ms\_willow\_network\_supplement

Matthew Barbour

January 31, 2015

Testing for whether gall size varies among willow genotypes. We were unable to use the mvabund framework for this analysis, so we conducted separate linear models to test for these effects.

## Warning: Removed 64 rows containing non-finite values (stat\_boxplot).

## Warning: Removed 79 rows containing non-finite values (stat\_boxplot).

## Warning: Removed 116 rows containing non-finite values (stat\_boxplot).

## Warning: Removed 134 rows containing non-finite values (stat\_boxplot).

There were too few data points to reliably test for differences in mid-Stem gall diameter (Rabdophaga salicisbattatus), but we used weighted linear models to test for differences in gall size among willow genotypes. We weighted models by the number of galls collected from each plant replicate, because a higher number would reflect a more accurate measure of mean gall size for that particular willow.

vLG.size.lm <- lm(log(vLG.height.mean) ~ Genotype, data = full.df, weights = vLG.gall.count)  
rG.size.lm <- lm(log(rG.height.mean) ~ Genotype, data = full.df, weights = rG.gall.count)  
aSG.size.lm <- lm(log(aSG.height.mean) ~ Genotype, data = full.df, weights = aSG.gall.count)

## Analysis of Variance Table  
##   
## Response: log(vLG.height.mean)  
## Df Sum Sq Mean Sq F value Pr(>F)   
## Genotype 23 4.5254 0.196757 2.1666 0.009437 \*\*  
## Residuals 57 5.1763 0.090812   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table  
##   
## Response: log(rG.height.mean)  
## Df Sum Sq Mean Sq F value Pr(>F)  
## Genotype 21 1.5181 0.072289 0.9798 0.5037  
## Residuals 44 3.2461 0.073776

## Analysis of Variance Table  
##   
## Response: log(aSG.height.mean)  
## Df Sum Sq Mean Sq F value Pr(>F)  
## Genotype 16 0.7123 0.044519 0.2905 0.9884  
## Residuals 12 1.8390 0.153249

We used multivariate GLMs to examine whether gall abundances varied among willow genotypes.

Boxplots of gall abundance among the different genotypes.

## Using Genotype as id variables

Assessing which error distribution is best to model the data. Negative binomial appear to provide the best fit.

## START SECTION 2   
## Plotting if overlay is TRUE

## using grouping variable full.df$Genotype 29 mean values were 0 and could   
## not be included in the log-plot  
## using grouping variable full.df$Genotype 29 variance values were 0 and could not   
## be included in the log-plot

## FINISHED SECTION 2

Tested whether genotype affected gall community composition. It appears that leaf and bud galls are the major determinants of variation in gall abundance, with apical-Stem galls contributing to a lesser extent.

anova.gall <- anova.manyglm(manyglm.gall, p.uni = "unadjusted")  
anova.gall

Test for quantitative differences in gall community composition.

##   
## \* A B D E F G H I J K L M N O P Q R S T U V W X Y Z   
## 5 4 6 5 4 4 7 4 5 0 6 5 3 0 5 3 5 6 5 3 0 5 3 5 5 9

##   
## Call:  
## adonis(formula = bray.gall.comm.sub ~ Genotype, data = gall.comm.sub)   
##   
## Permutation: free  
## Number of permutations: 999  
##   
## Terms added sequentially (first to last)  
##   
## Df SumsOfSqs MeanSqs F.Model R2 Pr(>F)   
## Genotype 22 9.8156 0.44616 1.9553 0.32584 0.001 \*\*\*  
## Residuals 89 20.3086 0.22819 0.67416   
## Total 111 30.1242 1.00000   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table  
##   
## Response: Distances  
## Df Sum Sq Mean Sq F value Pr(>F)  
## Groups 22 1.2001 0.054551 1.2846 0.2044  
## Residuals 89 3.7793 0.042464

##   
## Mean distances:  
## Average  
## within groups 0.6063920  
## between groups 0.6881157  
## overall 0.6849866  
##   
## Summary statistics:  
## Statistic  
## MRPP A weights n 0.09796736  
## MRPP A weights n-1 0.10320682  
## MRPP A weights n(n-1) 0.11473894  
## Classification strength 0.07023539

Determine which willow traits are resulting in variation in gall abundances.

