** |
| Linear Slope | 0.78  (-0.327 **to** 0.991) | **0.267  (0.185 to 0.382)** | **-0.078  (-0.114 to -0.0517)** |
| Quadratic Slope | -0.794  (-0.992 **to** 0.244) | **-0.933  (-0.994 to -0.811)** | **0.026  (0.016 to 0.041)** |
| *PE* | | *Residual* | *Residual Slope (SD)* |
| **0.065 (6.55e-05 to 0.00938)** | | **4.15  (3.97 to 4.34)** | -0.135 (-0.184 **to** -0.075) |

## 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 the same pattern as the raw variance estimates (Fig. S1-2). There were no treatment differences in , (Fig. S2). Both of which followed a quadratic relationship like the raw variance estimates in Fig. S1. We therefore conclude changes in mean mass did not affect estimation of variance components.

**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.

**![Chart, radar chart

Description automatically generated]()**

## 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 values (Table 1). The best supported model was the full model (Table S5), its *G* and *M* matrix is presented in Table S6 below. Model coefficients for the other three models are presented in Table S7-S9)

**Table S6.** *G* and *M* variance-covariance / correlation matrices between growth trajectory parameters (intercept, linear slope and quadratic slope) for the overall population (nlizards = 261, nobs = 2926). *PE* and Residual variance is also presented. Variances are represented along the diagonal, covariances are represented in the upper triangle and correlations are represented in the lower triangle. Bolded estimates are significantly different from zero. Values in the brackets represent the 95% credible intervals. Note that residual variance slope is in SD units.

|  |  |  |  |
| --- | --- | --- | --- |
| *G* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | **0.012  (0.007 to 0.019)** | 5.82e-05  (-0.0030**9 to 0**.00311) | **-0.00724  (-0.0108 to -0.00416)** |
| Linear Slope | 0.00484  (-0.237 to 0.238) | **0.014  (0.01 to 0.019)** | **0.0096  (0.00645 to 0.0139)** |
| Quadratic Slope | **-0.559  (-0.751 to -0.362)** | **0.689  (0.549 to 0.81)** | **0.014  (0.01 to 0.019)** |
| *M* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | **0.001  (0 to 0.004)** | -5.11e-05  (-0.00175 to 0.00165) | -0.000196  (-0.00169 to 0.000277) |
| Linear Slope | -0.0555  (-0.844 to 0.773) | **0.005  (0.002 to 0.01)** | 5.78e-05  (-0.00114 to 0.00176) |
| Quadratic Slope | -0.181  (-0.937 to 0.799) | -0.0121  (-0.865 to 0.845) | **0  (0 to 0.002)** |
| *PE* | | *Residual* | *Residual Slope (SD)* |
| **0.00333 (0.000317- 0.00653)** | | **4.36  (4.23 - 4.48)** | **-0.0483 (-0.0852 - -0.0105)** |

**Table S7** Estimates from model with interaction between treatment and age (linear growth rate) only. Bolded estimates are significantly different from zero. \* indicates that value is above zero prior to rounding. nobs = 2926. G is the additive genetic variance, M is maternal effects. r is the correlation between variance components. Age measured in days was z-transformed (mean = 361.34, SD = 185.16)

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| Intercept | **-0.995** | **-1.014** | **-0.977** |
| Treatment | **-0.072** | **-0.101** | **-0.045** |
| Age | **0.507** | **0.482** | **0.531** |
| Age2 | **-0.186** | **-0.199** | **-0.173** |
| Treatment Age | -0.005 | -0.028 | 0.018 |
| VM intercept | **0.024** | **0.001** | **0.064** |
| VM slope | **0.069** | **0.04** | **0.099** |
| VM curvature | **0.016** | **0.001** | **0.044** |
| Vpermanent environment | **0.055** | **0.017** | **0.08** |
| VG intercept | **0.109** | **0.08** | **0.137** |
| VG slope | **0.116** | **0.1** | **0.135** |
| VG curvature | **0.117** | **0.101** | **0.137** |
| *r*M intercept - slope | -0.058 | -0.845 | 0.776 |
| *r*M intercept - curvature | -0.157 | -0.921 | 0.849 |
| *r*M slope - curvature | -0.06 | -0.877 | 0.815 |
| *r*G intercept - slope | 0.014 | -0.233 | 0.242 |
| *r*G intercept - curvature | -0.549 | -0.742 | -0.356 |
| *r*G slope - curvature | **0.686** | **0.542** | **0.804** |
| Residual | **-2.087** | **-2.118** | **-2.057** |
| Residual Age | -0.048 | -0.084 | -0.011 |
|  |  |  |  |

