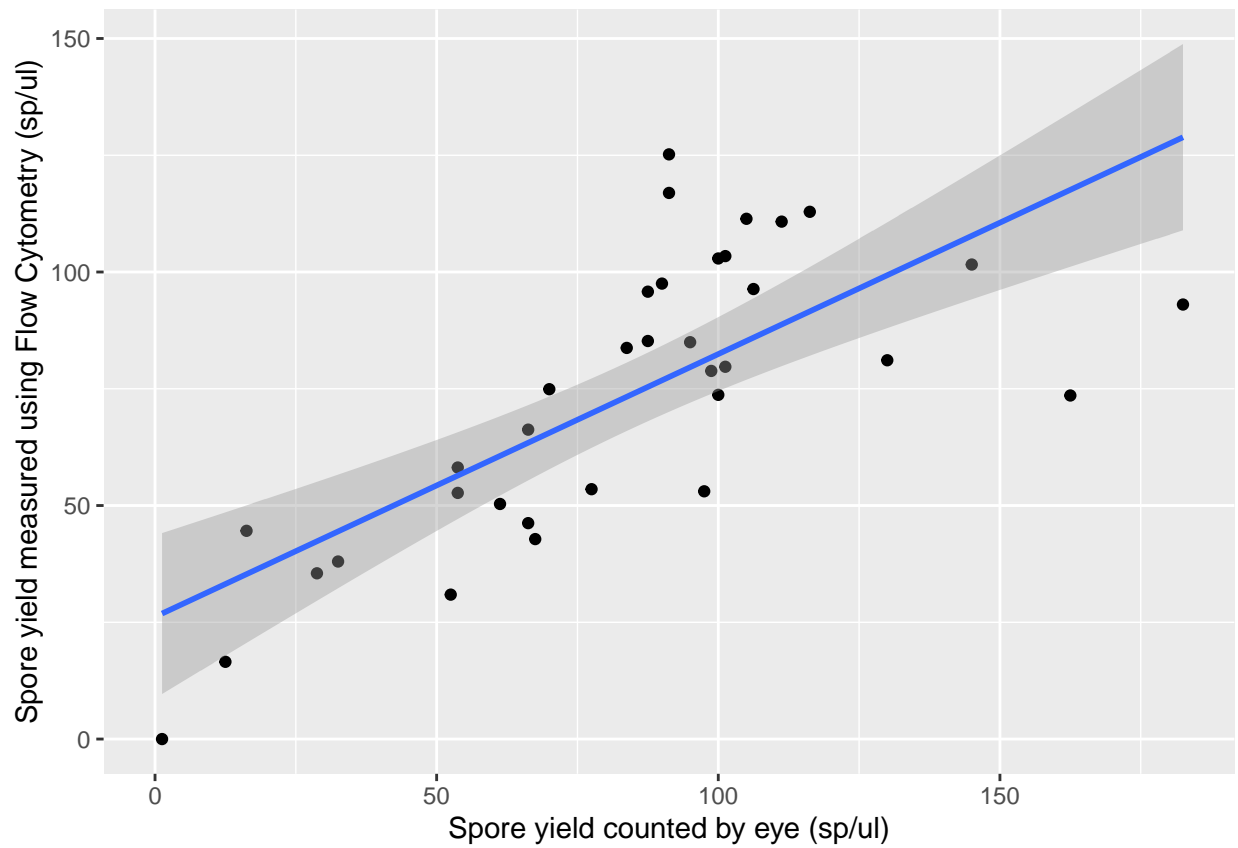


# Appendix

APB

7/23/2022

Comparison of spore counts using flow cytometry to traditional counts using a hemocytometer in 'Standard' genotype

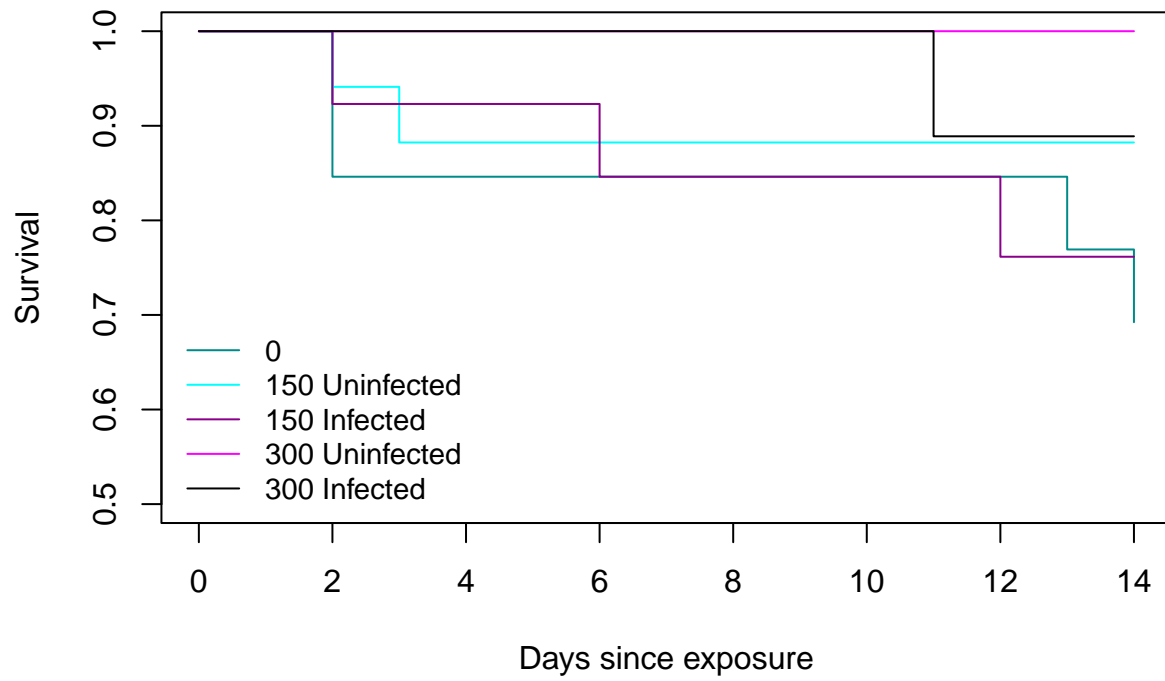


```
fit<-lm(sp.ul ~ flow_sp_ul - 1, data = sporecheck)
# R squared
summary(fit)$r.squared
```