Starting with the most complex model, we progressively dropped predictors from the model that resulted in the lowest AIC for the model. We continued this in stepwise fashion until we arrived at the null model (no predictors). Using AIC and likelihood ratio tests, we found that four of these models provided a better fit to the data than the null model. For clarity, we only interpret model 11 as this one had the second to lowest AIC value, yet likelihood ratio tests suggested that it provided a significantly better fit than the alternative models. Single term deletions

Model: galls\_galls.traits ~ C\_N\_imputed + water\_content + sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + Density\_resid + SLA\_resid Df AIC 1126.5 C\_N\_imputed 4 1127.4 water\_content 4 1121.0 sal\_tannin.PC1 4 1120.8 cinn.PC1 4 1121.4 cinn.PC2 4 1121.7 flavonOLES.PC1 4 1120.8 flavonOLES.PC2 4 1126.4 flavanonOLES.PC1 4 1133.0 log\_size 4 1127.4 log\_trichomes 4 1124.7 Height\_resid 4 1127.8 Density\_resid 4 1129.4 SLA\_resid 4 1124.4 Single term deletions

Model: galls\_galls.traits ~ C\_N\_imputed + water\_content + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + Density\_resid + SLA\_resid Df AIC 1120.8 C\_N\_imputed 4 1122.5 water\_content 4 1115.9 cinn.PC1 4 1115.9 cinn.PC2 4 1116.6 flavonOLES.PC1 4 1114.3 flavonOLES.PC2 4 1120.5 flavanonOLES.PC1 4 1127.5 log\_size 4 1121.3 log\_trichomes 4 1118.5 Height\_resid 4 1122.3 Density\_resid 4 1123.2 SLA\_resid 4 1118.9 Single term deletions

Model: galls\_galls.traits ~ C\_N\_imputed + water\_content + cinn.PC1 + cinn.PC2 + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + Density\_resid + SLA\_resid Df AIC 1114.3 C\_N\_imputed 4 1115.7 water\_content 4 1109.2 cinn.PC1 4 1110.2 cinn.PC2 4 1109.8 flavonOLES.PC2 4 1113.7 flavanonOLES.PC1 4 1121.4 log\_size 4 1114.8 log\_trichomes 4 1111.1 Height\_resid 4 1115.8 Density\_resid 4 1117.6 SLA\_resid 4 1112.0 Single term deletions

Model: galls\_galls.traits ~ C\_N\_imputed + cinn.PC1 + cinn.PC2 + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + Density\_resid + SLA\_resid Df AIC 1109.2 C\_N\_imputed 4 1110.3 cinn.PC1 4 1105.7 cinn.PC2 4 1104.5 flavonOLES.PC2 4 1108.1 flavanonOLES.PC1 4 1115.3 log\_size 4 1111.9 log\_trichomes 4 1105.5 Height\_resid 4 1110.2 Density\_resid 4 1112.4 SLA\_resid 4 1105.8 Single term deletions

Model: galls\_galls.traits ~ C\_N\_imputed + cinn.PC1 + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + Density\_resid + SLA\_resid Df AIC 1104.5 C\_N\_imputed 4 1103.7 cinn.PC1 4 1101.1 flavonOLES.PC2 4 1102.9 flavanonOLES.PC1 4 1114.7 log\_size 4 1109.4 log\_trichomes 4 1103.4 Height\_resid 4 1103.8 Density\_resid 4 1106.6 SLA\_resid 4 1100.6 Single term deletions

Model: galls\_galls.traits ~ C\_N\_imputed + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + Density\_resid + SLA\_resid Df AIC 1101.1 C\_N\_imputed 4 1099.8 flavonOLES.PC2 4 1099.8 flavanonOLES.PC1 4 1112.7 log\_size 4 1105.2 log\_trichomes 4 1099.7 Height\_resid 4 1099.8 Density\_resid 4 1101.5 SLA\_resid 4 1095.7 Single term deletions

Model: galls\_galls.traits ~ C\_N\_imputed + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + Density\_resid Df AIC 1095.7 C\_N\_imputed 4 1094.6 flavonOLES.PC2 4 1094.0 flavanonOLES.PC1 4 1105.9 log\_size 4 1099.0 log\_trichomes 4 1094.3 Height\_resid 4 1093.5 Density\_resid 4 1095.7 Single term deletions

