07_potted tree data analysis

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```
# rmarkdown::render("07_potted_tree_analysis.R", "pdf_document") Or press Cmd + Shift + K


# Load the required libraries
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(plotrix)
library(ggplot2)
library(vcd)
```

```
## Loading required package: grid
```

```
library(gdata)
```

```
## gdata: read.xls support for 'XLS' (Excel 97-2004) files ENABLED.
```

```
##
```

```
## gdata: read.xls support for 'XLSX' (Excel 2007+) files ENABLED.
```

```
##
## Attaching package: 'gdata'
```

```
## The following objects are masked from 'package:dplyr':
##
##     combine, first, last
```

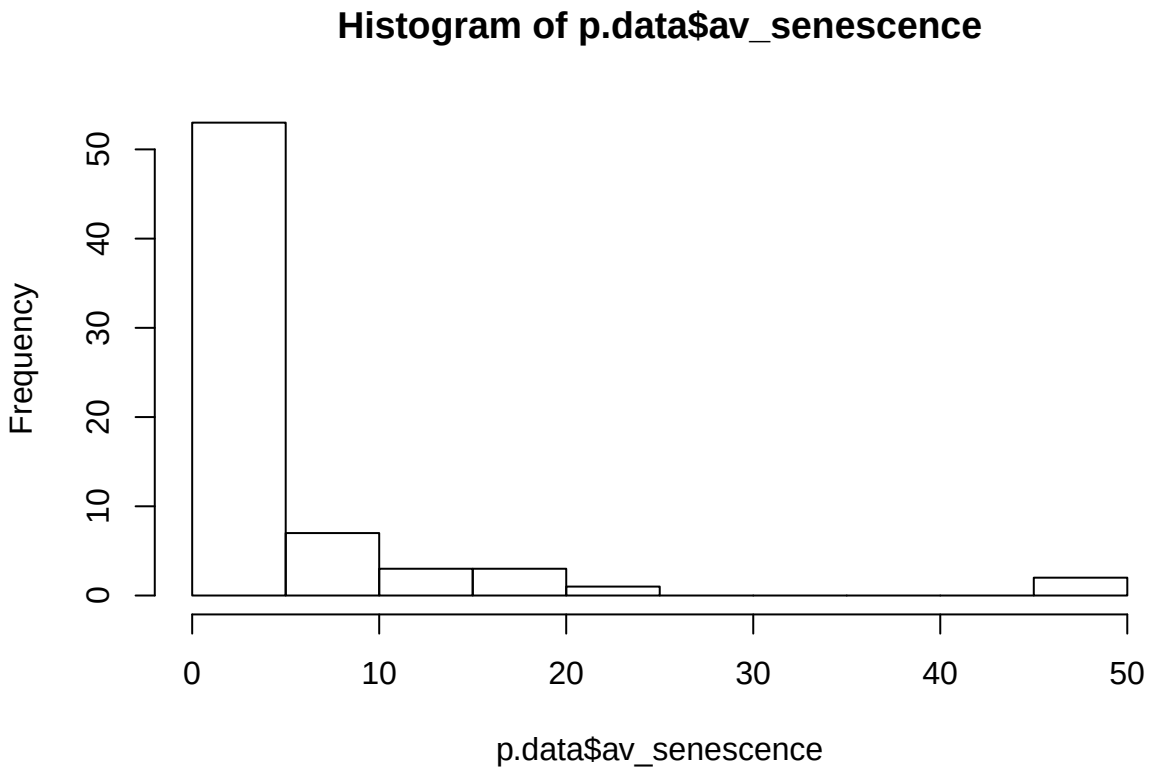
```
## The following object is masked from 'package:stats':
##
##     nobs
```

```
## The following object is masked from 'package:utils':
##
##     object.size
```

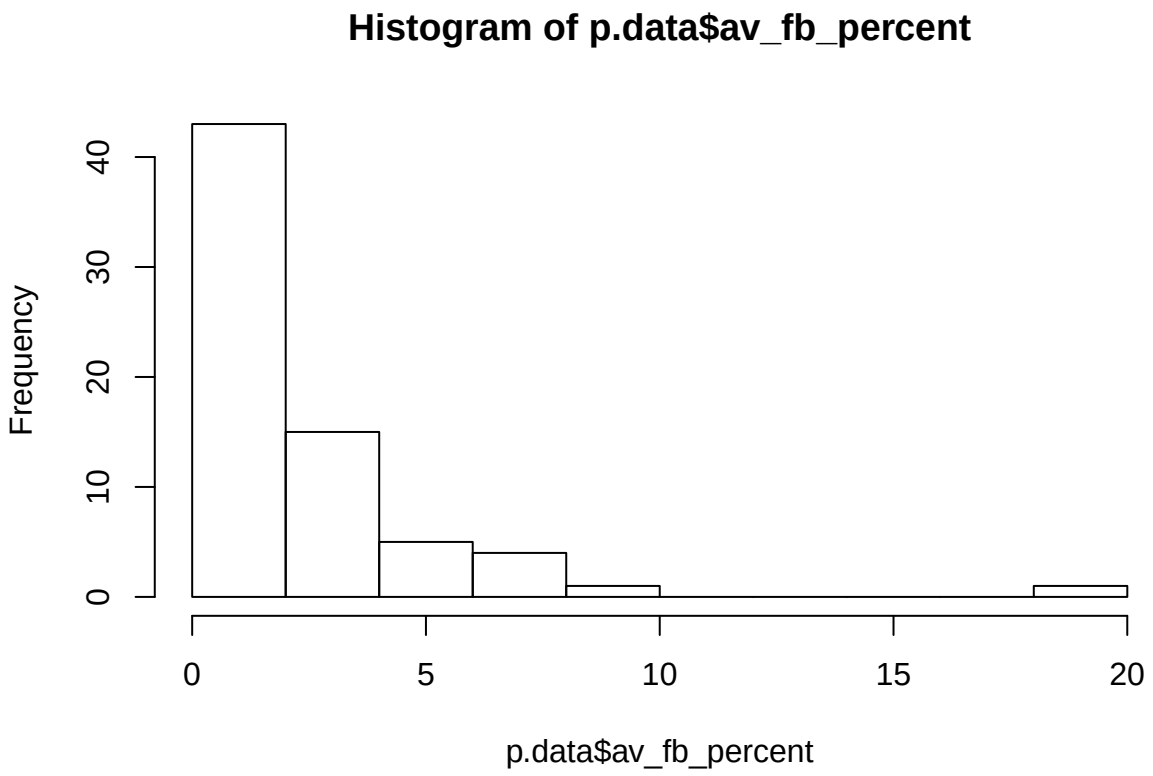
```
## The following object is masked from 'package:base':
##
##     startsWith
```

```
library(agricolae)
# library(RVAideMemoire) # dont need this, for post hoc chi squared
```

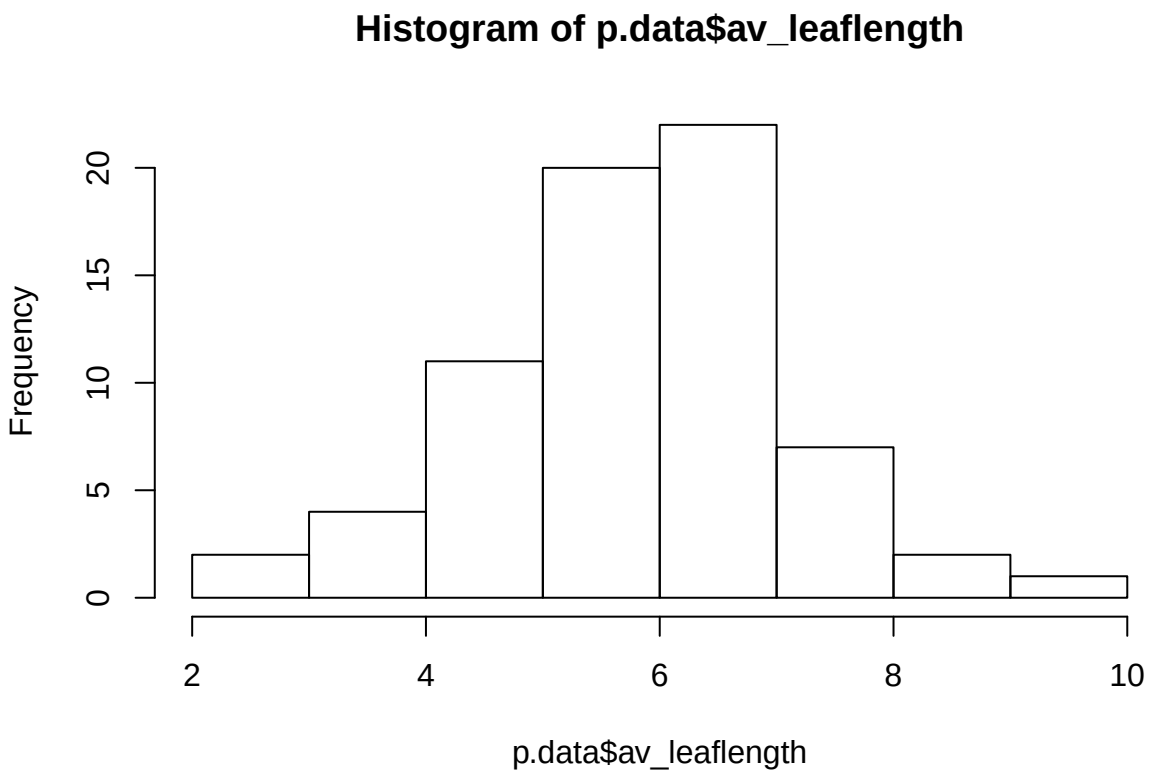
```r
# if get an error message "Error in library() : there is no package called.." you don't have them you c
# install.packages("dplyr")
# install.packages("plotrixr")
# install.packages("ggplot2")
# install.packages("vcd")
# install.packages("gdata")
# install.packages("agricolae")
# install.packages("RVAideMemoire")



# read in cleaned csv
p.data <- read.csv(file = "data/merged_leaf_summary_pot-level_2019clean.csv")


# look at some histograms of our continuous data
hist(p.data$av_senescence)
```



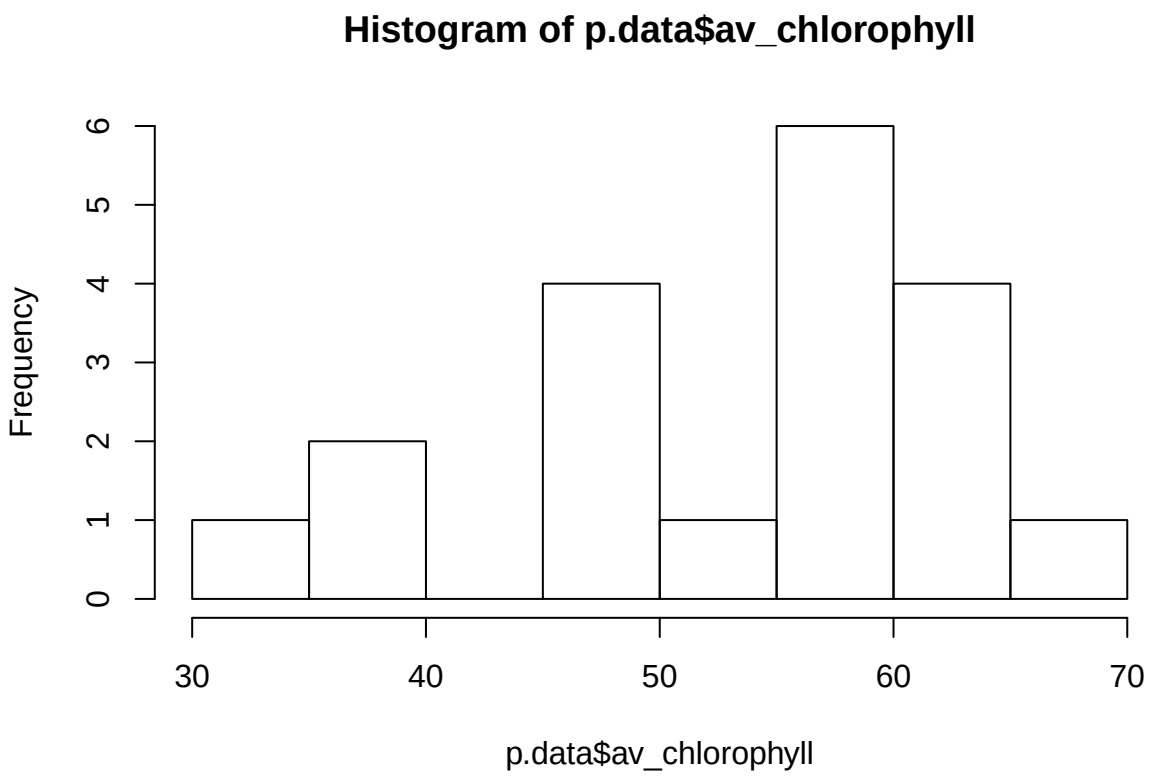

```r
hist(p.data$av_fb_percent)
```



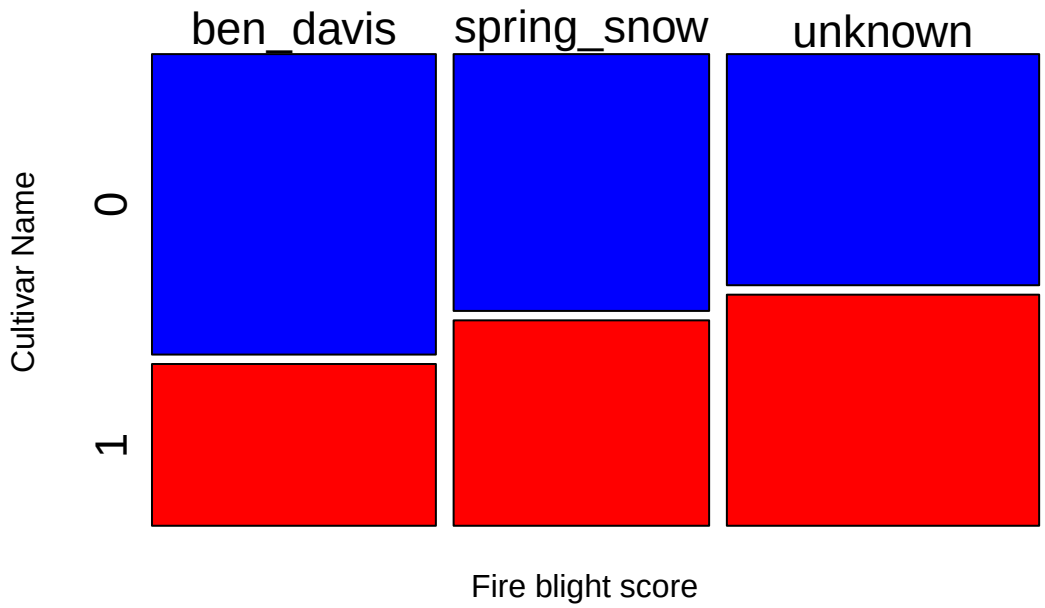

```
hist(p.data$av_leaflength)
```




```
hist(p.data$av_chlorophyll)
```




```
# create variables to use in some graphs below
treatment <- p.data$treatment_code
snip_density <- p.data$snip_density
inocula <- p.data$inocula_type
fb_strip <- p.data$fire_blight_strip_test
tree_ht <- p.data$X42_Tree_height_neare
fb_percent <- p.data$av_fb_percent
senescence <- p.data$av_senescence
l_length <- p.data$av_leaflength
chloro <- p.data$av_chlorophyll
leaf_num_ob <- p.data$num_leaves_obs
treatment_5 <- p.data$treatment_5
cultivar_name <-p.data$cultivar_name
cultivar_number <- p.data$cultivar

