

## Supporting Information

### Life-history trade-offs and limitations associated with phenotypic adaptation under future ocean warming and elevated salinity

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## MEAN RESPONSE ANALYSIS

### Statistical models and outputs for mean within-generation responses (C-C vs C-T vs C-TS) (Fig 4 and 5)

#### Longevity

```
> mod1.lme = lme(long~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1    61 219.92453  <.0001
treatment            2    61   2.92076   0.0615
transplant           1    61   2.38675   0.1275
treatment:transplant  2    61   7.65582   0.0011
>
> mdata$SHD<-interaction(mdata$treatment,mdata$transplant)
> mod1.lme = lme(long~ SHD, random=~1|shelf, data=mdata)
>
> comparison = glht(mod1.lme, linfct=mcp(SHD="Tukey"))
> summary(comparison)
```

#### Simultaneous Tests for General Linear Hypotheses

#### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = long ~ SHD, data = mdata, random = ~1 | shelf)
```

#### Linear Hypotheses:

|                           | Estimate | Std. Error | z value | Pr(> z )   |
|---------------------------|----------|------------|---------|------------|
| CT.egg - C.egg == 0       | -5.1667  | 4.5849     | -1.127  | 0.87028    |
| CTS.egg - C.egg == 0      | 6.4696   | 4.8148     | 1.344   | 0.76033    |
| C.hatch - C.egg == 0      | 7.0833   | 4.5849     | 1.545   | 0.63474    |
| CT.hatch - C.egg == 0     | 0.5000   | 4.5849     | 0.109   | 1.00000    |
| CTS.hatch - C.egg == 0    | -9.8333  | 4.5849     | -2.145  | 0.26418    |
| CTS.egg - CT.egg == 0     | 11.6363  | 4.8148     | 2.417   | 0.15023    |
| C.hatch - CT.egg == 0     | 12.2500  | 4.5849     | 2.672   | 0.08088 .  |
| CT.hatch - CT.egg == 0    | 5.6667   | 4.5849     | 1.236   | 0.81910    |
| CTS.hatch - CT.egg == 0   | -4.6667  | 4.5849     | -1.018  | 0.91212    |
| C.hatch - CTS.egg == 0    | 0.6137   | 4.8148     | 0.127   | 1.00000    |
| CT.hatch - CTS.egg == 0   | -5.9696  | 4.8148     | -1.240  | 0.81711    |
| CTS.hatch - CTS.egg == 0  | -16.3029 | 4.8148     | -3.386  | 0.00914 ** |
| CT.hatch - C.hatch == 0   | -6.5833  | 4.5849     | -1.436  | 0.70487    |
| CTS.hatch - C.hatch == 0  | -16.9167 | 4.5849     | -3.690  | 0.00306 ** |
| CTS.hatch - CT.hatch == 0 | -10.3333 | 4.5849     | -2.254  | 0.21321    |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## Max body size

```
> mod1.lme = lme(size~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1    61 1970.5353 <.0001
treatment            2    61   4.9795 0.0099
transplant           1    61   7.0923 0.0099
treatment:transplant 2    61   4.7968 0.0116
>
> mdata$SHD<-interaction(mdata$treatment,mdata$transplant)
> mod1.lme = lme(size~ SHD, random=~1|shelf, data=mdata)
>
> comparison = glht(mod1.lme, linfct=mcp(SHD="Tukey"))
> summary(comparison)
```

### Simultaneous Tests for General Linear Hypotheses

#### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = size ~ SHD, data = mdata, random = ~1 | shelf)
```

#### Linear Hypotheses:

|                           | Estimate | Std. Error | z value | Pr(> z ) |     |
|---------------------------|----------|------------|---------|----------|-----|
| CT.egg - C.egg == 0       | 1.2500   | 0.5765     | 2.168   | 0.25258  |     |
| CTS.egg - C.egg == 0      | -0.6433  | 0.6050     | -1.063  | 0.89587  |     |
| C.hatch - C.egg == 0      | 1.5000   | 0.5765     | 2.602   | 0.09651  | .   |
| CT.hatch - C.egg == 0     | 2.0833   | 0.5765     | 3.613   | 0.00406  | **  |
| CTS.hatch - C.egg == 0    | -1.5000  | 0.5765     | -2.602  | 0.09645  | .   |
| CTS.egg - CT.egg == 0     | -1.8933  | 0.6050     | -3.129  | 0.02167  | *   |
| C.hatch - CT.egg == 0     | 0.2500   | 0.5765     | 0.434   | 0.99806  |     |
| CT.hatch - CT.egg == 0    | 0.8333   | 0.5765     | 1.445   | 0.69895  |     |
| CTS.hatch - CT.egg == 0   | -2.7500  | 0.5765     | -4.770  | < 0.001  | *** |
| C.hatch - CTS.egg == 0    | 2.1433   | 0.6050     | 3.542   | 0.00533  | **  |
| CT.hatch - CTS.egg == 0   | 2.7266   | 0.6050     | 4.506   | < 0.001  | *** |
| CTS.hatch - CTS.egg == 0  | -0.8567  | 0.6050     | -1.416  | 0.71717  |     |
| CT.hatch - C.hatch == 0   | 0.5833   | 0.5765     | 1.012   | 0.91415  |     |
| CTS.hatch - C.hatch == 0  | -3.0000  | 0.5765     | -5.203  | < 0.001  | *** |
| CTS.hatch - CT.hatch == 0 | -3.5833  | 0.5765     | -6.215  | < 0.001  | *** |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## Fecundity

```
> mod1.lme = lme(FEC~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1     61 238.82033 <.0001
treatment            2     61 21.44745 <.0001
transplant           1     61  2.04540 0.1578
treatment:transplant 2     61  1.86896 0.1630
>
> comparison = glht(mod1.lme, linfct=mcp(treatment="Tukey", interaction_aver-
age = TRUE))
> summary(comparison)
```

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = FEC ~ treatment * transplant, data = mdata,
  random = ~1 | shelf)
```

Linear Hypotheses:

|               | Estimate | Std. Error | z value | Pr(> z ) |     |
|---------------|----------|------------|---------|----------|-----|
| CT - C == 0   | -29.711  | 3.956      | -7.511  | < 1e-04  | *** |
| CTS - C == 0  | -44.987  | 4.055      | -11.094 | < 1e-04  | *** |
| CTS - CT == 0 | -15.276  | 4.055      | -3.767  | 0.000472 | *** |

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## Juvenile survival

```
> mod1.lmer = glmer(prop ~ treatment*transplant + (1|shelf), family=binomial(), weights=N, data=mdata)
```

