**Title:** **Rodrigues et al. The genetic basis and adult reproductive consequences of developmental thermal plasticity**

**Summary:**

This data was used to assess how sublethal heat stress during development impacted subsequent multiple reproductive traits in both sexes and their plasticity and to identify candidate genes of reproductive traits sensitive to thermal stress. Using a subset of isogenic lines of the Drosophila Genetic Reference Panel (DGRP) reared at standardized densities in three temperatures (25°C, 27°C, 29°C), we quantified phenotypic variation in mating propensity, fertility, productivity and sex-ratio and obtained their respective thermal reaction norms when applicable.

**Files available:**

We provide 2 .txt files (MALE\_phenotypicdata; FEMALE\_phenotypicdata) and a .xls file (TableS4\_genomic\_analyses\_results\_productivity).

**MALE\_phenotypicdata:**

This file contains the raw data obtained for male DGRP under one of three constant temperatures.

Table headers are explained below:

*Block –* week in which the data were collected (1 or 2).

*LineDGRP -* line identity.

*Line\_Status* - classification based on the male reproductive performance across three temperatures tested in Zwoinska et al. (2020)\*. (High, lines whose fertility did not decline as temperature increased; Low, lines whose fertility declined substantially as temperature increased).

*Temperature* - mean developmental temperature experienced (25°C, 27°C or 29°C).

*Vial* – vial where each pair was kept.

*Mating* – mating propensity (1, if mating observed; 0, if no mating observed)

*Larvae* – fertility (1, if larvae present; 0, if no larvae present)

*Productivity (1,2 and 3)* – number of adult offspring counted on the first, second and third day of offspring counting.

*Daughters (1, 2 and 3)* – number of adult females counted on the first, second and third day of offspring counting.

*Sons (1, 2 and 3)* – number of adult males counted on the first, second and third day of offspring counting.

*daughtersTotal* – Total number of adult females counted.

*sonsTotal*– Total number of adult males counted.

*productivityTotal*– Total number of adult offspring counted.

**FEMALE\_phenotypicdata:**

This file contains the raw data obtained for female DGRP under one of three constant temperatures.

Table headers are explained below:

*LineDGRP -* line identity.

*Line\_Status* - classification based on the male reproductive performance across three temperatures tested in Zwoinska et al. (2020)\*. (High, lines whose fertility did not decline as temperature increased; Low, lines whose fertility declined substantially as temperature increased).

*Temperature* - mean developmental temperature experienced (25°C, 27°C or 29°C).

*Vial* – vial where each pair was kept.

*Larvae* – fertility (1, if larvae present; 0, if no larvae present)

*Productivity (1,2 and 3)* – number of adult offspring counted on the first, second and third day of offspring counting.

*Daughters (1, 2 and 3)* – number of adult females counted on the first, second and third day of offspring counting.

*Sons (1, 2 and 3)* – number of adult males counted on the first, second and third day of offspring counting.

*daughtersTotal* – Total number of adult females counted.

*sonsTotal*– Total number of adult males counted.

*productivityTotal*– Total number of adult offspring counted.

**TableS4\_genomic\_analyses\_results\_productivity:**

This table contains several individual sheets, the legends for these sheets are given below:

Top SNPs ANOVA Phenotype: Table of ANOVA results for the effect of genotype on phenotype

Chromosome=chromosome location of SNP

position=position on chromosome of the SNP

ID=SNP id, consisting of the chromosome followed by the position

F=F-value from an ANOVA of phenotype ~ genotype

d.f.=degrees of freedom for genotype and the residuals

P-value=p-value of an F-test for the effect of genotype

window=The coordinates of the 5kb genomic window in which this SNP can be found.

SNPEff: Table of DGRP annotations for 54 candidate SNPs

ID=SNP id, consisting of the chromosome followed by the position

Reference\_Allele=The reference allele at this SNP

Site\_Class=The site class of the SNP according to DGRP annotations

Transcript\_Annotation=The transcript annotation of the SNP according to DGRP annotations

TF\_binding\_site=TF binding site annotations of the SNP according to DGRP annotations

SNPEff Summary: Summary table of the DGRP site class annotations for 54 candidate SNPs

Annotation=Site class annotation category

N=Number of SNPs with this annotation

Percent=Percent of SNPs (out of 446) with this annotation

SNPEff Genes Coding: Table of genes with the site class annotations NON\_SYNONYMOUS\_CODING or SYNONYMOUS\_CODING

ID=SNP id, consisting of the chromosome followed by the position

FB\_gene\_ID=The FlyBase gene ID

Gene coordinates=The coordinates of the gene. On D. melanogaster genome r6.32

NAME=Gene name

SYMBOL=Gene symbol

SNPEff Annotation=The DGRP annotation for this gene from the candidate SNPs

Phenotypic\_terms=Phenotypic terms of interest associated with this gene obtained from the FlyBase entry for this gene.

Expression=Tissues for which expression is reported in FlyAtlas2 for males, females, and larvae.

ModPhEA Results (SNPEff Genes Coding): modPhEA results for genes in the table “SNPEff Genes Coding”. Cells that are filled in green have a BH FDR corrected p-value < 0.05.

Phenotype Name=Descriptive name for the phenotypic category

Phenotype ID=ID for the phenotypic category

% of genes with the term in "QueryGeneSet"=The percent of genes in the “query” set of genes that have this annotated phenotypic category.

% of genes with the term in "Background"=The percent of genes in the “backgroun” set of genes that have this annotated phenotypic category.

Fisher's Exact Test P-value=P-value from a Fisher’s Exact test of enrichment

BH FDR corrected P-value=Benjamini-Hochberg corrected p-value from Fisher’s Exact test

Bonferroni corrected P-value=Bonferroni corrected p-value from Fisher’s Exact test

Genes 2kb: Genes within 2kb up- and down- stream of a candidate SNP

FB\_gene\_ID=The FlyBase gene ID

annotation\_symbol=FlyBase gene annotation symbol

chromosome=chromosome location of gene

start=the start location of the gene on the chromosome. On the D. melanogaster genome r6.32

end=the end location of the gene on the chromosome. On the D. melanogaster genome r6.32

name=Gene name

symbol=Gene symbol

ModPhEA Results (Genes 2kb): modPhEA results for genes in the table “Genes 2kb”. Cells that are filled in green have a BH FDR corrected p-value < 0.05

Phenotype Name=Descriptive name for the phenotypic category

Phenotype ID=ID for the phenotypic category

% of genes with the term in "QueryGeneSet"=The percent of genes in the “query” set of genes that have this annotated phenotypic category.

% of genes with the term in "Background"=The percent of genes in the “backgroun” set of genes that have this annotated phenotypic category.

Fisher's Exact Test P-value=P-value from a Fisher’s Exact test of enrichment

BH FDR corrected P-value=Benjamini-Hochberg corrected p-value from Fisher’s Exact test

Bonferroni corrected P-value=Bonferroni corrected p-value from Fisher’s Exact test

\*Zwoinska, M. K., Rodrigues, L. R., Slate, J., & Snook, R. R. (2020). Phenotypic responses to and genetic architecture of sterility in response to sub-lethal temperature during development. Frontiers in Genetics, 11, 573. https://doi.org/10.3389/fgene.2020.00573