# load calc st error function
calcSE <- function(x){sd(x)/sqrt(length(x))}

# interesting analyses and graphs to answer the question about how cultivar and strain impacted tree re
##########################################################################################################


# mosaic plots - cultivar name
mosaicplot(~cultivar_name + fb_strip,
           xlab = "Fire blight score",
           ylab = "Cultivar Name",
           cex.axis = 1.4,
           main = "", # get rid of the main title
           color = c("blue", "red"))
```

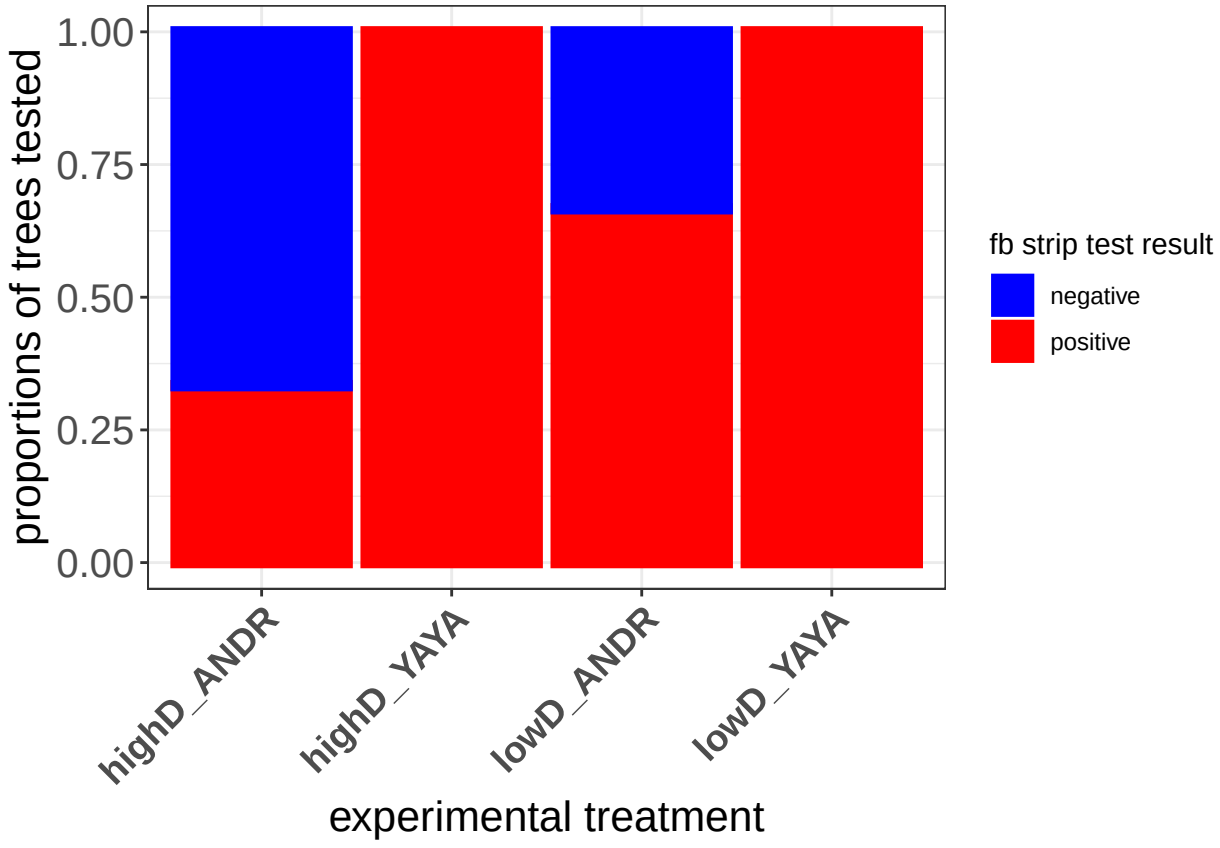



```
# chi square test looking at cultivar
cult_x_fb3 <- data.frame(
  positive_fb = c(length(which(p.data$cultivar == '105' & p.data$fire_blight_strip_test== 1)),
                  length(which(p.data$cultivar == '1030' & p.data$fire_blight_strip_test== 1)),
                  length(which(p.data$cultivar == '577' & p.data$fire_blight_strip_test== 1))),
  negative_fb = c(length(which(p.data$cultivar == '105' & p.data$fire_blight_strip_test== 1)),
                  length(which(p.data$cultivar == '1030' & p.data$fire_blight_strip_test== 0)),
                  length(which(p.data$cultivar == '577' & p.data$fire_blight_strip_test== 0))))

# run the Chi Squared test, no significant differences among cultivars
ch.x <- chisq.test(cult_x_fb3)


# check the Fishers test because of low sample size, this also yields non-significant differences among
fisher.test(cult_x_fb3,
            simulate.p.value = TRUE, # for when you have more than 2 x 2  variables
            hybrid = TRUE) # for when you have more than 2 x 2  variables
```

```
##
##  Fisher's Exact Test for Count Data with simulated p-value (based
##  on 2000 replicates)
##
## data:  cult_x_fb3
## p-value = 0.945
## alternative hypothesis: two.sided
```

```
# incoculated treatment groups for ben davis only
benD <- p.data%>%
  group_by(treatment_code, cultivar_name) %>%
  filter(!is.na(fire_blight_strip_test), cultivar == "105", treatment_code == "highD_ANDR" | treatment_

benD %>%
  ggplot(aes(x = treatment_code, fill = factor(fire_blight_strip_test),
             color = factor(fire_blight_strip_test))) +
  geom_bar(position = 'fill', size = 2) +
```

```
  ylab("proportions of trees tested") +  # yaxis labels
  xlab("experimental treatment") + # xaxis label
  theme_bw() +
  theme(axis.text.x = element_text(face = "bold", size = 14, angle = 45, hjust = 1),
        axis.text.y = element_text(size = 15),
        axis.title = element_text(size = 16)) +
  scale_color_manual(name = "fb strip test result",
                     labels = c("0" = "negative",
                                "1" = "positive"),
                     values = c("0" = "blue",
                                "1" = "red")) +
  scale_fill_manual(name = "fb strip test result",
                    labels = c("0" = "negative",
                               "1" = "positive"),
                    values = c("0" = "blue",
                               "1" = "red"))
```




```
# run a chi square test comparing the strains

benD_y_x_a <- p.data %>%
  filter(cultivar == "105")

benD_y_x_a <- data.frame(
  positive_fb = c(length(which(benD_y_x_a$inocula_type == 'andrus_Ea' & benD_y_x_a$fire_blight_strip_tes
                  length(which(benD_y_x_a$inocula_type == 'yaya_Ea' & benD_y_x_a$fire_blight_strip_test=
  negative_fb = c(length(which(benD_y_x_a$inocula_type == 'andrus_Ea' & benD_y_x_a$fire_blight_strip_tes
                  length(which(benD_y_x_a$inocula_type == 'yaya_Ea' & benD_y_x_a$fire_blight_strip_test=
```

```r
# chi square test looking at high low
chisq.test(benD_y_x_a)
```

```
## Warning in chisq.test(benD_y_x_a): Chi-squared approximation may be
## incorrect
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  benD_y_x_a
## X-squared = 0.97222, df = 1, p-value = 0.3241
```

```r
# check the Fishers test because of low sample size
fisher.test(benD_y_x_a,
            simulate.p.value = TRUE, # for when you have more than 2 x 2  variables
            hybrid = TRUE) # for when you have more than 2 x 2  variables
```

```
## Warning in fisher.test(benD_y_x_a, simulate.p.value = TRUE, hybrid = TRUE):
## 'hybrid' is ignored for a 2 x 2 table
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  benD_y_x_a
## p-value = 0.2
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.000000 3.405921
## sample estimates:
## odds ratio
##          0
```

```r
# run a chi square test comparing the strains and high low treatments

benD_y_x_a <- p.data %>%
  filter(cultivar == "105")

benD_y_x_a_x_hl <- data.frame(
  positive_fb = c(length(which(benD_y_x_a$treatment_code == 'highD_ANDR' & benD_y_x_a$fire_blight_strip
                  length(which(benD_y_x_a$treatment_code == 'highD_YAYA' & benD_y_x_a$fire_blight_strip
                  length(which(benD_y_x_a$treatment_code == 'lowD_ANDR' & benD_y_x_a$fire_blight_strip_
                  length(which(benD_y_x_a$treatment_code == 'lowD_YAYA' & benD_y_x_a$fire_blight_strip_
  negative_fb = c(length(which(benD_y_x_a$treatment_codee == 'highD_ANDR' & benD_y_x_a$fire_blight_stri
                  length(which(benD_y_x_a$treatment_code == 'highD_YAYA' & benD_y_x_a$fire_blight_strip
                  length(which(benD_y_x_a$treatment_code == 'lowD_ANDR' & benD_y_x_a$fire_blight_strip_
                  length(which(benD_y_x_a$treatment_code == 'lowD_YAYA' & benD_y_x_a$fire_blight_strip_

# chi square test looking at high low, not significant
chisq.test(benD_y_x_a_x_hl)
```

```
## Warning in chisq.test(benD_y_x_a_x_hl): Chi-squared approximation may be
## incorrect
```

```
##
##  Pearson's Chi-squared test
##
```

```
## data:  benD_y_x_a_x_hl
## X-squared = 1.9048, df = 3, p-value = 0.5924
```

```
# check the Fishers test because of low sample size, also not significant
fisher.test(benD_y_x_a_x_hl,
            simulate.p.value = TRUE, # for when you have more than 2 x 2  variables
            hybrid = TRUE) # for when you have more than 2 x 2  variables
```

```
##
##  Fisher's Exact Test for Count Data with simulated p-value (based
##  on 2000 replicates)
##
## data:  benD_y_x_a_x_hl
## p-value = 1
## alternative hypothesis: two.sided
```

```
# check treatment comparisons with ANOVA with cultivar as predictors **this test shows a significant di
anova_model4 <- aov(senescence~cultivar_name, data= p.data)
summary(anova_model4) # view the results
```

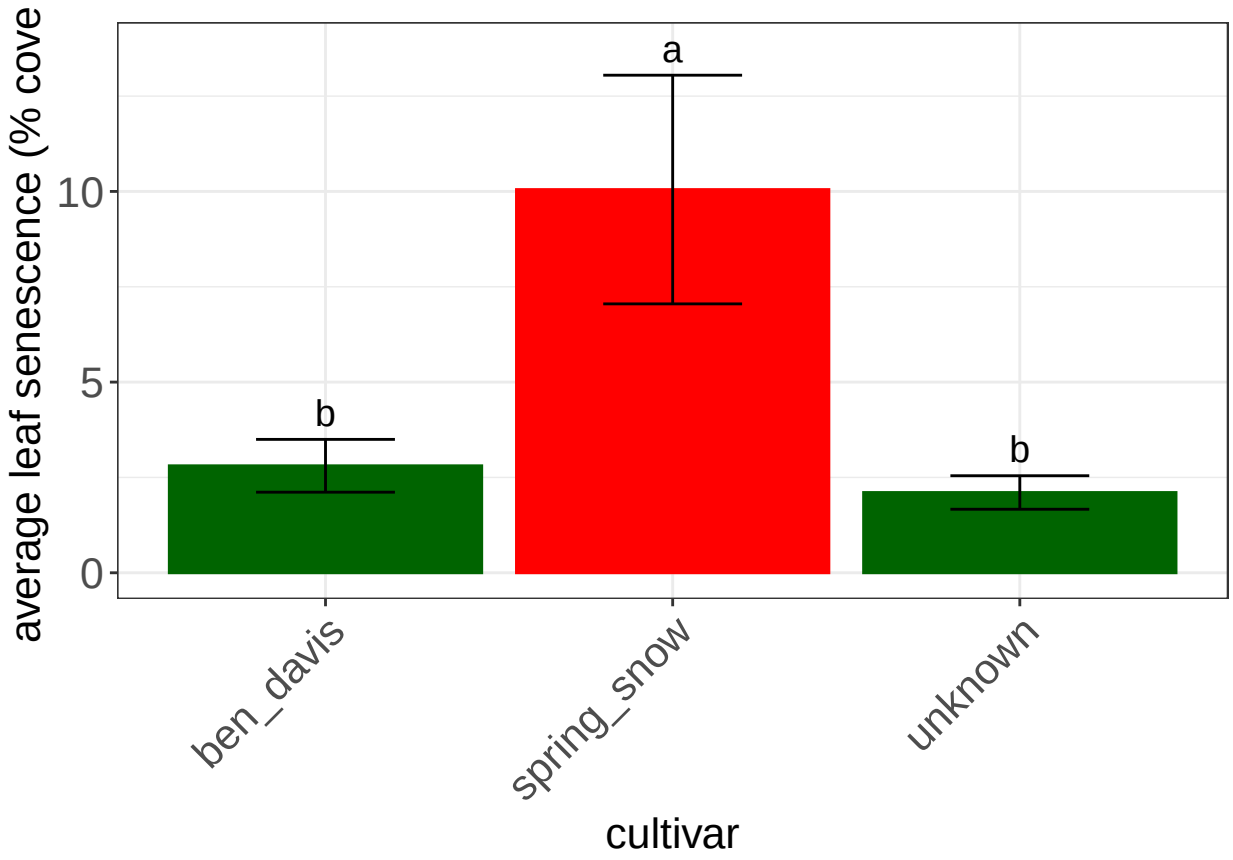
```
##               Df Sum Sq Mean Sq F value  Pr(>F)
## cultivar_name  2    886   443.2   5.966 0.00415 **
## Residuals     66   4903    74.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3 observations deleted due to missingness
```