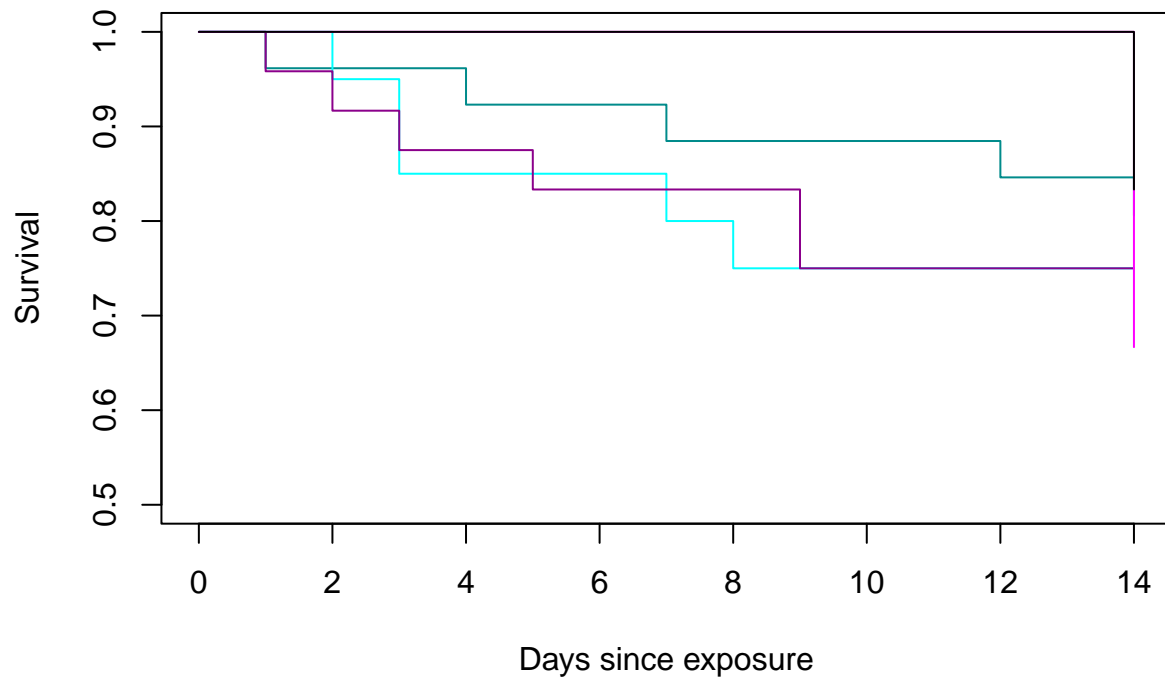
```
## [1] 0.9130979
```

## Survival Analyses

**A45**