Model: galls\_galls.traits ~ C\_N\_imputed + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes + Density\_resid Df AIC 1093.5 C\_N\_imputed 4 1094.2 flavonOLES.PC2 4 1092.2 flavanonOLES.PC1 4 1104.3 log\_size 4 1096.5 log\_trichomes 4 1093.9 Density\_resid 4 1091.2 Single term deletions

Model: galls\_galls.traits ~ C\_N\_imputed + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes Df AIC 1091.2 C\_N\_imputed 4 1092.3 flavonOLES.PC2 4 1087.9 flavanonOLES.PC1 4 1102.1 log\_size 4 1095.4 log\_trichomes 4 1092.1 Single term deletions

Model: galls\_galls.traits ~ C\_N\_imputed + flavanonOLES.PC1 + log\_size + log\_trichomes Df AIC 1087.9 C\_N\_imputed 4 1089.8 flavanonOLES.PC1 4 1098.6 log\_size 4 1091.3 log\_trichomes 4 1085.5 Single term deletions

Model: galls\_galls.traits ~ C\_N\_imputed + flavanonOLES.PC1 + log\_size Df AIC 1085.5 C\_N\_imputed 4 1086.5 flavanonOLES.PC1 4 1095.6 log\_size 4 1087.0 Single term deletions

Model: galls\_galls.traits ~ flavanonOLES.PC1 + log\_size Df AIC 1086.5 flavanonOLES.PC1 4 1096.5 log\_size 4 1084.3 Single term deletions

Model: galls\_galls.traits ~ flavanonOLES.PC1 Df AIC 1084.3 flavanonOLES.PC1 4 1089.9

|  |  |  |
| --- | --- | --- |
| Model | Formula | AIC |
| 13 | flavanonOLES.PC1 | 1084.293 |
| 11 | C\_N\_imputed + flavanonOLES.PC1 + log\_size | 1085.454 |
| 12 | flavanonOLES.PC1 + log\_size | 1086.498 |
| 10 | C\_N\_imputed + flavanonOLES.PC1 + log\_size + log\_trichomes | 1087.898 |
| 14 | 1 | 1089.898 |

Time elapsed: 0 hr 0 min 10 sec Analysis of Deviance Table

mod14.null: galls\_galls.traits ~ 1 mod13: galls\_galls.traits ~ flavanonOLES.PC1

Multivariate test: Res.Df Df.diff Dev Pr(>Dev)  
mod14.null 107  
mod13 106 1 13.61 0.005  **--- Signif. codes: 0 '**\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1 Arguments: Test statistics calculated assuming uncorrelated response (for faster computation) P-value calculated using 999 resampling iterations via resampling (to account for correlation in testing).

Time elapsed: 0 hr 0 min 10 sec Analysis of Deviance Table

mod14.null: galls\_galls.traits ~ 1 mod12: galls\_galls.traits ~ flavanonOLES.PC1 + log\_size

Multivariate test: Res.Df Df.diff Dev Pr(>Dev)  
mod14.null 107  
mod12 105 2 19.4 0.014  *--- Signif. codes: 0 '***' 0.001 '**' 0.01 '\*' 0.05 '.' 0.1 ' ' 1 Arguments: Test statistics calculated assuming uncorrelated response (for faster computation) P-value calculated using 999 resampling iterations via resampling (to account for correlation in testing).

Time elapsed: 0 hr 0 min 11 sec Analysis of Deviance Table

mod14.null: galls\_galls.traits ~ 1 mod11: galls\_galls.traits ~ C\_N\_imputed + flavanonOLES.PC1 + log\_size

Multivariate test: Res.Df Df.diff Dev Pr(>Dev)  
mod14.null 107  
mod11 104 3 28.44 0.006  **--- Signif. codes: 0 '**\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1 Arguments: Test statistics calculated assuming uncorrelated response (for faster computation) P-value calculated using 999 resampling iterations via resampling (to account for correlation in testing).