```
TukeyHSD(anova_model4) # check the group comparisons, we see that spring snow is significantly more sen
```

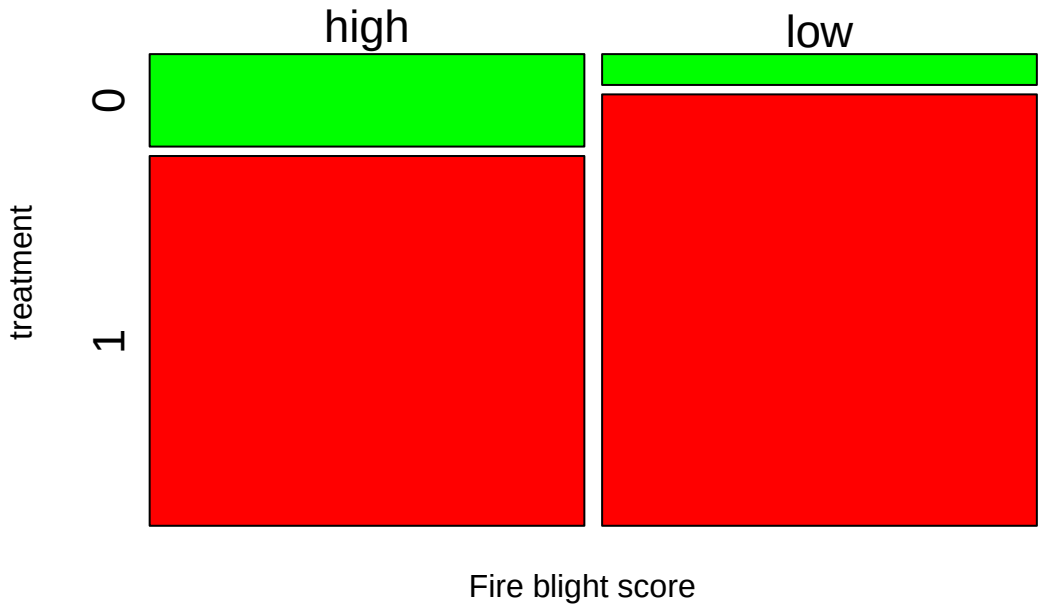
```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = senescence ~ cultivar_name, data = p.data)
##
## $cultivar_name
##                              diff        lwr       upr     p adj
## spring_snow-ben_davis  7.2441556   1.213795 13.274516 0.0146116
## unknown-ben_davis     -0.7006972  -6.800641  5.399246 0.9590719
## unknown-spring_snow   -7.9448528 -14.107891 -1.781815 0.0081131
```

```
# chi square test looking snip density and cultivar

# prepare a dataset with the summarized group variables
results1 <- HSD.test(anova_model4, "cultivar_name", group = TRUE) # save the output of the post hoc tes
results1 <- results1$groups[order(rownames(results1$groups)), ] # make sure that the cultivars match th
sen_means1 <- aggregate(av_senescence ~ cultivar_name, data = p.data, mean) # calc group means
sen_SE1 <- aggregate(av_senescence ~ cultivar_name, data = p.data, calcSE) # calc group st. errors
sen_means1$SE_lower <- sen_means1$av_senescence - sen_SE1$av_senescence # create upper bound of st. err
sen_means1$SE_upper <- sen_means1$av_senescence + sen_SE1$av_senescence # create lower bound of st. err
sen_means1$letters <- results1$groups # save the letter, which represent which groups are statistically

# grpah the differences in senescence between cultivars
area.color1 <- c("darkgreen", "red", "darkgreen") # save colors to use, you could change these, but red

ggplot(data = sen_means1, mapping = aes(x = cultivar_name, y = av_senescence)) +
  geom_bar(stat = "identity", color = area.color1, fill = area.color1) +
  geom_errorbar(aes(ymin = SE_lower, ymax = SE_upper), width = 0.4) +
```

```
  geom_text(aes(x = cultivar_name, y = SE_upper+.7, label = letters), size = 5)+
  ylab("average leaf senescence (% cover)") +
  xlab("cultivar") +
  theme_bw() +
  theme(axis.text.x = element_text(size = 16, angle = 45, hjust = 1),
        axis.title.x = element_text(size = 16),
        axis.title.y = element_text(size = 16),
        axis.text.y = element_text(size = 16))
```




```
##########################################################################################################
##########################################################################################################
# interesting analyses and graphs to answer the question about how the high low snip density treatments

# mosaic plots - compare high and low density inoculated treatments
densit.d <- p.data %>%
  filter(treatment_5 == "highD_inoc" | treatment_5 == "lowD_inoc") %>%
  filter(snip_density != "no_snip")
densit.d <- gdata::drop.levels(densit.d) # drop the unused level using gdata package
mosaicplot(~densit.d$snip_density + densit.d$fire_blight_strip_test,
           xlab = "Fire blight score",
           ylab = "treatment",
           cex.axis = 1.4,
           main = "", # get rid of the main title
           color = c("green", "red"))
```




```
# chi square test to compare high and low density inoculated treatments
high_x_low <- data.frame(
  positive_fb = c(length(which(p.data$treatment_5 == 'highD_inoc' & p.data$fire_blight_strip_test== 1))
                  length(which(p.data$treatment_5 == 'lowD_inoc' & p.data$fire_blight_strip_test== 1)))
  negative_fb = c(length(which(p.data$treatment_5 == 'highD_inoc' & p.data$fire_blight_strip_test== 0))
                  length(which(p.data$treatment_5 == 'lowD_inoc' & p.data$fire_blight_strip_test== 0))))


# run the Chi Squared test
chisq.test(high_x_low)
```

```
## Warning in chisq.test(high_x_low): Chi-squared approximation may be
## incorrect
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  high_x_low
## X-squared = 0.28846, df = 1, p-value = 0.5912
```

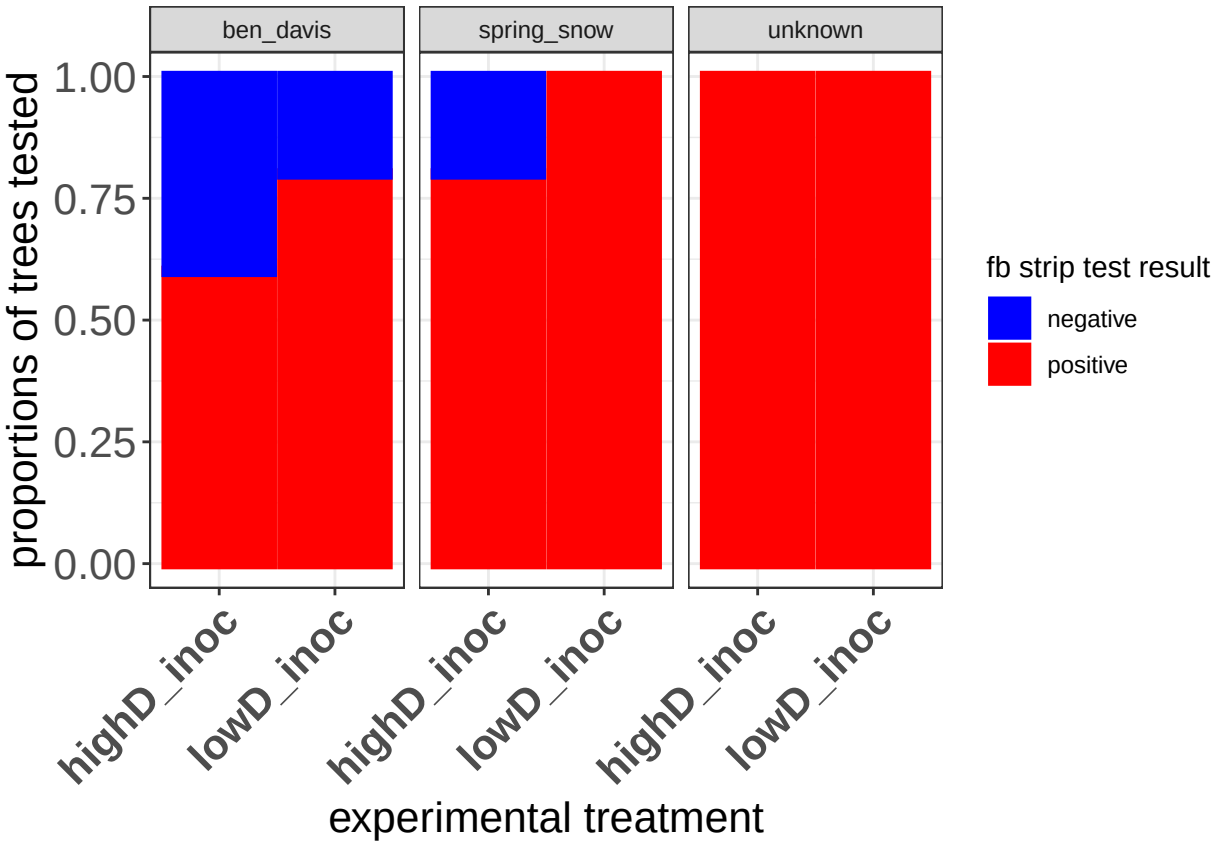
```
# check the Fishers test because of low sample size
fisher.test(high_x_low,
            simulate.p.value = TRUE, # for when you have more than 2 x 2  variables
            hybrid = TRUE) # for when you have more than 2 x 2  variables
```

```
## Warning in fisher.test(high_x_low, simulate.p.value = TRUE, hybrid = TRUE):
## 'hybrid' is ignored for a 2 x 2 table
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  high_x_low
## p-value = 0.5977
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.005092481 4.276366213
## sample estimates:
```

```
## odds ratio
##  0.2972859
```

```
#  count the # of fb strip test positive and negatives for high and low snip inculated treatment groups
p.data%>%
  group_by(treatment_5, cultivar_name) %>%
  filter(!is.na(fire_blight_strip_test)) %>%
  filter(treatment_5 == "highD_inoc" | treatment_5 == "lowD_inoc") %>%
  ggplot(aes(x = treatment_5, fill = factor(fire_blight_strip_test),
             color = factor(fire_blight_strip_test))) +
  geom_bar(position = 'fill', size = 2) +
  facet_wrap(facets = ~cultivar_name)+
  ylab("proportions of trees tested") +  # yaxis labels
  xlab("experimental treatment") + # xaxis label
  theme_bw() +
  theme(axis.text.x = element_text(face = "bold", size = 16, angle = 45, hjust = 1),
        axis.title = element_text(size = 16),
        axis.text.y = element_text(size = 16)) +
  scale_color_manual(name = "fb strip test result",
                     labels = c("0" = "negative",
                                "1" = "positive"),
                     values = c("0" = "blue",
                                "1" = "red")) +
  scale_fill_manual(name = "fb strip test result",
                    labels = c("0" = "negative",
                               "1" = "positive"),
                    values = c("0" = "blue",
                               "1" = "red"))
```




```
# chi square test looking snip density and cultivar
# filter to look at high and low inoculated data only
high.low.data <- p.data %>%
  filter(treatment_5 == "highD_inoc" | treatment_5 == "lowD_inoc" ) %>%
  mutate(treatment_cultivar = as.factor(paste0(cultivar,"-",treatment_5)))

# build the contigency table
cult_x_highlow <- data.frame(
  positive_fb = c(length(which(high.low.data$treatment_cultivar == '105-highD_inoc' & high.low.data$fir
                  length(which(high.low.data$treatment_cultivar == '105-lowD_inoc' & high.low.data$fire
                  length(which(high.low.data$treatment_cultivar == '577-highD_inoc' & high.low.data$fir
                  length(which(high.low.data$treatment_cultivar == '577-lowD_inoc' & high.low.data$fire
                  length(which(high.low.data$treatment_cultivar == '1030-highD_inoc' & high.low.data$fi
                  length(which(high.low.data$treatment_cultivar == '1030-lowD_inoc' & high.low.data$fir
  negative_fb = c(length(which(high.low.data$treatment_cultivar == '105-highD_inoc' & high.low.data$fir
                  length(which(high.low.data$treatment_cultivar == '105-lowD_inoc' & high.low.data$fire
                  length(which(high.low.data$treatment_cultivar == '577-highD_inoc' & high.low.data$fir
                  length(which(high.low.data$treatment_cultivar == '577-lowD_inoc' & high.low.data$fire
                  length(which(high.low.data$treatment_cultivar == '1030-highD_inoc' & high.low.data$fi
                  length(which(high.low.data$treatment_cultivar == '1030-lowD_inoc' & high.low.data$fir

# view contingency table
cult_x_highlow
```

```
##   positive_fb negative_fb
## 1           3           2
## 2           4           1
```

```
## 3           5           0
## 4           6           0
## 5           4           1
## 6           4           0
```

```
# run the Chi Squared test
chisq.test(cult_x_highlow)
```

```
## Warning in chisq.test(cult_x_highlow): Chi-squared approximation may be
## incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  cult_x_highlow
## X-squared = 5.7692, df = 5, p-value = 0.3293
```

```
# check the Fishers test because of low sample size
fisher.test(cult_x_highlow,
            simulate.p.value = TRUE, # for when you have more than 2 x 2  variables
            hybrid = TRUE) # for when you have more than 2 x 2  variables
```

```
##
##  Fisher's Exact Test for Count Data with simulated p-value (based
##  on 2000 replicates)
##
## data:  cult_x_highlow
## p-value = 0.3888
## alternative hypothesis: two.sided
```

```
# not significant, even though the graph appears like #577 unknown would be different than ben davis an