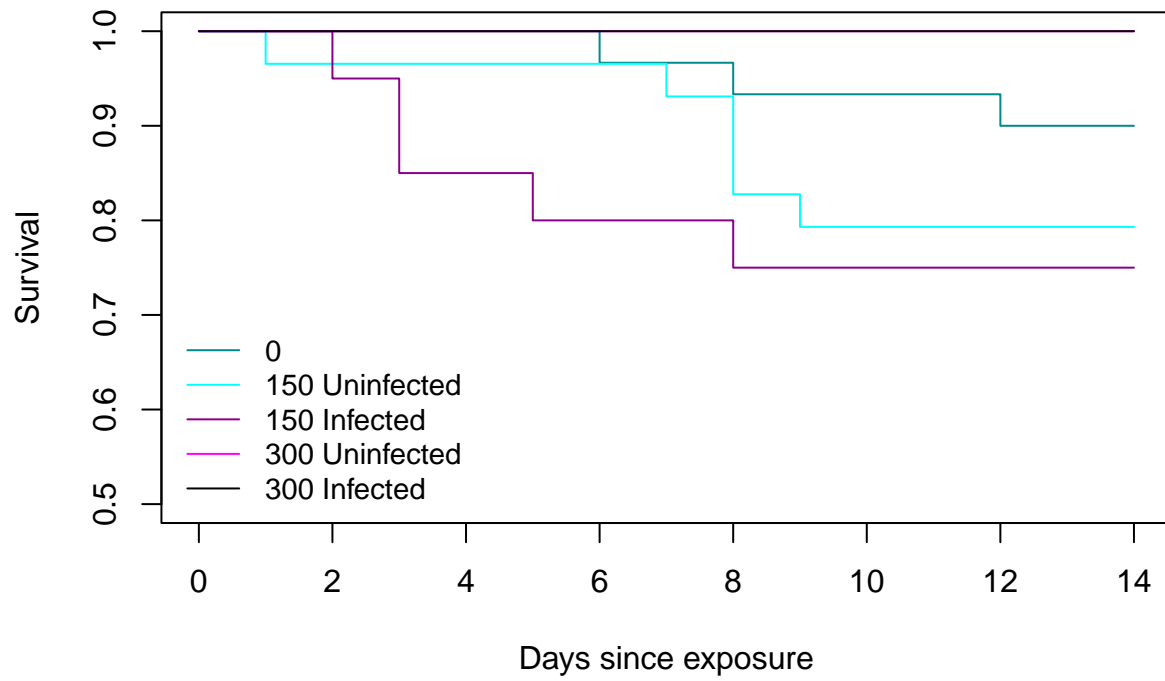


**M252**

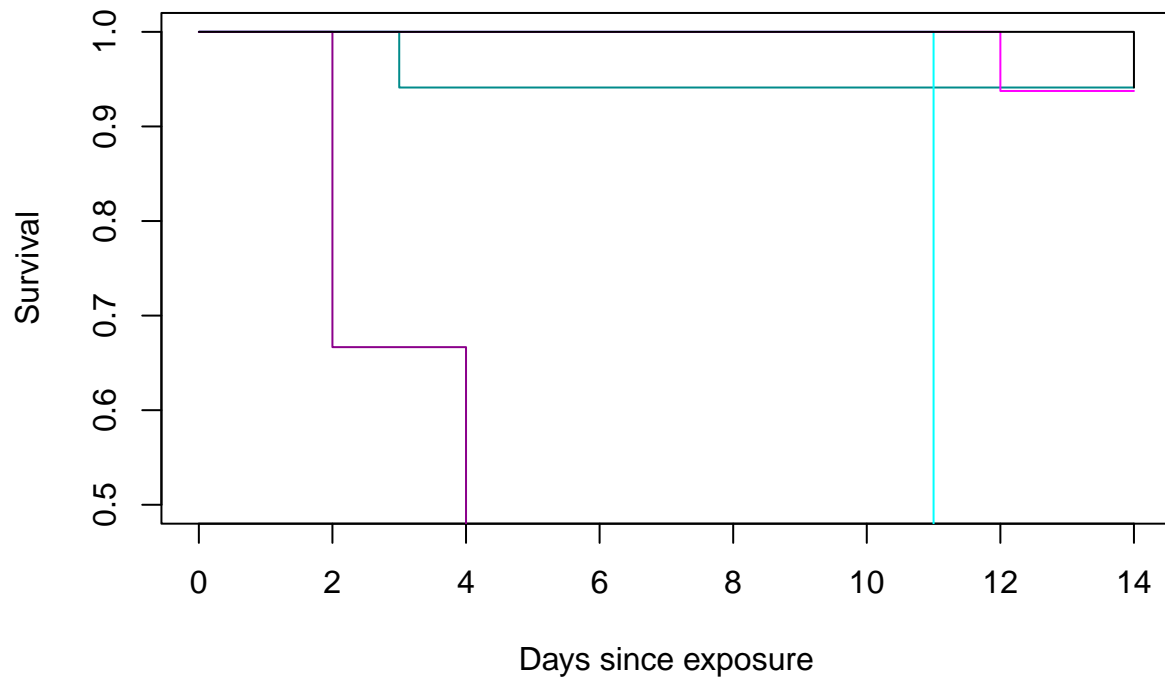


## Survival Analyses