

Bioassay screen of Arjen

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Data import

Background information

This is the data of the whitefly development bioassay performed by Arjen van Doorn. Only MM and LA1840 will be used.

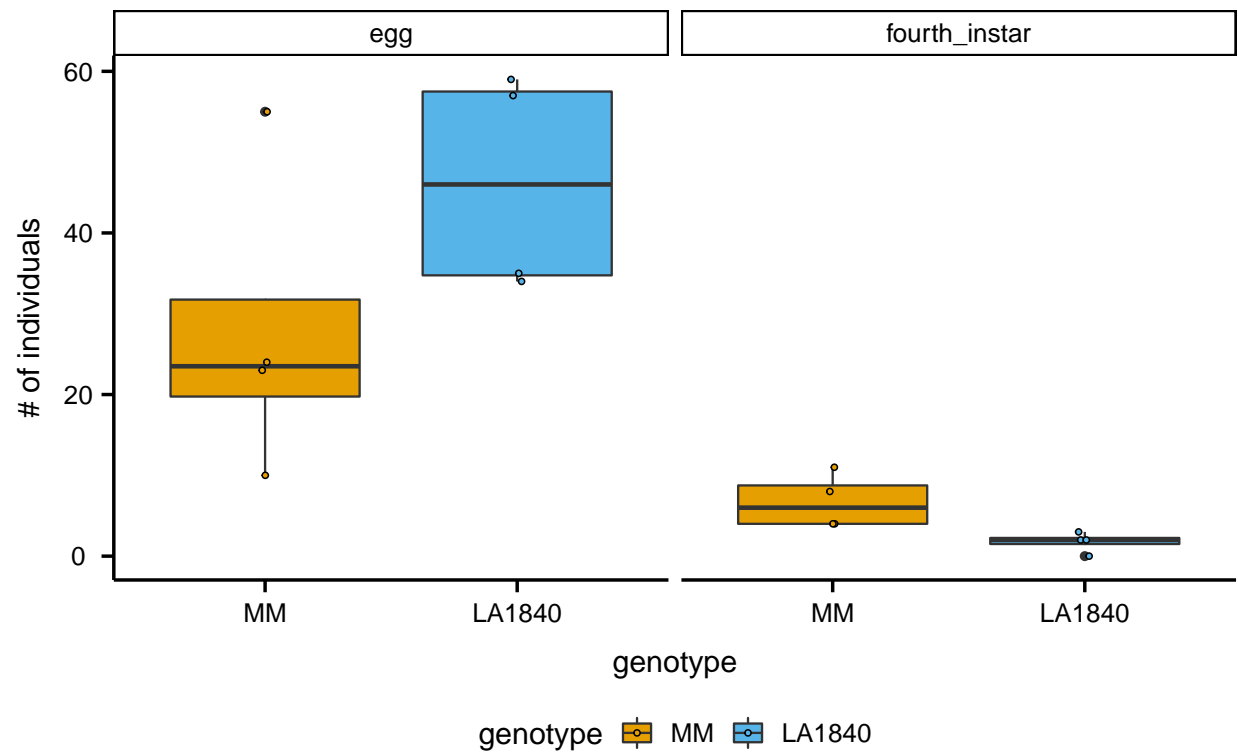
The raw data

genotype	replicate	stage	number
MM	3	fourth_instar	8
MM	4	fourth_instar	11
MM	5	fourth_instar	4
MM	6	fourth_instar	4
LA1840	1	fourth_instar	3
LA1840	2	fourth_instar	2
LA1840	3	fourth_instar	0
LA1840	5	fourth_instar	2
MM	3	egg	23
MM	4	egg	24

