

“Big 5” aphid genotype experiment

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Data

Due to very low infection rate (effectively zero) BLRV can be removed from this study below if necessary

```
bf <- read.csv("../Data/big five.csv")
str(bf)
```

```
## 'data.frame':    527 obs. of  15 variables:
## $ Run           : chr  "One" "One" "One" "One" ...
## $ ID..          : chr  "AB1" "AB1" "A1" "A1" ...
## $ count.of.plants : int  5 6 2 3 13 14 9 11 21 22 ...
## $ Plant         : chr  "Alfalfa" "Alfalfa" "Alfalfa" "Alfalfa" ...
## $ Genotype      : int  1 1 1 1 2 2 2 2 3 3 ...
## $ Biotype       : chr  "pea" "pea" "pea" "pea" ...
## $ virus         : chr  "BLRV" "BLRV" "Sham" "Sham" ...
## $ Counts        : int  113 134 106 40 3 147 0 4 95 229 ...
## $ absorbance    : num  1.173 0.918 0.433 0.588 0.761 ...
## $ log.Counts    : num  4.74 4.91 4.67 3.71 1.39 ...
## $ sqrt_rel_increase: num  3.21 3.52 3.1 1.73 NA ...
## $ Infection.status : chr  "YES" "YES" "NO" "NO" ...
## $ relative.increase: num  10.3 12.4 9.6 3 -0.7 13.7 -1 -0.6 8.5 21.9 ...
## $ Retain.       : chr  "Keep" "Keep" "Keep" "Keep" ...
## $ Bean.Aphids   : int  NA NA NA NA NA NA NA NA NA NA ...
```

```
bf$Genotype <- as.factor(bf$Genotype)
```

```
# BLRV is now included, but can be suppressed here with this line
# bf <- subset(bf, virus != "BLRV")
```

Remaining code and plots

Figure 1

```
##
## Call:
## glm.nb(formula = Counts ~ Biotype * Plant * virus + Run, data = bf,
##       init.theta = 0.5258337382, link = log)
##
## Deviance Residuals:
```

```

##      Min      1Q   Median      3Q      Max
## -2.6199 -1.0464 -0.3972  0.2470  2.5600
##
## Coefficients: (2 not defined because of singularities)
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      5.79498    0.40758  14.218 < 2e-16 ***
## Biotypepea      -1.91181    0.50985  -3.750 0.000177 ***
## PlantFaba       -0.86007    0.56374  -1.526 0.127098
## PlantHairy Vetch -3.13878    0.56835  -5.523 3.34e-08 ***
## PlantLentil     -1.16193    0.56393  -2.060 0.039359 *
## PlantPea        -1.03575    0.56385  -1.837 0.066220 .
## PlantRed Clover -1.84701    0.56463  -3.271 0.001071 **
## virusPEMV        0.50102    0.56527   0.886 0.375433
## virusSham       -1.05951    0.56386  -1.879 0.060242 .
## RunThree        -0.36034    0.14671  -2.456 0.014042 *
## RunTwo          0.58260    0.14991   3.886 0.000102 ***
## Biotypepea:PlantFaba 2.47297    0.72064   3.432 0.000600 ***
## Biotypepea:PlantHairy Vetch 4.07072    0.72439   5.620 1.91e-08 ***
## Biotypepea:PlantLentil 2.24334    0.72089   3.112 0.001859 **
## Biotypepea:PlantPea 2.45191    0.72075   3.402 0.000669 ***
## Biotypepea:PlantRed Clover 2.84315    0.72146   3.941 8.12e-05 ***
## Biotypepea:virusPEMV -1.18742    0.72176  -1.645 0.099932 .
## Biotypepea:virusSham -0.01189    0.72280  -0.016 0.986875
## PlantFaba:virusPEMV 0.09189    0.79838   0.115 0.908367
## PlantHairy Vetch:virusPEMV 2.63862    0.80159   3.292 0.000996 ***
## PlantLentil:virusPEMV 0.54036    0.79849   0.677 0.498574
## PlantPea:virusPEMV -0.08419    0.79854  -0.105 0.916035
## PlantRed Clover:virusPEMV NA         NA         NA         NA
## PlantFaba:virusSham 1.75899    0.79736   2.206 0.027384 *
## PlantHairy Vetch:virusSham 3.70338    0.80070   4.625 3.74e-06 ***
## PlantLentil:virusSham 1.48938    0.79764   1.867 0.061869 .
## PlantPea:virusSham 0.69535    0.79789   0.871 0.383491
## PlantRed Clover:virusSham 1.47348    0.79847   1.845 0.064983 .
## Biotypepea:PlantFaba:virusPEMV 0.36175    1.01956   0.355 0.722732
## Biotypepea:PlantHairy Vetch:virusPEMV -0.57183    1.02210  -0.559 0.575845
## Biotypepea:PlantLentil:virusPEMV 1.21029    1.01964   1.187 0.235236
## Biotypepea:PlantPea:virusPEMV 1.20000    1.01965   1.177 0.239246
## Biotypepea:PlantRed Clover:virusPEMV NA         NA         NA         NA
## Biotypepea:PlantFaba:virusSham -0.93321    1.02028  -0.915 0.360369
## Biotypepea:PlantHairy Vetch:virusSham -1.51534    1.02293  -1.481 0.138508
## Biotypepea:PlantLentil:virusSham -0.18686    1.02058  -0.183 0.854729
## Biotypepea:PlantPea:virusSham 0.77330    1.02067   0.758 0.448664
## Biotypepea:PlantRed Clover:virusSham -1.47968    1.02169  -1.448 0.147541
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.5258) family taken to be 1)
##
##      Null deviance: 823.47  on 526  degrees of freedom
## Residual deviance: 644.82  on 491  degrees of freedom
## AIC: 6288
##
## Number of Fisher Scoring iterations: 1
##

```

```

##
##          Theta: 0.5258
##        Std. Err.: 0.0304
##
## 2 x log-likelihood: -6214.0350

## Analysis of Deviance Table (Type II tests)
##
## Response: Counts
##          LR Chisq Df Pr(>Chisq)
## Biotype          0.533 1 0.465493
## Plant          33.301 5 3.279e-06 ***
## virus           9.308 2 0.009523 **
## Run            34.098 2 3.943e-08 ***
## Biotype:Plant    44.727 5 1.649e-08 ***
## Biotype:virus     4.983 2 0.082776 .
## Plant:virus      39.445 9 9.573e-06 ***
## Biotype:Plant:virus 9.336 9 0.406835
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Plant = Alfalfa, virus = BLRV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf          353.9 141.01 Inf    162.10    772.7  a
## pea           52.3  16.64 Inf     28.04     97.6  b
##
## Plant = Faba, virus = BLRV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf          149.8  59.73 Inf     68.53    327.2  a
## pea          262.5  83.14 Inf    141.08    488.3  a
##
## Plant = Hairy Vetch, virus = BLRV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf           15.3   6.22 Inf      6.93     33.9  a
## pea          132.8  42.12 Inf     71.36    247.3  b
##
## Plant = Lentil, virus = BLRV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf          110.7  44.20 Inf     50.65    242.1  a
## pea          154.3  48.90 Inf     82.88    287.1  a
##
## Plant = Pea, virus = BLRV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf          125.6  50.12 Inf     57.47    274.6  a
## pea          215.6  68.31 Inf    115.87    401.2  a
##
## Plant = Red Clover, virus = BLRV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf           55.8  22.33 Inf     25.48    122.3  a
## pea          141.7  44.91 Inf     76.10    263.7  a
##
## Plant = Alfalfa, virus = PEMV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf          nonEst   NA  NA         NA         NA

```

```

## pea      nonEst      NA NA      NA      NA
##
## Plant = Faba, virus = PEMV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf      270.9 107.97 Inf    124.07    591.7 a
## pea      208.0  65.89 Inf    111.77    387.0 a
##
## Plant = Hairy Vetch, virus = PEMV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf      354.2 141.13 Inf    162.24    773.4 a
## pea      528.3 167.24 Inf    284.04    982.5 a
##
## Plant = Lentil, virus = PEMV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf      313.7 125.01 Inf    143.68    685.0 a
## pea      447.2 141.58 Inf    240.42    831.7 a
##
## Plant = Pea, virus = PEMV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf      190.6  75.99 Inf     87.25    416.4 a
## pea      331.2 104.90 Inf    178.07    616.2 a
##
## Plant = Red Clover, virus = PEMV:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf      92.1  36.78 Inf     42.12    201.5 a
## pea      71.3  22.65 Inf     38.26    132.9 a
##
## Plant = Alfalfa, virus = Sham:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf      122.7  48.95 Inf     56.12    268.2 a
## pea      17.9   5.76 Inf      9.54     33.6 b
##
## Plant = Faba, virus = Sham:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf      301.4 120.10 Inf    138.03    658.2 a
## pea      205.3  65.05 Inf    110.34    382.1 a
##
## Plant = Hairy Vetch, virus = Sham:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf      215.8  86.00 Inf     98.78    471.3 a
## pea      405.8 128.49 Inf    218.17    754.8 a
##
## Plant = Lentil, virus = Sham:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf      170.2  67.87 Inf     77.90    371.9 a
## pea      194.4  61.59 Inf    104.45    361.7 a
##
## Plant = Pea, virus = Sham:
## Biotype response      SE df asymp.LCL asymp.UCL .group
## alf      87.3  34.86 Inf     39.90    190.9 a
## pea      320.8 101.58 Inf    172.43    596.7 b
##
## Plant = Red Clover, virus = Sham:
## Biotype response      SE df asymp.LCL asymp.UCL .group

```

```
## alf      84.4  33.73 Inf    38.60    184.7  a
## pea      48.2  15.35 Inf    25.84     90.0  a
##
## Results are averaged over the levels of: Run
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
## Tests are performed on the log scale
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.

## Warning: The 'size' argument of 'element_line()' is deprecated as of ggplot2 3.4.0.
## i Please use the 'linewidth' argument instead.

## Warning: Removed 2 rows containing missing values ('geom_bar()').

## Warning: Removed 2 rows containing missing values ('geom_text()').
```