Continued

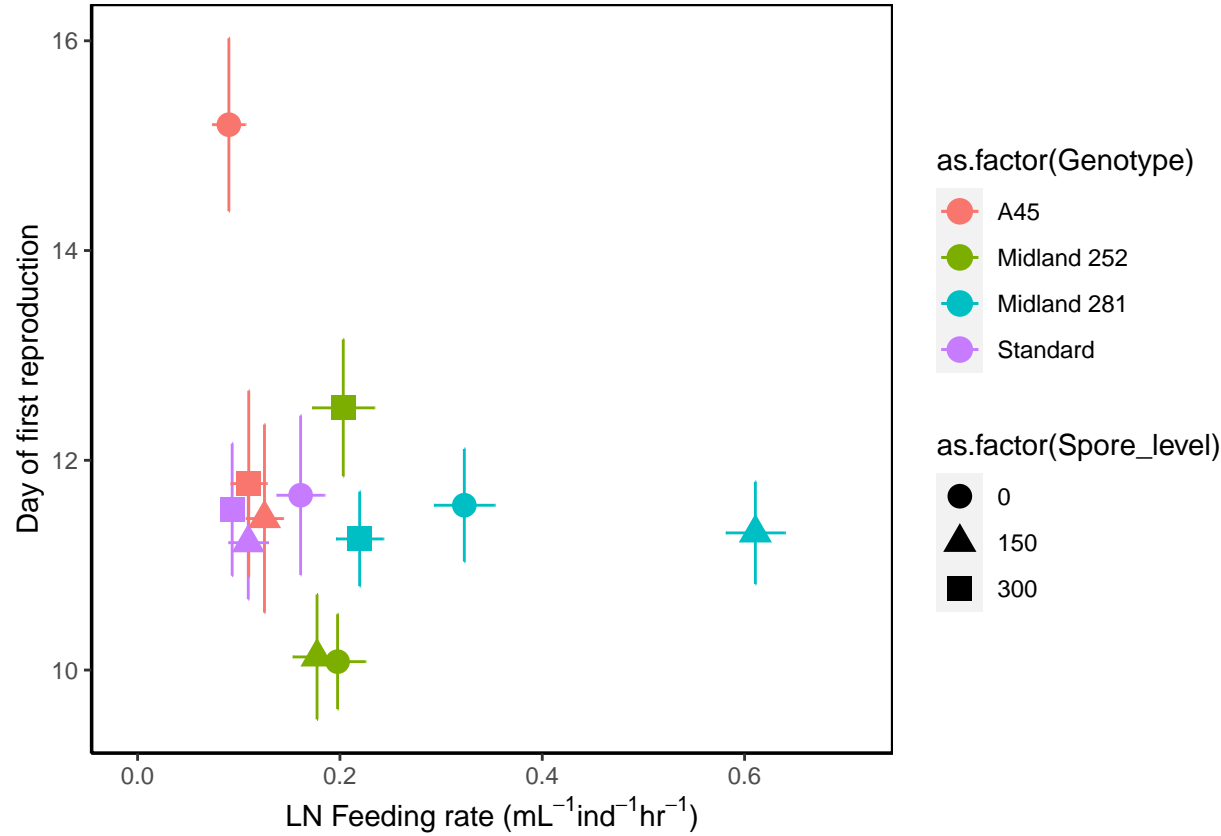
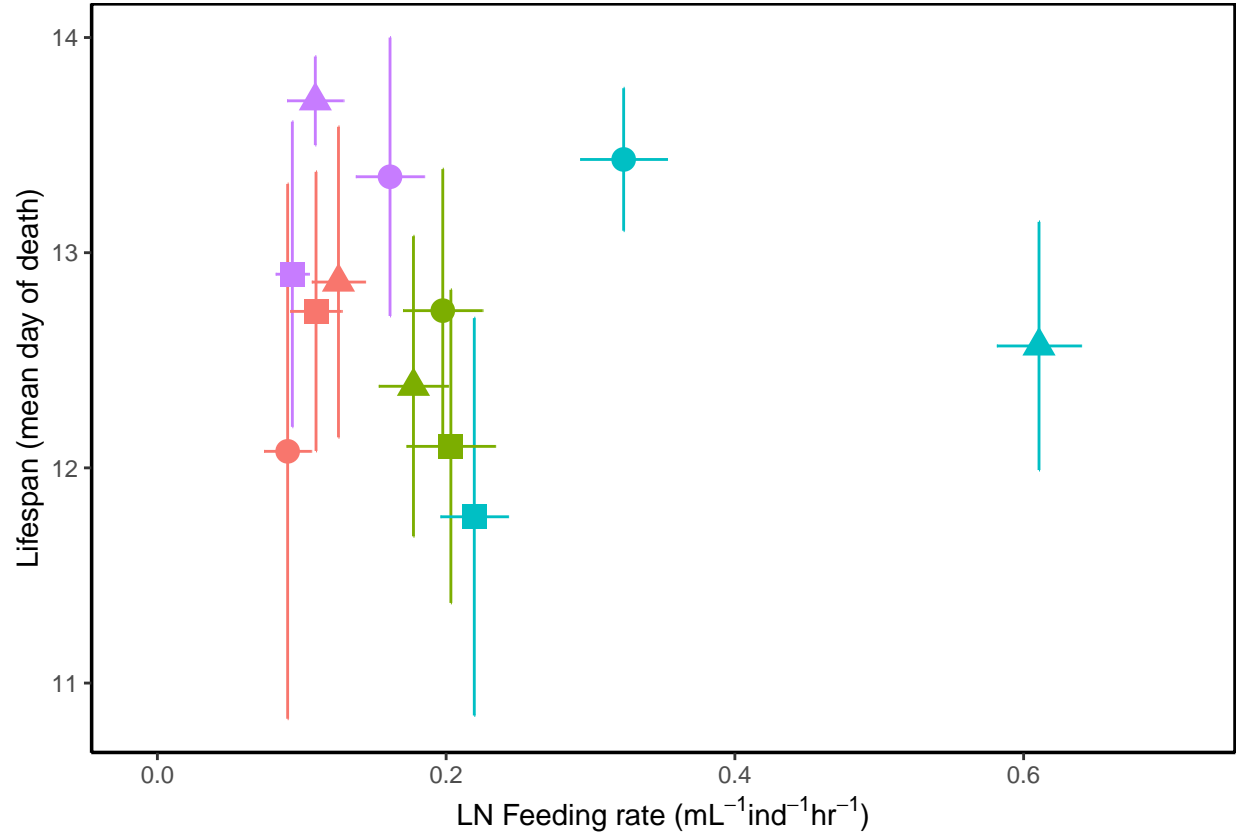
### M281