Time elapsed: 0 hr 0 min 12 sec Analysis of Deviance Table

mod14.null: galls\_galls.traits ~ 1 mod10: galls\_galls.traits ~ C\_N\_imputed + flavanonOLES.PC1 + log\_size + log\_trichomes

Multivariate test: Res.Df Df.diff Dev Pr(>Dev)  
mod14.null 107  
mod10 103 4 34 0.004  **--- Signif. codes: 0 '**\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1 Arguments: Test statistics calculated assuming uncorrelated response (for faster computation) P-value calculated using 999 resampling iterations via resampling (to account for correlation in testing).

Time elapsed: 0 hr 0 min 11 sec Analysis of Deviance Table

mod13: galls\_galls.traits ~ flavanonOLES.PC1 mod11: galls\_galls.traits ~ C\_N\_imputed + flavanonOLES.PC1 + log\_size

Multivariate test: Res.Df Df.diff Dev Pr(>Dev)  
mod13 106  
mod11 104 2 23.23 0.006  **--- Signif. codes: 0 '**\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1 Arguments: Test statistics calculated assuming uncorrelated response (for faster computation) P-value calculated using 999 resampling iterations via resampling (to account for correlation in testing).

Time elapsed: 0 hr 0 min 13 sec Analysis of Deviance Table

mod12: galls\_galls.traits ~ flavanonOLES.PC1 + log\_size mod11: galls\_galls.traits ~ C\_N\_imputed + flavanonOLES.PC1 + log\_size

Multivariate test: Res.Df Df.diff Dev Pr(>Dev)  
mod12 105  
mod11 104 1 9.587 0.056 . --- Signif. codes: 0 '***' 0.001 '****' 0.01 '*' 0.05 '.' 0.1 ' ' 1 Arguments: Test statistics calculated assuming uncorrelated response (for faster computation) P-value calculated using 999 resampling iterations via resampling (to account for correlation in testing).

Time elapsed: 0 hr 0 min 17 sec Analysis of Deviance Table

mod11: galls\_galls.traits ~ C\_N\_imputed + flavanonOLES.PC1 + log\_size mod10: galls\_galls.traits ~ C\_N\_imputed + flavanonOLES.PC1 + log\_size + log\_trichomes

Multivariate test: Res.Df Df.diff Dev Pr(>Dev) mod11 104  
mod10 103 1 5.556 0.275 Arguments: Test statistics calculated assuming uncorrelated response (for faster computation) P-value calculated using 999 resampling iterations via resampling (to account for correlation in testing).

Time elapsed: 0 hr 0 min 52 sec Analysis of Deviance Table

mod14.null: galls\_galls.traits ~ 1 mod13: galls\_galls.traits ~ flavanonOLES.PC1 mod12: galls\_galls.traits ~ flavanonOLES.PC1 + log\_size mod11: galls\_galls.traits ~ C\_N\_imputed + flavanonOLES.PC1 + log\_size mod10: galls\_galls.traits ~ C\_N\_imputed + flavanonOLES.PC1 + log\_size + log\_trichomes

Multivariate test: Res.Df Df.diff Dev Pr(>Dev)  
mod14.null 107  
mod13 106 1 5.215 0.179  
mod12 105 1 13.641 0.011  *mod11 104 1 9.587 0.042*  mod10 103 1 5.556 0.245  
--- Signif. codes: 0 '***' 0.001 '****' 0.01 '*' 0.05 '.' 0.1 ' ' 1 Arguments: Test statistics calculated assuming uncorrelated response (for faster computation) P-value calculated using 999 resampling iterations via resampling (to account for correlation in testing).

# identify gall-trait associations. C\_N\_imputed has a marginally significant effect on Iteomyia and R. salicisbrassicoides abundance. FlavononOLES.PC1 has a signficiant effect on Cecidomyiid sp. A abundance, and plant size as a significant effect on R. salicisbrassicoides and a marginal effect on R. salicisbattatus abundance.  
uni.galls.traits <-anova.manyglm(mod11, p.uni = "unadjusted")  
  
coef.df <- data.frame(coef(mod11))  
  
range.flavanonOLES.PC1 <- with(gall.density.df, max(flavanonOLES.PC1) - min(flavanonOLES.PC1))  
exp(coef.df["flavanonOLES.PC1","aSG\_abund"]\*range.flavanonOLES.PC1) # over the range of flavanonOLES.PC1, Cecidomyiid sp. A abundance increased 15-fold  
  