# check treatment comparisons with ANOVA with snip density as predictors **this test shows a significan
anova_model12 <- aov(av_fb_percent~treatment_5, data= p.data)
summary(anova_model12) # view the results
```

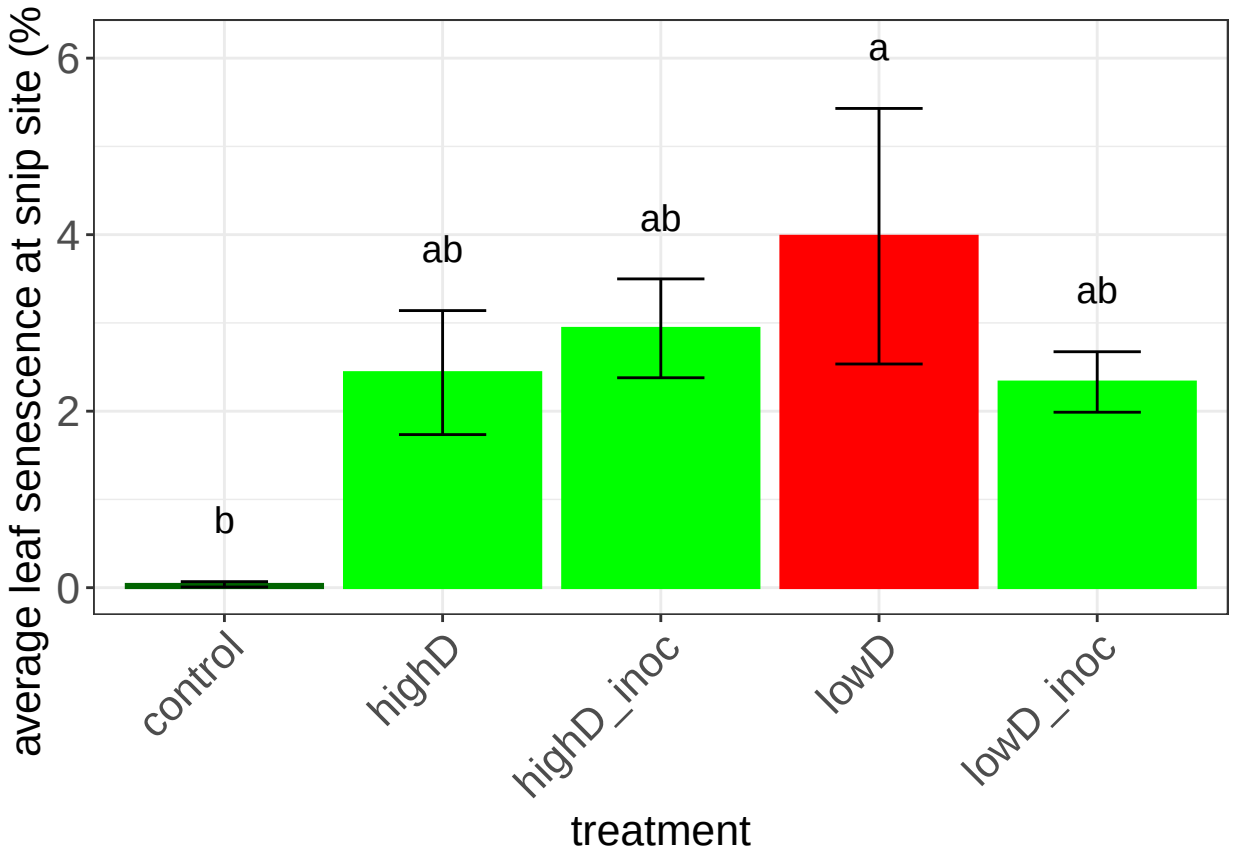
```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treatment_5  4   96.4  24.105   3.359 0.0147 *
## Residuals   64  459.3   7.177
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3 observations deleted due to missingness
```

```
TukeyHSD(anova_model12) # check the group comparisons, we see that spring snow is significantly more se
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = av_fb_percent ~ treatment_5, data = p.data)
##
## $treatment_5
##                           diff          lwr      upr     p adj
## highD-control         2.3991751 -0.739804122 5.538154 0.2140090
## highD_inoc-control    2.9006925 -0.009151484 5.810537 0.0511139
## lowD-control          3.9444349  0.805455683 7.083414 0.0067764
## lowD_inoc-control     2.2929353 -0.616908671 5.202779 0.1885435
## highD_inoc-highD      0.5015174 -2.333759070 3.336794 0.9874151
```

```
## lowD-highD             1.5452598 -1.524722480 4.615242 0.6217298
## lowD_inoc-highD       -0.1062398 -2.941516257 2.729037 0.9999716
## lowD-highD_inoc        1.0437424 -1.791534015 3.879019 0.8389594
## lowD_inoc-highD_inoc -0.6077572 -3.187058218 1.971544 0.9638426
## lowD_inoc-lowD       -1.6514996 -4.486776062 1.183777 0.4810191
```

```r
# prepare a dataset with the summarized group variables
results2 <- HSD.test(anova_model12, "treatment_5", group = TRUE) # save the output of the post hoc test
results2 <- results2$groups[order(rownames(results2$groups)), ] # make sure that the cultivars match th
sen_means2 <- aggregate(av_fb_percent ~ treatment_5, data = p.data, mean) # calc group means
sen_SE2 <- aggregate(av_fb_percent ~ treatment_5, data = p.data, calcSE) # calc group st. errors
sen_means2$SE_lower <- sen_means2$av_fb_percent - sen_SE2$av_fb_percent # create upper bound of st. err
sen_means2$SE_upper <- sen_means2$av_fb_percent + sen_SE2$av_fb_percent # create lower bound of st. err
sen_means2$letters <- results2$groups # save the letter, which represent which groups are statistically

# grpah the differences in senescence between cultivars
area.color2 <- c("darkgreen", "green", "green", "red", "green") # save colors to use, you could change

ggplot(data = sen_means2, mapping = aes(x = treatment_5, y = av_fb_percent)) +
  geom_bar(stat = "identity", color = area.color2, fill = area.color2) +
  geom_errorbar(aes(ymin = SE_lower, ymax = SE_upper), width = 0.4) +
  geom_text(aes(x = treatment_5, y = SE_upper+.7, label = letters), size = 5)+
  ylab("average leaf senescence at snip site (% cover)") +
  xlab("treatment") +
  theme_bw() +
  theme(axis.text.x = element_text(size = 16, angle = 45, hjust = 1),
        axis.title.x = element_text(size = 16),
        axis.title.y = element_text(size = 16),
        axis.text.y = element_text(size = 16))
```




```
# So here we are looking at total senescence as predicted by treatment and cultivar, this test yielded
anova_model7 <- aov(fb_percent~treatment_5 + cultivar_name, data= p.data)
summary(anova_model7) # view the results
```

```
##                Df Sum Sq Mean Sq F value Pr(>F)
## treatment_5     4   96.4  24.105   3.279 0.0167 *
## cultivar_name   2    3.5   1.757   0.239 0.7881
## Residuals      62  455.8   7.351
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3 observations deleted due to missingness
```

```
# post hoc test to see what differed
TukeyHSD(anova_model7) #its really just the lowD compared to the control, which isn't super interesting
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = fb_percent ~ treatment_5 + cultivar_name, data = p.data)
##
## $treatment_5
##                             diff         lwr      upr     p adj
## highD-control          2.3991751 -0.78075741 5.579108 0.2248641
## highD_inoc-control     2.9006925 -0.04711532 5.848500 0.0558738
## lowD-control           3.9444349  0.76450240 7.124368 0.0078127
## lowD_inoc-control      2.2929353 -0.65487250 5.240743 0.1988245
## highD_inoc-highD       0.5015174 -2.37075004 3.373785 0.9879632
## lowD-highD             1.5452598 -1.56477559 4.655295 0.6324933
```

```
## lowD_inoc-highD      -0.1062398 -2.97850723 2.766028 0.9999729
## lowD-highD_inoc       1.0437424 -1.82852499 3.916010 0.8447388
## lowD_inoc-highD_inoc -0.6077572 -3.22070956 2.005195 0.9653495
## lowD_inoc-lowD       -1.6514996 -4.52376703 1.220768 0.4933792
##
## $cultivar_name
##                              diff       lwr      upr     p adj
## spring_snow-ben_davis -0.5433066 -2.443086 1.356472 0.7720905
## unknown-ben_davis     -0.3207478 -2.242448 1.600952 0.9153907
## unknown-spring_snow    0.2225587 -1.719019 2.164136 0.9591236
```

```
# lets check if this is signficant after taking out the control trees
treatment_4 <- p.data %>%
  filter(treatment_5 != "control")
anova_model8 <- aov(av_fb_percent~treatment_5 + cultivar_name, data= treatment_4)
summary(anova_model8) # view the results, not significant among high and low density snip trees
```

```
##               Df Sum Sq Mean Sq F value Pr(>F)
## treatment_5    3   22.1   7.373   0.843  0.477
## cultivar_name  2    4.3   2.137   0.244  0.784
## Residuals     52  454.9   8.749
## 2 observations deleted due to missingness
```

```
# lets check differences in total senescence with treatment and cultivar as predictors
anova_model11 <- aov(av_senescence~treatment_cultivar, data= high.low.data)
summary(anova_model11) # view the results, not significant among high and low density snip tree treatme
```

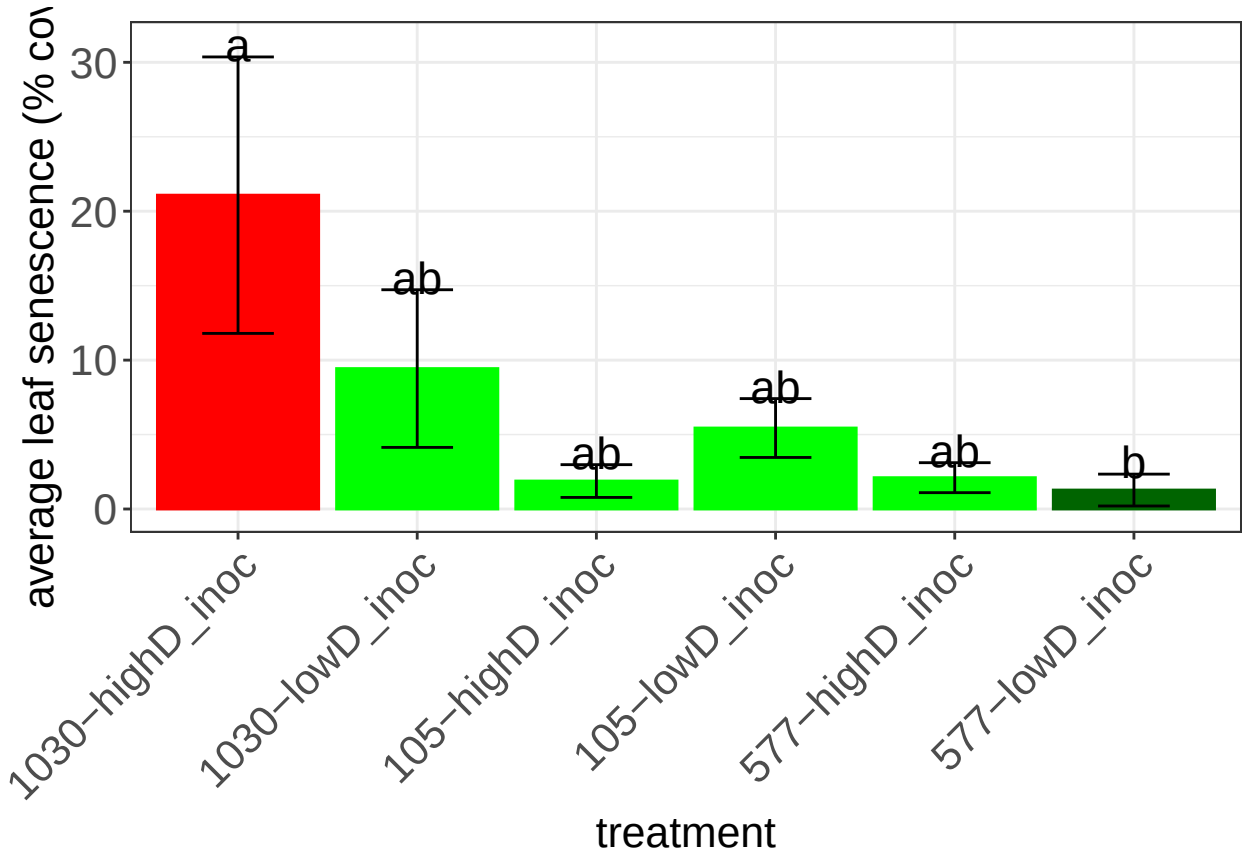
```
##                   Df Sum Sq Mean Sq F value Pr(>F)
## treatment_cultivar  5   1707   341.5    2.85 0.0334 *
## Residuals          28   3355   119.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 2 observations deleted due to missingness
```