### STD



Impacts of Feeding Behavior



## Table 2

```
##
## Call:
## glm(formula = mean_feeding_rate ~ Genotype * Size_mm2 + Infected_Uninfected +
##       Spore_level, family = gaussian(link = "log"), data = total)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.28232  -0.07199  -0.00455   0.07947   0.63002
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -3.6790349   1.3734430  -2.679  0.00786 **
## GenotypeMidland 252   0.4129904   1.4218075   0.290  0.77169
## GenotypeMidland 281   1.7544277   1.3921475   1.260  0.20870
## GenotypeStandard     0.8783600   1.8305967   0.480  0.63175
## Size_mm2           0.8337302   0.8508144   0.980  0.32803
## Infected_UninfectedExposed 1.1843364  0.1265402   9.359 < 2e-16 ***
## Infected_UninfectedInfected 0.9761503  0.1852444   5.270 2.85e-07 ***
## Spore_level        -0.0046333  0.0006209  -7.462 1.25e-12 ***
## GenotypeMidland 252:Size_mm2 0.1153302  0.8790541   0.131  0.89572
## GenotypeMidland 281:Size_mm2 -0.2638278  0.8628215  -0.306  0.76002
## GenotypeStandard:Size_mm2 -0.4227152  1.1498522  -0.368  0.71345
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.01640027)
##
##      Null deviance: 10.296  on 273  degrees of freedom
## Residual deviance:  4.313  on 263  degrees of freedom
## (7 observations deleted due to missingness)
## AIC: -335.93
##
## Number of Fisher Scoring iterations: 9

## Analysis of Deviance Table (Type III tests)
##
## Response: mean_feeding_rate
##              LR Chisq Df Pr(>Chisq)
## Genotype           9.269  3  0.02592 *
## Size_mm2           0.789  1  0.37434
## Infected_Uninfected 91.087  2 < 2e-16 ***
## Spore_level        77.146  1 < 2e-16 ***
## Genotype:Size_mm2   1.833  3  0.60772
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type II tests)
##
## Response: mean_feeding_rate
##              LR Chisq Df Pr(>Chisq)
## Genotype      218.487  3 < 2.2e-16 ***
```



```
## contrast      estimate      SE  df t.ratio p.value
## Control - Exposed    -1.178 0.126 266  -9.345 <.0001
## Control - Infected   -0.965 0.185 266  -5.229 <.0001
## Exposed - Infected    0.212 0.140 266   1.512 0.2867
##
## Genotype = Midland 252:
## contrast      estimate      SE  df t.ratio p.value
## Control - Exposed    -1.178 0.126 266  -9.345 <.0001
## Control - Infected   -0.965 0.185 266  -5.229 <.0001
## Exposed - Infected    0.212 0.140 266   1.512 0.2867
##
## Genotype = Midland 281:
## contrast      estimate      SE  df t.ratio p.value
## Control - Exposed    -1.178 0.126 266  -9.345 <.0001
## Control - Infected   -0.965 0.185 266  -5.229 <.0001
## Exposed - Infected    0.212 0.140 266   1.512 0.2867
##
## Genotype = Standard:
## contrast      estimate      SE  df t.ratio p.value
## Control - Exposed    -1.178 0.126 266  -9.345 <.0001
## Control - Infected   -0.965 0.185 266  -5.229 <.0001
## Exposed - Infected    0.212 0.140 266   1.512 0.2867
##
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 3 estimates
```

## with size correction

```
## Analysis of Deviance Table (Type III tests)
##
## Response: meanfeedrate
##          LR Chisq Df Pr(>Chisq)
## probinf      3.527  1  0.06038 .
## finalsize     2.749  1  0.09729 .
## Spore_level    0.964  1  0.32623
## Genotype    105.966  3  < 2e-16 ***
## probinf:finalsize  3.566  1  0.05898 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Deviance Table (Type III tests)
##
## Response: meanfeedrate
##          LR Chisq Df Pr(>Chisq)
## probinf      3.230  1  0.07232 .
## finalsize     2.748  1  0.09737 .
## Genotype    105.663  3  < 2e-16 ***
## probinf:finalsize  3.466  1  0.06263 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Deviance Table (Type III tests)
```

```

##
## Response: meanfeedrate
##           LR Chisq Df Pr(>Chisq)
## probinf      3.527  1  0.06038 .
## finalsize     2.749  1  0.09729 .
## Spore_level    0.964  1  0.32623
## Genotype    105.966  3  < 2e-16 ***
## probinf:finalsize  3.566  1  0.05898 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type III tests)
##
## Response: meanfeedrate
##           LR Chisq Df Pr(>Chisq)
## probinf      3.081  1  0.07920 .
## finalsize     1.369  1  0.24192
## Genotype    105.706  3  < 2e-16 ***
## probinf:finalsize  3.384  1  0.06583 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##           dAICc df
## modfeedinfb 0.0  8
## modfeedinfd 0.4  8
## modfeedinf  1.2  9
## modfeedinfc 1.2  9

##
## Call:
## glm(formula = meanfeedrate ~ probinf * finalsize + Genotype,
##      family = gaussian(link = "identity"), data = inf1)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.39125 -0.08163 -0.01700  0.07431  0.53012
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.17391    0.17409  -0.999  0.31894
## probinf         0.37294    0.20752   1.797  0.07373 .
## finalsize      0.10804    0.06518   1.658  0.09884 .
## GenotypeMidland 252  0.11927    0.03774   3.160  0.00181 **
## GenotypeMidland 281  0.30358    0.03335   9.102 < 2e-16 ***
## GenotypeStandard  0.03748    0.03485   1.075  0.28337
## probinf:finalsize -0.15923    0.08552  -1.862  0.06401 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.02436518)
##
##      Null deviance: 8.3950  on 220  degrees of freedom
## Residual deviance: 5.2141  on 214  degrees of freedom

