IL bioassay

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Data import

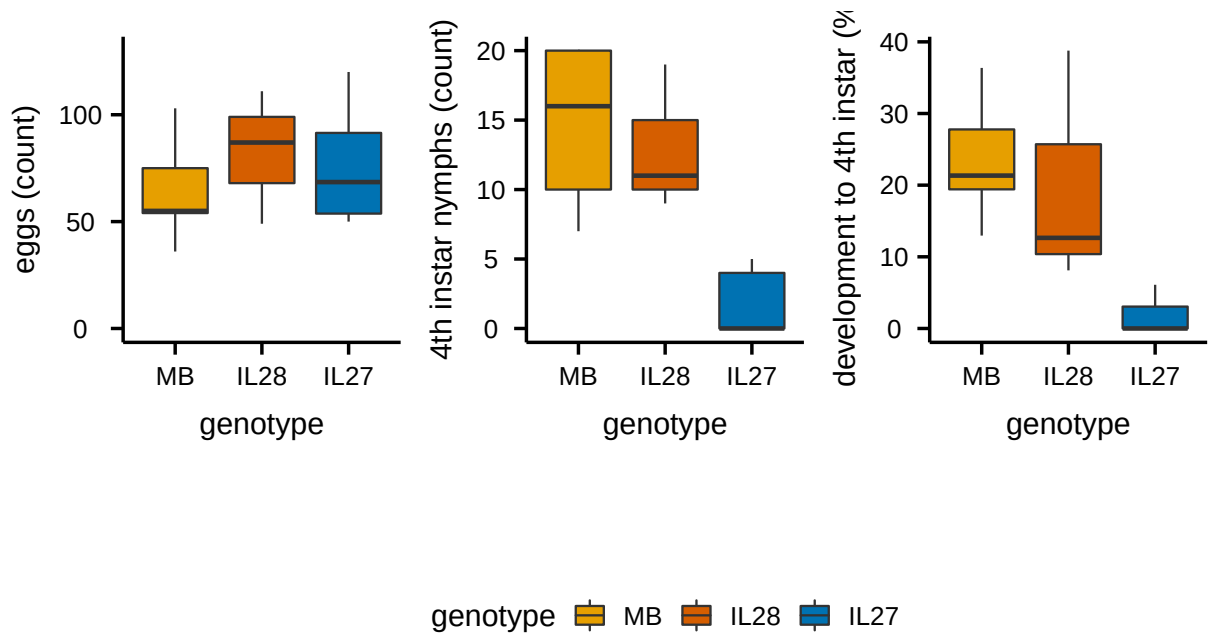
Background information

This is the the whitefly development bioassay on the ILs performed by Arjen van Doorn. Only the cultivated parent (MB) is included, not LA1840. IL29 will be excluded from the data, because it is not part of the metabolomics data.

The raw data

genotype	id	number	stage
IL27	1927-1	0	fourth_instar
IL27	1927-2	5	fourth_instar
IL27	1927-3	0	fourth_instar
IL27	1927-4	4	fourth_instar
IL27	1927-5	0	fourth_instar
IL28	1928-1	11	fourth_instar
IL28	1928-2	9	fourth_instar
IL28	1928-3	19	fourth_instar
MB	1955-1	16	fourth_instar
MB	1955-2	10	fourth_instar

plots



statistics

Are the number of 4th instars lower than the number of eggs per genotype?

```
## # A tibble: 3 x 11
##   genotype .y.    group1 group2          n1    n2 statistic    df      p p.adj
## * <fct>    <chr>  <chr>  <chr>        <int> <int>     <dbl> <dbl>  <dbl> <dbl>
## 1 MB       number egg    fourth_instar     5     5      5.03     4 0.007 0.007
## 2 IL28     number egg    fourth_instar     3     3      3.29     2 0.081 0.081
## 3 IL27     number egg    fourth_instar     5     5      5.33     4 0.006 0.006
## # ... with 1 more variable: p.adj.signif <chr>
```