```
> resid=sum(residuals(mod1.lmer, 'pearson', level=0)^2)
```

```
> rdf=nrow(mdata) - length(fixef(mod1.lmer))-1
```

```
> resid/rdf
```

```
[1] 1.265676 - model dispersion OK
```

```
>
```

```
> Anova(mod1.lmer)
```

Analysis of Deviance Table (Type II Wald chisquare tests)

Response: prop

|                      | Chisq  | Df | Pr(>Chisq) |
|----------------------|--------|----|------------|
| treatment            | 8.1366 | 2  | 0.01711 *  |
| transplant           | 0.4350 | 1  | 0.50955    |
| treatment:transplant | 3.1015 | 2  | 0.21209    |

```
---
```

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
> comparison = glht(mod1.lmer, linfct=mcp(treatment="Tukey", interaction_averages = TRUE))
```

```
> summary(comparison)
```

### Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: glmer(formula = prop ~ treatment \* transplant + (1 | shelf),  
data = mdata, family = binomial(), weights = N)

Linear Hypotheses:

|               | Estimate | Std. Error | z value | Pr(> z )   |
|---------------|----------|------------|---------|------------|
| CT - C == 0   | -0.3002  | 0.2026     | -1.482  | 0.29958    |
| CTS - C == 0  | -0.5855  | 0.2003     | -2.923  | 0.00986 ** |
| CTS - CT == 0 | -0.2853  | 0.1965     | -1.452  | 0.31437    |

```
---
```

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Adjusted p values reported -- single-step method)

## CS activity

```
> mod1.lme = lme(CS.activity~ treatment*transplant, random=~1|shelf, data=
mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1    45  291.75965  <.0001
treatment            2    45   3.16155  0.0519
transplant           1    45   0.97395  0.3290
treatment:transplant 2    45   3.93400  0.0266
>
> mdata$SHD<-interaction(mdata$treatment,mdata$transplant)
> mod1.lme = lme(CS.activity~ SHD, random=~1|shelf, data=mdata)
>
> comparison = glht(mod1.lme, linfct=mcp(SHD="Tukey", interaction_average
= TRUE))
> summary(comparison)
```

## Simultaneous Tests for General Linear Hypotheses

### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = CS.activity ~ SHD, data = mdata, random = ~1 |
shelf)
```

#### Linear Hypotheses:

|                           | Estimate   | Std. Error | z value | Pr(> z ) |
|---------------------------|------------|------------|---------|----------|
| CT.egg - C.egg == 0       | -0.0045541 | 0.0020039  | -2.273  | 0.2041   |
| CTS.egg - C.egg == 0      | -0.0047379 | 0.0023497  | -2.016  | 0.3314   |
| C.hatch - C.egg == 0      | -0.0020741 | 0.0021017  | -0.987  | 0.9218   |
| CT.hatch - C.egg == 0     | -0.0042939 | 0.0021017  | -2.043  | 0.3163   |
| CTS.hatch - C.egg == 0    | 0.0017229  | 0.0020484  | 0.841   | 0.9595   |
| CTS.egg - CT.egg == 0     | -0.0001838 | 0.0022627  | -0.081  | 1.0000   |
| C.hatch - CT.egg == 0     | 0.0024800  | 0.0020039  | 1.238   | 0.8174   |
| CT.hatch - CT.egg == 0    | 0.0002602  | 0.0020039  | 0.130   | 1.0000   |
| CTS.hatch - CT.egg == 0   | 0.0062771  | 0.0019480  | 3.222   | 0.0160 * |
| C.hatch - CTS.egg == 0    | 0.0026638  | 0.0023497  | 1.134   | 0.8667   |
| CT.hatch - CTS.egg == 0   | 0.0004440  | 0.0023497  | 0.189   | 1.0000   |
| CTS.hatch - CTS.egg == 0  | 0.0064608  | 0.0023023  | 2.806   | 0.0561 . |
| CT.hatch - C.hatch == 0   | -0.0022198 | 0.0021017  | -1.056  | 0.8979   |
| CTS.hatch - C.hatch == 0  | 0.0037970  | 0.0020484  | 1.854   | 0.4296   |
| CTS.hatch - CT.hatch == 0 | 0.0060168  | 0.0020484  | 2.937   | 0.0385 * |

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Adjusted p values reported -- single-step method)

## ETS activity

```
> mod1.lme = lme(ETS.activity~ treatment*transplant, random=~1|shelf, data
=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1    54  181.94097  <.0001
treatment            2    54   2.05703  0.1377
transplant           1    54   0.16086  0.6899
treatment:transplant 2    54   1.90669  0.1584
```

## Juvenile growth rates

```
> mod1.lme = lme(growth~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1   341 2864.9347 <.0001
treatment            2   341  46.4223 <.0001
transplant           1   341   2.0562  0.1525
treatment:transplant 2   341   3.4100  0.0342
>
> mdata$SHD<-interaction(mdata$treatment,mdata$transplant)
> mod1.lme = lme(growth~ SHD, random=~1|shelf, data=mdata)
>
> comparison = glht(mod1.lme, linfct=mcp(SHD="Tukey", interaction_average
= TRUE))
> summary(comparison)
```

## Simultaneous Tests for General Linear Hypotheses

### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = growth ~ SHD, data = mdata, random = ~1 |
shelf)
```

#### Linear Hypotheses:

|                           | Estimate | Std. Error | z value | Pr(> z ) |     |
|---------------------------|----------|------------|---------|----------|-----|
| CT.egg - C.egg == 0       | 0.10714  | 0.03487    | 3.073   | 0.02584  | *   |
| CTS.egg - C.egg == 0      | -0.24020 | 0.03659    | -6.565  | < 0.001  | *** |
| C.hatch - C.egg == 0      | 0.05000  | 0.03487    | 1.434   | 0.70609  |     |
| CT.hatch - C.egg == 0     | 0.15476  | 0.03487    | 4.438   | < 0.001  | *** |
| CTS.hatch - C.egg == 0    | -0.07619 | 0.03487    | -2.185  | 0.24453  |     |
| CTS.egg - CT.egg == 0     | -0.34735 | 0.03659    | -9.493  | < 0.001  | *** |
| C.hatch - CT.egg == 0     | -0.05714 | 0.03487    | -1.639  | 0.57245  |     |
| CT.hatch - CT.egg == 0    | 0.04762  | 0.03487    | 1.366   | 0.74747  |     |
| CTS.hatch - CT.egg == 0   | -0.18333 | 0.03487    | -5.258  | < 0.001  | *** |
| C.hatch - CTS.egg == 0    | 0.29020  | 0.03659    | 7.931   | < 0.001  | *** |
| CT.hatch - CTS.egg == 0   | 0.39496  | 0.03659    | 10.795  | < 0.001  | *** |
| CTS.hatch - CTS.egg == 0  | 0.16401  | 0.03659    | 4.483   | < 0.001  | *** |
| CT.hatch - C.hatch == 0   | 0.10476  | 0.03487    | 3.004   | 0.03175  | *   |
| CTS.hatch - C.hatch == 0  | -0.12619 | 0.03487    | -3.619  | 0.00392  | **  |
| CTS.hatch - CT.hatch == 0 | -0.23095 | 0.03487    | -6.623  | < 0.001  | *** |