```



```

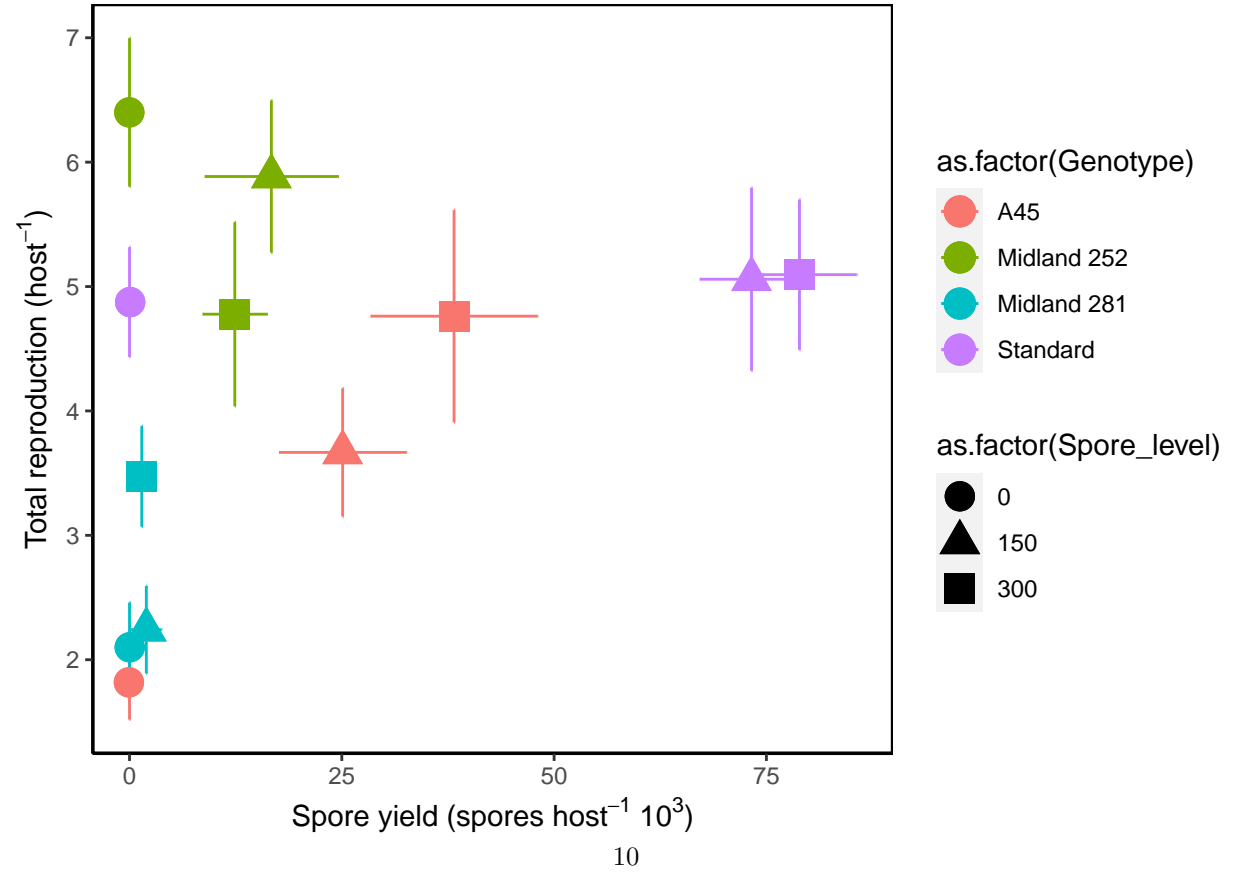
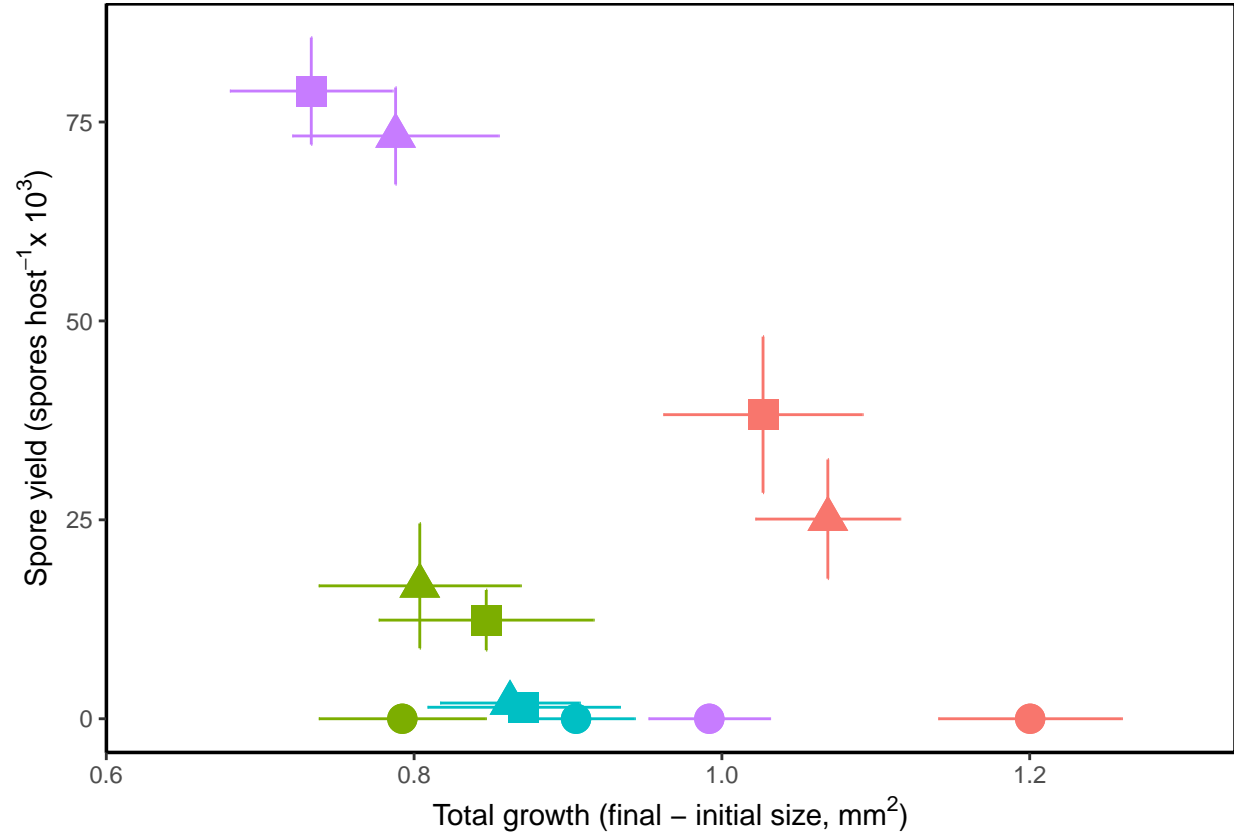
## (60 observations deleted due to missingness)
## AIC: -184.87
##
## Number of Fisher Scoring iterations: 2

## Analysis of Deviance Table (Type III tests)
##
## Response: meanfeedrate
##              LR Chisq Df Pr(>Chisq)
## probinf          3.230  1  0.07232 .
## finalsize        2.748  1  0.09737 .
## Genotype       105.663  3  < 2e-16 ***
## probinf:finalsize  3.466  1  0.06263 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Term	LR Chisq	Df	Pr(>Chisq)
probinf	3.229664	1	0.07231552365034664420218035730
finalsize	2.748078	1	0.09737143128251564416775210020
Genotype	105.662556	3	0.000000000000000000009410693
probinf:finalsize	3.466209	1	0.06263468621257345381181380617

Impacts of Infection



## Table 5a