**Table S8** Estimates from model with interaction between treatment and quadratic age paramater only. Bolded estimates are significantly different from zero. \* indicates that value is above zero prior to rounding. nobs = 2926. G is the additive genetic variance, M is maternal effects. r is the correlation between variance components. Age measured in days was z-transformed (mean = 361.34, SD = 185.16)

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| Intercept | **-0.99** | **-1.009** | **-0.97** |
| Age | **0.504** | **0.482** | **0.525** |
| Treatment | **-0.083** | **-0.116** | **-0.053** |
| Age2 | **-0.194** | **-0.212** | **-0.177** |
| Treatment x Age2 | 0.017 | -0.007 | 0.042 |
| VM intercept | **0.025** | **0.001** | **0.064** |
| VM slope | **0.069** | **0.041** | **0.098** |
| VM curvature | **0.016** | **0.001** | **0.047** |
| Vpermanent environment | **0.056** | **0.02** | **0.081** |
| VG intercept | **0.109** | **0.077** | **0.135** |
| VG slope | **0.116** | **0.099** | **0.135** |
| VG curvature | **0.118** | **0.102** | **0.135** |
| *r*M intercept - slope | -0.091 | -0.868 | 0.765 |
| *r*M intercept - curvature | -0.175 | -0.929 | 0.826 |
| *r*M slope - curvature | -0.047 | -0.902 | 0.835 |
| *r*G intercept - slope | 0.006 | -0.233 | 0.249 |
| *r*G intercept - curvature | -0.559 | -0.755 | -0.352 |
| *r*G slope - curvature | **0.687** | **0.544** | **0.8** |
| Residual | **-2.087** | **-2.119** | **-2.055** |
| Residual x Age | **-0.047** | **-0.084** | **-0.01** |

**Table S9** Estimates from model with main effects of treatment and age only. Bolded estimates are significantly different from zero. \* indicates that value is above zero prior to rounding. nobs = 2926. G is the additive genetic variance, M is maternal effects. r is the correlation between variance components. Age measured in days was z-transformed (mean = 361.34, SD = 185.16)

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Estimate | Lower | Upper |
| Intercept | **-0.997** | **-1.015** | **-0.979** |
| Treatment | **-0.069** | **-0.095** | **-0.046** |
| Age | **0.504** | **0.481** | **0.526** |
| Age2 | **-0.186** | **-0.198** | **-0.172** |
| VM intercept | **0.025** | **0.001** | **0.064** |
| VM slope | **0.07** | **0.042** | **0.099** |
| VM curvature | **0.017** | **0.001** | **0.047** |
| Vpermanent environment | **0.055** | **0.017** | **0.081** |
| VG intercept | **0.109** | **0.077** | **0.136** |
| VG slope | **0.115** | **0.098** | **0.134** |
| VG curvature | **0.117** | **0.101** | **0.134** |
| *r*M intercept - slope | -0.057 | -0.871 | 0.811 |
| *r*M intercept - curvature | -0.163 | -0.924 | 0.84 |
| *r*M slope - curvature | -0.02 | -0.865 | 0.814 |
| *r*G intercept - slope | 0.021 | -0.218 | 0.265 |
| *r*G intercept - curvature | -0.552 | -0.737 | -0.357 |
| *r*G slope - curvature | **0.68** | **0.529** | **0.794** |
| Residual | **-2.087** | **-2.118** | **-2.057** |
| Residual x Age | **-0.048** | **-0.085** | **-0.013** |

**Table S10** Estimates from model testing the effects of incubation treatment on changes in mass over age. Note that individual variation is not accounted for in random effects, only variation among different mothers to account for non-independence among siblings. Bolded estimates are significantly different from zero. \* indicates that value is above zero prior to rounding. nobs = 2926. G is the additive genetic variance, M is maternal effects. r is the correlation between variance components. Age measured in days was z-transformed (mean = 361.34, SD = 185.16). \* indicates that value is very small but does not overlap zero prior to rounding

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Q2.5 | Q97.5 |
| Intercept | **-0.77** | **-0.85** | **-0.68** |
| Treatment | **-0.01** | **-0.01** | **-0.01** |
| Age | 0.63 | 0.57 | 0.7 |
| Age2 | -0.05 | -0.1 | 0.01 |
| Treatment Age | **-0\*** | **-0.01** | **-0\*** |
| Treatment Age2 | **-0\*** | **-0\*** | **-0\*** |
| VM intercept | **0.08** | **0.06** | **0.09** |
| Residual | **0.18** | **0.18** | **0.19** |