range.C\_N\_imputed <- with(gall.density.df, max(C\_N\_imputed) - min(C\_N\_imputed))  
exp(coef.df["C\_N\_imputed", "vLG\_abund"]\*range.C\_N\_imputed) # over the range of C:N ratio, Iteomyia abundance increased 3-fold (2.9)  
  
exp(coef.df["C\_N\_imputed", "rG\_abund"]\*range.C\_N\_imputed) # over the range of C:N ratio, R. salicisbrassicoides abundance increased 8-fold (7.6)  
  
1 - 1.10^coef.df["log\_size","rG\_abund"] # for every 10% increase in plant size, R. salicisbrassicoides density decreased 9%  
  
1 - 1.10^coef.df["log\_size","SG\_abund"] # for every 10% increase in plant size, R. salicisbattatus density decreasted by 37%

# include model with all of the traits, but only examine one of the variables  
vLG.trait <- MASS::glm.nb(vLG\_abund ~ C\_N\_imputed + log\_size + flavanonOLES.PC1, gall.density.df)  
summary(vLG.trait)   
visreg(vLG.trait, xvar = "C\_N\_imputed", scale = "response")  
  
aSG.trait <- MASS::glm.nb(aSG\_abund ~ C\_N\_imputed + log\_size + flavanonOLES.PC1, gall.density.df)  
summary(aSG.trait)  
visreg(aSG.trait, xvar = "flavanonOLES.PC1", scale = "response") # may or may not be too important  
  
rG.trait <- MASS::glm.nb(rG\_abund ~ C\_N\_imputed + log\_size + flavanonOLES.PC1, gall.density.df)  
summary(rG.trait)  
visreg(rG.trait, xvar = "log\_size", scale = "response")  
visreg(rG.trait, xvar = "C\_N\_imputed", scale = "response")  
  
SG.trait <- MASS::glm.nb(SG\_abund ~ C\_N\_imputed + log\_size + flavanonOLES.PC1, gall.density.df)  
summary(SG.trait) # some warnings about lack of convergence  
visreg(SG.trait, xvar = "log\_size", scale = "response") # not a great fit. Outlier seems to be driving most of this relationship.

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ C\_N\_imputed + water\_content + sal\_tannin.PC1 +   
## cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + flavonOLES.PC2 + flavanonOLES.PC1 +   
## log\_size + log\_trichomes + Height\_resid + Density\_resid +   
## SLA\_resid  
## Df Sum of Sq RSS AIC  
## <none> 339.76 133.47  
## C\_N\_imputed 1 0.0007 339.76 131.47  
## water\_content 1 5.9091 345.67 132.54  
## sal\_tannin.PC1 1 20.8414 360.60 135.16  
## cinn.PC1 1 7.4141 347.18 132.81  
## cinn.PC2 1 10.6408 350.40 133.38  
## flavonOLES.PC1 1 18.7226 358.49 134.79  
## flavonOLES.PC2 1 0.1061 339.87 131.49  
## flavanonOLES.PC1 1 0.5069 340.27 131.56  
## log\_size 1 6.1888 345.95 132.59  
## log\_trichomes 1 0.1086 339.87 131.49  
## Height\_resid 1 4.0852 343.85 132.21  
## Density\_resid 1 0.0001 339.76 131.47  
## SLA\_resid 1 1.1356 340.90 131.68

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ water\_content + sal\_tannin.PC1 + cinn.PC1 +   
## cinn.PC2 + flavonOLES.PC1 + flavonOLES.PC2 + flavanonOLES.PC1 +   
## log\_size + log\_trichomes + Height\_resid + Density\_resid +   
## SLA\_resid  
## Df Sum of Sq RSS AIC  
## <none> 339.76 131.47  
## water\_content 1 5.9112 345.68 130.54  
## sal\_tannin.PC1 1 20.8409 360.61 133.16  
## cinn.PC1 1 7.4929 347.26 130.82  
## cinn.PC2 1 10.8337 350.60 131.41  
## flavonOLES.PC1 1 18.7219 358.49 132.79  
## flavonOLES.PC2 1 0.1069 339.87 129.49  
## flavanonOLES.PC1 1 0.5106 340.27 129.56  
## log\_size 1 6.5677 346.33 130.66  
## log\_trichomes 1 0.1199 339.88 129.49  
## Height\_resid 1 4.2463 344.01 130.24  
## Density\_resid 1 0.0000 339.76 129.47  
## SLA\_resid 1 1.2194 340.98 129.69