```
TukeyHSD(anova_model11)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = av_senescence ~ treatment_cultivar, data = high.low.data)
##
## $treatment_cultivar
##                                         diff       lwr        upr     p adj
## 1030-lowD_inoc-1030-highD_inoc -11.6473883 -31.90189  8.6071135 0.5077720
## 105-highD_inoc-1030-highD_inoc -19.2008803 -38.51279  0.1110294 0.0519980
## 105-lowD_inoc-1030-highD_inoc  -15.6399524 -34.95186  3.6719573 0.1660122
## 577-highD_inoc-1030-highD_inoc -18.9751351 -39.22964  1.2793667 0.0762121
## 577-lowD_inoc-1030-highD_inoc  -19.8059780 -39.11789 -0.4940683 0.0419220
## 105-highD_inoc-1030-lowD_inoc   -7.5534921 -27.80799 12.7010097 0.8605784
## 105-lowD_inoc-1030-lowD_inoc    -3.9925641 -24.24707 16.2619377 0.9899947
## 577-highD_inoc-1030-lowD_inoc   -7.3277468 -28.48288 13.8273903 0.8934100
## 577-lowD_inoc-1030-lowD_inoc    -8.1585897 -28.41309 12.0959120 0.8181145
## 105-lowD_inoc-105-highD_inoc     3.5609280 -15.75098 22.8728377 0.9926273
## 577-highD_inoc-105-highD_inoc    0.2257452 -20.02876 20.4802470 1.0000000
## 577-lowD_inoc-105-highD_inoc    -0.6050977 -19.91701 18.7068120 0.9999987
## 577-highD_inoc-105-lowD_inoc    -3.3351827 -23.58968 16.9193190 0.9956391
```

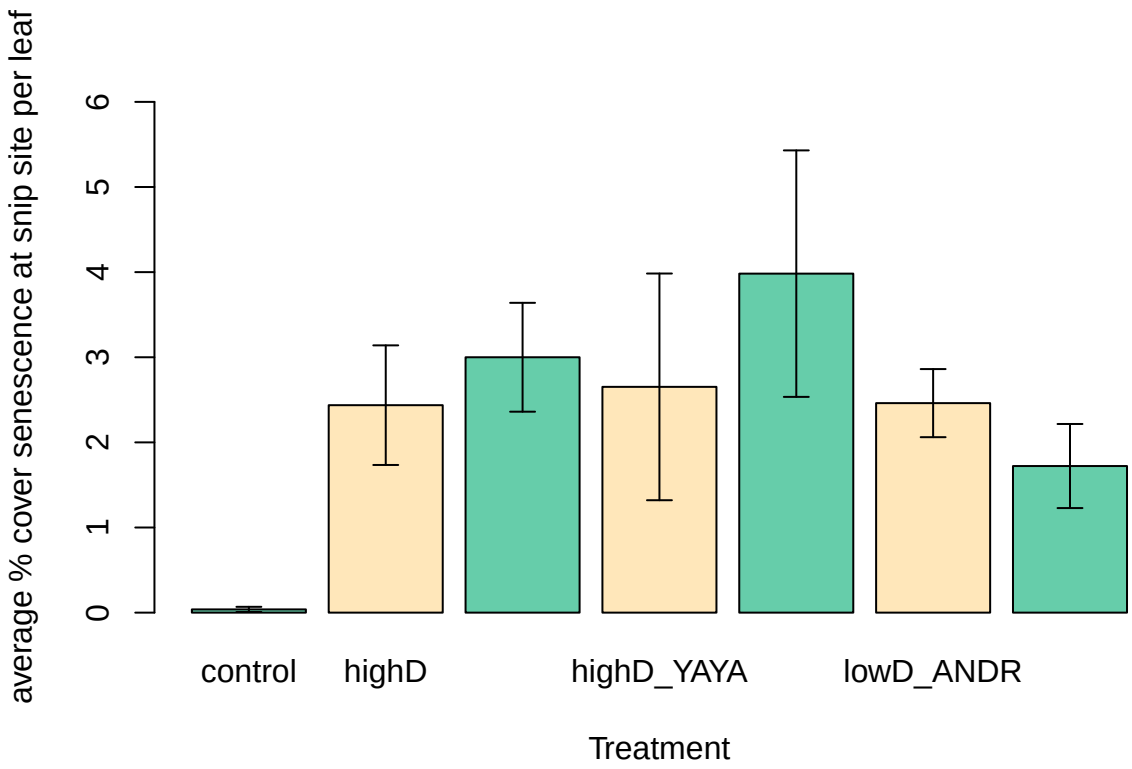
```
## 577-lowD_inoc-105-lowD_inoc     -4.1660256 -23.47794 15.1458841 0.9849803
## 577-lowD_inoc-577-highD_inoc    -0.8308429 -21.08534 19.4236588 0.9999951
```

```r
results <- HSD.test(anova_model11, "treatment_cultivar", group = TRUE)
results <- results$groups[order(rownames(results$groups)), ]
sen_means <- aggregate(av_senescence ~ treatment_cultivar, data = high.low.data, mean)
sen_SE <- aggregate(av_senescence ~ treatment_cultivar, data = high.low.data, calcSE)
sen_means$SE_lower <- sen_means$av_senescence - sen_SE$av_senescence
sen_means$SE_upper <- sen_means$av_senescence + sen_SE$av_senescence
sen_means$letters <- results$groups

#
area.color <- c("red", "green", "green", "green", "green", "darkgreen")

ggplot(data = sen_means, mapping = aes(x = treatment_cultivar, y = av_senescence)) +
  geom_bar(stat = "identity", color = area.color, fill = area.color) +
  geom_errorbar(aes(ymin = SE_lower, ymax = SE_upper), width = 0.4) +
  geom_text(aes(x = treatment_cultivar, y = SE_upper+.8, label = letters), size = 6)+
  ylab("average leaf senescence (% cover)") +
  xlab("treatment") +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1, size = 16),
        axis.text.y = element_text(size = 16),
        axis.title = element_text(size = 16))
```




```r
# OTHER GRAPHS/TESTS that aren't super interesting, or that are graphed in a better way above.
##########################################################################################################
##########################################################################################################
```

```
# 4.3 Bar graph- fireblight % coverage with all 7 treatment groups
htMean <- aggregate(fb_percent~treatment, data=p.data, mean)
htSE <- aggregate(fb_percent~treatment, data=p.data, calcSE)
plotCI(barplot(htMean[,2], beside=T,
               ylim=c(0,6),
               ylab="average % cover senescence at snip site per leaf",
               xlab="Treatment",
               col=c("aquamarine3","wheat1"),
               names.arg=c(levels(p.data$treatment_code))), # name the levels of categories
       htMean[,2], uiw=htSE[,2], add=T, pch=NA)
```

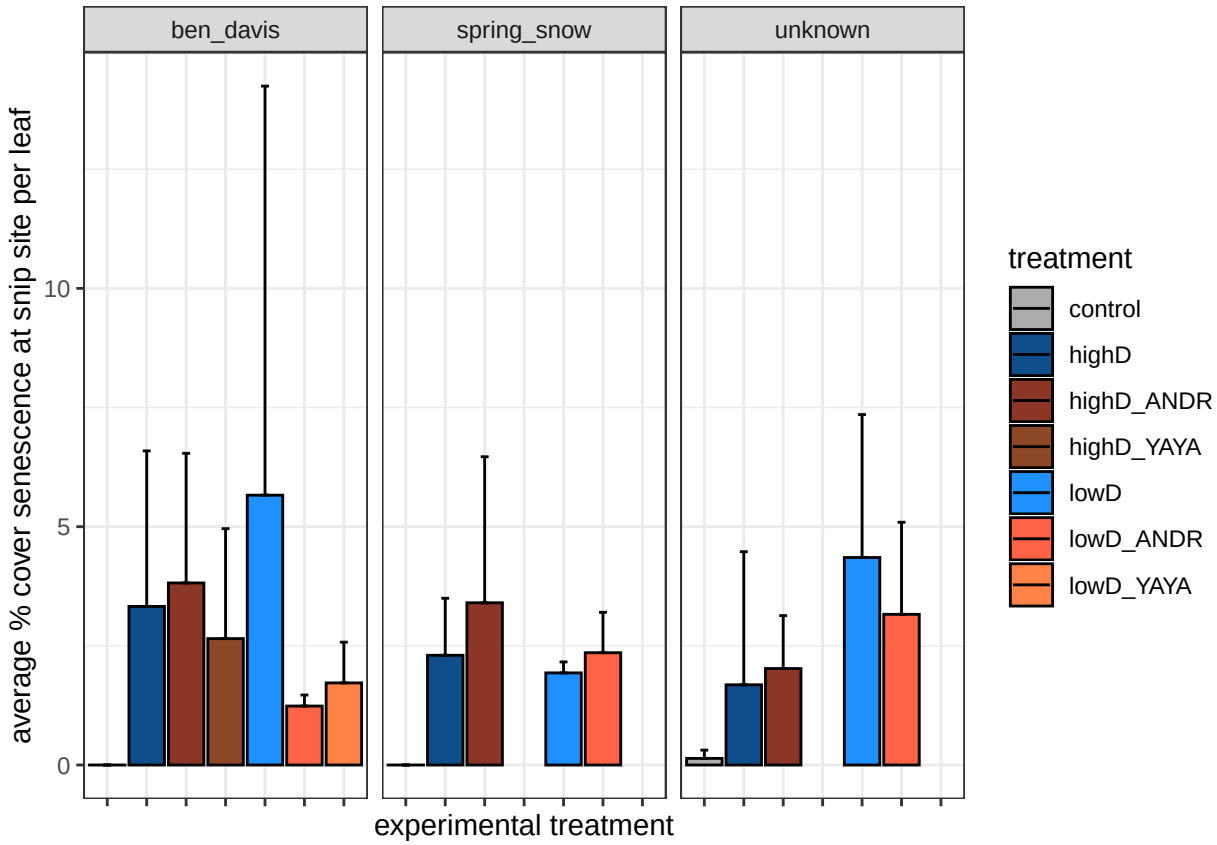



```
# check treatment comparisons with ANOVA

# So here we are looking at fire blight % as predicted by treatment
anova_model2 <- aov(fb_percent~treatment, data= p.data)
summary(anova_model2) # view the results
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treatment    6   98.1  16.345   2.214 0.0533 .
## Residuals   62  457.7   7.382
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3 observations deleted due to missingness
```

```
#  add means and se error bars for snip site with 7 treatment groups
p.data %>%
  group_by(treatment_code, cultivar_name) %>%
  summarize("av_fb_me" = mean(av_fb_percent, na.rm = TRUE), "av_fb_sd"= sd(av_fb_percent, na.rm = TRUE)
  ggplot(aes(x = treatment_code, y = av_fb_me,
             color = treatment_code,
```

```
            fill = treatment_code)) +
  geom_bar(stat = 'identity') +
  facet_wrap(facets = ~cultivar_name)+
  ylab("average % cover senescence at snip site per leaf") +  # yaxis labels
  xlab("experimental treatment") + # xaxis label
  theme_bw() +
  theme(axis.text.x = element_blank()) +
  scale_color_manual(name = "treatment",
                     labels = c("control",
                                "highD",
                                "highD_ANDR",
                                "highD_YAYA",
                                "lowD",
                                "lowD_ANDR",
                                "lowD_YAYA"),
                     values = c("control" = "black",
                                "highD" = "black",
                                "highD_ANDR" = "black",
                                "highD_YAYA" = "black",
                                "lowD" = "black",
                                "lowD_ANDR" = "black",
                                "lowD_YAYA" = "black")) +
  scale_fill_manual(name = "treatment",
                    labels = c("control",
                               "highD",
                               "highD_ANDR",
                               "highD_YAYA",
                               "lowD",
                               "lowD_ANDR",
                               "lowD_YAYA"),
                    values = c("control" = "grey68",
                               "highD" = "dodgerblue4",
                               "highD_ANDR" = "tomato4",
                               "highD_YAYA" = "sienna4",
                               "lowD" = "dodgerblue1",
                               "lowD_ANDR" = "tomato1",
                               "lowD_YAYA" = "sienna1")) +
  geom_errorbar(aes(ymin = av_fb_me, ymax = av_fb_me + av_fb_sd), width = 0.2, position = position_dodg
```

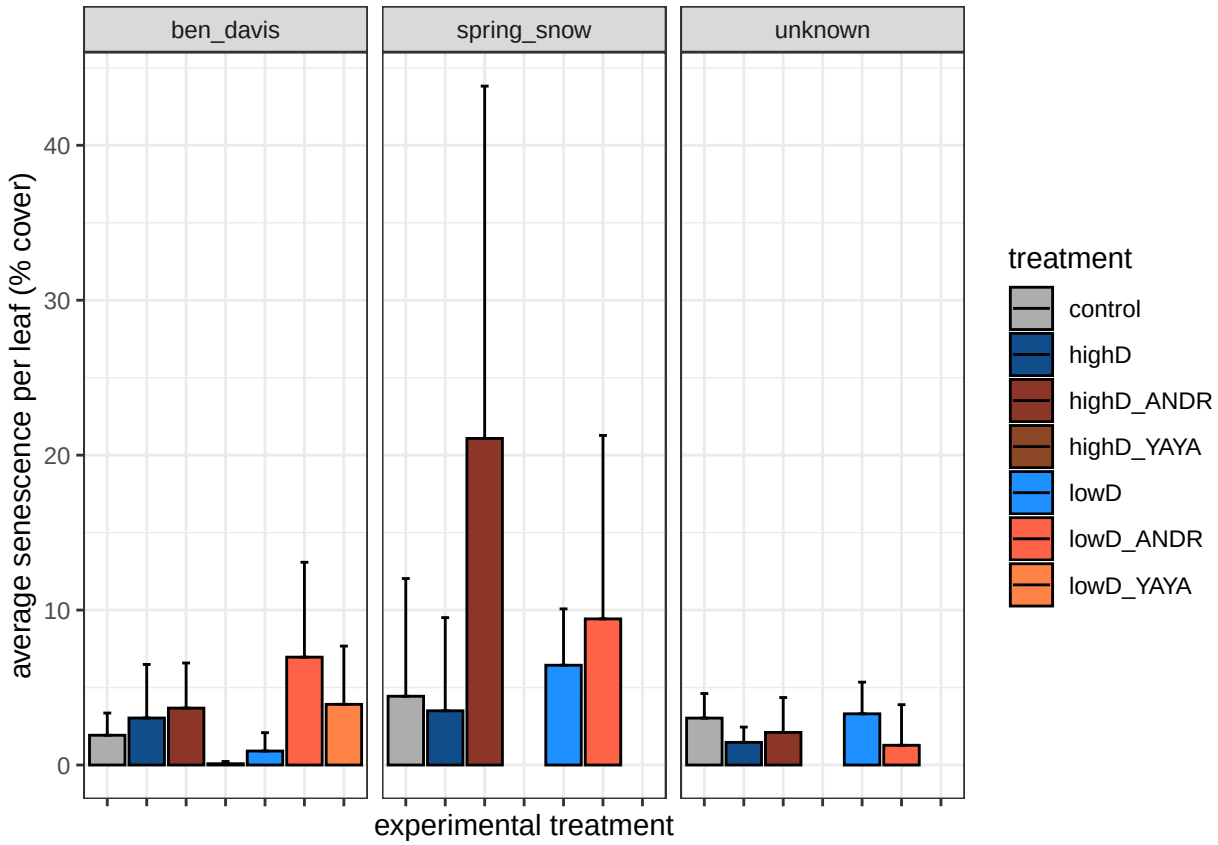



```
# check treatment comparisons with ANOVA with treatment and cultivar as predictors
anova_model1 <- aov(fb_percent~treatment + cultivar, data= p.data)
summary(anova_model1) # view the results
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treatment    6   98.1  16.345   2.209 0.0541 .
## cultivar     1    6.4   6.359   0.860 0.3575
## Residuals   61  451.3   7.398
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3 observations deleted due to missingness
```