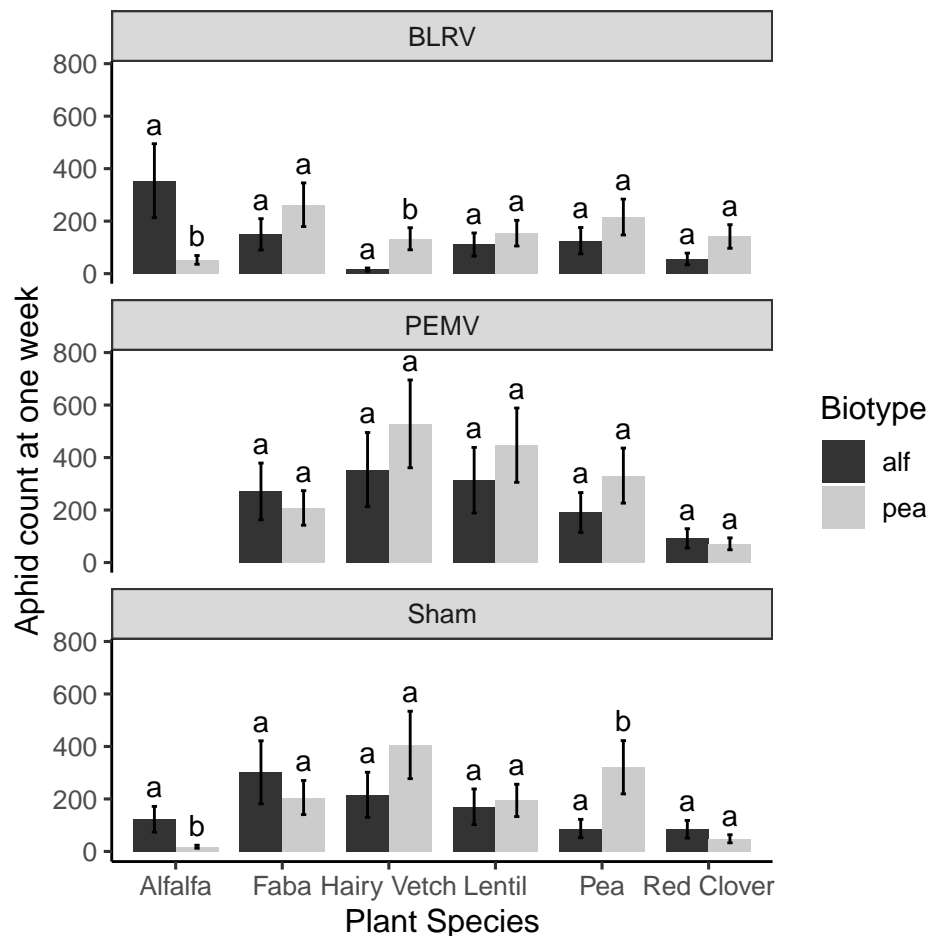


Figure 2

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

```
##
## Response: Counts
##              LR Chisq Df Pr(>Chisq)
## Biotype      0.147  1    0.7014
## Plant_sp     73.862  5   1.607e-14 ***
## Virus        1.779  2    0.4108
## Biotype:Plant_sp 29.810  5   1.607e-05 ***
## Biotype:Virus  0.459  2    0.7950
## Plant_sp:Virus  6.001  9    0.7398
## Biotype:Plant_sp:Virus 6.678  9    0.6706
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Plant_sp = Alfalfa, Virus = BLRV:
## Biotype emmean SE df lower.CL upper.CL .group
## Alfalfa  6.00 1.511 306  3.026  8.97  1
## Pea       2.71 0.989 306  0.767  4.66  1
##
## Plant_sp = Fava, Virus = BLRV:
## Biotype emmean SE df lower.CL upper.CL .group
## Alfalfa  9.83 1.511 306  6.859 12.81  1
## Pea       8.86 0.989 306  6.910 10.80  1
##
## Plant_sp = Hairy Vetch, Virus = BLRV:
## Biotype emmean SE df lower.CL upper.CL .group
## Alfalfa  6.20 1.656 306  2.942  9.46  1
## Pea      10.07 0.989 306  8.124 12.02  2
##
## Plant_sp = Lentil, Virus = BLRV:
## Biotype emmean SE df lower.CL upper.CL .group
## Alfalfa  9.50 1.511 306  6.526 12.47  1
## Pea       7.14 0.989 306  5.196  9.09  1
##
## Plant_sp = Pea, Virus = BLRV:
## Biotype emmean SE df lower.CL upper.CL .group
## Alfalfa  6.29 1.399 306  3.532  9.04  1
## Pea       7.64 0.989 306  5.696  9.59  1
##
## Plant_sp = Red Clover, Virus = BLRV:
## Biotype emmean SE df lower.CL upper.CL .group
## Alfalfa  6.33 1.511 306  3.359  9.31  1
## Pea       8.50 0.989 306  6.553 10.45  1
##
## Plant_sp = Alfalfa, Virus = PEMV:
## Biotype emmean SE df lower.CL upper.CL .group
## Alfalfa nonEst NA NA      NA      NA
## Pea      nonEst NA NA      NA      NA
##
## Plant_sp = Fava, Virus = PEMV:
## Biotype emmean SE df lower.CL upper.CL .group
## Alfalfa 12.86 1.399 306 10.104 15.61  1
## Pea      8.92 1.027 306  6.903 10.94  2
##
## Plant_sp = Hairy Vetch, Virus = PEMV:
```

```

## Biotype emmean    SE  df lower.CL upper.CL .group
## Alfalfa   7.14 1.399 306    4.389    9.90  1
## Pea       10.00 1.027 306    7.980   12.02  1
##
## Plant_sp = Lentil, Virus = PEMV:
## Biotype emmean    SE  df lower.CL upper.CL .group
## Alfalfa   6.88 1.309 306    4.299    9.45  1
## Pea       8.00 1.027 306    5.980   10.02  1
##
## Plant_sp = Pea, Virus = PEMV:
## Biotype emmean    SE  df lower.CL upper.CL .group
## Alfalfa   9.17 1.511 306    6.193   12.14  1
## Pea       8.38 1.027 306    6.364   10.41  1
##
## Plant_sp = Red Clover, Virus = PEMV:
## Biotype emmean    SE  df lower.CL upper.CL .group
## Alfalfa   6.71 1.399 306    3.961    9.47  1
## Pea       9.00 1.027 306    6.980   11.02  1
##
## Plant_sp = Alfalfa, Virus = SHAM:
## Biotype emmean    SE  df lower.CL upper.CL .group
## Alfalfa   6.43 1.399 306    3.675    9.18  1
## Pea       1.15 1.027 306   -0.867    3.17  2
##
## Plant_sp = Fava, Virus = SHAM:
## Biotype emmean    SE  df lower.CL upper.CL .group
## Alfalfa   9.86 1.399 306    7.104   12.61  1
## Pea      10.15 1.027 306    8.133   12.17  1
##
## Plant_sp = Hairy Vetch, Virus = SHAM:
## Biotype emmean    SE  df lower.CL upper.CL .group
## Alfalfa   6.43 1.399 306    3.675    9.18  1
## Pea       9.00 1.027 306    6.980   11.02  1
##
## Plant_sp = Lentil, Virus = SHAM:
## Biotype emmean    SE  df lower.CL upper.CL .group
## Alfalfa   7.29 1.399 306    4.532   10.04  1
## Pea       7.23 1.027 306    5.210    9.25  1
##
## Plant_sp = Pea, Virus = SHAM:
## Biotype emmean    SE  df lower.CL upper.CL .group
## Alfalfa   6.43 1.399 306    3.675    9.18  1
## Pea       6.15 1.027 306    4.133    8.17  1
##
## Plant_sp = Red Clover, Virus = SHAM:
## Biotype emmean    SE  df lower.CL upper.CL .group
## Alfalfa   6.86 1.399 306    4.104    9.61  1
## Pea      10.15 1.027 306    8.133   12.17  1
##
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.

```

```
## Warning: Removed 2 rows containing missing values ('geom_bar()').
```

```
## Warning: Removed 2 rows containing missing values ('geom_text()').
```

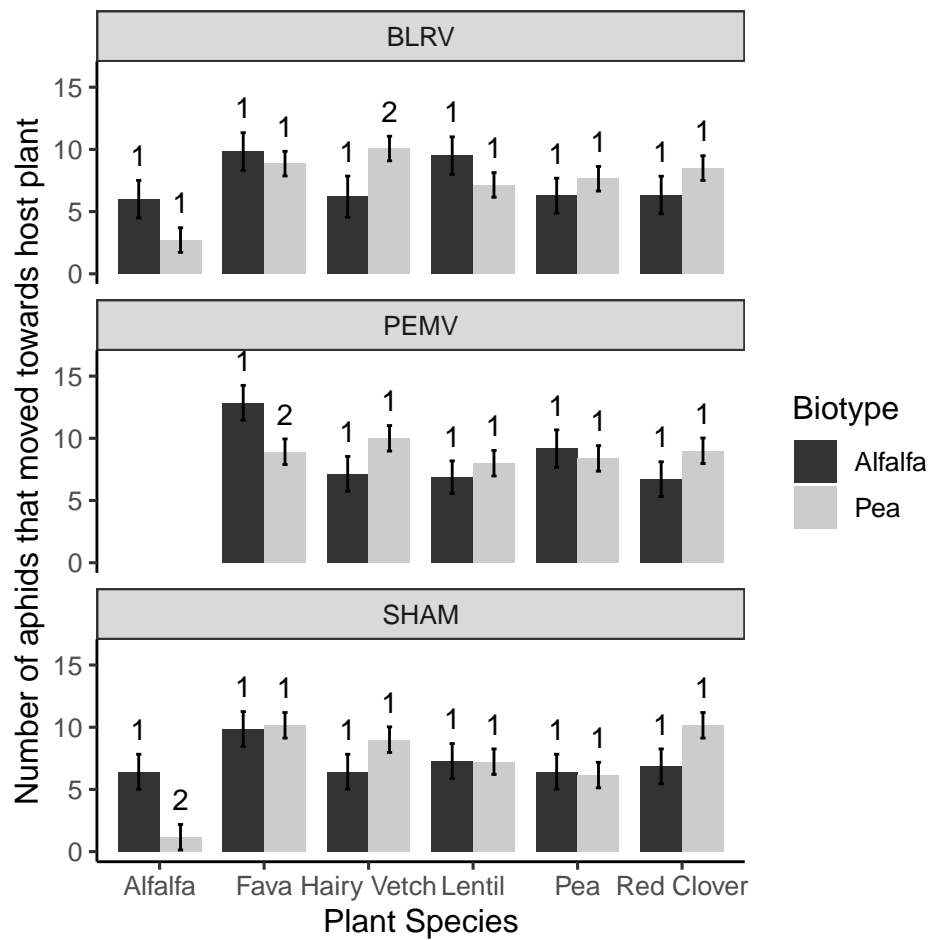


Figure 3

```
# Fig 3 ####
# Fig 3 should be preference by performance assay with BLRV excluded. perhaps two models can be run, con

# make a data frame that has the lsm/cld for preference and performance
pxp <- as.data.frame(count.lsm)

#compare to order from both.bio.cld (performance assay)
bbc.dat <- as.data.frame(both.bio.cld)

pxp$performance <- bbc.dat$response
pxp$preference <- count.lsm$emmean

# glm for preference by performance
```



```
pxp.glm <- glm(preference ~ performance*Virus, data=pxp)
Anova(pxp.glm)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: preference
##              LR Chisq Df Pr(>Chisq)
## performance    2.14180  1   0.1433
## Virus           0.98682  2   0.6105
## performance:Virus 1.10541  2   0.5754
```

```
plot_model(pxp.glm, type="int", ci.lvl = 0.90)
```