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signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## Egg volume

```
> mod1.lme = lme(egg~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF  F-value p-value
(Intercept)         1   671 731.0722 <.0001
treatment            2   671   6.9104  0.0011
transplant           1   671   0.0009  0.9760
treatment:transplant 2   671   0.1445  0.8655
>
> comparison = glht(mod1.lme, linfct=mcp(treatment="Tukey", interaction_aver-
age = TRUE))
> summary(comparison)
```

### Simultaneous Tests for General Linear Hypotheses

#### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = egg ~ treatment * transplant, data = mdata,
  random = ~1 | shelf)
```

#### Linear Hypotheses:

|               | Estimate  | Std. Error | z value | Pr(> z ) |     |
|---------------|-----------|------------|---------|----------|-----|
| CT - C == 0   | -0.063539 | 0.011988   | -5.300  | <1e-04   | *** |
| CTS - C == 0  | -0.056038 | 0.011967   | -4.683  | <1e-04   | *** |
| CTS - CT == 0 | 0.007501  | 0.012298   | 0.610   | 0.815    |     |

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)



## Statistical models and outputs for mean within- vs trans-generation responses to elevated temperature (C-C vs C-T vs T-T) (Fig 4 and 5)

### Longevity

```
> mod1.lme = lme(long~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1    63 247.98143  <.0001
treatment            2    63   6.19446  0.0035
transplant           1    63   2.04597  0.1576
treatment:transplant  2    63   2.82925  0.0666
>
> comparison = glht(mod1.lme, linfct=mcp(treatment="Tukey", interaction_aver-
age = TRUE))
> summary(comparison)
```

### Simultaneous Tests for General Linear Hypotheses

#### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = long ~ treatment * transplant, data = mdata,
  random = ~1 | shelf)
```

#### Linear Hypotheses:

|              | Estimate | Std. Error | z value | Pr(> z ) |
|--------------|----------|------------|---------|----------|
| CT - C == 0  | -5.875   | 3.502      | -1.678  | 0.2138   |
| TT - C == 0  | 4.292    | 3.502      | 1.226   | 0.4380   |
| TT - CT == 0 | 10.167   | 3.502      | 2.903   | 0.0102 * |

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## Maximum body size

```
> mod1.lme = lme(size~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1    63 2218.6255 <.0001
treatment            2    63  10.5325 0.0001
transplant           1    63   7.0996 0.0098
treatment:transplant 2    63   1.0810 0.3455
>
>
> comparison = glht(mod1.lme, linfct=mcp(treatment="Tukey", interaction_aver-
age = TRUE))
> summary(comparison)
```

### Simultaneous Tests for General Linear Hypotheses

#### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = size ~ treatment * transplant, data = mdata,
  random = ~1 | shelf)
```

#### Linear Hypotheses:

|              | Estimate | Std. Error | z value | Pr(> z ) |     |
|--------------|----------|------------|---------|----------|-----|
| CT - C == 0  | 0.9167   | 0.3981     | 2.303   | 0.0554   | .   |
| TT - C == 0  | 2.0000   | 0.3981     | 5.024   | <0.001   | *** |
| TT - CT == 0 | 1.0833   | 0.3981     | 2.721   | 0.0179   | *   |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## Fecundity

```
> mod1.lme = lme(fec2~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1    63  205.19677 <.0001
treatment            2    63   8.33843  0.0006
transplant           1    63   1.82215  0.1819
treatment:transplant  2    63   0.96796  0.3854
>
> comparison = glht(mod1.lme, linfct=mcp(treatment="Tukey", interaction_aver-
age = TRUE))
> summary(comparison)
```

Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = fec2 ~ treatment * transplant, data = mdata,
  random = ~1 | shelf)
```

Linear Hypotheses:

|              | Estimate | Std. Error | z value | Pr(> z )    |
|--------------|----------|------------|---------|-------------|
| CT - C == 0  | -29.711  | 4.191      | -7.089  | < 0.001 *** |
| TT - C == 0  | -15.941  | 4.191      | -3.803  | < 0.001 *** |
| TT - CT == 0 | 13.770   | 4.191      | 3.285   | 0.00298 **  |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## Juvenile survival

```
> mod1.lmer = glmer(prop ~ treatment*transplant + (1|shelf), family=binom-
ial(), weights=N, data=mdata)

> resid=sum(residuals(mod1.lmer, 'pearson', level=0)^2)
> rdf=nrow(mdata) - length(fixef(mod1.lmer))-1
> resid/rdf
[1] 1.305359 - model dispersion OK
>
> Anova(mod1.lmer)
Analysis of Deviance Table (Type II Wald chisquare tests)
```

Response: prop

|                      | Chisq  | Df | Pr(>Chisq) |
|----------------------|--------|----|------------|
| treatment            | 5.1795 | 2  | 0.07504 .  |
| transplant           | 0.2874 | 1  | 0.59187    |
| treatment:transplant | 3.5658 | 2  | 0.16815    |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Juvenile growth rates

```
> mod1.lme = lme(growth~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1   351 1882.4609  <.0001
treatment            2   351   7.1637  0.0009
transplant           1   351   1.8403  0.1758
treatment:transplant  2   351   0.7052  0.4947
>
> comparison = glht(mod1.lme, linfct=mcp(treatment="Tukey", interaction_aver-
age = TRUE))
> summary(comparison)
```

### Simultaneous Tests for General Linear Hypotheses

#### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = growth ~ treatment * transplant, data = mdata,
  random = ~1 | shelf)
```

#### Linear Hypotheses:

|              | Estimate  | Std. Error | z value | Pr(> z ) |     |
|--------------|-----------|------------|---------|----------|-----|
| CT - C == 0  | 0.105952  | 0.026062   | 4.065   | 0.000184 | *** |
| TT - C == 0  | 0.103571  | 0.026062   | 3.974   | 0.000220 | *** |
| TT - CT == 0 | -0.002381 | 0.026062   | -0.091  | 0.995409 |     |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## Egg volume

```
> mod1.lme = lme(egg~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1   691  1179.7886  <.0001
treatment            2   691    5.1311  0.0061
transplant           1   691    0.0008  0.9768
treatment:transplant  2   691    0.2677  0.7652
>
> comparison = glht(mod1.lme, linfct=mcp(treatment="Tukey", interaction_aver-
age = TRUE))
> summary(comparison)
```

### Simultaneous Tests for General Linear Hypotheses

#### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = egg ~ treatment * transplant, data = mdata,
  random = ~1 | shelf)
```