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ water\_content + sal\_tannin.PC1 + cinn.PC1 +   
## cinn.PC2 + flavonOLES.PC1 + flavonOLES.PC2 + flavanonOLES.PC1 +   
## log\_size + log\_trichomes + Height\_resid + SLA\_resid  
## Df Sum of Sq RSS AIC  
## <none> 339.76 129.47  
## water\_content 1 6.0910 345.86 128.57  
## sal\_tannin.PC1 1 20.8417 360.61 131.16  
## cinn.PC1 1 8.1160 347.88 128.93  
## cinn.PC2 1 10.8471 350.61 129.42  
## flavonOLES.PC1 1 18.9111 358.68 130.83  
## flavonOLES.PC2 1 0.1091 339.87 127.49  
## flavanonOLES.PC1 1 0.5194 340.28 127.56  
## log\_size 1 6.5782 346.34 128.66  
## log\_trichomes 1 0.1204 339.88 127.49  
## Height\_resid 1 4.5713 344.34 128.30  
## SLA\_resid 1 1.2793 341.04 127.70

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ water\_content + sal\_tannin.PC1 + cinn.PC1 +   
## cinn.PC2 + flavonOLES.PC1 + flavanonOLES.PC1 + log\_size +   
## log\_trichomes + Height\_resid + SLA\_resid  
## Df Sum of Sq RSS AIC  
## <none> 339.87 127.49  
## water\_content 1 6.2170 346.09 126.61  
## sal\_tannin.PC1 1 20.9949 360.87 129.21  
## cinn.PC1 1 8.2429 348.12 126.97  
## cinn.PC2 1 10.9826 350.86 127.46  
## flavonOLES.PC1 1 19.2771 359.15 128.91  
## flavanonOLES.PC1 1 0.5435 340.42 125.59  
## log\_size 1 6.7734 346.65 126.71  
## log\_trichomes 1 0.3017 340.17 125.54  
## Height\_resid 1 4.6092 344.48 126.32  
## SLA\_resid 1 1.5463 341.42 125.77

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ water\_content + sal\_tannin.PC1 + cinn.PC1 +   
## cinn.PC2 + flavonOLES.PC1 + log\_size + log\_trichomes + Height\_resid +   
## SLA\_resid  
## Df Sum of Sq RSS AIC  
## <none> 340.42 125.59  
## water\_content 1 6.2834 346.70 124.72  
## sal\_tannin.PC1 1 20.7073 361.12 127.25  
## cinn.PC1 1 7.7004 348.12 124.97  
## cinn.PC2 1 13.7884 354.21 126.05  
## flavonOLES.PC1 1 20.0367 360.45 127.13  
## log\_size 1 6.7746 347.19 124.81  
## log\_trichomes 1 0.0823 340.50 123.60  
## Height\_resid 1 4.0671 344.48 124.33  
## SLA\_resid 1 2.3349 342.75 124.01

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ water\_content + sal\_tannin.PC1 + cinn.PC1 +   
## cinn.PC2 + flavonOLES.PC1 + log\_size + Height\_resid + SLA\_resid  
## Df Sum of Sq RSS AIC  
## <none> 340.50 123.60  
## water\_content 1 6.4074 346.91 122.76  
## sal\_tannin.PC1 1 27.2095 367.71 126.37  
## cinn.PC1 1 7.8734 348.37 123.02  
## cinn.PC2 1 14.4894 354.99 124.19  
## flavonOLES.PC1 1 25.0785 365.58 126.01  
## log\_size 1 6.6980 347.20 122.81  
## Height\_resid 1 4.5889 345.09 122.43  
## SLA\_resid 1 2.3232 342.82 122.03