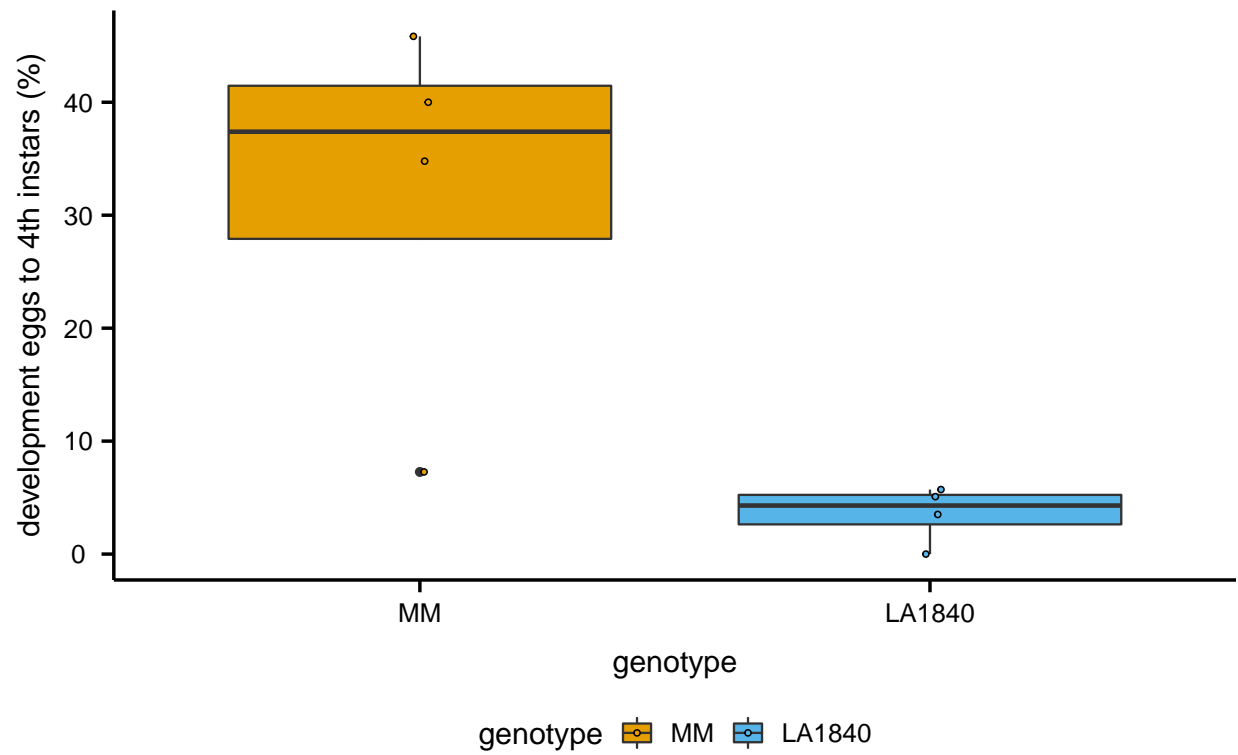
plots

I'm doubting whether I should use the absolute or relative number of 4th instars for the plot, so I will try both.