```
#  add means and se error bars for total * senescence* with 7 treatment groups
p.data %>%
  group_by(treatment_code, cultivar_name) %>%
  summarize("av_sen_me" = mean(av_senescence, na.rm = TRUE), "av_sen_sd"= sd(av_senescence, na.rm = TRU
  ggplot(aes(x = treatment_code, y = av_sen_me,
             color = treatment_code,
             fill = treatment_code)) +
  geom_bar(stat = 'identity') +
  facet_wrap(facets = ~cultivar_name)+
  ylab("average senescence per leaf (% cover)") +  # yaxis labels
  xlab("experimental treatment") + # xaxis label
  theme_bw() +
  theme(axis.text.x = element_blank()) +
  scale_color_manual(name = "treatment",
                     labels = c("control",
                                "highD",
```

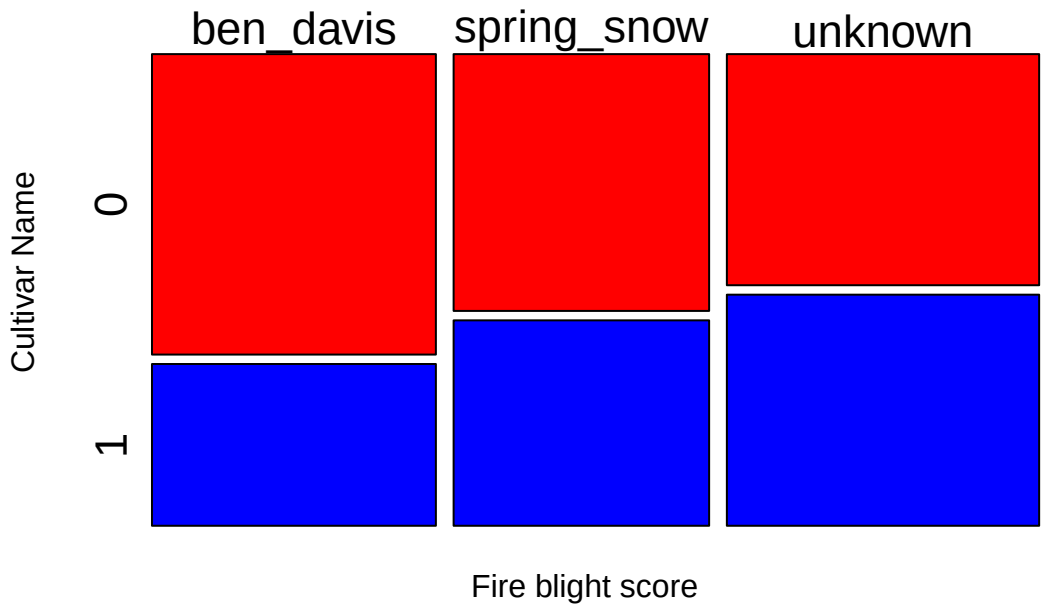
```
                                "highD_ANDR",
                                "highD_YAYA",
                                "lowD",
                                "lowD_ANDR",
                                "lowD_YAYA"),
                     values = c("control" = "black",
                                "highD" = "black",
                                "highD_ANDR" = "black",
                                "highD_YAYA" = "black",
                                "lowD" = "black",
                                "lowD_ANDR" = "black",
                                "lowD_YAYA" = "black")) +
  scale_fill_manual(name = "treatment",
                    labels = c("control",
                               "highD",
                               "highD_ANDR",
                               "highD_YAYA",
                               "lowD",
                               "lowD_ANDR",
                               "lowD_YAYA"),
                    values = c("control" = "grey68",
                               "highD" = "dodgerblue4",
                               "highD_ANDR" = "tomato4",
                               "highD_YAYA" = "sienna4",
                               "lowD" = "dodgerblue1",
                               "lowD_ANDR" = "tomato1",
                               "lowD_YAYA" = "sienna1")) +
  geom_errorbar(aes(ymin = av_sen_me, ymax = av_sen_me + av_sen_sd), width = 0.2, position = position_d
```




```
# check treatment comparisons with ANOVA with treatment as predictor
anova_model3 <- aov(senescence~treatment, data= p.data)
summary(anova_model3) # view the results
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treatment    6    642  106.99   1.289  0.276
## Residuals   62   5148   83.03
## 3 observations deleted due to missingness
```

```
# mosaic plots - cultivar name
mosaicplot(~cultivar_name + fb_strip,
           xlab = "Fire blight score",
           ylab = "Cultivar Name",
           cex.axis = 1.4,
           main = "", # get rid of the main title
           color = c("red", "blue", "green"))
```




```
# chi square test looking at cultivar
cult_x_fb3 <- data.frame(
  positive_fb = c(length(which(p.data$cultivar == '105' & p.data$fire_blight_strip_test== 1)),
                  length(which(p.data$cultivar == '1030' & p.data$fire_blight_strip_test== 1)),
                  length(which(p.data$cultivar == '577' & p.data$fire_blight_strip_test== 1))),
  negative_fb = c(length(which(p.data$cultivar == '105' & p.data$fire_blight_strip_test== 1)),
                  length(which(p.data$cultivar == '1030' & p.data$fire_blight_strip_test== 0)),
                  length(which(p.data$cultivar == '577' & p.data$fire_blight_strip_test== 0))))

# run the Chi Squared test
chisq.test(cult_x_fb3)
```

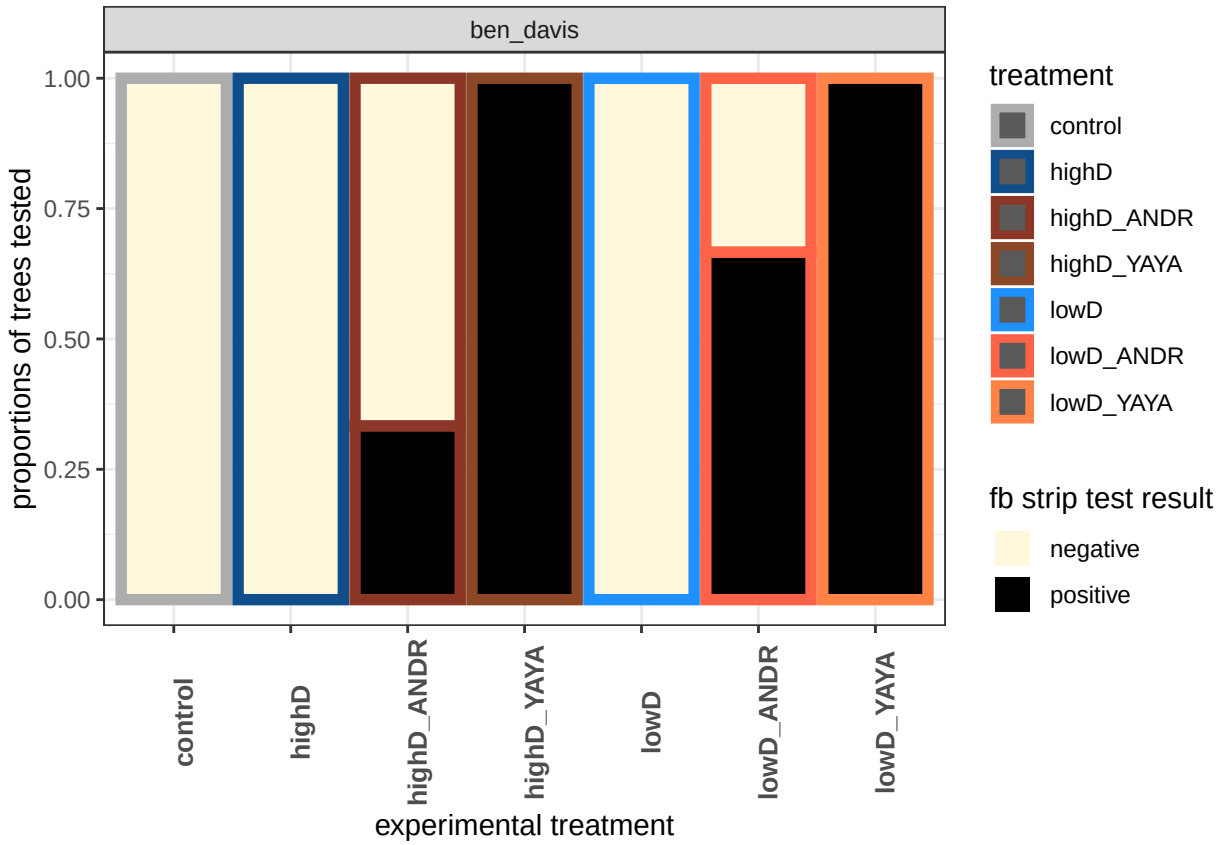
```
##
##  Pearson's Chi-squared test
##
## data:  cult_x_fb3
## X-squared = 0.14835, df = 2, p-value = 0.9285
```

```
# check the Fishers test because of low sample size
fisher.test(cult_x_fb3,
            simulate.p.value = TRUE, # for when you have more than 2 x 2  variables
            hybrid = TRUE) # for when you have more than 2 x 2  variables
```

```
##
##  Fisher's Exact Test for Count Data with simulated p-value (based
##  on 2000 replicates)
##
## data:  cult_x_fb3
## p-value = 0.942
## alternative hypothesis: two.sided
```

```
# 7 treatment grouops for ben davis only
p.data%>%
  group_by(treatment_code, cultivar_name) %>%
  filter(!is.na(fire_blight_strip_test), cultivar == "105") %>%
  ggplot(aes(x = treatment_code, fill = factor(fire_blight_strip_test),
```

```
            color = treatment_code)) +
  geom_bar(position = 'fill', size = 2) +
  facet_wrap(facets = ~cultivar_name)+
  ylab("proportions of trees tested") +  # yaxis labels
  xlab("experimental treatment") + # xaxis label
  theme_bw() +
  theme(axis.text.x = element_text(face = "bold", size = 10, angle = 90)) +
  scale_color_manual(name = "treatment",
                     labels = c("control",
                                "highD",
                                "highD_ANDR",
                                "highD_YAYA",
                                "lowD",
                                "lowD_ANDR",
                                "lowD_YAYA"),
                     values = c("control" = "grey68",
                                "highD" = "dodgerblue4",
                                "highD_ANDR" = "tomato4",
                                "highD_YAYA" = "sienna4",
                                "lowD" = "dodgerblue1",
                                "lowD_ANDR" = "tomato1",
                                "lowD_YAYA" = "sienna1"))   +
  scale_fill_manual(name = "fb strip test result",
                    labels = c("0" = "negative",
                               "1" = "positive"),
                    values = c("0" = "cornsilk",
                               "1" = "black"))
```




```
# run a chi square test comparing the strains

benD_y_x_a <- p.data %>%
  filter(cultivar == "105")

benD_y_x_a <- data.frame(
  positive_fb = c(length(which(benD_y_x_a$inocula_type == 'andrus_Ea' & p.data$fire_blight_strip_test==
                  length(which(benD_y_x_a$inocula_type == 'yaya_Ea' & p.data$fire_blight_strip_test== 1
  negative_fb = c(length(which(benD_y_x_a$inocula_type == 'andrus_Ea' & p.data$fire_blight_strip_test==
                  length(which(benD_y_x_a$inocula_type == 'yaya_Ea' & p.data$fire_blight_strip_test== 0

# chi square test looking at high low
chisq.test(benD_y_x_a)
```

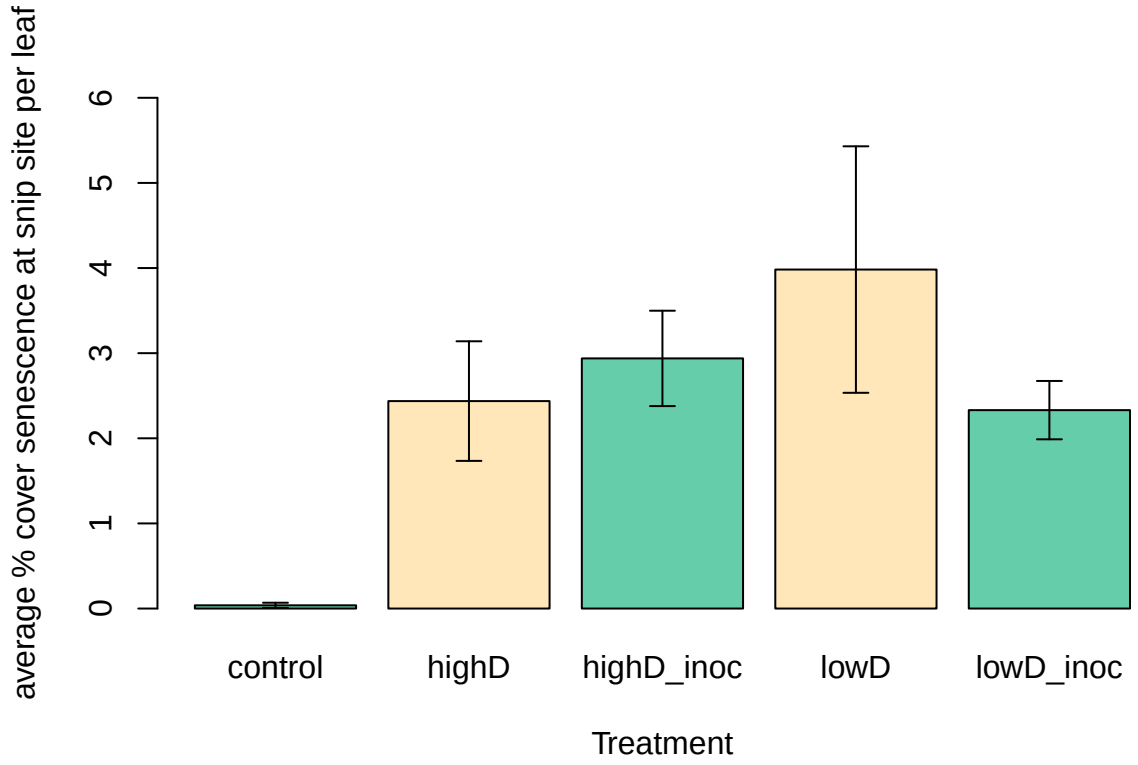
```
##
##  Pearson's Chi-squared test
##
## data:  benD_y_x_a
## X-squared = 0, df = 1, p-value = 1
```

```
# check the Fishers test because of low sample size
fisher.test(benD_y_x_a,
            simulate.p.value = TRUE, # for when you have more than 2 x 2  variables
            hybrid = TRUE) # for when you have more than 2 x 2  variables
```

```
## Warning in fisher.test(benD_y_x_a, simulate.p.value = TRUE, hybrid = TRUE):
## 'hybrid' is ignored for a 2 x 2 table
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  benD_y_x_a
## p-value = 1
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.1657209 6.0342427
## sample estimates:
## odds ratio
##          1
```