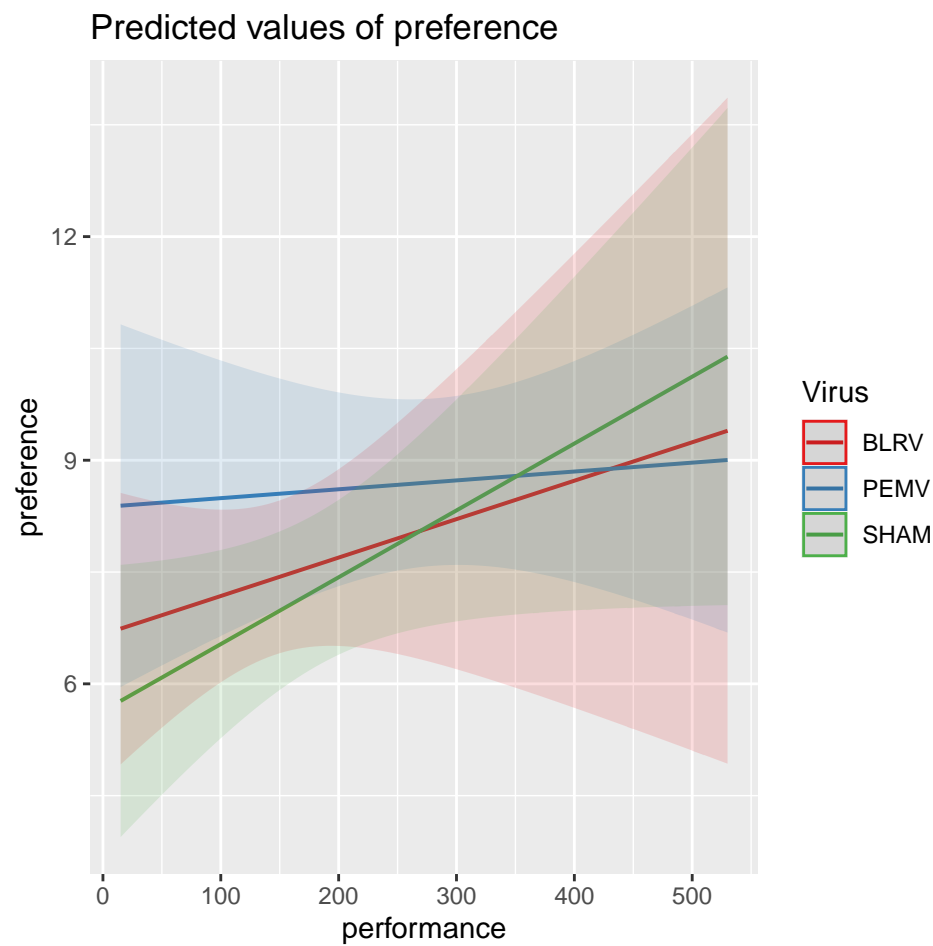


Figure s1-3

```
# Fig S1 ####
# Fig S1 should show infection rate of PEMV
choice.pcr <- read.csv("../Data/test choice pcr.csv", header = TRUE)
str(choice.pcr)
```

```
## 'data.frame': 170 obs. of 15 variables:
## $ Plant_sp : chr "Alfalfa" "Alfalfa" "Alfalfa" "Alfalfa" ...
## $ Genotype : int 3 5 5 3 3 5 3 5 3 3 ...
## $ Biotype : chr "alfalfa" "pea" "pea" "alfalfa" ...
## $ Rep : int 1 1 1 1 2 2 2 2 3 3 ...
## $ Virus : chr "BLRV" "SHAM" "BLRV" "SHAM" ...
## $ PEMV.test : chr "" "Sham" "" "Sham" ...
## $ Aphid.counts : int 4 2 2 8 11 2 9 2 4 1 ...
## $ Dead.aphids.IN.REP: int 1 3 4 2 3 5 1 6 4 3 ...
## $ Fresh.Weight : num 12.9 18.6 16.5 18.1 18.6 20.9 16.3 19.8 19.9 25 ...
## $ Proportion_.50 : num 0.08 0.04 0.04 0.16 0.22 0.04 0.18 0.04 0.08 0.02 ...
## $ Proportion_living : num 0.082 0.043 0.043 0.167 0.234 0.044 0.184 0.045 0.087 0.021 ...
## $ Primers.used : chr "PEMV+BLRV" "PEMV+BLRV" "PEMV+BLRV" "PEMV+BLRV" ...
## $ PCR.outcome : chr "Negative" "Negative" "Negative" "Negative" ...
## $ PEMV : int 0 0 0 0 0 1 0 0 0 0 ...
## $ BLRV : int 0 0 0 0 0 0 0 0 0 0 ...
```

```
#choice glm to see if treatment increases likelihood of infection
choice.pcr.PEMV <- glm(PEMV ~ Virus, family=binomial, data=choice.pcr)
#not promising at all
Anova(choice.pcr.PEMV)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: PEMV
## LR Chisq Df Pr(>Chisq)
## Virus 34.329 2 3.511e-08 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(choice.pcr.PEMV)
```

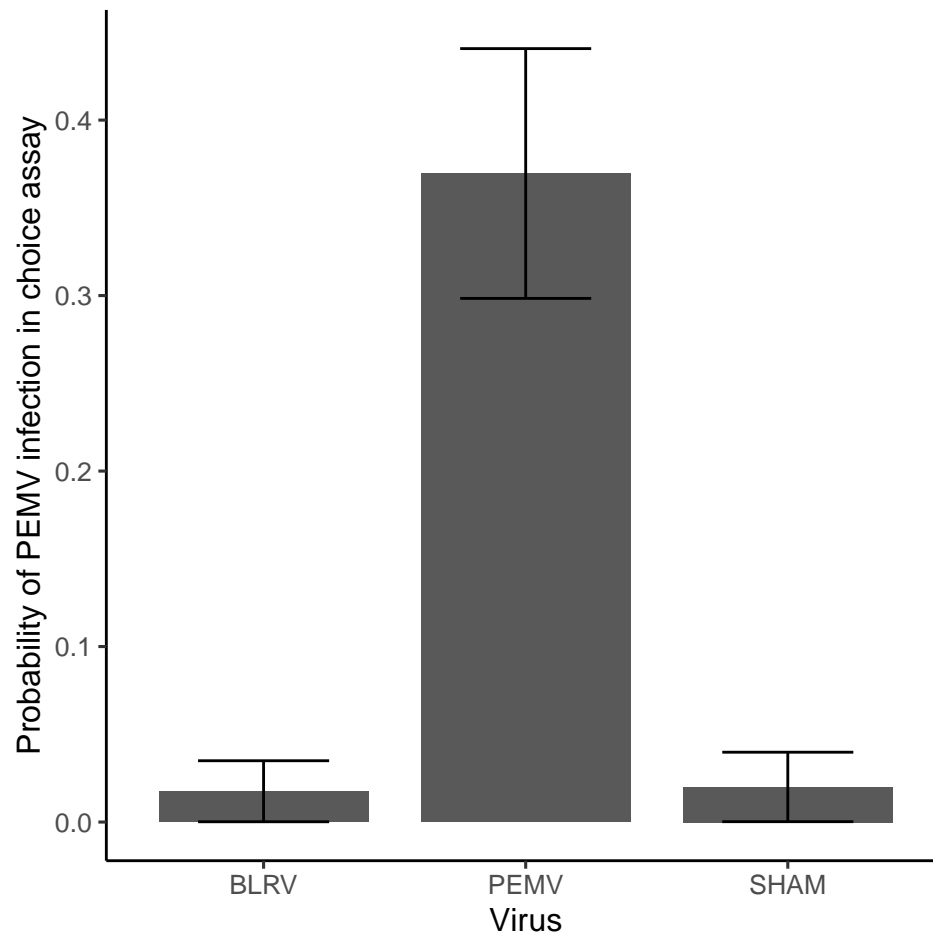
```
##
## Call:
## glm(formula = PEMV ~ Virus, family = binomial, data = choice.pcr)
##
## Deviance Residuals:
## Min 1Q Median 3Q Max
## -0.9606 -0.2010 -0.2010 -0.1882 2.8436
##
## Coefficients:
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) -4.0254 1.0087 -3.990 6.59e-05 ***
## VirusPEMV 3.4913 1.0540 3.312 0.000925 ***
## VirusSHAM 0.1335 1.4275 0.094 0.925474
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 114.804 on 152 degrees of freedom
## Residual deviance: 80.475 on 150 degrees of freedom
## (17 observations deleted due to missingness)
```

```
## AIC: 86.475
##
## Number of Fisher Scoring iterations: 6
```

```
choice.pemv.lsm <- cld(emmeans(choice.pcr.PEMV, ~ Virus), type="response")
choice.pemv.lsm
```

```
## Virus   prob   SE  df asymp.LCL asymp.UCL .group
## BLRV  0.0175 0.0174 Inf   0.00247   0.114   1
## SHAM  0.0200 0.0198 Inf   0.00281   0.129   1
## PEMV  0.3696 0.0712 Inf   0.24365   0.516   2
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
## P value adjustment: tukey method for comparing a family of 3 estimates
## Tests are performed on the log odds ratio scale
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
choice.pemv.fig <- ggplot(choice.pemv.lsm, aes(x=Virus, y=prob)) +
  geom_bar(stat="identity", width=0.8, position="dodge") +
  geom_errorbar(aes(ymin=prob-(SE), ymax=prob+(SE)), position=position_dodge(0.8), width=0.5) +
  theme_bw(base_size = 12) +
  theme(panel.border = element_blank(), panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) +
  labs(y="Probability of PEMV infection in choice assay", x="Virus") +
  scale_fill_grey() +
  theme(axis.line.x = element_line(color="black", size = 0.5),
        axis.line.y = element_line(color="black", size = 0.5))
#ylim(0,7.5) +
#facet_wrap( ~ virus, nrow=3)
choice.pemv.fig
```



```
#can run, but one positive in a sham treatment does not really instill confidence
choice.pcr.BLRV <- glm(BLRV ~ Virus, family=binomial, data=choice.pcr)
Anova(choice.pcr.BLRV)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: BLRV
##      LR Chisq Df Pr(>Chisq)
## Virus   2.2504  2    0.3246
```

```
summary(choice.pcr.BLRV)
```

```
##
## Call:
## glm(formula = BLRV ~ Virus, family = binomial, data = choice.pcr)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.20101 -0.20101 -0.00002 -0.00002  2.79715
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept) -2.257e+01  6.384e+03 -0.004    0.997
## VirusPEMV   -7.332e-11  9.552e+03  0.000    1.000
## VirusSHAM    1.867e+01  6.384e+03  0.003    0.998
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 12.0543 on 152 degrees of freedom
## Residual deviance: 9.8039 on 150 degrees of freedom
## (17 observations deleted due to missingness)
## AIC: 15.804
##
## Number of Fisher Scoring iterations: 21

# test to see if positive, negative, or sham pemv alters behavior
choice.pcr.2 <- subset(choice.pcr, Virus != "BLRV")

test.count.mod <- glm(Aphid.counts ~ PEMV.test*Plant_sp, data=choice.pcr.2)
Anova(test.count.mod)

## Analysis of Deviance Table (Type II tests)
##
## Response: Aphid.counts
##
##          LR Chisq Df Pr(>Chisq)
## PEMV.test      1.8671  2  0.393160
## Plant_sp      17.5472  5  0.003571 **
## PEMV.test:Plant_sp  2.1378  7  0.951820
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

holy.lsm <- cld(emmeans(test.count.mod, ~ PEMV.test|Plant_sp), adjust="none")
holy.lsm

## Plant_sp = Alfalfa:
## PEMV.test emmean SE df lower.CL upper.CL .group
## Sham      5.00 1.32 95      2.38      7.62  1
## Negative  nonEst NA NA      NA      NA
## Postive   nonEst NA NA      NA      NA
##
## Plant_sp = Fava:
## PEMV.test emmean SE df lower.CL upper.CL .group
## Sham      9.20 1.32 95      6.58     11.82  1
## Negative  11.12 1.48 95      8.19     14.06  1
## Postive   12.50 2.96 95      6.63     18.37  1
##
## Plant_sp = Hairy Vetch:
## PEMV.test emmean SE df lower.CL upper.CL .group
## Sham      6.50 1.32 95      3.88      9.12  1
## Negative   6.88 1.48 95      3.94      9.81  1
## Postive    8.00 2.96 95      2.13     13.87  1
##
## Plant_sp = Lentil:
## PEMV.test emmean SE df lower.CL upper.CL .group
## Sham      6.50 1.32 95      3.88      9.12  1
```

```
## Postive      7.14 1.58 95      4.01      10.28  1
## Negative     7.25 2.09 95      3.10      11.40  1
##
## Plant_sp = Pea:
## PEMV.test emmean    SE df lower.CL upper.CL .group
## Sham       5.80 1.32 95      3.18      8.42  1
## Negative    7.00 4.18 95     -1.30     15.30  1
## Postive     8.25 1.48 95      5.32     11.18  1
##
## Plant_sp = Red Clover:
## PEMV.test emmean    SE df lower.CL upper.CL .group
## Negative    8.90 1.32 95      6.28     11.52  1
## Sham       10.30 1.32 95      7.68     12.92  1
## Postive    nonEst    NA NA      NA      NA
##
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
# test to see if preference thingy can work this way
```

```
pref.mod.3 <- glm(Aphid.counts ~ PEMV.test*Plant_sp*Biotype, data=choice.pcr.2)
Anova(pref.mod.3)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Aphid.counts
##              LR Chisq Df Pr(>Chisq)
## PEMV.test           2.709  2    0.25812
## Plant_sp           28.540  5   2.854e-05 ***
## Biotype              0.006  1    0.93842
## PEMV.test:Plant_sp   4.496  7    0.72121
## PEMV.test:Biotype    2.671  2    0.26300
## Plant_sp:Biotype    59.705  5   1.399e-11 ***
## PEMV.test:Plant_sp:Biotype  9.582  5    0.08799 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# nah, it doesnt look like this will work. there isnt any positive hits for most combinations of biotype
holy.lsm.3 <- cld(emmeans(pref.mod.3, ~ PEMV.test|Plant_sp|Biotype), adjust="none")
holy.lsm.3
```

```
## Plant_sp = Alfalfa, Biotype = alfalfa:
## PEMV.test emmean    SE df lower.CL upper.CL .group
## Sham       7.17 1.35 82      4.482      9.85  1
## Negative    nonEst    NA NA      NA      NA
## Postive     nonEst    NA NA      NA      NA
##
## Plant_sp = Fava, Biotype = alfalfa:
## PEMV.test emmean    SE df lower.CL upper.CL .group
## Postive     9.00 3.31 82      2.423     15.58  1
```

```

## Sham      10.33 1.35 82      7.648      13.02 1
## Negative  13.00 1.48 82     10.059      15.94 1
##
## Plant_sp = Hairy Vetch, Biotype = alfalfa:
## PEMV.test emmean   SE df lower.CL upper.CL .group
## Sham      7.00 1.35 82      4.315       9.68 1
## Negative  7.75 1.65 82      4.462      11.04 1
## Postive   8.00 2.34 82      3.350      12.65 1
##
## Plant_sp = Lentil, Biotype = alfalfa:
## PEMV.test emmean   SE df lower.CL upper.CL .group
## Postive   6.20 1.48 82      3.259       9.14 1
## Negative  6.50 2.34 82      1.850      11.15 1
## Sham      7.33 1.35 82      4.648      10.02 1
##
## Plant_sp = Pea, Biotype = alfalfa:
## PEMV.test emmean   SE df lower.CL upper.CL .group
## Sham      6.50 1.35 82      3.815       9.18 1
## Postive   10.40 1.48 82      7.459      13.34 1
## Negative  nonEst   NA NA         NA         NA
##
## Plant_sp = Red Clover, Biotype = alfalfa:
## PEMV.test emmean   SE df lower.CL upper.CL .group
## Sham      5.33 1.35 82      2.648       8.02 1
## Negative  6.00 1.35 82      3.315       8.68 1
## Postive   nonEst   NA NA         NA         NA
##
## Plant_sp = Alfalfa, Biotype = pea:
## PEMV.test emmean   SE df lower.CL upper.CL .group
## Sham      1.75 1.65 82     -1.538       5.04 1
## Negative  nonEst   NA NA         NA         NA
## Postive   nonEst   NA NA         NA         NA
##
## Plant_sp = Fava, Biotype = pea:
## PEMV.test emmean   SE df lower.CL upper.CL .group
## Sham      7.50 1.65 82      4.212      10.79 1
## Negative  8.00 1.91 82      4.203      11.80 1
## Postive   16.00 3.31 82      9.423      22.58 2
##
## Plant_sp = Hairy Vetch, Biotype = pea:
## PEMV.test emmean   SE df lower.CL upper.CL .group
## Sham      5.75 1.65 82      2.462       9.04 1
## Negative  6.00 1.65 82      2.712       9.29 1
## Postive   nonEst   NA NA         NA         NA
##
## Plant_sp = Lentil, Biotype = pea:
## PEMV.test emmean   SE df lower.CL upper.CL .group
## Sham      5.25 1.65 82      1.962       8.54 1
## Negative  8.00 2.34 82      3.350      12.65 1
## Postive   9.50 2.34 82      4.850      14.15 1
##
## Plant_sp = Pea, Biotype = pea:
## PEMV.test emmean   SE df lower.CL upper.CL .group
## Postive   4.67 1.91 82      0.870       8.46 1