plot with absolute numbers

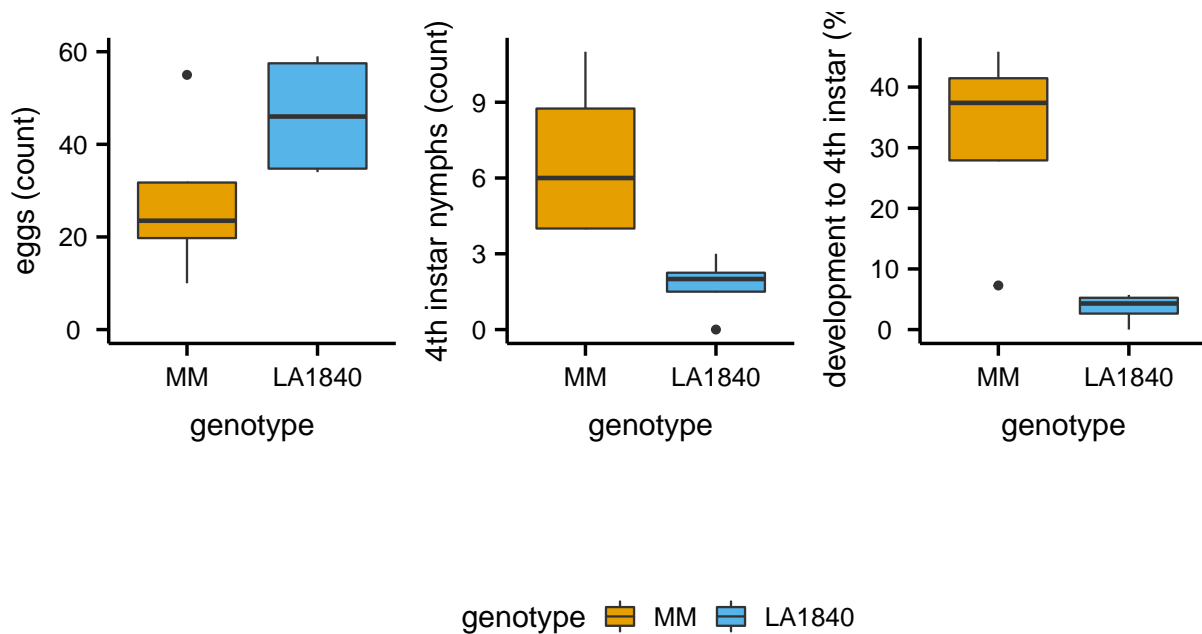


plot with relative 4th instar numbers



combined

It might be best to use both for the most complete view of the phenotype.



statistics

Are the number of 4th instars lower than the number of eggs for MM and LA1840?

```
## # A tibble: 2 x 11
##   genotype .y. group1 group2      n1      n2 statistic    df      p p.adj
## * <fct>   <chr> <chr> <chr>    <int> <int>    <dbl> <dbl> <dbl> <dbl>
## 1 MM      number egg    fourth_instar    4      4      2.10     3 0.126 0.126
## 2 LA1840  number egg    fourth_instar    4      4      7.00     3 0.006 0.006
## # ... with 1 more variable: p.adj.signif <chr>
```

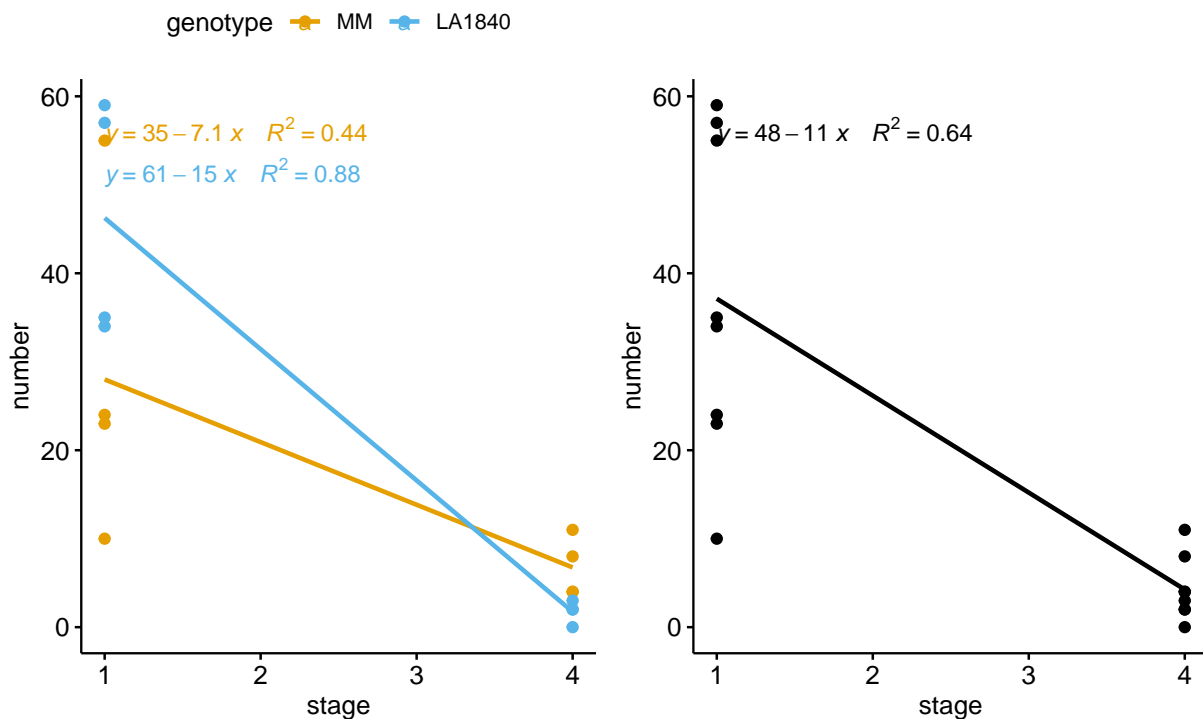
For MM not. On LA1840, there were significantly less 4th instars than eggs.