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ water\_content + sal\_tannin.PC1 + cinn.PC1 +   
## cinn.PC2 + flavonOLES.PC1 + log\_size + Height\_resid  
## Df Sum of Sq RSS AIC  
## <none> 342.82 122.03  
## water\_content 1 7.180 350.00 121.31  
## sal\_tannin.PC1 1 40.319 383.14 126.92  
## cinn.PC1 1 9.260 352.08 121.68  
## cinn.PC2 1 22.330 365.15 123.94  
## flavonOLES.PC1 1 29.746 372.57 125.18  
## log\_size 1 7.788 350.61 121.42  
## Height\_resid 1 6.137 348.96 121.12

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ water\_content + sal\_tannin.PC1 + cinn.PC1 +   
## cinn.PC2 + flavonOLES.PC1 + log\_size  
## Df Sum of Sq RSS AIC  
## <none> 348.96 121.12  
## water\_content 1 6.259 355.22 120.23  
## sal\_tannin.PC1 1 43.012 391.97 126.33  
## cinn.PC1 1 9.429 358.39 120.78  
## cinn.PC2 1 17.334 366.29 122.13  
## flavonOLES.PC1 1 30.004 378.96 124.24  
## log\_size 1 9.881 358.84 120.86

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 +   
## log\_size  
## Df Sum of Sq RSS AIC  
## <none> 355.22 120.23  
## sal\_tannin.PC1 1 42.626 397.84 125.25  
## cinn.PC1 1 12.506 367.72 120.37  
## cinn.PC2 1 13.199 368.42 120.49  
## flavonOLES.PC1 1 29.059 384.28 123.10  
## log\_size 1 8.203 363.42 119.64

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1  
## Df Sum of Sq RSS AIC  
## <none> 363.42 119.64  
## sal\_tannin.PC1 1 45.331 408.75 124.93  
## cinn.PC1 1 11.828 375.25 119.63  
## cinn.PC2 1 12.362 375.78 119.72  
## flavonOLES.PC1 1 26.130 389.55 121.95

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ sal\_tannin.PC1 + cinn.PC2 + flavonOLES.PC1  
## Df Sum of Sq RSS AIC  
## <none> 375.25 119.63  
## sal\_tannin.PC1 1 34.272 409.52 123.05  
## cinn.PC2 1 15.110 390.36 120.08  
## flavonOLES.PC1 1 41.413 416.66 124.12

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ sal\_tannin.PC1 + flavonOLES.PC1  
## Df Sum of Sq RSS AIC  
## <none> 390.36 120.08  
## sal\_tannin.PC1 1 32.428 422.79 123.02  
## flavonOLES.PC1 1 28.597 418.96 122.46

## Single term deletions  
##   
## Model:  
## vLG.height.mean ~ sal\_tannin.PC1  
## Df Sum of Sq RSS AIC  
## <none> 418.96 122.46  
## sal\_tannin.PC1 1 80.891 499.85 131.40

## Models  
## 1 11  
## 2 10  
## 3 12  
## 4 9  
## 5 8  
## 6 7  
## 7 13  
## 8 6  
## 9 5  
## 10 4  
## 11 3  
## 12 14  
## 13 2  
## 14 1  
## Formula  
## 1 sal\_tannin.PC1 + cinn.PC2 + flavonOLES.PC1  
## 2 sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1  
## 3 sal\_tannin.PC1 + flavonOLES.PC1  
## 4 sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + log\_size  
## 5 water\_content + sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + log\_size  
## 6 water\_content + sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + log\_size + Height\_resid  
## 7 sal\_tannin.PC1  
## 8 water\_content + sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + log\_size + Height\_resid + SLA\_resid  
## 9 water\_content + sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + SLA\_resid  
## 10 water\_content + sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + flavanonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + SLA\_resid  
## 11 water\_content + sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + SLA\_resid  
## 12 1  
## 13 water\_content + sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + Density\_resid + SLA\_resid  
## 14 C\_N\_imputed + water\_content + sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 + flavonOLES.PC1 + flavonOLES.PC2 + flavanonOLES.PC1 + log\_size + log\_trichomes + Height\_resid + Density\_resid + SLA\_resid  
## AIC  
## 1 245.2773  
## 2 245.2916  
## 3 245.7249  
## 4 245.8761  
## 5 246.7740  
## 6 247.6740  
## 7 248.1083  
## 8 249.2524  
## 9 251.2374  
## 10 253.1384  
## 11 255.1185  
## 12 257.0535  
## 13 257.1185  
## 14 259.1183