```

```
## Sham      4.75 1.65 82    1.462    8.04 1
## Negative  7.00 3.31 82    0.423   13.58 1
##
## Plant_sp = Red Clover, Biotype = pea:
## PEMV.test emmean  SE df lower.CL upper.CL .group
## Negative  13.25 1.65 82    9.962    16.54 1
## Sham      17.75 1.65 82   14.462    21.04 1
## Postive   nonEst  NA NA      NA      NA
##
## Confidence level used: 0.95
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
# Fig S2 ####
```

```
# Fig S2 should show that aphid abundance for infective aphids vs. positive PCR infection are more simi
```

```
repro.pcr <-read.csv("../Data/test reproduction pcr.csv", header=TRUE)
str(repro.pcr)
```

```
## 'data.frame': 168 obs. of 9 variables:
## $ Plant.Species: chr "Lentil" "Clover" "Pea" "Fava" ...
## $ Virus : chr "BLRV" "BLRV" "Sham" "Sham" ...
## $ Biotype : chr "B3" "B3" "B4" "B4" ...
## $ Plant.Number : chr "A" "A" "B" "A" ...
## $ Primers.used : chr "" "" "PEMV" "PEMV" ...
## $ PCR.hit : chr "missing" "missing" "Negative" "Negative" ...
## $ PEMV : int NA NA 0 0 0 0 0 0 1 0 ...
## $ BLRV : int NA NA 0 0 0 0 0 0 0 0 ...
## $ Virus.test : chr "" "" "Sham" "" ...
```

```
#pemv infection higher here
```

```
repro.pcr.PEMV <- glm(PEMV ~ Virus, family=binomial, data=repro.pcr)
Anova(repro.pcr.PEMV)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: PEMV
##      LR Chisq Df Pr(>Chisq)
## Virus  16.286  2  0.0002908 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(repro.pcr.PEMV)
```

```
##
## Call:
## glm(formula = PEMV ~ Virus, family = binomial, data = repro.pcr)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
```



```
## -0.8141 -0.4001 -0.4001 -0.1933 2.8245
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -3.970      1.009  -3.934 8.36e-05 ***
## VirusPEMV      3.036      1.070   2.837 0.00456 **
## VirusSham      1.485      1.111   1.336 0.18141
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##    Null deviance: 107.900  on 157  degrees of freedom
## Residual deviance:  91.615  on 155  degrees of freedom
## (10 observations deleted due to missingness)
## AIC: 97.615
##
## Number of Fisher Scoring iterations: 6
```

```
repro.pcr.lsm <- cld(emmeans(repro.pcr.PEMV, ~ Virus), type="response")

repro.pemv.fig <- ggplot(repro.pcr.lsm, aes(x=Virus, y=prob)) +
  geom_bar(stat="identity", width=0.8, position="dodge") +
  geom_errorbar(aes(ymin=prob-(SE), ymax=prob+(SE)), position=position_dodge(0.8), width=0.5) +
  theme_bw(base_size = 12) +
  theme(panel.border = element_blank(), panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) +
  labs(y="Probability of PEMV infection in reproduction assay", x="Virus") +
  scale_fill_grey() +
  theme(axis.line.x = element_line(color="black", size = 0.5),
        axis.line.y = element_line(color="black", size = 0.5))
repro.pemv.fig
```

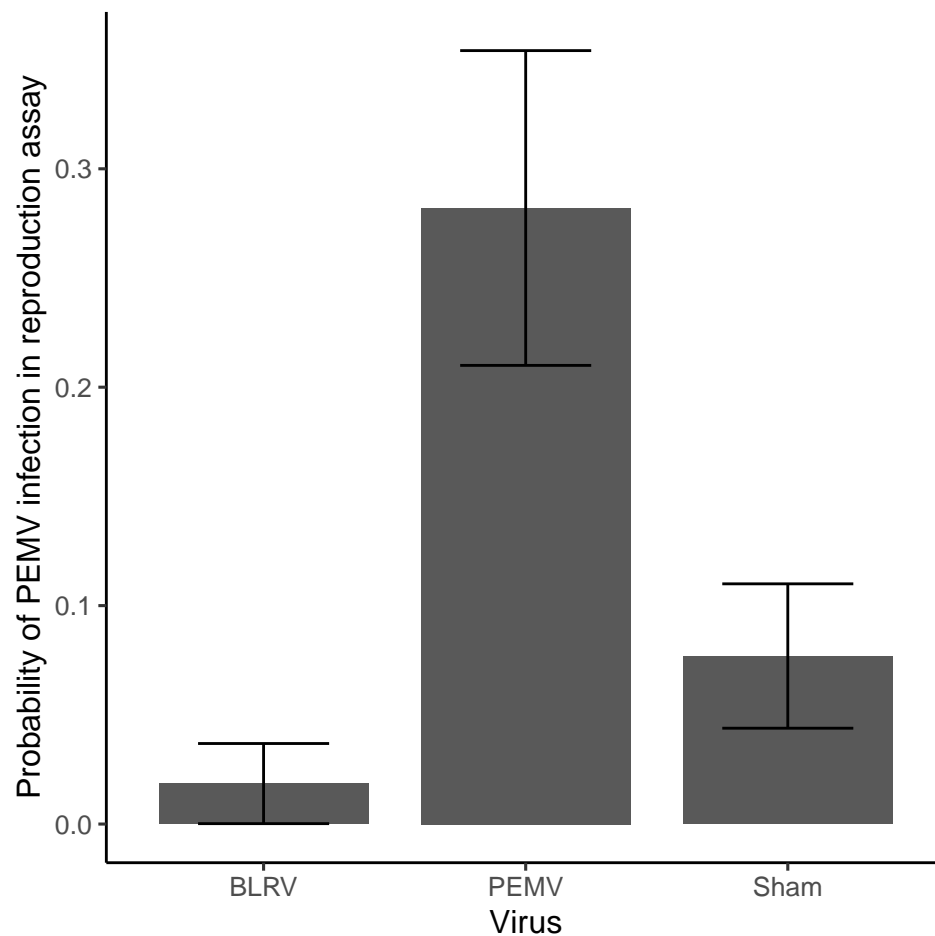


Fig S3

Fig S3 should show that aphid abundance for infective aphids vs. positive PCR infection are more similar