#### Linear Hypotheses:

|              | Estimate | Std. Error | z value | Pr(> z )    |
|--------------|----------|------------|---------|-------------|
| CT - C == 0  | -0.06233 | 0.01241    | -5.023  | < 1e-04 *** |
| TT - C == 0  | -0.02519 | 0.01208    | -2.085  | 0.09290 .   |
| TT - CT == 0 | 0.03715  | 0.01241    | 2.994   | 0.00772 **  |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## CS activity

```
> mod1.lme = lme(CS.activity ~ treatment*transplant, random=~1|shelf, data=
mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1    51  253.39924  <.0001
treatment            2    51   3.16621  0.0506
transplant           1    51   0.84005  0.3637
treatment:transplant  2    51   0.67735  0.5125
```

## ETS activity

```
> mod1.lme = lme(ETS.activity ~ treatment*transplant, random=~1|shelf, dat
a=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1    57  156.02778  <.0001
treatment            2    57   0.92164  0.4037
transplant           1    57   0.10094  0.7519
treatment:transplant  2    57   0.24174  0.7861
```

# **Statistical models and outputs for mean within- vs trans-generation responses to elevated temperature and elevated salinity (C-C vs C-TS vs TS-TS) (Fig 4 and 5)**

## **Longevity**

```

> mod1.lme = lme(long ~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')

```

|                      | numDF | denDF | F-value   | p-value |
|----------------------|-------|-------|-----------|---------|
| (Intercept)          | 1     | 60    | 277.89133 | <.0001  |
| treatment            | 2     | 60    | 0.99110   | 0.3772  |
| transplant           | 1     | 60    | 1.97819   | 0.1647  |
| treatment:transplant | 2     | 60    | 5.24491   | 0.0080  |

```

>
> mdata$SHD<-interaction(mdata$treatment,mdata$transplant)
> mod1.lme = lme(long~ SHD, random=~1|shelf, data=mdata)
>
> comparison = glht(mod1.lme, linfct=mcp(SHD="Tukey"))
> summary(comparison)

```

## Simultaneous Tests for General Linear Hypotheses

### Multiple Comparisons of Means: Tukey Contrasts

Fit: lme.formula(fixed = long ~ SHD, data = mdata, random = ~1 | shelf)

#### Linear Hypotheses:

|                           | Estimate | Std. Error | z value | Pr(> z ) |
|---------------------------|----------|------------|---------|----------|
| CTS.egg - C.egg == 0      | 6.6577   | 5.2855     | 1.260   | 0.8069   |
| TS.egg - C.egg == 0       | 5.8925   | 5.1517     | 1.144   | 0.8629   |
| C.hatch - C.egg == 0      | 7.0833   | 5.0362     | 1.406   | 0.7230   |
| CTS.hatch - C.egg == 0    | -9.8333  | 5.0362     | -1.953  | 0.3699   |
| TS.hatch - C.egg == 0     | 0.1667   | 5.0362     | 0.033   | 1.0000   |
| TS.egg - CTS.egg == 0     | -0.7652  | 5.3925     | -0.142  | 1.0000   |
| C.hatch - CTS.egg == 0    | 0.4256   | 5.2855     | 0.081   | 1.0000   |
| CTS.hatch - CTS.egg == 0  | -16.4910 | 5.2855     | -3.120  | 0.0223 * |
| TS.hatch - CTS.egg == 0   | -6.4910  | 5.2855     | -1.228  | 0.8231   |
| C.hatch - TS.egg == 0     | 1.1909   | 5.1517     | 0.231   | 0.9999   |
| CTS.hatch - TS.egg == 0   | -15.7258 | 5.1517     | -3.053  | 0.0275 * |
| TS.hatch - TS.egg == 0    | -5.7258  | 5.1517     | -1.111  | 0.8768   |
| CTS.hatch - C.hatch == 0  | -16.9167 | 5.0362     | -3.359  | 0.0101 * |
| TS.hatch - C.hatch == 0   | -6.9167  | 5.0362     | -1.373  | 0.7430   |
| TS.hatch - CTS.hatch == 0 | 10.0000  | 5.0362     | 1.986   | 0.3503   |

---  
signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## Maximum body size

```
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1     60 2061.7347  <.0001
treatment            2     60   0.4450  0.6429
transplant           1     60   7.4768  0.0082
treatment:transplant 2     60   5.0696  0.0092
>
> mdata$SHD<-interaction(mdata$treatment,mdata$transplant)
> mod1.lme = lme(size~ SHD, random=~1|shelf, data=mdata)
>
> comparison = glht(mod1.lme, linfct=mcp(SHD="Tukey"))
> summary(comparison)
```

## Simultaneous Tests for General Linear Hypotheses

### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = size ~ SHD, data = mdata, random = ~1 | shelf)
```

#### Linear Hypotheses:

|                           | Estimate | Std. Error | z value | Pr(> z ) |     |
|---------------------------|----------|------------|---------|----------|-----|
| CTS.egg - C.egg == 0      | -0.6270  | 0.5898     | -1.063  | 0.89591  |     |
| TS.egg - C.egg == 0       | -0.1153  | 0.5749     | -0.201  | 0.99996  |     |
| C.hatch - C.egg == 0      | 1.5000   | 0.5620     | 2.669   | 0.08174  | .   |
| CTS.hatch - C.egg == 0    | -1.5000  | 0.5620     | -2.669  | 0.08136  | .   |
| TS.hatch - C.egg == 0     | -0.2500  | 0.5620     | -0.445  | 0.99781  |     |
| TS.egg - CTS.egg == 0     | 0.5117   | 0.6017     | 0.850   | 0.95787  |     |
| C.hatch - CTS.egg == 0    | 2.1270   | 0.5898     | 3.606   | 0.00425  | **  |
| CTS.hatch - CTS.egg == 0  | -0.8730  | 0.5898     | -1.480  | 0.67685  |     |
| TS.hatch - CTS.egg == 0   | 0.3770   | 0.5898     | 0.639   | 0.98804  |     |
| C.hatch - TS.egg == 0     | 1.6153   | 0.5749     | 2.810   | 0.05573  | .   |
| CTS.hatch - TS.egg == 0   | -1.3847  | 0.5749     | -2.409  | 0.15291  |     |
| TS.hatch - TS.egg == 0    | -0.1347  | 0.5749     | -0.234  | 0.99990  |     |
| CTS.hatch - C.hatch == 0  | -3.0000  | 0.5620     | -5.338  | < 0.001  | *** |
| TS.hatch - C.hatch == 0   | -1.7500  | 0.5620     | -3.114  | 0.02279  | *   |
| TS.hatch - CTS.hatch == 0 | 1.2500   | 0.5620     | 2.224   | 0.22625  |     |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## Fecundity