For comparing the genotypes: dunnett's

```
## # A tibble: 2 x 7
##   stage         .y.        n statistic    df      p method
## * <fct>         <chr>  <int>     <dbl> <int>  <dbl> <chr>
## 1 egg           number    13      1.32     2 0.516  Kruskal-Wallis
## 2 fourth_instar number    13      8.77     2 0.0125 Kruskal-Wallis
```

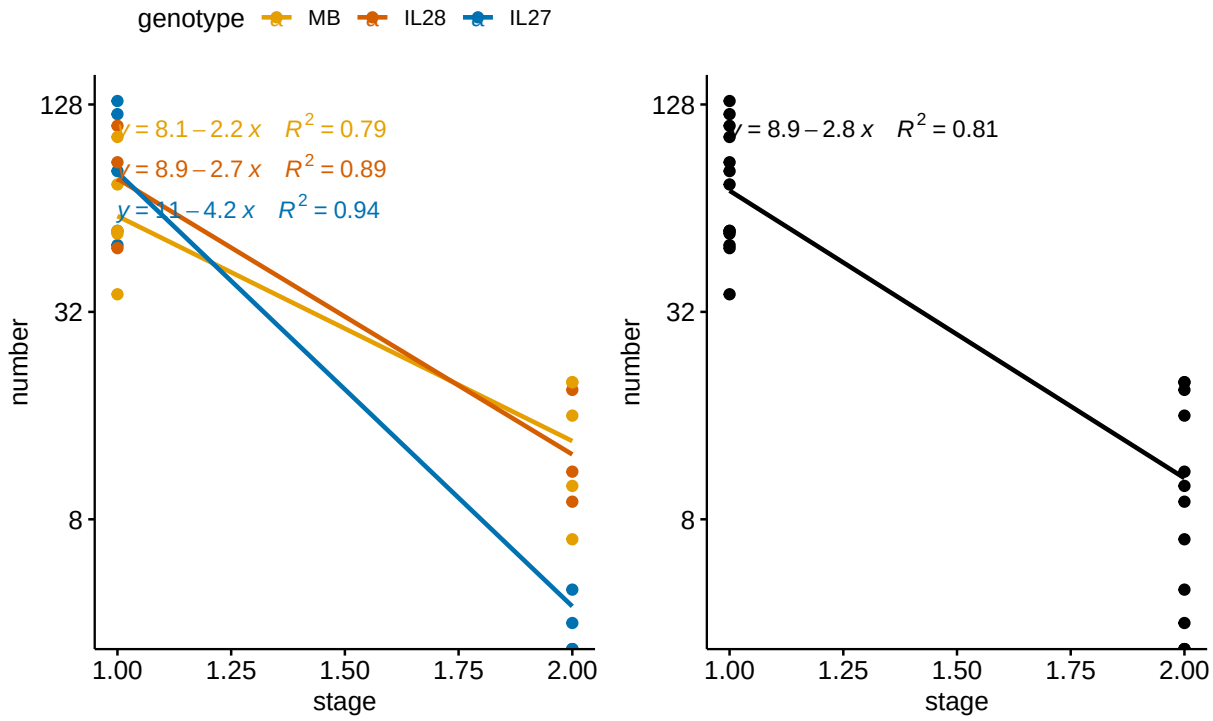
```
## # A tibble: 6 x 10
##   stage    .y.   group1 group2    n1    n2 statistic       p  p.adj p.adj.signif
## * <fct>    <chr> <chr>  <chr>  <int> <int>     <dbl>   <dbl>  <dbl> <chr>
```

```
## 1 egg       numb~ MB     IL28       5     3     0.645 0.519   1      ns
## 2 egg       numb~ MB     IL27       5     5     1.14  0.255   0.765  ns
## 3 egg       numb~ IL28   IL27       3     5     0.340 0.734   1      ns
## 4 fourth_~ numb~ MB     IL28       5     3    -0.283 0.777   0.777  ns
## 5 fourth_~ numb~ MB     IL27       5     5    -2.78  0.00544 0.0163 *
## 6 fourth_~ numb~ IL28   IL27       3     5    -2.12  0.0336  0.0673 ns
```