requires cleaned data from Logan Dean made on sept 12

```
bflc <- read.csv("../Data/big five Logan check.csv", header = TRUE)
str(bflc)
```

```
## 'data.frame': 527 obs. of 16 variables:
## $ Run : chr "One" "One" "One" "One" ...
## $ ID.. : chr "AB1" "AB1" "A1" "A1" ...
## $ count.of.plants : chr "5" "6" "2" "3" ...
## $ Plant : chr "Alfalfa" "Alfalfa" "Alfalfa" "Alfalfa" ...
## $ Genotype : int 1 1 1 1 2 2 2 2 3 3 ...
## $ Biotype : chr "pea" "pea" "pea" "pea" ...
## $ virus : chr "BLRV" "BLRV" "Sham" "Sham" ...
## $ PEMV.PCR : chr "" "" "" "" ...
## $ Counts : int 113 134 106 40 3 147 0 4 95 229 ...
## $ absorbance : chr "1.173" "0.918" "0.433" "0.588" ...
## $ log.Counts : num 4.74 4.91 4.67 3.71 1.39 ...
## $ sqrt_rel_increase: num 3.21 3.52 3.1 1.73 NA ...
```

```
## $ Infection.status : chr "YES" "YES" "NO" "NO" ...
## $ relative.increase: num 10.3 12.4 9.6 3 -0.7 13.7 -1 -0.6 8.5 21.9 ...
## $ Retain. : chr "Keep" "Keep" "Keep" "Keep" ...
## $ Bean.Aphids : int NA NA NA NA NA NA NA NA NA NA ...
```

```
bf$Genotype <- as.factor(bf$Genotype)
```

```
# make all blanks NA
```

```
bflc[bflc==""] <- NA
```

```
# exclude all but block 3 (because that has pcr tests)
```

```
bflc.mod <- glm(Counts ~ PEMV.PCR, data=bflc)
```

```
summary(bflc.mod)
```

```
##
```

```
## Call:
```

```
## glm(formula = Counts ~ PEMV.PCR, data = bflc)
```

```
##
```

```
## Deviance Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -271.45 -143.54  -68.49   65.26  1172.71
```

```
##
```

```
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      68.49      31.91   2.147  0.03350 *
## PEMV.PCRNegative  153.36      55.60   2.758  0.00657 **
## PEMV.PCRPositive  202.96      78.15   2.597  0.01038 *
## PEMV.PCRSham       85.80      45.12   1.902  0.05923 .
```

```
## ---
```

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

```
##
```

```
## (Dispersion parameter for gaussian family taken to be 55989.41)
```

```
##
```

```
## Null deviance: 8724178 on 147 degrees of freedom
```

```
## Residual deviance: 8062475 on 144 degrees of freedom
```

```
## (379 observations deleted due to missingness)
```

```
## AIC: 2044
```

```
##
```

```
## Number of Fisher Scoring iterations: 2
```

```
cld(emmeans(bflc.mod, ~ PEMV.PCR))
```

```
## PEMV.PCR emmean SE df lower.CL upper.CL .group
## BLRV      68.5 31.9 144      5.43      132  1
## Sham     154.3 31.9 144     91.23      217  12
## Negative 221.9 45.5 144    131.84      312  2
## Positive 271.5 71.3 144    130.44      412  12
##
```

```
## Confidence level used: 0.95
```

```
## P value adjustment: tukey method for comparing a family of 4 estimates
```

```
## significance level used: alpha = 0.05
```

```
## NOTE: If two or more means share the same grouping symbol,
```

```
##      then we cannot show them to be different.
##      But we also did not show them to be the same.
```

```
# Run again excluded BLRV to solve some model problems and include host plant species
```

```
bflc.2 <- subset(bflc, virus != "BLRV")
```

```
bflc.mod.2 <- glm(Counts ~ PEMV.PCR*Plant, data=bflc.2)
summary(bflc.mod.2)
```

```
##
## Call:
## glm(formula = Counts ~ PEMV.PCR * Plant, data = bflc.2)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -387.40  -155.25   -7.67   30.33   986.27
##
## Coefficients: (4 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      227.556      87.827   2.591  0.0113 *
## PEMV.PCRPositive -157.250     165.145  -0.952  0.3438
## PEMV.PCRSham       7.717     118.426   0.065  0.9482
## PlantHairy Vetch   105.455     112.348   0.939  0.3507
## PlantLentil       257.844     146.962   1.754  0.0831 .
## PlantPea          131.694     158.332   0.832  0.4080
## PlantRed Clover  -218.889     124.206  -1.762  0.0817 .
## PEMV.PCRPositive:PlantHairy Vetch    NA         NA      NA      NA
## PEMV.PCRSham:PlantHairy Vetch        NA         NA      NA      NA
## PEMV.PCRPositive:PlantLentil      64.850     241.894   0.268  0.7893
## PEMV.PCRSham:PlantLentil    -354.208     184.987  -1.915  0.0590 .
## PEMV.PCRPositive:PlantPea         NA         NA      NA      NA
## PEMV.PCRSham:PlantPea    -314.422     194.142  -1.620  0.1092
## PEMV.PCRPositive:PlantRed Clover    NA         NA      NA      NA
## PEMV.PCRSham:PlantRed Clover   -12.384     167.479  -0.074  0.9412
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 69421.83)
##
##      Null deviance: 7607039  on 92  degrees of freedom
## Residual deviance: 5692590  on 82  degrees of freedom
## (248 observations deleted due to missingness)
## AIC: 1313
##
## Number of Fisher Scoring iterations: 2
```

```
logan.lsm <- cld(emmeans(bflc.mod.2, ~ Plant|PEMV.PCR), adjust="none")
```

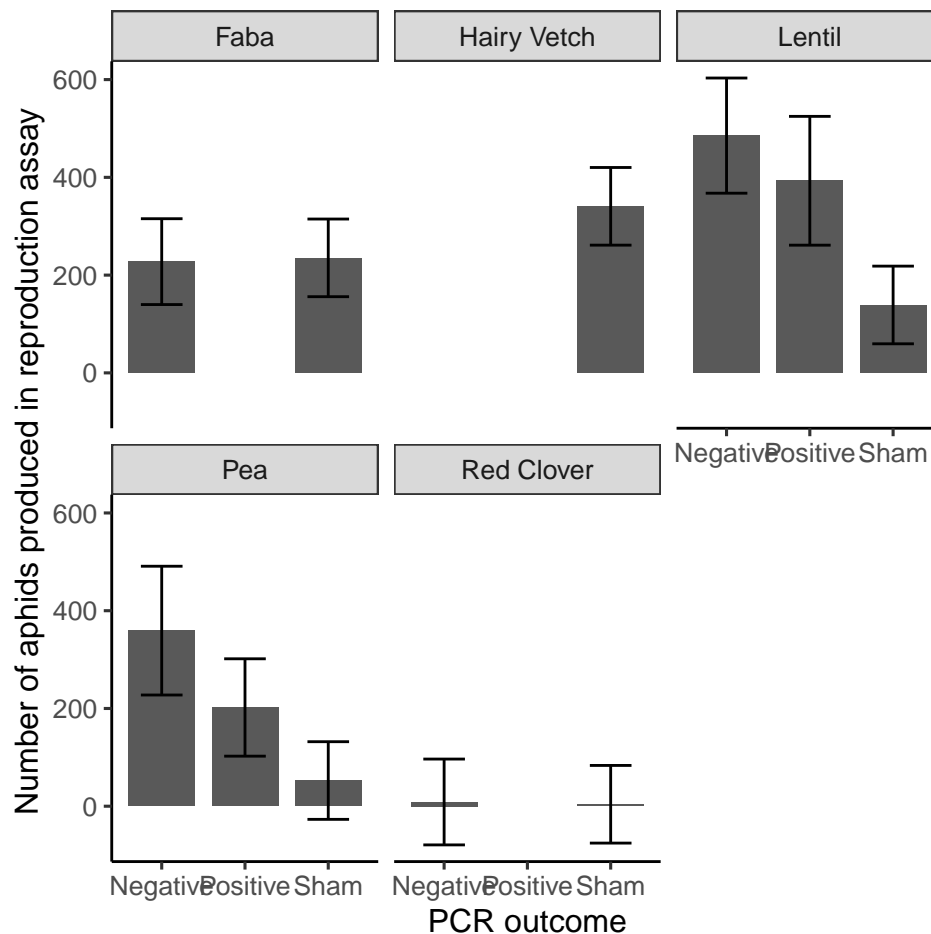
```
logan.pcr <- ggplot(logan.lsm, aes(x=PEMV.PCR, y=emmean)) +
  geom_bar(stat="identity", width=0.8, position="dodge") +
  geom_errorbar(aes(ymin=emmean-(SE), ymax=emmean+(SE)), position=position_dodge(0.8), width=0.5) +
```

```

theme_bw(base_size = 12) +
theme(panel.border = element_blank(), panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) +
labs(y="Number of aphids produced in reproduction assay", x="PCR outcome") +
scale_fill_grey() +
theme(axis.line.x = element_line(color="black", size = 0.5),
      axis.line.y = element_line(color="black", size = 0.5)) +
facet_wrap(. ~ Plant)
logan.pcr

```

Warning: Removed 4 rows containing missing values ('geom_bar()').



Extra plant focused figures

```

## Note: adjust = "tukey" was changed to "sidak"
## because "tukey" is only appropriate for one set of pairwise comparisons

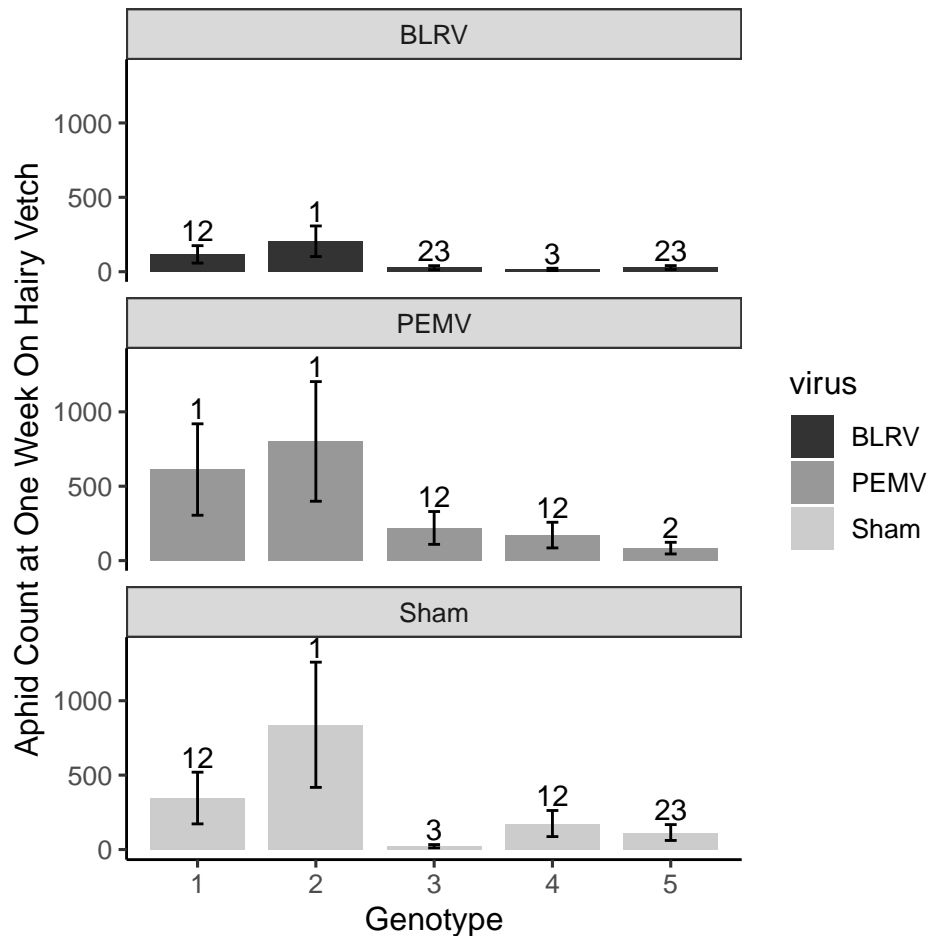
```

```

## Analysis of Deviance Table (Type II tests)
##
## Response: Counts