```
> mod1.lme = lme(fec2~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1     60 219.57550 <.0001
treatment            2     60  18.49638 <.0001
transplant           1     60   1.71416 0.1954
treatment:transplant 2     60   1.46314 0.2396
>
> comparison = glht(mod1.lme, linfct=mcp(treatment="Tukey", interaction_aver-
age = TRUE))
> summary(comparison)
```

Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed =fec2 ~ treatment * transplant, data = mdata,
  random = ~1 | shelf)
```

Linear Hypotheses:

|               | Estimate | Std. Error | z value | Pr(> z ) |     |
|---------------|----------|------------|---------|----------|-----|
| CTS - C == 0  | -44.929  | 4.428      | -10.146 | <1e-04   | *** |
| TS - C == 0   | -30.635  | 4.370      | -7.010  | <1e-04   | *** |
| TS - CTS == 0 | 14.295   | 4.476      | 3.194   | 0.0039   | **  |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Adjusted p values reported -- single-step method)

Survival



## Juvenile survival

```
> mod1.lmer = glmer(prop ~ treatment*transplant + (1|shelf), family=binomial(), weights=N, data=mdata)
```

```
> resid=sum(residuals(mod1.lmer, 'pearson', level=0)^2)
```

```
> rdf=nrow(mdata) - length(fixef(mod1.lmer))-1
```

```
> resid/rdf
```

```
[1] 1.030909 - model dispersion OK
```

```
> Anova(mod1.lmer)
```

Analysis of Deviance Table (Type II Wald chisquare tests)

Response: prop

|                      | Chisq   | Df | Pr(>Chisq)  |
|----------------------|---------|----|-------------|
| treatment            | 10.9304 | 2  | 0.004232 ** |
| transplant           | 1.7657  | 1  | 0.183913    |
| treatment:transplant | 1.8927  | 2  | 0.388150    |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
>
```

```
> comparison = glht(mod1.lmer, linfct=mcp(treatment="Tukey", interaction_average = TRUE))
```

```
> summary(comparison)
```

### Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: glmer(formula = prop ~ treatment \* transplant + (1 | shelf),  
data = mdata, family = binomial(), weights = N)

Linear Hypotheses:

|               | Estimate | Std. Error | z value | Pr(> z ) |
|---------------|----------|------------|---------|----------|
| CTS - C == 0  | -0.58389 | 0.20005    | -2.919  | 0.0100 * |
| TS - C == 0   | -0.57017 | 0.20716    | -2.752  | 0.0162 * |
| TS - CTS == 0 | 0.01372  | 0.20111    | 0.068   | 0.9974   |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## Juvenile growth rates

```
> mod1.lme = lme(growth~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF    F-value p-value
(Intercept)         1   336 2933.8094 <.0001
treatment            2   336  29.1148 <.0001
transplant           1   336   1.9498 0.1635
treatment:transplant 2   336   5.2855 0.0055
>
> mdata$SHD<-interaction(mdata$treatment,mdata$transplant)
> mod1.lme = lme(growth~ SHD, random=~1|shelf, data=mdata)
>
> comparison = glht(mod1.lme, linfct=mcp(SHD="Tukey"))
> summary(comparison)
```

## Simultaneous Tests for General Linear Hypotheses

### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lme.formula(fixed = growth ~ SHD, data = mdata, random = ~1 |
shelf)
```

#### Linear Hypotheses:

|                           | Estimate  | Std. Error | z value | Pr(> z ) |     |
|---------------------------|-----------|------------|---------|----------|-----|
| CTS.egg - C.egg == 0      | -0.240000 | 0.037555   | -6.391  | < 0.001  | *** |
| TS.egg - C.egg == 0       | -0.244156 | 0.036612   | -6.669  | < 0.001  | *** |
| C.hatch - C.egg == 0      | 0.050000  | 0.035807   | 1.396   | 0.72915  |     |
| CTS.hatch - C.egg == 0    | -0.076190 | 0.035807   | -2.128  | 0.27260  |     |
| TS.hatch - C.egg == 0     | -0.247619 | 0.035807   | -6.915  | < 0.001  | *** |
| TS.egg - CTS.egg == 0     | -0.004156 | 0.038323   | -0.108  | 1.00000  |     |
| C.hatch - CTS.egg == 0    | 0.290000  | 0.037555   | 7.722   | < 0.001  | *** |
| CTS.hatch - CTS.egg == 0  | 0.163810  | 0.037555   | 4.362   | < 0.001  | *** |
| TS.hatch - CTS.egg == 0   | -0.007619 | 0.037555   | -0.203  | 0.99995  |     |
| C.hatch - TS.egg == 0     | 0.294156  | 0.036612   | 8.034   | < 0.001  | *** |
| CTS.hatch - TS.egg == 0   | 0.167965  | 0.036612   | 4.588   | < 0.001  | *** |
| TS.hatch - TS.egg == 0    | -0.003463 | 0.036612   | -0.095  | 1.00000  |     |
| CTS.hatch - C.hatch == 0  | -0.126190 | 0.035807   | -3.524  | 0.00571  | **  |
| TS.hatch - C.hatch == 0   | -0.297619 | 0.035807   | -8.312  | < 0.001  | *** |
| TS.hatch - CTS.hatch == 0 | -0.171429 | 0.035807   | -4.788  | < 0.001  | *** |

## Egg volume

```
> mod1.lme = lme(egg~ treatment*transplant, random=~1|shelf, data=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF  F-value p-value
(Intercept)         1   681 885.9101  <.0001
treatment            2   681   7.1629  0.0008
transplant           1   681   0.0009  0.9767
treatment:transplant 2   681   2.6417  0.0720
>
> comparison = glht(mod1.lmer, linfct=mcp(treatment="Tukey", interaction_aver-
age = TRUE))
> summary(comparison)
```

## Simultaneous Tests for General Linear Hypotheses

### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: glmer(formula = prop ~ treatment * transplant + (1 | shelf),
  data = mdata, family = binomial(), weights = N)
```

#### Linear Hypotheses:

|               | Estimate | Std. Error | z value | Pr(> z ) |    |
|---------------|----------|------------|---------|----------|----|
| CTS - C == 0  | -0.58389 | 0.20005    | -2.919  | 0.00998  | ** |
| TS - C == 0   | -0.57017 | 0.20716    | -2.752  | 0.01634  | *  |
| TS - CTS == 0 | 0.01372  | 0.20111    | 0.068   | 0.99744  |    |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## CS activity

```
> mod1.lme = lme(CS.activity~ treatment*transplant, random=~1|shelf, data=
mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF  F-value p-value
(Intercept)         1   40 208.75195  <.0001
treatment            2   40   1.70238  0.1952
transplant           1   40   0.81533  0.3720
treatment:transplant 2   40   3.34806  0.0452
```

## ETS activity