```
##          dAICc df
## mod3m 0      3
## mod2m 1      5

##
## Call:
## glm(formula = y ~ mean_feeding_rate + Size_mm2, family = binomial,
##      data = infected)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0168  -0.7848  -0.5477   0.4820   1.8138
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -1.4615     0.8171  -1.789  0.07368 .
## mean_feeding_rate -3.2139     1.0594  -3.034  0.00242 **
## Size_mm2         0.6494     0.5396   1.204  0.22877
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 108.639  on 188  degrees of freedom
## Residual deviance:  95.683  on 186  degrees of freedom
##      (6 observations deleted due to missingness)
## AIC: 193.18
##
## Number of Fisher Scoring iterations: 5

## Analysis of Deviance Table (Type III tests)
##
## Response: y
##              LR Chisq Df Pr(>Chisq)
## mean_feeding_rate  12.272  1  0.0004597 ***
## Size_mm2           1.494  1  0.2215954
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Term	LR Chisq	Df	Pr(>Chisq)
mean_feeding_rate	12.27225	1	0.000459744
Size_mm2	1.49401	1	0.221595370

## Table 5b (accounting for genetic variation)

```
## Analysis of Deviance Table (Type II tests)
##
```

```

## Response: y
##               Df    Chisq Pr(>Chisq)
## mean_feeding_rate      1  0.0219  0.8823744
## Size_mm2                1  0.3861  0.5343357
## as.factor(Genotype)     3 16.7564  0.0007931 ***
## as.factor(Spore_level)  1  0.1030  0.7482329
## mean_feeding_rate:Size_mm2 1  3.6375  0.0564906 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type II tests)
##
## Response: y
##               Df    Chisq Pr(>Chisq)
## mean_feeding_rate      1  0.1860  0.6662878
## Size_mm2                1  0.5353  0.4643890
## as.factor(Genotype)     3 16.6723  0.0008253 ***
## as.factor(Spore_level)  1  0.0310  0.8602011
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##          dAICc df
## mod2h 0.0    8
## mod2i 1.4    7

## Analysis of Deviance Table (Type III tests)
##
## Response: y
##               LR Chisq Df Pr(>Chisq)
## mean_feeding_rate      3.1284  1  0.0769370 .
## Size_mm2                3.6215  1  0.0570377 .
## as.factor(Genotype)    19.3611  3  0.0002302 ***
## as.factor(Spore_level)  0.1031  1  0.7481421
## mean_feeding_rate:Size_mm2 3.5805  1  0.0584600 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type III tests)
##
## Response: y
##               LR Chisq Df Pr(>Chisq)
## mean_feeding_rate      3.1284  1  0.0769370 .
## Size_mm2                3.6215  1  0.0570377 .
## as.factor(Genotype)    19.3611  3  0.0002302 ***
## as.factor(Spore_level)  0.1031  1  0.7481421
## mean_feeding_rate:Size_mm2 3.5805  1  0.0584600 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Term	LR Chisq	Df	Pr(>Chisq)
mean_feeding_rate	3.1284463	1	0.0769370344
Size_mm2	3.6214925	1	0.0570376833
as.factor(Genotype)	19.3610810	3	0.0002302002
as.factor(Spore_level)	0.1030989	1	0.7481420645
mean_feeding_rate:Size_mm2	3.5805454	1	0.0584599561

**Table 5a Spore yield**

```
##
## Call:
## glm(formula = Spores_ul ~ mean_feeding_rate + as.factor(Spore_level),
##      data = total)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -39.925  -24.637   -3.703   11.404   138.041
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      10.216      4.128   2.475   0.014 *
## mean_feeding_rate    -46.881     10.760  -4.357 1.95e-05 ***
## as.factor(Spore_level)150    27.941      4.932   5.665 4.20e-08 ***
## as.factor(Spore_level)300    30.621      4.991   6.135 3.49e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 992.8513)
##
##      Null deviance: 307338  on 243  degrees of freedom
## Residual deviance: 238284  on 240  degrees of freedom
## (37 observations deleted due to missingness)
## AIC: 2382.2
##
## Number of Fisher Scoring iterations: 2

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##              LR Chisq Df Pr(>Chisq)
## mean_feeding_rate    18.984  1 1.318e-05 ***
## as.factor(Spore_level) 48.256  2 3.321e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Call:
##      aov(formula = mod2k)
##
```

```

## Terms:
##               mean_feeding_rate as.factor(Spore_level) Residuals
## Sum of Squares      21142.83      47911.20 238284.30
## Deg. of Freedom      1          2      240
##
## Residual standard error: 31.50954
## Estimated effects may be unbalanced
## 37 observations deleted due to missingness