```

```
##          LR Chisq Df Pr(>Chisq)
## Genotype    45.165  4  3.674e-09 ***
## virus       23.871  2  6.552e-06 ***
## Run         5.733  2   0.05691 .
## Genotype:virus  9.499  8   0.30193
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
## 'data.frame': 93 obs. of 15 variables:
## $ Run : chr "One" "One" "One" "One" ...
## $ ID.. : chr "PB1" "PB1" "PP1" "PP1" ...
## $ count.of.plants : int 5 6 9 10 1 4 17 18 21 22 ...
## $ Plant : chr "Pea" "Pea" "Pea" "Pea" ...
## $ Genotype : Factor w/ 5 levels "1","2","3","4",...: 1 1 1 1 1 1 2 2 2 2 ...
## $ Biotype : chr "pea" "pea" "pea" "pea" ...
## $ virus : chr "BLRV" "BLRV" "PEMV" "PEMV" ...
## $ Counts : int 341 427 248 131 111 266 406 176 413 223 ...
## $ absorbance : num 0.809 0.843 3.499 3.493 0.644 ...
## $ log.Counts : num 5.83 6.06 5.52 4.88 4.72 ...
## $ sqrt_rel_increase: num 5.75 6.46 4.88 3.48 3.18 ...
## $ Infection.status : chr "YES" "YES" "YES" "YES" ...
## $ relative.increase: num 33.1 41.7 23.8 12.1 10.1 25.6 39.6 16.6 40.3 21.3 ...
```

```

## $ Retain.          : chr  "Keep" "Keep" "Keep" "Keep" ...
## $ Bean.Aphids      : int   NA NA NA NA NA NA NA NA NA NA ...

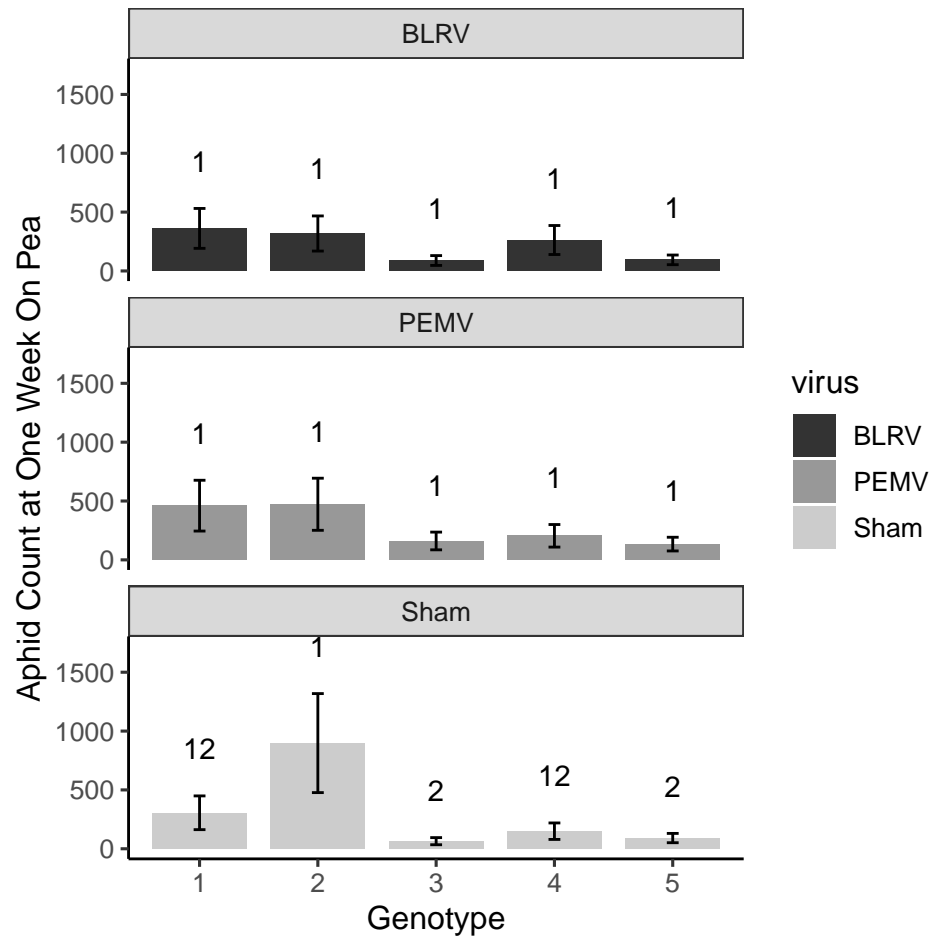
##
## Call:
## glm.nb(formula = Counts ~ Genotype * virus, data = pea.dat, init.theta = 0.7598600045,
##        link = log)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.1269  -0.9042  -0.3523   0.4750   1.7272
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      5.8907     0.4688  12.565  <2e-16 ***
## Genotype2        -0.1281     0.6631   -0.193   0.8468
## Genotype3        -1.4058     0.6641   -2.117   0.0343 *
## Genotype4        -0.3192     0.6632   -0.481   0.6303
## Genotype5        -1.3444     0.6398   -2.101   0.0356 *
## virusPEMV         0.2416     0.6629    0.364   0.7155
## virusSham        -0.1682     0.6631   -0.254   0.7997
## Genotype2:virusPEMV 0.1535     0.9376    0.164   0.8699
## Genotype3:virusPEMV 0.3518     0.9387    0.375   0.7078
## Genotype4:virusPEMV -0.4934     0.9379   -0.526   0.5989
## Genotype5:virusPEMV 0.1089     0.9045    0.120   0.9042
## Genotype2:virusSham 1.2056     0.9376    1.286   0.1985
## Genotype3:virusSham -0.1526     0.9396   -0.162   0.8710
## Genotype4:virusSham -0.3982     0.9381   -0.424   0.6712
## Genotype5:virusSham 0.1312     0.9049    0.145   0.8847
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.7599) family taken to be 1)
##
##      Null deviance: 150.23  on 92  degrees of freedom
## Residual deviance: 112.44  on 78  degrees of freedom
## AIC: 1202.7
##
## Number of Fisher Scoring iterations: 1
##
##              Theta: 0.760
##      Std. Err.: 0.104
##
## 2 x log-likelihood: -1170.681

## Note: adjust = "tukey" was changed to "sidak"
## because "tukey" is only appropriate for one set of pairwise comparisons

## Analysis of Deviance Table (Type II tests)
##
## Response: Counts
##              LR Chisq Df Pr(>Chisq)

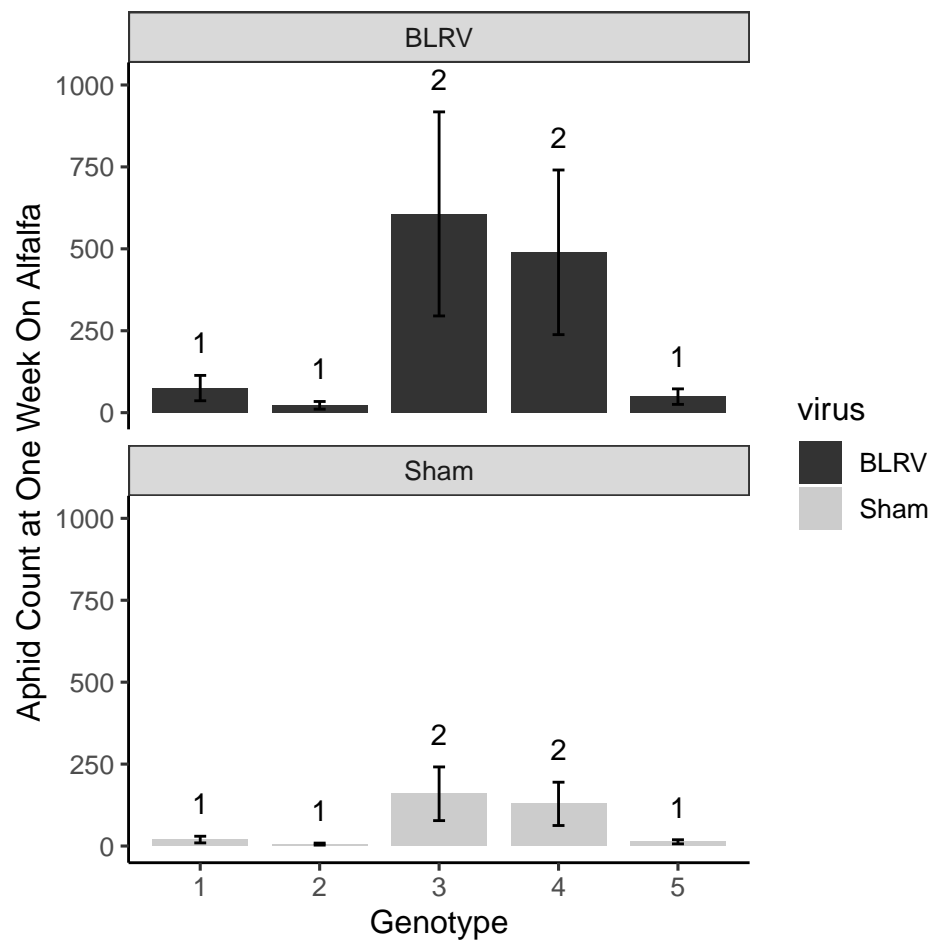
```

```
## Genotype      31.5867  4  2.324e-06 ***
## virus         1.0306  2    0.5973
## Genotype:virus 5.1072  8    0.7461
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
## Note: adjust = "tukey" was changed to "sidak"
## because "tukey" is only appropriate for one set of pairwise comparisons
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Counts
##      LR Chisq Df Pr(>Chisq)
## Genotype  34.125  4  7.024e-07 ***
## virus       8.263  1  0.004047 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Call:
## glm.nb(formula = Counts ~ Genotype * virus + Run, data = Faba.dat,
##       init.theta = 0.9429077872, link = log)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3301  -0.7779  -0.1555   0.3520   1.7414
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      5.59594    0.44801  12.491  <2e-16 ***
## Genotype2         0.32487    0.59541   0.546   0.585
## Genotype3        -0.52446    0.59588  -0.880   0.379
## Genotype4        -0.84970    0.59620  -1.425   0.154
## Genotype5        -0.89747    0.57493  -1.561   0.119
## virusPEMV        -0.52795    0.59588  -0.886   0.376
## virusSham        -0.13803    0.59562  -0.232   0.817
## RunThree         -0.10188    0.26121  -0.390   0.697
## RunTwo           0.35713    0.26651   1.340   0.180
## Genotype2:virusPEMV 0.06479    0.84242   0.077   0.939
## Genotype3:virusPEMV 0.98628    0.84273   1.170   0.242
## Genotype4:virusPEMV 1.14516    0.84302   1.358   0.174
```