```
> mod1.lme = lme(ETS.activity~ treatment*transplant, random=~1|shelf, data
=mdata)
> anova(mod1.lme, type = 'marginal')
              numDF denDF  F-value p-value
(Intercept)         1   53 154.75065  <.0001
treatment            2   53   1.70626  0.1914
transplant           1   53   0.11667  0.7340
treatment:transplant 2   53   1.30772  0.2790
```

# TRADE-OFF ANALYSIS

## Within-generation

### Statistical models and outputs for within-generation relationship between juvenile growth rates and adult life-history traits (C-C, C-T and C-TS) (Fig 6 and S1)

#### C-C - MANOVA

```
> manova<-manova(matrix~ growth, data=mdata)
> summary(manova)
```

|           | Df | Pillai   | approx F | num Df | den Df | Pr(>F) |
|-----------|----|----------|----------|--------|--------|--------|
| growth    | 1  | 0.025683 | 0.17574  | 3      | 20     | 0.9116 |
| Residuals | 22 |          |          |        |        |        |

```
> summary.aov(manova)
```

Response long :

|           | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|-----------|----|--------|---------|---------|--------|
| growth    | 1  | 27.8   | 27.785  | 0.1706  | 0.6835 |
| Residuals | 22 | 3582.2 | 162.826 |         |        |

Response size :

|           | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|-----------|----|--------|---------|---------|--------|
| growth    | 1  | 0.654  | 0.65396 | 0.2271  | 0.6384 |
| Residuals | 22 | 63.346 | 2.87937 |         |        |

Response fec2 : # fec2 = fecundity

|           | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|-----------|----|--------|---------|---------|--------|
| growth    | 1  | 203.0  | 203.01  | 0.555   | 0.4642 |
| Residuals | 22 | 8047.5 | 365.80  |         |        |

#### C-T - MANOVA

```
> manova<-manova(matrix~ growth, data=mdata)
> summary(manova)
```

|           | Df | Pillai  | approx F | num Df | den Df | Pr(>F) |
|-----------|----|---------|----------|--------|--------|--------|
| growth    | 1  | 0.12791 | 0.9778   | 3      | 20     | 0.4229 |
| Residuals | 22 |         |          |        |        |        |

```
> summary.aov(manova)
```

Response long :

|           | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|-----------|----|--------|---------|---------|--------|
| growth    | 1  | 190.4  | 190.42  | 1.1299  | 0.2993 |
| Residuals | 22 | 3707.4 | 168.52  |         |        |

Response size :

|           | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|-----------|----|--------|---------|---------|--------|
| growth    | 1  | 0.728  | 0.72845 | 0.3136  | 0.5811 |
| Residuals | 22 | 51.105 | 2.32295 |         |        |

Response fec2 : # fec2 = fecundity

|           | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|-----------|----|--------|---------|---------|--------|
| growth    | 1  | 104.6  | 104.60  | 0.8093  | 0.3781 |
| Residuals | 22 | 2843.3 | 129.24  |         |        |

### C-TS - Three ANOVAs with Bonferroni correction ( $\alpha = 0.017$ )

```
> lm = lm(longevity ~ growth, mdata)
> summary(lm)
```

Call:

```
lm(formula = longevity ~ growth, data = mdata)
```

Residuals:

| Min     | 1Q     | Median | 3Q     | Max    |
|---------|--------|--------|--------|--------|
| -29.660 | -4.985 | -1.082 | 10.304 | 17.313 |

Coefficients:

|             | Estimate | Std. Error | t value | Pr(> t )     |
|-------------|----------|------------|---------|--------------|
| (Intercept) | 133.15   | 21.73      | 6.127   | 5.49e-06 *** |
| growth      | -59.40   | 17.69      | -3.358  | 0.00313 **   |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 11.53 on 20 degrees of freedom

Multiple R-squared: 0.3606, Adjusted R-squared: 0.3286

F-statistic: 11.28 on 1 and 20 DF, p-value: 0.003128

```
> lm = lm(max.body.size ~ growth, mdata)
> summary(lm)
```

Call:

```
lm(formula = max.body.size ~ growth, data = mdata)
```

Residuals:

| Min      | 1Q       | Median   | 3Q      | Max     |
|----------|----------|----------|---------|---------|
| -1.51083 | -1.01463 | -0.04822 | 0.98917 | 1.62352 |

Coefficients:

|             | Estimate | Std. Error | t value | Pr(> t )     |
|-------------|----------|------------|---------|--------------|
| (Intercept) | 23.422   | 2.038      | 11.491  | 2.91e-10 *** |
| growth      | -4.702   | 1.659      | -2.834  | 0.0102 *     |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.081 on 20 degrees of freedom

Multiple R-squared: 0.2866, Adjusted R-squared: 0.2509

F-statistic: 8.034 on 1 and 20 DF, p-value: 0.01025

```
> lm = lm(fec2 ~ growth, mdata) # FEC2 = fecundity
> summary(lm)
```

Call:

```
lm(formula = fec2 ~ growth, data = mdata)
```

Residuals:

| Min      | 1Q      | Median  | 3Q     | Max     |
|----------|---------|---------|--------|---------|
| -15.1625 | -7.9505 | -0.4448 | 7.4889 | 20.8403 |

Coefficients:

|             | Estimate | Std. Error | t value | Pr(> t ) |
|-------------|----------|------------|---------|----------|
| (Intercept) | 28.519   | 18.646     | 1.529   | 0.142    |
| growth      | -3.909   | 15.176     | -0.258  | 0.799    |

Residual standard error: 9.891 on 20 degrees of freedom  
Multiple R-squared: 0.003307, Adjusted R-squared: -0.04653  
F-statistic: 0.06636 on 1 and 20 DF, p-value: 0.7993

**Statistical models and outputs for within-generation relationship between  
Longevity/max body size and CS/ETS activity in the C-TS treatment  
(Fig 6 and S2)**

```
> lm = lm(longevity ~ CS.activity, mdata)
> summary(lm)
```

```
Call:
lm(formula = longevity ~ CS.activity, data = mdata)
```

```
Residuals:
    Min       1Q   Median       3Q      Max
-26.325  -7.556   2.859   5.477  15.462
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    88.71      12.22   7.257 4.18e-06 ***
CS.activity  -1234.14     482.03  -2.560  0.0227 *
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Residual standard error: 11.22 on 14 degrees of freedom  
Multiple R-squared: 0.3189, Adjusted R-squared: 0.2703  
F-statistic: 6.555 on 1 and 14 DF, p-value: 0.02266

```
> lm = lm(max.body.size ~ CS.activity, mdata)
> summary(lm)
```

```
Call:
lm(formula = max.body.size ~ CS.activity, data = mdata)
```

```
Residuals:
    Min       1Q   Median       3Q      Max
-1.4049 -0.9425 -0.2202  0.8384  1.9974
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   18.833      1.242  15.161 4.42e-10 ***
CS.activity   -56.522     48.979  -1.154  0.268
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Residual standard error: 1.14 on 14 degrees of freedom  
Multiple R-squared: 0.08686, Adjusted R-squared: 0.02164  
F-statistic: 1.332 on 1 and 14 DF, p-value: 0.2678