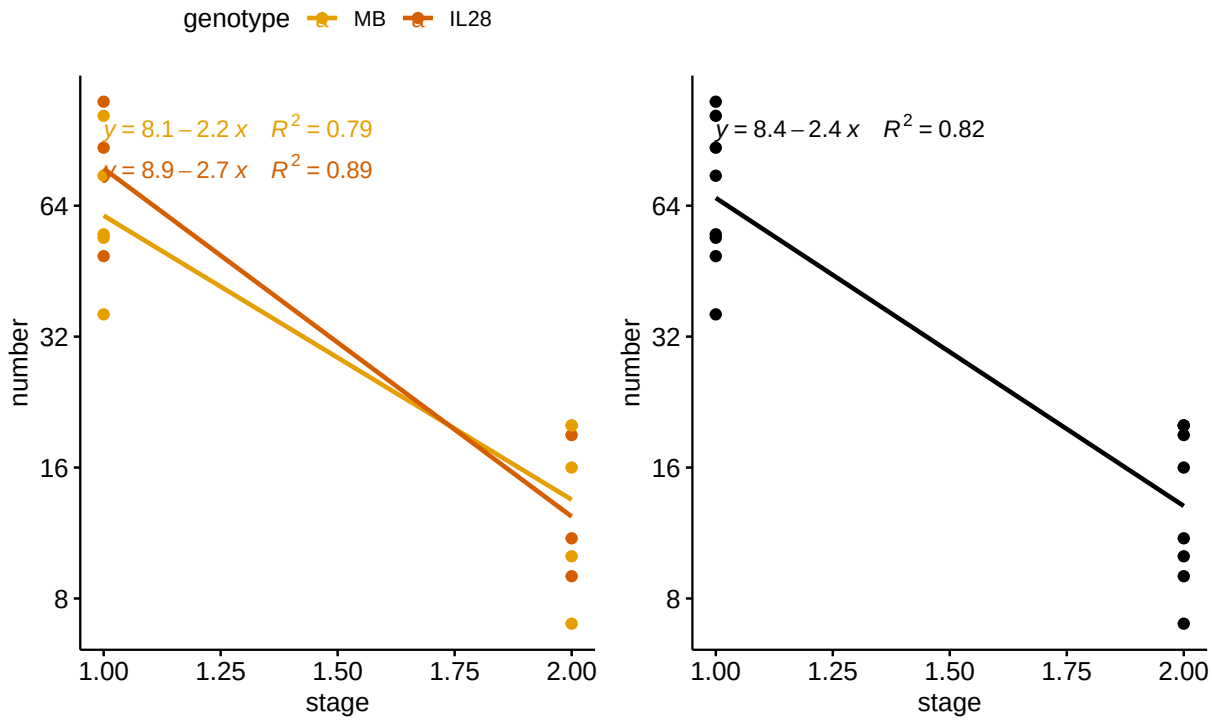
The number of eggs is simmilar for all genotypes. The number of fourth instars is lower on IL27 than on MB, but equal on IL28 and MB.

Linear model for comparison of regression

note: for 'stage' on the x-axis: 1 is eggs and 4 is 4th instars (the '4' became '2' in the graphs, I don't know why)