```
#########################################################################################################

# 4.3 Bar graphs of snip site senscense using the 5 treatment aggregates (so lumping YAYA and ANDRUS)
htMean <- aggregate(fb_percent~treatment_5, data=p.data, mean)
htSE <- aggregate(fb_percent~treatment_5, data=p.data, calcSE)
plotCI(barplot(htMean[,2], beside=T,
               ylim=c(0,6),
               ylab="average % cover senescence at snip site per leaf",
               xlab="Treatment",
               col=c("aquamarine3","wheat1"),
               names.arg=c(levels(p.data$treatment_5))), # name the levels of categories
       htMean[,2], uiw=htSE[,2], add=T, pch=NA)
```




```
# So here we are looking at fire blight % at snip site as predicted by treatment, this test yielded sig
anova_model6 <- aov(fb_percent~treatment_5, data= p.data)
summary(anova_model6) # view the results
```

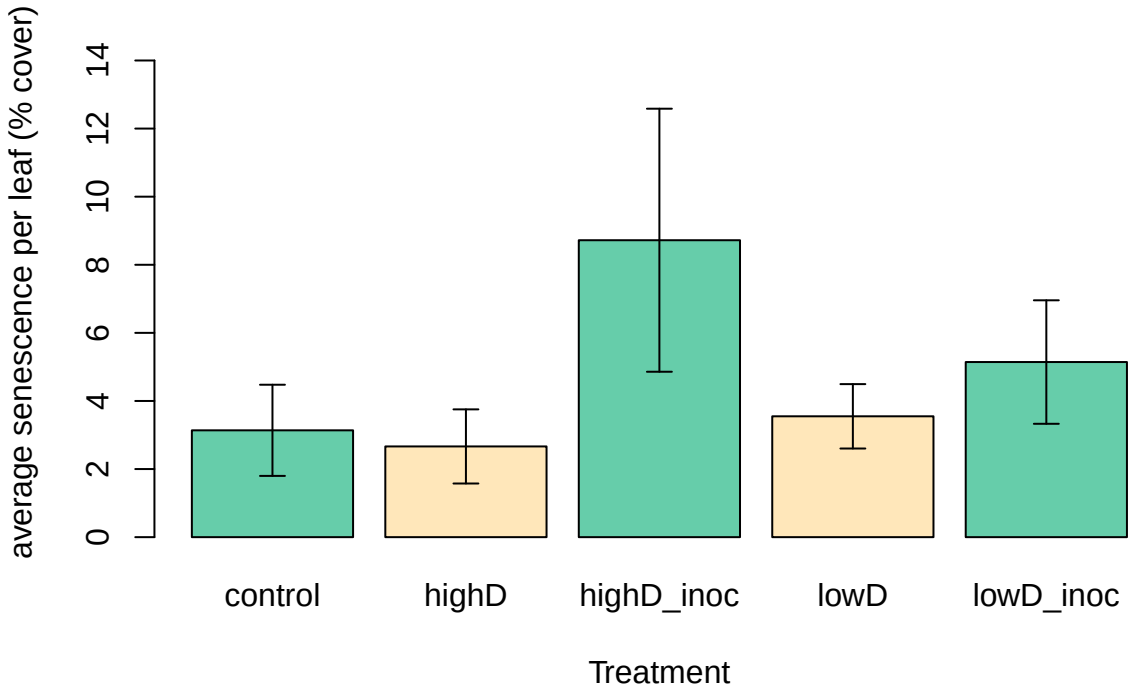
```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treatment_5  4   96.4  24.105   3.359 0.0147 *
```

```
## Residuals   64  459.3   7.177
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3 observations deleted due to missingness
```

```
# post hoc test to see what differed
TukeyHSD(anova_model6) #its really just the lowD compared to the control, which isn't super interesting
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = fb_percent ~ treatment_5, data = p.data)
##
## $treatment_5
##                             diff          lwr      upr     p adj
## highD-control          2.3991751 -0.739804122 5.538154 0.2140090
## highD_inoc-control     2.9006925 -0.009151484 5.810537 0.0511139
## lowD-control           3.9444349  0.805455683 7.083414 0.0067764
## lowD_inoc-control      2.2929353 -0.616908671 5.202779 0.1885435
## highD_inoc-highD       0.5015174 -2.333759070 3.336794 0.9874151
## lowD-highD             1.5452598 -1.524722480 4.615242 0.6217298
## lowD_inoc-highD       -0.1062398 -2.941516257 2.729037 0.9999716
## lowD-highD_inoc        1.0437424 -1.791534015 3.879019 0.8389594
## lowD_inoc-highD_inoc -0.6077572 -3.187058218 1.971544 0.9638426
## lowD_inoc-lowD       -1.6514996 -4.486776062 1.183777 0.4810191
```

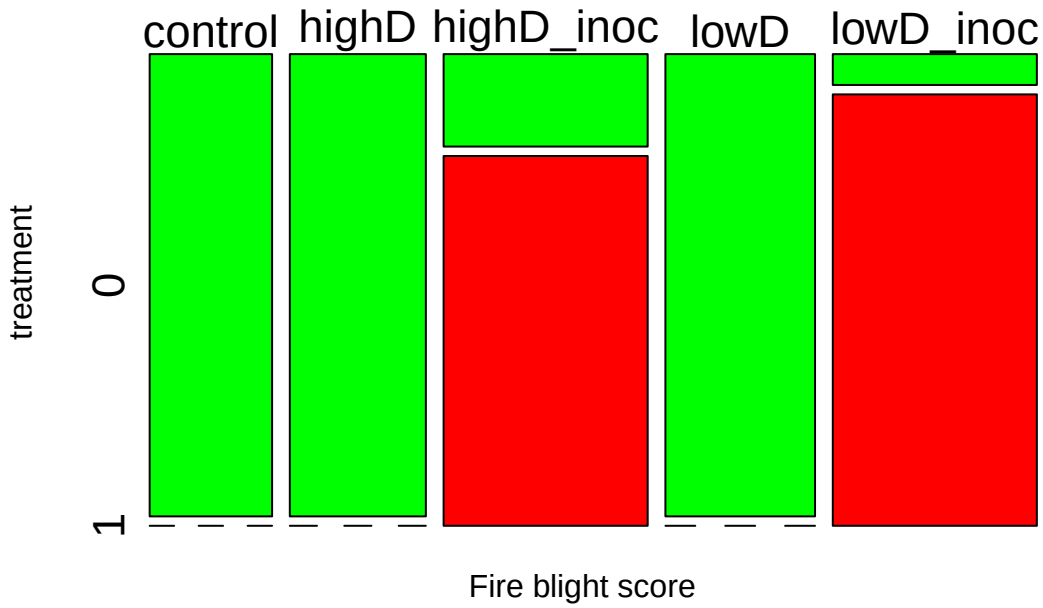
```
# 4.3 Bar graphs of total senscense using the 5 treatment aggregates (so lumping YAYA and ANDRUS)
htMean2 <- aggregate(av_senescence~treatment_5, data=p.data, mean)
htSE2 <- aggregate(av_senescence~treatment_5, data=p.data, calcSE)
plotCI(barplot(htMean2[,2], beside=T,
               ylim=c(0,15),
               ylab="average senescence per leaf (% cover)",
               xlab="Treatment",
               col=c("aquamarine3","wheat1"),
               names.arg=c(levels(p.data$treatment_5))), # name the levels of categories
       htMean2[,2], uiw=htSE2[,2], add=T, pch=NA)
```




```
# So here we are looking at total senescence as predicted by treatment
anova_model10 <- aov(av_senescence~treatment_5, data= p.data)
summary(anova_model10) # view the results
```

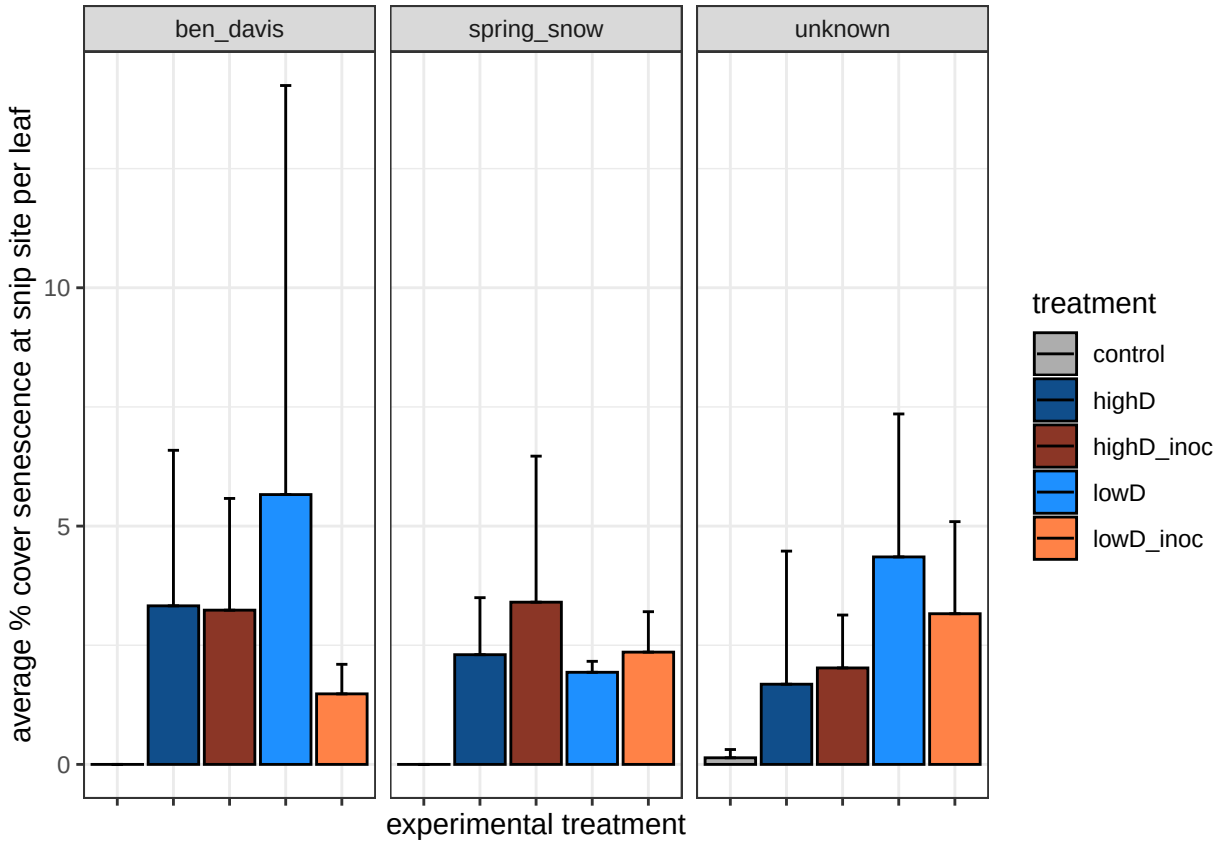
```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treatment_5  4    365   91.16   1.075  0.376
## Residuals   64   5425   84.77
## 3 observations deleted due to missingness
```

```
# mosaic plots - 5 treatments
mosaicplot(~treatment_5 + fb_strip,
           xlab = "Fire blight score",
           ylab = "treatment",
           cex.axis = 1.4,
           main = "", # get rid of the main title
           color = c("green", "red"))
```




```
#  add means and se error bars for *snip site senscense* with 5 treatment groups
p.data %>%
  group_by(treatment_5, cultivar_name) %>%
  summarize("av_fb_me" = mean(av_fb_percent, na.rm = TRUE), "av_fb_sd"= sd(av_fb_percent, na.rm = TRUE)
  ggplot(aes(x = treatment_5, y = av_fb_me,
             color = treatment_5,
             fill = treatment_5)) +
  geom_bar(stat = 'identity') +
  facet_wrap(facets = ~cultivar_name)+
  ylab("average % cover senescence at snip site per leaf") +  # yaxis labels
  xlab("experimental treatment") + # xaxis label
  theme_bw() +
  theme(axis.text.x = element_blank()) +
  scale_color_manual(name = "treatment",
                     labels = c("control",
                                "highD",
                                "highD_inoc",
                                "lowD",
                                "lowD_inoc"),
                     values = c("control" = "black",
                                "highD" = "black",
                                "highD_inoc" = "black",
                                "lowD" = "black",
                                "lowD_inoc" = "black")) +
  scale_fill_manual(name = "treatment",
                    labels = c("control",
                               "highD",
                               "highD_inoc",
                               "lowD",
                               "lowD_inoc"),
                    values = c("control" = "grey68",
                               "highD" = "dodgerblue4",
                               "highD_inoc" = "tomato4",
                               "lowD" = "dodgerblue1",
```

```
                                "lowD_inoc" = "sienna1"))  +
  geom_errorbar(aes(ymin = av_fb_me, ymax = av_fb_me + av_fb_sd), width = 0.2, position = position_dodg
```




```
# So here we are looking at total senescence as predicted by treatment and cultivar, this test yielded
anova_model7 <- aov(fb_percent~treatment_5 + cultivar_name, data= p.data)
summary(anova_model7) # view the results
```

```
##                Df Sum Sq Mean Sq F value Pr(>F)
## treatment_5     4   96.4  24.105   3.279 0.0167 *
## cultivar_name   2    3.5   1.757   0.239 0.7881
## Residuals      62  455.8   7.351
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3 observations deleted due to missingness
```