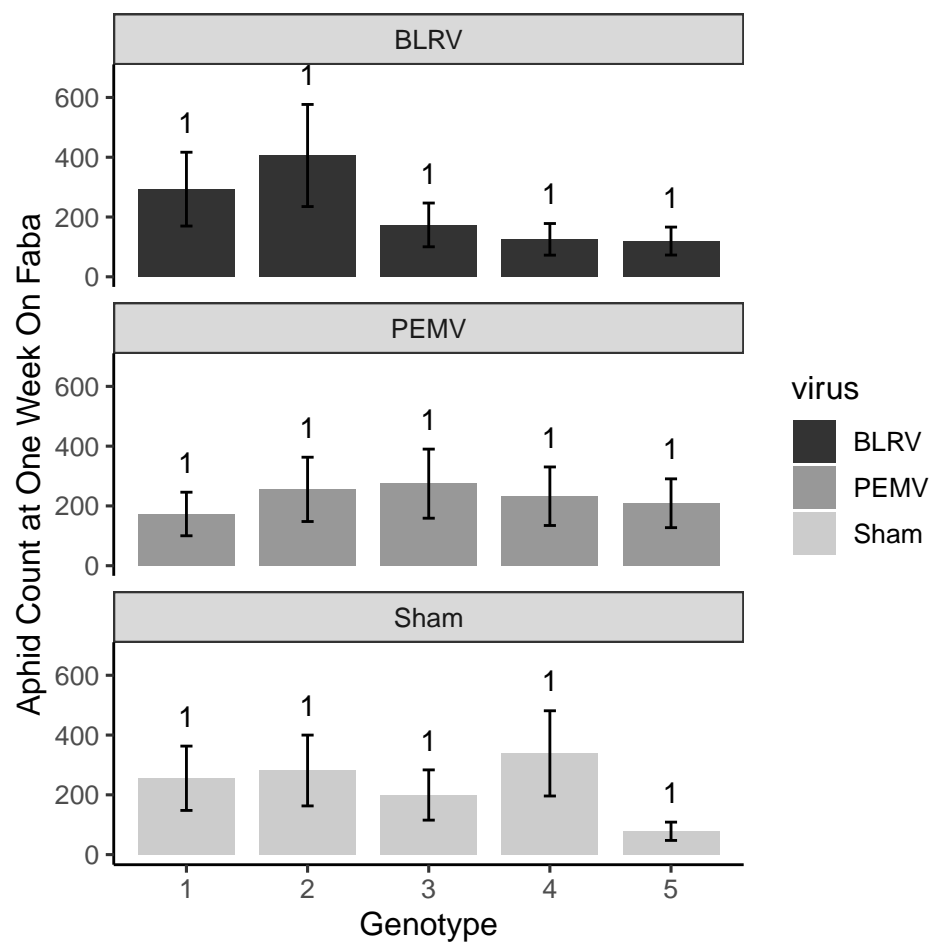
```

## Genotype5:virusPEMV  1.08652    0.81244    1.337    0.181
## Genotype2:virusSham -0.22824    0.84220   -0.271    0.786
## Genotype3:virusSham  0.27677    0.84268    0.328    0.743
## Genotype4:virusSham  1.13174    0.84269    1.343    0.179
## Genotype5:virusSham -0.28839    0.81298   -0.355    0.723
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.9429) family taken to be 1)
##
##      Null deviance: 130.95  on 92  degrees of freedom
## Residual deviance: 112.69  on 76  degrees of freedom
## AIC: 1212.8
##
## Number of Fisher Scoring iterations: 1
##
##
##           Theta:  0.943
##          Std. Err.:  0.134
##
## 2 x log-likelihood: -1176.819

## Analysis of Deviance Table (Type II tests)
##
## Response: Counts
##           LR Chisq Df Pr(>Chisq)
## Genotype      7.5654  4    0.1089
## virus         0.3260  2    0.8496
## Run           3.0833  2    0.2140
## Genotype:virus 6.9098  8    0.5464

## Note: adjust = "tukey" was changed to "sidak"
## because "tukey" is only appropriate for one set of pairwise comparisons

```



##	Run ID..	count.of.plants	Plant	Genotype	Biotype	virus	Counts
## 141	One RCB1	9	Red Clover	1	pea	BLRV	161
## 142	One RCB1	10	Red Clover	1	pea	BLRV	41
## 143	One RCP1	1	Red Clover	1	pea	PEMV	71
## 144	One RCP1	2	Red Clover	1	pea	PEMV	1
## 145	One RC1	5	Red Clover	1	pea	Sham	15
## 146	One RC1	6	Red Clover	1	pea	Sham	31
## 147	One RCB2	21	Red Clover	2	pea	BLRV	168
## 148	One RCB2	22	Red Clover	2	pea	BLRV	1
## 149	One RCP2	15	Red Clover	2	pea	PEMV	8
## 150	One RCP2	16	Red Clover	2	pea	PEMV	4
## 151	One RC2	13	Red Clover	2	pea	Sham	0
## 152	One RC2	19	Red Clover	2	pea	Sham	8
## 153	One RCB3	25	Red Clover	3	alf	BLRV	236
## 154	One RCB3	26	Red Clover	3	alf	BLRV	22
## 155	One RCP3	29	Red Clover	3	alf	PEMV	201
## 156	One RCP3	30	Red Clover	3	alf	PEMV	38
## 157	One RC3	33	Red Clover	3	alf	Sham	118
## 158	One RC3	34	Red Clover	3	alf	Sham	49
## 159	One RCB4	45	Red Clover	4	alf	BLRV	16
## 160	One RCB4	46	Red Clover	4	alf	BLRV	141
## 161	One RCP4	37	Red Clover	4	alf	PEMV	273
## 162	One RCP4	38	Red Clover	4	alf	PEMV	93

## 163	One	RC4	41 Red Clover	4	alf	Sham	373
## 164	One	RC4	42 Red Clover	4	alf	Sham	54
## 165	One	RCB5	49 Red Clover	5	pea	BLRV	842
## 166	One	RCB5	58 Red Clover	5	pea	BLRV	590
## 167	One	RCP5	50 Red Clover	5	pea	PEMV	91
## 168	One	RCP5	51 Red Clover	5	pea	PEMV	273
## 169	One	RC5	54 Red Clover	5	pea	Sham	189
## 170	One	RC5	55 Red Clover	5	pea	Sham	133
## 311	Two	RCB1	11 Red Clover	1	pea	BLRV	121
## 312	Two	RCB1	12 Red Clover	1	pea	BLRV	141
## 313	Two	RCP1	3 Red Clover	1	pea	PEMV	25
## 314	Two	RCP1	4 Red Clover	1	pea	PEMV	28
## 315	Two	RC1	7 Red Clover	1	pea	Sham	342
## 316	Two	RC1	8 Red Clover	1	pea	Sham	51
## 317	Two	RCB2	23 Red Clover	2	pea	BLRV	0
## 318	Two	RCB2	24 Red Clover	2	pea	BLRV	21
## 319	Two	RCP2	17 Red Clover	2	pea	PEMV	59
## 320	Two	RCP2	18 Red Clover	2	pea	PEMV	4
## 321	Two	RC2	14 Red Clover	2	pea	Sham	86
## 322	Two	RC2	20 Red Clover	2	pea	Sham	0
## 323	Two	RCB3	27 Red Clover	3	alf	BLRV	202
## 324	Two	RCB3	28 Red Clover	3	alf	BLRV	41
## 325	Two	RCP3	31 Red Clover	3	alf	PEMV	232
## 326	Two	RCP3	32 Red Clover	3	alf	PEMV	94
## 327	Two	RC3	35 Red Clover	3	alf	Sham	36
## 328	Two	RC3	36 Red Clover	3	alf	Sham	166
## 329	Two	RCB4	47 Red Clover	4	alf	BLRV	52
## 330	Two	RCB4	48 Red Clover	4	alf	BLRV	74
## 331	Two	RCP4	39 Red Clover	4	alf	PEMV	191
## 332	Two	RCP4	40 Red Clover	4	alf	PEMV	200
## 333	Two	RC4	43 Red Clover	4	alf	Sham	373
## 334	Two	RC4	44 Red Clover	4	alf	Sham	24
## 335	Two	RCB5	59 Red Clover	5	pea	BLRV	452
## 336	Two	RCB5	60 Red Clover	5	pea	BLRV	476
## 337	Two	RCP5	52 Red Clover	5	pea	PEMV	229
## 338	Two	RCP5	53 Red Clover	5	pea	PEMV	909
## 339	Two	RC5	56 Red Clover	5	pea	Sham	230
## 340	Two	RC5	57 Red Clover	5	pea	Sham	45
## 495	Three		NA Red Clover	1	pea	BLRV	0
## 496	Three		NA Red Clover	1	pea	BLRV	13
## 497	Three		NA Red Clover	1	pea	PEMV	0
## 498	Three		NA Red Clover	1	pea	PEMV	12
## 499	Three		NA Red Clover	1	pea	Sham	2
## 500	Three		NA Red Clover	1	pea	Sham	0
## 501	Three		NA Red Clover	2	pea	BLRV	0
## 502	Three		NA Red Clover	2	pea	BLRV	0
## 503	Three		NA Red Clover	2	pea	PEMV	12
## 504	Three		NA Red Clover	2	pea	PEMV	1
## 505	Three		NA Red Clover	2	pea	Sham	0
## 506	Three		NA Red Clover	2	pea	Sham	2
## 507	Three		NA Red Clover	3	alf	BLRV	0
## 508	Three		NA Red Clover	3	alf	BLRV	0
## 509	Three		NA Red Clover	3	alf	PEMV	6
## 510	Three		NA Red Clover	3	alf	PEMV	7