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##               LR Chisq Df Pr(>Chisq)
## mean_feeding_rate      0.22312 1    0.6367
## Size_mm2                2.19853 1    0.1381
## Spore_level_fct         0.06526 1    0.7984
## mean_feeding_rate:Size_mm2 0.65240 1    0.4193

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##               LR Chisq Df Pr(>Chisq)
## mean_feeding_rate      0.79702 1    0.3720
## Size_mm2                0.08375 1    0.7723
## Spore_level_fct         1.05072 1    0.3053
## Final_Size_mm2          0.55722 1    0.4554
## Spore_level_fct:Final_Size_mm2 1.28394 1    0.2572

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##               LR Chisq Df Pr(>Chisq)
## Spore_level_fct      0.4621 1    0.4967
## Final_Size_mm2       5.2617 1    0.0218 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##               df      AIC
## modfeedspores1  6 644.8335
## modfeedspores2  7 610.9386
## modfeedspores3  6 610.3441
## modfeedspores4  4 607.3463

```

## Table 5b Spore yield

```

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##               LR Chisq Df Pr(>Chisq)
## mean_feeding_rate      1.4557 1    0.22762
## Size_mm2                0.0266 1    0.87046
## Spore_level_fct         1.0240 1    0.31158

```

```

## Final_Size_mm2          6.6193  1    0.01009 *
## Genotype                6.7155  3    0.08154 .
## mean_feeding_rate:Size_mm2  1.4536  1    0.22796
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##          LR Chisq Df Pr(>Chisq)
## mean_feeding_rate  0.0253  1    0.87353
## Size_mm2          0.8198  1    0.36524
## Spore_level_fct    0.7896  1    0.37421
## Final_Size_mm2     6.2452  1    0.01245 *
## Genotype          5.6513  3    0.12986
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##          LR Chisq Df Pr(>Chisq)
## mean_feeding_rate  0.2142  1    0.6435
## Size_mm2          0.6809  1    0.4093
## Spore_level_fct    0.0722  1    0.7881
## Genotype          3.2987  3    0.3478

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##          LR Chisq Df Pr(>Chisq)
## mean_feeding_rate   1.214  1    0.2705
## Spore_level_fct     52.335  2  4.320e-12 ***
## Genotype           74.429  3  4.804e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##          LR Chisq Df Pr(>Chisq)
## Spore_level_fct     51.567  2  6.343e-12 ***
## Genotype           97.760  3 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Call:
## glm(formula = Spores_ul ~ mean_feeding_rate + Size_mm2 + Spore_level_fct +
##      Final_Size_mm2 + Genotype, family = gaussian(link = "identity"),
##      data = totalpos)
##
## Deviance Residuals:

```

```

##      Min      1Q   Median      3Q      Max
## -52.833 -23.933  -0.319   20.326   95.758
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -12.719     37.399  -0.340   0.7351
## mean_feeding_rate      5.891     37.012   0.159   0.8741
## Size_mm2       -16.291     17.993  -0.905   0.3693
## Spore_level_fct300      7.395      8.322   0.889   0.3782
## Final_Size_mm2     40.740     16.302   2.499   0.0155 *
## GenotypeMidland 252      5.831     14.571   0.400   0.6906
## GenotypeMidland 281    -27.677     26.048  -1.063   0.2927
## GenotypeStandard      18.712     10.329   1.811   0.0756 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 945.2518)
##
##      Null deviance: 62483  on 61  degrees of freedom
## Residual deviance: 51044  on 54  degrees of freedom
## (3 observations deleted due to missingness)
## AIC: 610.17
##
## Number of Fisher Scoring iterations: 2

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##              LR Chisq Df Pr(>Chisq)
## mean_feeding_rate  0.0253  1  0.87353
## Size_mm2           0.8198  1  0.36524
## Spore_level_fct    0.7896  1  0.37421
## Final_Size_mm2     6.2452  1  0.01245 *
## Genotype           5.6513  3  0.12986
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Term	LR Chisq	Df	Pr(>Chisq)
mean_feeding_rate	0.02533612	1	0.87353240
Size_mm2	0.81979692	1	0.36523955
Spore_level_fct	0.78963588	1	0.37421025
Final_Size_mm2	6.24521611	1	0.01245292
Genotype	5.65134086	3	0.12986181

```

## Spore_level_fct = 150:
## contrast      estimate    SE df t.ratio p.value
## A45 - Midland 252      -5.83 14.6 54  -0.400  0.9781
## A45 - Midland 281      27.68 26.0 54   1.063  0.7135
## A45 - Standard     -18.71 10.3 54  -1.811  0.2792

```



```

## Midland 252 - Midland 281    33.51 25.2 54    1.327 0.5500
## Midland 252 - Standard      -12.88 12.6 54   -1.024 0.7363
## Midland 281 - Standard      -46.39 25.8 54   -1.801 0.2840
##
## Spore_level_fct = 300:
## contrast          estimate    SE df t.ratio p.value
## A45 - Midland 252         -5.83 14.6 54   -0.400 0.9781
## A45 - Midland 281         27.68 26.0 54    1.063 0.7135
## A45 - Standard          -18.71 10.3 54   -1.811 0.2792
## Midland 252 - Midland 281    33.51 25.2 54    1.327 0.5500
## Midland 252 - Standard      -12.88 12.6 54   -1.024 0.7363
## Midland 281 - Standard      -46.39 25.8 54   -1.801 0.2840
##
## P value adjustment: tukey method for comparing a family of 4 estimates

```