```
> lm =lm(longevity ~ ETS.activity, mdata)
> summary(lm)
```

Call:

```
lm(formula = longevity ~ ETS.activity, data = mdata)
```

Residuals:

|  | Min     | 1Q     | Median | 3Q    | Max    |
|--|---------|--------|--------|-------|--------|
|  | -26.467 | -8.704 | 1.421  | 8.854 | 22.157 |

Coefficients:

|              | Estimate | Std. Error | t value | Pr(> t )     |
|--------------|----------|------------|---------|--------------|
| (Intercept)  | 80.67    | 10.78      | 7.485   | 6.24e-07 *** |
| ETS.activity | -723.89  | 387.93     | -1.866  | 0.0784 .     |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 12.96 on 18 degrees of freedom

Multiple R-squared: 0.1621, Adjusted R-squared: 0.1155

F-statistic: 3.482 on 1 and 18 DF, p-value: 0.07842

```
> lm =lm(max.body.size ~ ETS.activity, mdata)
> summary(lm)
```

Call:

```
lm(formula = max.body.size ~ ETS.activity, data = mdata)
```

Residuals:

|  | Min     | 1Q      | Median  | 3Q     | Max    |
|--|---------|---------|---------|--------|--------|
|  | -1.9014 | -0.7402 | -0.1648 | 0.9645 | 1.7576 |

Coefficients:

|              | Estimate | Std. Error | t value | Pr(> t )     |
|--------------|----------|------------|---------|--------------|
| (Intercept)  | 19.8149  | 0.9818     | 20.182  | 8.23e-14 *** |
| ETS.activity | -77.1647 | 35.3374    | -2.184  | 0.0425 *     |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.181 on 18 degrees of freedom

Multiple R-squared: 0.2094, Adjusted R-squared: 0.1655

F-statistic: 4.768 on 1 and 18 DF, p-value: 0.04247

## Within- vs trans-generation

### Statistical models and outputs for within- vs trans-generation relationship between juvenile growth rates and adult life-history traits (Fig 7 and S3)

#### C-T vs T-T - MANOVA

```
> manova<-manova(matrix~growth*treatment, data=mdata)
> summary(manova)
```

|                  | Df | Pillai  | approx F | num Df | den Df | Pr(>F)    |
|------------------|----|---------|----------|--------|--------|-----------|
| growth           | 1  | 0.12943 | 0.8920   | 3      | 18     | 0.46423   |
| treatment        | 1  | 0.42150 | 4.3716   | 3      | 18     | 0.01768 * |
| growth:treatment | 1  | 0.25203 | 2.0217   | 3      | 18     | 0.14692   |
| Residuals        | 20 |         |          |        |        |           |

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
> summary.aov(manova)
```

Response long :

|                  | Df | Sum Sq  | Mean Sq | F value | Pr(>F)      |
|------------------|----|---------|---------|---------|-------------|
| growth           | 1  | 341.88  | 341.88  | 2.3750  | 0.138962    |
| treatment        | 1  | 1605.48 | 1605.48 | 11.1534 | 0.003265 ** |
| growth:treatment | 1  | 78.23   | 78.23   | 0.5435  | 0.469559    |
| Residuals        | 20 | 2878.91 | 143.95  |         |             |

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Response size :

|                  | Df | Sum Sq | Mean Sq | F value | Pr(>F)    |
|------------------|----|--------|---------|---------|-----------|
| growth           | 1  | 0.047  | 0.0470  | 0.0293  | 0.86592   |
| treatment        | 1  | 10.899 | 10.8994 | 6.7830  | 0.01696 * |
| growth:treatment | 1  | 0.250  | 0.2497  | 0.1554  | 0.69757   |
| Residuals        | 20 | 32.137 | 1.6069  |         |           |

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Response FEC2 : # FEC2 = fecundity

|                  | Df | Sum Sq  | Mean Sq | F value | Pr(>F)      |
|------------------|----|---------|---------|---------|-------------|
| growth           | 1  | 35.66   | 35.66   | 0.3359  | 0.568694    |
| treatment        | 1  | 934.63  | 934.63  | 8.8030  | 0.007621 ** |
| growth:treatment | 1  | 641.38  | 641.38  | 6.0410  | 0.023228 *  |
| Residuals        | 20 | 2123.45 | 106.17  |         |             |

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1



### C-TS vs TS-TS - Three ANOVAs with Bonferroni correction ( $\alpha = 0.017$ )

```
> lm = lm(longevity ~ growth, mdata)
> summary(lm)
```

Call:

```
lm(formula = longevity ~ growth, data = mdata)
```

Residuals:

|  | Min      | 1Q      | Median | 3Q     | Max     |
|--|----------|---------|--------|--------|---------|
|  | -19.4996 | -4.0152 | 0.8859 | 7.5317 | 12.5004 |

Coefficients:

|             | Estimate | Std. Error | t value | Pr(> t )    |
|-------------|----------|------------|---------|-------------|
| (Intercept) | 115.09   | 17.84      | 6.449   | 3.5e-06 *** |
| growth      | -40.65   | 15.71      | -2.587  | 0.0181 *    |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.62 on 19 degrees of freedom

Multiple R-squared: 0.2605, Adjusted R-squared: 0.2216

F-statistic: 6.694 on 1 and 19 DF, p-value: 0.01807

```
> lm = lm(max.body.size ~ growth, mdata)
> summary(lm)
```

Call:

```
lm(formula = max.body.size ~ growth, data = mdata)
```

Residuals:

|  | Min     | 1Q      | Median  | 3Q     | Max    |
|--|---------|---------|---------|--------|--------|
|  | -2.3075 | -1.2273 | -0.4146 | 0.7727 | 2.8530 |

Coefficients:

|             | Estimate | Std. Error | t value | Pr(> t )     |
|-------------|----------|------------|---------|--------------|
| (Intercept) | 19.4847  | 2.5110     | 7.760   | 2.63e-07 *** |
| growth      | -0.9363  | 2.2108     | -0.424  | 0.677        |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.354 on 19 degrees of freedom

Multiple R-squared: 0.009353, Adjusted R-squared: -0.04279

F-statistic: 0.1794 on 1 and 19 DF, p-value: 0.6767

```
> lm = lm(FEC2 ~ growth, mdata) # FEC2 = fecundity
> summary(lm)
```