## 511 Three	NA Red Clover	3	alf Sham	3	
## 512 Three	NA Red Clover	3	alf Sham	0	
## 513 Three	NA Red Clover	4	alf BLRV	0	
## 514 Three	NA Red Clover	4	alf BLRV	0	
## 515 Three	NA Red Clover	4	alf PEMV	1	
## 516 Three	NA Red Clover	4	alf PEMV	0	
## 517 Three	NA Red Clover	4	alf Sham	0	
## 518 Three	NA Red Clover	4	alf Sham	5	
## 519 Three	NA Red Clover	5	pea BLRV	0	
## 520 Three	NA Red Clover	5	pea BLRV	0	
## 521 Three	NA Red Clover	5	pea BLRV	0	
## 522 Three	NA Red Clover	5	pea PEMV	39	
## 523 Three	NA Red Clover	5	pea PEMV	11	
## 524 Three	NA Red Clover	5	pea PEMV	0	
## 525 Three	NA Red Clover	5	pea Sham	15	
## 526 Three	NA Red Clover	5	pea Sham	4	
## 527 Three	NA Red Clover	5	pea Sham	13	
##	absorbance	log.Counts	sqrt_rel_increase	Infection.status	relative.increase
## 141	0.779	5.0875963	3.8858718	YES	15.1
## 142	0.684	3.7376696	1.7606817	YES	3.1
## 143	0.387	4.2766661	2.4698178	NO	6.1
## 144	0.414	0.6931472	NA	NO	-0.9
## 145	0.506	2.7725887	0.7071068	NO	0.5
## 146	0.279	3.4657359	1.4491377	NO	2.1
## 147	0.672	5.1298987	3.9749214	YES	15.8
## 148	0.662	0.6931472	NA	YES	-0.9
## 149	0.380	2.1972246	NA	NO	-0.2
## 150	0.264	1.6094379	NA	NO	-0.6
## 151	0.626	0.0000000	NA	YES	-1.0
## 152	0.279	2.1972246	NA	NO	-0.2
## 153	0.424	5.4680601	4.7539457	NO	22.6
## 154	0.559	3.1354942	1.0954451	NO	1.2
## 155	0.323	5.3082677	4.3703547	NO	19.1
## 156	0.302	3.6635616	1.6733201	NO	2.8
## 157	0.452	4.7791235	3.2863353	NO	10.8
## 158	0.299	3.9120230	1.9748418	NO	3.9
## 159	0.680	2.8332133	0.7745967	YES	0.6
## 160	0.697	4.9558271	3.6193922	YES	13.1
## 161	0.276	5.6131281	5.1283526	NO	26.3
## 162	0.298	4.5432948	2.8809721	NO	8.3
## 163	0.494	5.9242558	6.0249481	NO	36.3
## 164	0.374	4.0073332	2.0976177	NO	4.4
## 165	0.569	6.7369670	9.1214034	NO	83.2
## 166	0.637	6.3818160	7.6157731	YES	58.0
## 167	0.282	4.5217886	2.8460499	NO	8.1
## 168	0.227	5.6131281	5.1283526	NO	26.3
## 169	0.505	5.2470241	4.2308392	NO	17.9
## 170	0.369	4.8978398	3.5071356	NO	12.3
## 311	0.952	4.8040210	3.3316663	YES	11.1
## 312	0.739	4.9558271	3.6193922	YES	13.1
## 313	0.482	3.2580965	1.2247449	NO	1.5
## 314	0.519	3.3672958	1.3416408	NO	1.8
## 315	0.558	5.8377304	5.7619441	NO	33.2
## 316	0.345	3.9512437	2.0248457	NO	4.1

## 317	0.750	0.0000000	NA	YES	-1.0
## 318	0.738	3.0910425	1.0488088	YES	1.1
## 319	0.479	4.0943446	2.2135944	NO	4.9
## 320	0.314	1.6094379	NA	NO	-0.6
## 321	0.700	4.4659081	2.7568097	YES	7.6
## 322	0.338	0.0000000	NA	NO	-1.0
## 323	0.461	5.3132060	4.3817805	NO	19.2
## 324	0.595	3.7376696	1.7606817	NO	3.1
## 325	0.389	5.4510385	4.7116876	NO	22.2
## 326	0.368	4.5538769	2.8982753	NO	8.4
## 327	0.493	3.6109179	1.6124516	NO	2.6
## 328	0.361	5.1179938	3.9496835	NO	15.6
## 329	0.764	3.9702919	2.0493902	YES	4.2
## 330	0.764	4.3174881	2.5298221	YES	6.4
## 331	0.338	5.2574954	4.2544095	NO	18.1
## 332	0.365	5.3033049	4.3588989	NO	19.0
## 333	0.550	5.9242558	6.0249481	NO	36.3
## 334	0.480	3.2188758	1.1832160	NO	1.4
## 335	0.632	6.1158921	6.6483081	YES	44.2
## 336	0.712	6.1675165	6.8264193	YES	46.6
## 337	0.345	5.4380793	4.6797436	NO	21.9
## 338	0.269	6.8134446	9.4815611	NO	89.9
## 339	0.566	5.4424177	4.6904158	NO	22.0
## 340	0.464	3.8286414	1.8708287	NO	3.5
## 495	NA	0.0000000	NA		NA
## 496	NA	2.6390573	NA		NA
## 497	NA	0.0000000	NA		NA
## 498	NA	2.5649494	NA		NA
## 499	NA	1.0986123	NA		NA
## 500	NA	0.0000000	NA		NA
## 501	NA	0.0000000	NA		NA
## 502	NA	0.0000000	NA		NA
## 503	NA	2.5649494	NA		NA
## 504	NA	0.6931472	NA		NA
## 505	NA	0.0000000	NA		NA
## 506	NA	1.0986123	NA		NA
## 507	NA	0.0000000	NA		NA
## 508	NA	0.0000000	NA		NA
## 509	NA	1.9459101	NA		NA
## 510	NA	2.0794415	NA		NA
## 511	NA	1.3862944	NA		NA
## 512	NA	0.0000000	NA		NA
## 513	NA	0.0000000	NA		NA
## 514	NA	0.0000000	NA		NA
## 515	NA	0.6931472	NA		NA
## 516	NA	0.0000000	NA		NA
## 517	NA	0.0000000	NA		NA
## 518	NA	1.7917595	NA		NA
## 519	NA	0.0000000	NA		NA
## 520	NA	0.0000000	NA		NA
## 521	NA	0.0000000	NA		NA
## 522	NA	3.6888795	NA		NA
## 523	NA	2.4849067	NA		NA
## 524	NA	0.0000000	NA		NA

## 525	NA	2.7725887	NA	NA
## 526	NA	1.6094379	NA	NA
## 527	NA	2.6390573	NA	NA
##	Retain.	Bean.Aphids		
## 141	Keep	NA		
## 142	Keep	NA		
## 143	Drop	NA		
## 144	Drop	NA		
## 145	Keep	NA		
## 146	Keep	NA		
## 147	Keep	NA		
## 148	Keep	NA		
## 149	Drop	NA		
## 150	Drop	NA		
## 151	Drop	NA		
## 152	Keep	NA		
## 153	Drop	NA		
## 154	Drop	NA		
## 155	Drop	NA		
## 156	Drop	NA		
## 157	Keep	NA		
## 158	Keep	NA		
## 159	Keep	NA		
## 160	Keep	NA		
## 161	Drop	NA		
## 162	Drop	NA		
## 163	Keep	NA		
## 164	Keep	NA		
## 165	Drop	NA		
## 166	Keep	NA		
## 167	Drop	NA		
## 168	Drop	NA		
## 169	Keep	NA		
## 170	Keep	NA		
## 311	Keep	NA		
## 312	Keep	NA		
## 313	Drop	NA		
## 314	Drop	NA		
## 315	Keep	NA		
## 316	Keep	NA		
## 317	Keep	NA		
## 318	Keep	NA		
## 319	Drop	NA		
## 320	Drop	NA		
## 321	Drop	NA		
## 322	Keep	NA		
## 323	Drop	NA		
## 324	Drop	NA		
## 325	Drop	NA		
## 326	Drop	NA		
## 327	Keep	NA		
## 328	Keep	NA		
## 329	Keep	NA		
## 330	Keep	NA		

```

## 331      Drop      NA
## 332      Drop      NA
## 333      Keep      NA
## 334      Keep      NA
## 335      Keep      NA
## 336      Keep      NA
## 337      Drop      NA
## 338      Drop      NA
## 339      Keep      NA
## 340      Keep      NA
## 495              6
## 496              0
## 497             84
## 498            214
## 499              8
## 500            46
## 501              0
## 502              0
## 503              0
## 504              0
## 505              1
## 506              1
## 507              0
## 508              0
## 509            68
## 510            22
## 511              0
## 512              0
## 513              0
## 514              0
## 515              2
## 516            51
## 517              4
## 518            44
## 519              0
## 520              0
## 521              0
## 522              0
## 523              0
## 524              0
## 525            41
## 526              6
## 527            76

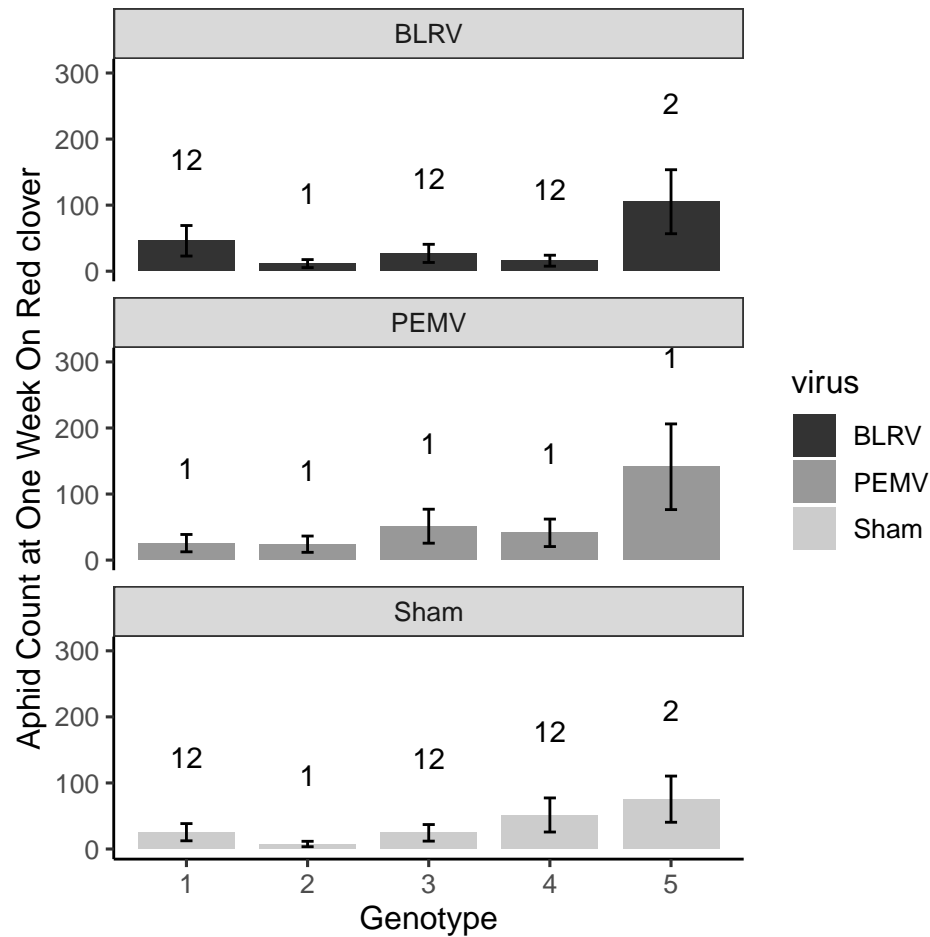
## Note: adjust = "tukey" was changed to "sidak"
## because "tukey" is only appropriate for one set of pairwise comparisons

## Analysis of Deviance Table (Type II tests)
##
## Response: Counts
##              LR Chisq Df Pr(>Chisq)
## Genotype      27.600  4  1.503e-05 ***
## virus          1.991  2    0.3696
## Run           94.688  2 < 2.2e-16 ***

```



```
## Genotype:virus      5.961  8      0.6516
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



#lentil figure

```
## Note: adjust = "tukey" was changed to "sidak"
## because "tukey" is only appropriate for one set of pairwise comparisons
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Counts
##          LR Chisq Df Pr(>Chisq)
## Genotype    19.6913  4  0.0005746 ***
## virus        11.0785  2  0.0039294 **
## Genotype:virus  5.7736  8  0.6725757
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