```
# post hoc test to see what differed
TukeyHSD(anova_model7) #its really just the lowD compared to the control, which isn't super interesting
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = fb_percent ~ treatment_5 + cultivar_name, data = p.data)
##
## $treatment_5
##                           diff         lwr      upr     p adj
## highD-control         2.3991751 -0.78075741 5.579108 0.2248641
## highD_inoc-control    2.9006925 -0.04711532 5.848500 0.0558738
## lowD-control          3.9444349  0.76450240 7.124368 0.0078127
```

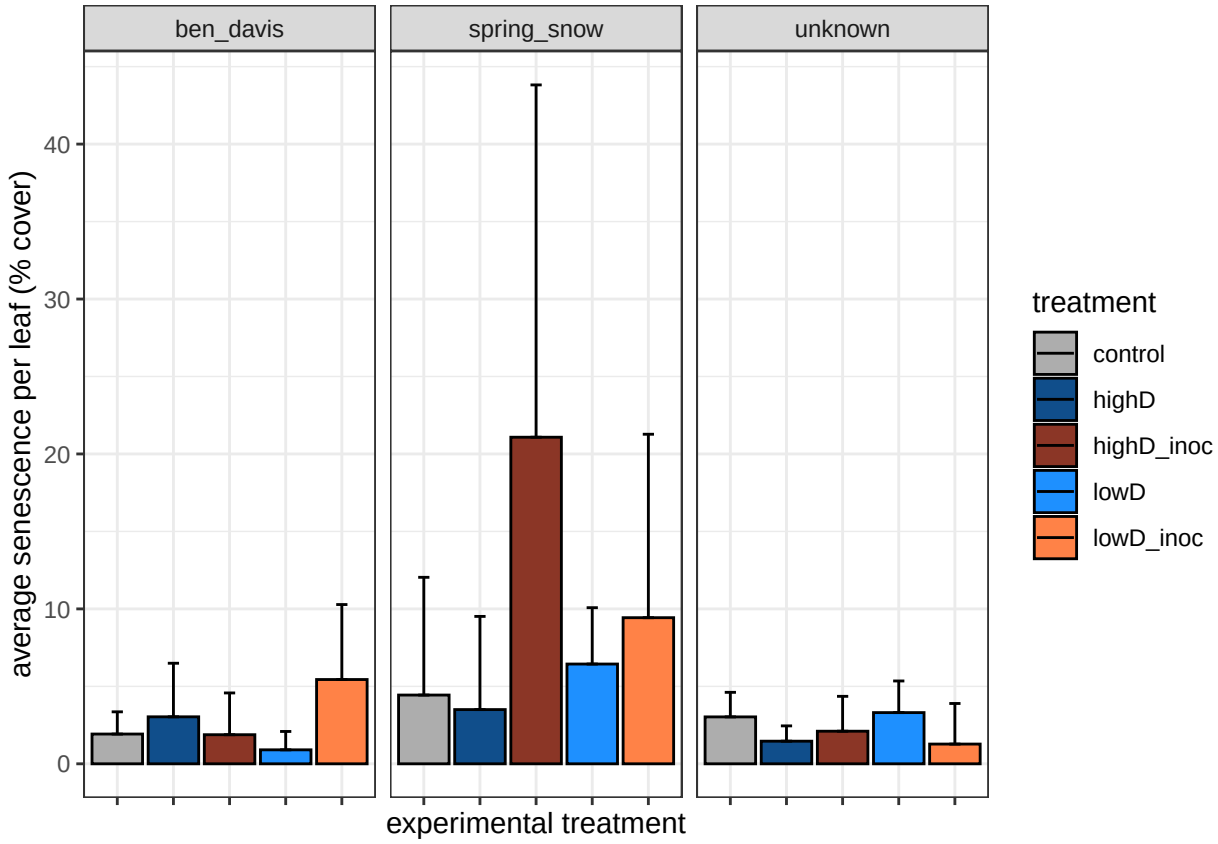
```
## lowD_inoc-control     2.2929353 -0.65487250 5.240743 0.1988245
## highD_inoc-highD      0.5015174 -2.37075004 3.373785 0.9879632
## lowD-highD            1.5452598 -1.56477559 4.655295 0.6324933
## lowD_inoc-highD      -0.1062398 -2.97850723 2.766028 0.9999729
## lowD-highD_inoc       1.0437424 -1.82852499 3.916010 0.8447388
## lowD_inoc-highD_inoc -0.6077572 -3.22070956 2.005195 0.9653495
## lowD_inoc-lowD       -1.6514996 -4.52376703 1.220768 0.4933792
##
## $cultivar_name
##                              diff       lwr      upr     p adj
## spring_snow-ben_davis -0.5433066 -2.443086 1.356472 0.7720905
## unknown-ben_davis     -0.3207478 -2.242448 1.600952 0.9153907
## unknown-spring_snow    0.2225587 -1.719019 2.164136 0.9591236
```

```
# lets check if this is signficant after taking out the control trees
treatment_4 <- p.data %>%
  filter(treatment_5 != "control")
anova_model8 <- aov(av_fb_percent~treatment_5 + cultivar_name, data= treatment_4)
summary(anova_model8) # view the results, not significant among high and low density snip trees
```

```
##               Df Sum Sq Mean Sq F value Pr(>F)
## treatment_5    3   22.1   7.373   0.843  0.477
## cultivar_name  2    4.3   2.137   0.244  0.784
## Residuals     52  454.9   8.749
## 2 observations deleted due to missingness
```

```
#  look at  * total senescence* between high and low density treatments and cultivars
p.data %>%
  group_by(treatment_5, cultivar_name) %>%
  summarize("av_sen_me" = mean(av_senescence, na.rm = TRUE), "av_sen_sd"= sd(av_senescence, na.rm = TRU
  ggplot(aes(x = treatment_5, y = av_sen_me,
             color = treatment_5,
             fill = treatment_5)) +
  geom_bar(stat = 'identity') +
  facet_wrap(facets = ~cultivar_name)+
  ylab("average senescence per leaf (% cover)") +  # yaxis labels
  xlab("experimental treatment") + # xaxis label
  theme_bw() +
  theme(axis.text.x = element_blank()) +
  scale_color_manual(name = "treatment",
                     labels = c("control",
                                "highD",
                                "highD_inoc",
                                "lowD",
                                "lowD_inoc"),
                     values = c("control" = "black",
                                "highD" = "black",
                                "highD_inoc" = "black",
                                "lowD" = "black",
                                "lowD_inoc" = "black")) +
  scale_fill_manual(name = "treatment",
                    labels = c("control",
                               "highD",
                               "highD_inoc",
                               "lowD",
```

```
                                "lowD_inoc"),
                     values = c("control" = "grey68",
                                "highD" = "dodgerblue4",
                                "highD_inoc" = "tomato4",
                                "lowD" = "dodgerblue1",
                                "lowD_inoc" = "sienna1"))  +
  geom_errorbar(aes(ymin = av_sen_me, ymax = av_sen_me + av_sen_sd), width = 0.2, position = position_d
```




```
# lets check differences in total senescence with treatment and cultivar as predictors
anova_model9 <- aov(av_senescence~treatment_5 + cultivar_name, data= p.data)
summary(anova_model9) # view the results, not significant among high and low density snip tree treatmen
```

```
##                Df Sum Sq Mean Sq F value  Pr(>F)
## treatment_5     4    365    91.2   1.243 0.30191
## cultivar_name   2    880   440.0   6.002 0.00414 **
## Residuals      62   4545    73.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 3 observations deleted due to missingness
```

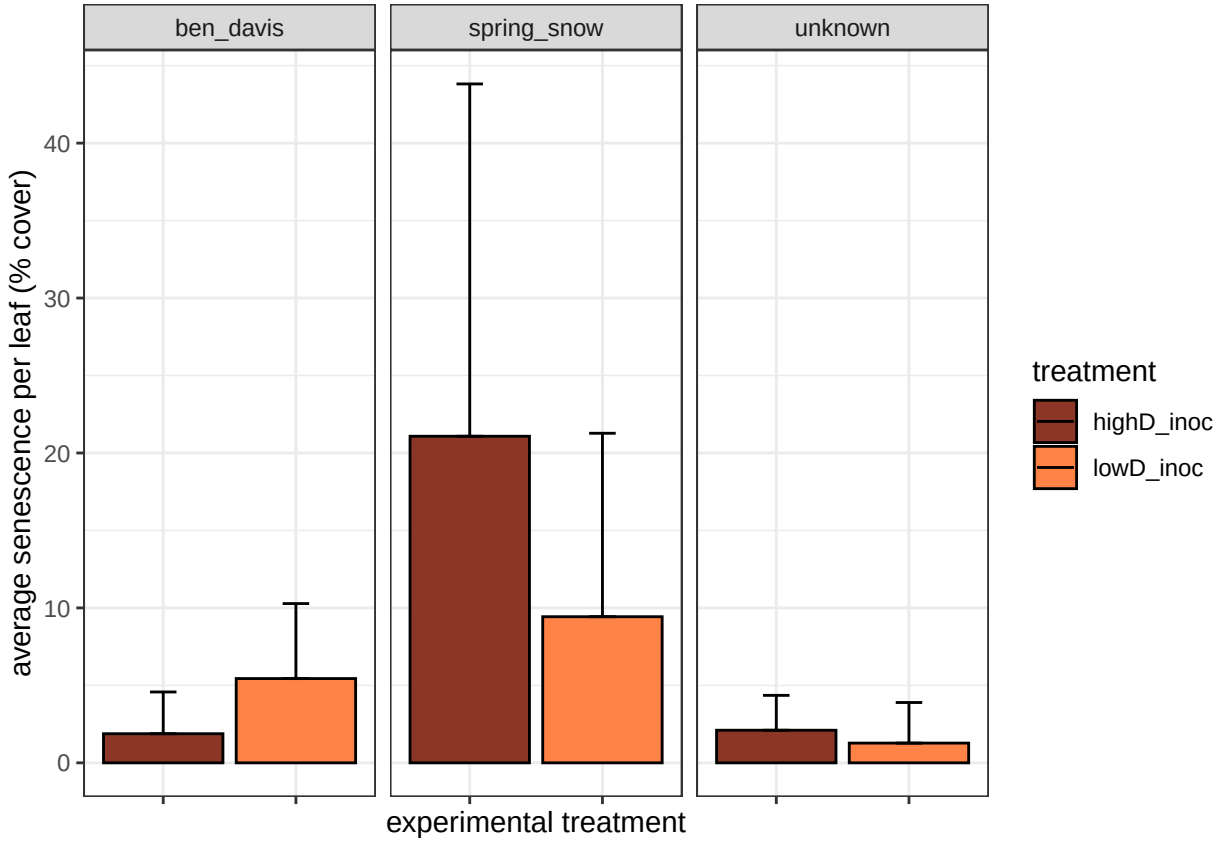
```
TukeyHSD(anova_model9) # spring snow is sig dif from ben davis and the unknown tree... but this is comp
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = av_senescence ~ treatment_5 + cultivar_name, data = p.data)
##
## $treatment_5
```

```
##                              diff        lwr       upr     p adj
## highD-control          -0.4734061 -10.515111  9.568299 0.9999286
## highD_inoc-control      5.5834728  -3.725220 14.892166 0.4503927
## lowD-control            0.4114351  -9.630270 10.453140 0.9999592
## lowD_inoc-control       2.0051453  -7.303548 11.313838 0.9737597
## highD_inoc-highD        6.0568788  -3.013270 15.127028 0.3407800
## lowD-highD              0.8848412  -8.936140 10.705822 0.9990696
## lowD_inoc-highD         2.4785514  -6.591597 11.548700 0.9388671
## lowD-highD_inoc        -5.1720376 -14.242186  3.898111 0.5017326
## lowD_inoc-highD_inoc   -3.5783274 -11.829602  4.672947 0.7407224
## lowD_inoc-lowD          1.5937102  -7.476439 10.663859 0.9876746
##
## $cultivar_name
##                               diff        lwr       upr     p adj
## spring_snow-ben_davis  7.2492999   1.250110 13.248490 0.0140188
## unknown-ben_davis     -0.6184327  -6.686847  5.449981 0.9675444
## unknown-spring_snow   -7.8677325 -13.998915 -1.736550 0.0085126
```

```
# let's just compare the high and low snip density groups with total senescence
high.low.data <- p.data %>%
  filter(treatment_5 == "highD_inoc" | treatment_5 == "lowD_inoc" ) %>%
  mutate(treatment_cultivar = as.factor(paste0(cultivar,"-",treatment_5)))

#  look at  * total senescence* between high and low density treatments and cultivars
high.low.data %>%
  group_by(treatment_5, cultivar_name) %>%
  summarize("av_sen_me" = mean(av_senescence, na.rm = TRUE), "av_sen_sd"= sd(av_senescence, na.rm = TRU
  ggplot(aes(x = treatment_5, y = av_sen_me,
             color = treatment_5,
             fill = treatment_5)) +
  geom_bar(stat = 'identity') +
  facet_wrap(facets = ~cultivar_name)+
  ylab("average senescence per leaf (% cover)") +  # yaxis labels
  xlab("experimental treatment") + # xaxis label
  theme_bw() +
  theme(axis.text.x = element_blank()) +
  scale_color_manual(name = "treatment",
                     labels = c(
                                "highD_inoc",

                                "lowD_inoc"),
                     values = c(

                                "highD_inoc" = "black",

                                "lowD_inoc" = "black")) +
  scale_fill_manual(name = "treatment",
                    labels = c(
                               "highD_inoc",

                               "lowD_inoc"),
                    values = c(

                               "highD_inoc" = "tomato4",
```

```
                                "lowD_inoc" = "sienna1"))  +
  geom_errorbar(aes(ymin = av_sen_me, ymax = av_sen_me + av_sen_sd), width = 0.2, position = position_d
```




```
#  add means and se error bars for *snip site senscense* with 5 treatment groups
p.data %>%
  group_by(treatment_5) %>%
  summarize("av_fb_me" = mean(av_fb_percent, na.rm = TRUE), "av_fb_sd"= sd(av_fb_percent, na.rm = TRUE)


  ggplot(aes(x = treatment_5, y = av_fb_me,
             color = treatment_5,
             fill = treatment_5)) +
  geom_bar(stat = 'identity') +
  ylab("average % cover senescence at snip site per leaf") +  # yaxis labels
  xlab("experimental treatment") + # xaxis label
  theme_bw() +
  theme(axis.text.x = element_blank()) +
  scale_color_manual(name = "treatment",
                     labels = c("control",
                                "highD",
                                "highD_inoc",
                                "lowD",
                                "lowD_inoc"),
                     values = c("control" = "black",
                                "highD" = "black",
                                "highD_inoc" = "black",
```

```
                                "lowD" = "black",
                                "lowD_inoc" = "black")) +
  scale_fill_manual(name = "treatment",
                    labels = c("control",
                               "highD",
                               "highD_inoc",
                               "lowD",
                               "lowD_inoc"),
                    values = c("control" = "grey68",
                               "highD" = "dodgerblue4",
                               "highD_inoc" = "tomato4",
                               "lowD" = "dodgerblue1",
                               "lowD_inoc" = "sienna1"))  +
  geom_errorbar(aes(ymin = av_fb_me, ymax = av_fb_me + av_fb_sd), width = 0.2, position = position_dodg
```