Call:

```
lm(formula = FEC2 ~ growth, data = mdata)
```

Residuals:

|  | Min     | 1Q     | Median | 3Q    | Max    |
|--|---------|--------|--------|-------|--------|
|  | -24.808 | -7.864 | 0.527  | 9.247 | 34.055 |

Coefficients:

|             | Estimate | Std. Error | t value | Pr(> t ) |
|-------------|----------|------------|---------|----------|
| (Intercept) | 0.8808   | 28.9729    | 0.030   | 0.976    |
| growth      | 28.7140  | 25.5093    | 1.126   | 0.274    |

Residual standard error: 15.62 on 19 degrees of freedom  
Multiple R-squared: 0.06252, Adjusted R-squared: 0.01318  
F-statistic: 1.267 on 1 and 19 DF, p-value: 0.2743

## Statistical models and outputs for within- vs trans-generation relationship between adult life-history traits (Fig 7 and S5)

### C-T vs T-T - MANOVA

```
> manova<-manova(matrix~FEC2 * treatment, data=mdata) # FEC2 = fecundity
> summary(manova)
```

|                | Df | Pillai  | approx F | num Df | den Df | Pr(>F)        |
|----------------|----|---------|----------|--------|--------|---------------|
| FEC2           | 1  | 0.65382 | 17.9427  | 2      | 19     | 4.201e-05 *** |
| treatment      | 1  | 0.28077 | 3.7086   | 2      | 19     | 0.04368 *     |
| FEC2:treatment | 1  | 0.35254 | 5.1726   | 2      | 19     | 0.01609 *     |
| Residuals      | 20 |         |          |        |        |               |

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> summary.aov(manova)
```

Response longevity :

|                | Df | Sum Sq  | Mean Sq | F value | Pr(>F)        |
|----------------|----|---------|---------|---------|---------------|
| FEC2           | 1  | 2189.75 | 2189.75 | 27.7488 | 3.726e-05 *** |
| treatment      | 1  | 431.66  | 431.66  | 5.4700  | 0.02984 *     |
| FEC2:treatment | 1  | 704.83  | 704.83  | 8.9317  | 0.00726 **    |
| Residuals      | 20 | 1578.26 | 78.91   |         |               |

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Response max.body.size :
```

|                | Df | Sum Sq  | Mean Sq | F value | Pr(>F)     |
|----------------|----|---------|---------|---------|------------|
| FEC2           | 1  | 12.5004 | 12.5004 | 9.8093  | 0.00525 ** |
| treatment      | 1  | 2.9198  | 2.9198  | 2.2912  | 0.14575    |
| FEC2:treatment | 1  | 2.4264  | 2.4264  | 1.9040  | 0.18286    |
| Residuals      | 20 | 25.4868 | 1.2743  |         |            |

### C-TS vs TS-TS - Two ANOVAs with Bonferroni correction ( $\alpha = 0.025$ )

```
> lm =lm(longevity ~ FEC2, mdata) # FEC2 = fecundity
> summary(lm)
```

Call:

```
lm(formula = long ~ FEC2, data = mdata)
```

Residuals:

| Min     | 1Q     | Median | 3Q    | Max    |
|---------|--------|--------|-------|--------|
| -26.103 | -1.944 | 3.616  | 4.350 | 19.083 |

Coefficients:

|             | Estimate | Std. Error | t value | Pr(> t )     |
|-------------|----------|------------|---------|--------------|
| (Intercept) | 63.0380  | 5.6142     | 11.228  | 7.89e-10 *** |
| FEC2        | 0.1864   | 0.1532     | 1.216   | 0.239        |

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 10.78 on 19 degrees of freedom
Multiple R-squared:  0.07222, Adjusted R-squared:  0.02339
F-statistic: 1.479 on 1 and 19 DF, p-value: 0.2388
```

```
> lm = lm(size ~ FEC2, mdata) # FEC2 = fecundity
```

```
> summary(lm)
```

Call:

```
lm(formula = size ~ FEC2, data = mdata)
```

Residuals:

|  | Min      | 1Q       | Median   | 3Q      | Max     |
|--|----------|----------|----------|---------|---------|
|  | -2.43389 | -1.15181 | -0.00116 | 0.63759 | 2.37929 |

Coefficients:

|             | Estimate | Std. Error | t value | Pr(> t )    |
|-------------|----------|------------|---------|-------------|
| (Intercept) | 17.73086 | 0.68631    | 25.84   | 2.9e-16 *** |
| FEC2        | 0.02097  | 0.01873    | 1.12    | 0.277       |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.317 on 19 degrees of freedom

Multiple R-squared: 0.06188, Adjusted R-squared: 0.01251

F-statistic: 1.253 on 1 and 19 DF, p-value: 0.2769

## Statistical models and outputs for within- vs trans-generation relationship between fecundity and CS/ETS activity under T conditions (Fig S4)

```
> lm =lm(fecundity ~ CS.activity, mdata)
> summary(lm)
```

Call:

```
lm(formula = fecundity ~ CS.activity, data = mdata)
```

Residuals:

| Min      | 1Q      | Median  | 3Q     | Max     |
|----------|---------|---------|--------|---------|
| -21.7059 | -8.1917 | -0.3083 | 9.0516 | 21.8045 |

Coefficients:

|             | Estimate | Std. Error | t value | Pr(> t ) |
|-------------|----------|------------|---------|----------|
| (Intercept) | 21.06    | 13.62      | 1.547   | 0.1376   |
| CS.activity | 1239.80  | 646.92     | 1.916   | 0.0697 . |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 12.24 on 20 degrees of freedom

Multiple R-squared: 0.1552, Adjusted R-squared: 0.1129

F-statistic: 3.673 on 1 and 20 DF, p-value: 0.06971

```
> lm =lm(fecundity ~ ETS.activity, mdata)
> summary(lm)
```

Call:

```
lm(formula = fecundity ~ ETS.activity, data = mdata)
```

Residuals:

| Min     | 1Q     | Median | 3Q    | Max    |
|---------|--------|--------|-------|--------|
| -24.123 | -7.074 | 1.714  | 8.862 | 18.064 |

Coefficients:

|              | Estimate | Std. Error | t value | Pr(> t )     |
|--------------|----------|------------|---------|--------------|
| (Intercept)  | 33.320   | 8.278      | 4.025   | 0.000612 *** |
| ETS.activity | 582.915  | 315.416    | 1.848   | 0.078724 .   |

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 11.79 on 21 degrees of freedom

Multiple R-squared: 0.1399, Adjusted R-squared: 0.09893

F-statistic: 3.415 on 1 and 21 DF, p-value: 0.07872