comparing MB and IL28



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

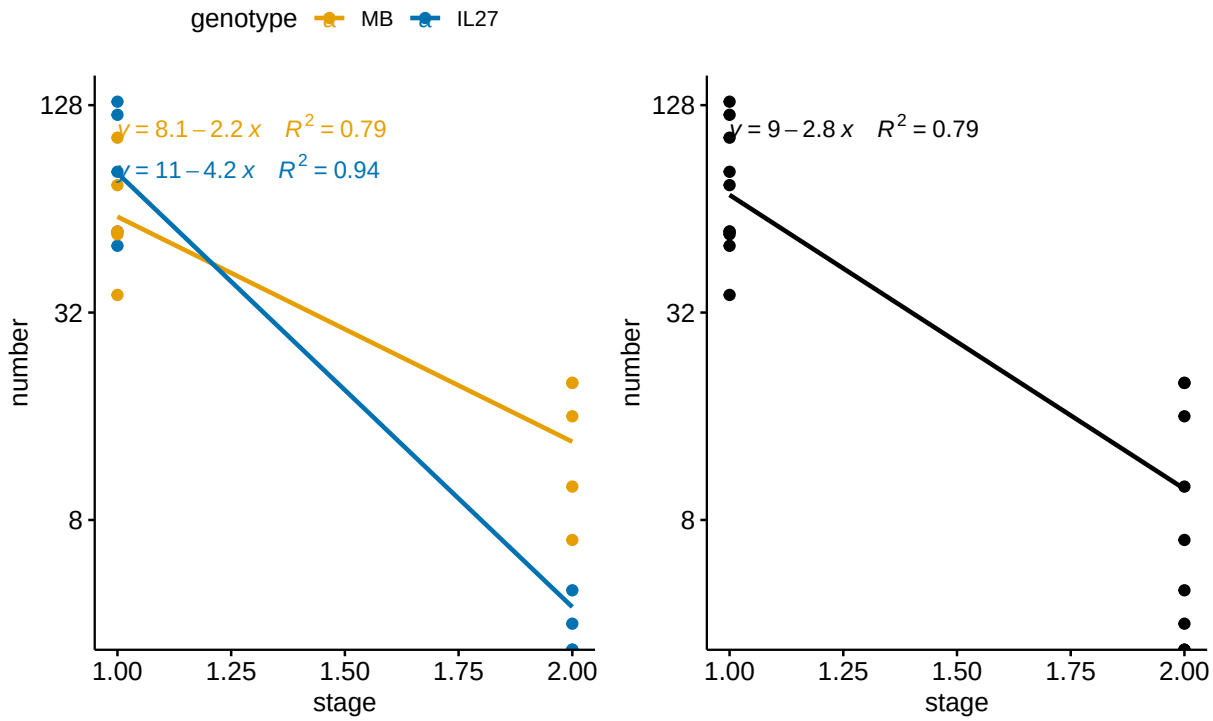
```
## # A tibble: 1 x 5
##   adj.r.squared sigma   AIC   BIC  p.value
##           <dbl> <dbl> <dbl> <dbl>    <dbl>
## 1         0.678  19.9  147.  150. 0.000756
```

Now a model without the genotype effect

```
## # A tibble: 1 x 5
##   adj.r.squared sigma   AIC   BIC   p.value
##           <dbl> <dbl> <dbl> <dbl>     <dbl>
## 1         0.690  19.5  144.  147. 0.0000416
```

The second model (without the genotype interaction) fits better. The survival/development from egg to 4th instar is simmilar for IL28 and MB.

comparing MB and IL27



Again, fit a model with interaction an interaction term for genotype:

```
## # A tibble: 1 x 5
##   adj.r.squared sigma   AIC   BIC   p.value
##           <dbl> <dbl> <dbl> <dbl>     <dbl>
## 1         0.705  22.7  187.  192. 0.0000433
```

And a model without the genotype effect

```
## # A tibble: 1 x 5
##   adj.r.squared sigma   AIC   BIC    p.value
##           <dbl> <dbl> <dbl> <dbl>      <dbl>
## 1         0.682  23.5  187.  190. 0.00000445
```

The first model (with genotype effect) fits better. The survival/development from egg to 4th instar is hampered on IL28 compared to MB.

note: I used a log2 y axis for the graphs, but not for the models I compared.

conclusion

IL27 has the nymph development phenotype of LA1840. IL28 has the MM/MB phenotype.