Are the number off eggs and 4th instars the same on MM and LA1840?

```
## # A tibble: 2 x 11
##   stage .y. group1 group2      n1      n2 statistic    df      p p.adj p.adj.signif
## * <chr> <chr> <chr> <chr>    <int> <int>    <dbl> <dbl> <dbl> <dbl> <chr>
## 1 egg  numb~ MM      LA1840    4      4     -1.37     3 0.263 0.263 ns
## 2 four~ numb~ MM      LA1840    4      4      3.40     3 0.043 0.043 *
```

The number of eggs are equal on MM and LA1840. The 4th instars are less on LA1840.

What does this look like? note: for 'stage' on the x-axis: 1 is eggs and 4 is 4th instars



Comparing the regression of the nymph development on the two genotypes:

First fit a model with interaction an interaction term for genotype:

```
##
## Call:
## lm(formula = number ~ stage + genotype + stage:genotype, data = mod)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.00  -4.25  -0.75   2.00  27.00
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      35.083      8.151   4.304  0.00102 **
## stage           -7.083      2.796  -2.534  0.02624 *
## genotypeLA1840    26.000     11.527   2.256  0.04356 *
## stage:genotypeLA1840 -7.750      3.954  -1.960  0.07361 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.86 on 12 degrees of freedom
## Multiple R-squared:  0.7491, Adjusted R-squared:  0.6863
## F-statistic: 11.94 on 3 and 12 DF,  p-value: 0.0006488
```

Now a model without the genotype effect

```
##
```

```
## Call:
## lm(formula = number ~ stage, data = mod)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -27.125  -3.406  -1.688   4.500  21.875
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   48.083     6.368   7.551 2.67e-06 ***
## stage        -10.958     2.184  -5.017 0.000188 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 13.11 on 14 degrees of freedom
## Multiple R-squared:  0.6426, Adjusted R-squared:  0.6171
## F-statistic: 25.17 on 1 and 14 DF,  p-value: 0.0001884
```

comparing the performance

model1:

```
## # A tibble: 1 x 5
##   adj.r.squared sigma    AIC    BIC p.value
##   <dbl> <dbl> <dbl> <dbl>   <dbl>
## 1      0.686  11.9  130.  134. 0.000649
```

model2:

```
## # A tibble: 1 x 5
##   adj.r.squared sigma    AIC    BIC p.value
##   <dbl> <dbl> <dbl> <dbl>   <dbl>
## 1      0.617  13.1  132.  134. 0.000188
```

The first model (with genotype interaction) has a better fit.

The nymph survival during the development from egg to 4th instar is higher on MM than on LA1840.