##   
## Call:  
## lm(formula = vLG.height.mean ~ sal\_tannin.PC1 + cinn.PC2 + flavonOLES.PC1,   
## data = select(gall.size.df, -vLG.gall.count), weights = gall.size.df$vLG.gall.count)  
##   
## Weighted Residuals:  
## Min 1Q Median 3Q Max   
## -5.2761 -1.4903 0.0275 1.3865 5.8311   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 8.83848 0.19138 46.184 <2e-16 \*\*\*  
## sal\_tannin.PC1 -0.20211 0.08782 -2.302 0.0250 \*   
## cinn.PC2 0.22268 0.14571 1.528 0.1319   
## flavonOLES.PC1 -0.33346 0.13180 -2.530 0.0141 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 2.544 on 58 degrees of freedom  
## Multiple R-squared: 0.2493, Adjusted R-squared: 0.2104   
## F-statistic: 6.419 on 3 and 58 DF, p-value: 0.0007887

##   
## Call:  
## lm(formula = vLG.height.mean ~ sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 +   
## flavonOLES.PC1, data = select(gall.size.df, -vLG.gall.count),   
## weights = gall.size.df$vLG.gall.count)  
##   
## Weighted Residuals:  
## Min 1Q Median 3Q Max   
## -5.534 -1.210 -0.058 1.354 5.641   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 8.82827 0.19013 46.433 < 2e-16 \*\*\*  
## sal\_tannin.PC1 -0.25255 0.09472 -2.666 0.00996 \*\*   
## cinn.PC1 -0.15638 0.11481 -1.362 0.17855   
## cinn.PC2 0.20248 0.14541 1.392 0.16919   
## flavonOLES.PC1 -0.27759 0.13712 -2.024 0.04762 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 2.525 on 57 degrees of freedom  
## Multiple R-squared: 0.2729, Adjusted R-squared: 0.2219   
## F-statistic: 5.349 on 4 and 57 DF, p-value: 0.000996

##   
## Call:  
## lm(formula = vLG.height.mean ~ sal\_tannin.PC1 + flavonOLES.PC1,   
## data = select(gall.size.df, -vLG.gall.count), weights = gall.size.df$vLG.gall.count)  
##   
## Weighted Residuals:  
## Min 1Q Median 3Q Max   
## -6.0972 -1.2772 -0.3961 1.7911 6.1227   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 8.82724 0.19339 45.645 <2e-16 \*\*\*  
## sal\_tannin.PC1 -0.19643 0.08872 -2.214 0.0307 \*   
## flavonOLES.PC1 -0.25551 0.12290 -2.079 0.0420 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 2.572 on 59 degrees of freedom  
## Multiple R-squared: 0.219, Adjusted R-squared: 0.1926   
## F-statistic: 8.274 on 2 and 59 DF, p-value: 0.00068

##   
## Call:  
## lm(formula = vLG.height.mean ~ sal\_tannin.PC1 + cinn.PC1 + cinn.PC2 +   
## flavonOLES.PC1 + log\_size, data = select(gall.size.df, -vLG.gall.count),   
## weights = gall.size.df$vLG.gall.count)  
##   
## Weighted Residuals:  
## Min 1Q Median 3Q Max   
## -5.455 -1.253 -0.092 1.693 5.521   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 8.57335 0.29362 29.198 <2e-16 \*\*\*  
## sal\_tannin.PC1 -0.24544 0.09468 -2.592 0.0121 \*   
## cinn.PC1 -0.16090 0.11459 -1.404 0.1658   
## cinn.PC2 0.20940 0.14516 1.443 0.1547   
## flavonOLES.PC1 -0.29445 0.13757 -2.140 0.0367 \*   
## log\_size 0.49767 0.43763 1.137 0.2603   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 2.519 on 56 degrees of freedom  
## Multiple R-squared: 0.2893, Adjusted R-squared: 0.2259   
## F-statistic: 4.56 on 5 and 56 DF, p-value: 0.001472

## Warning in max(vLG.size.predict$sal\_tannin.PC1$y$fit): no non-missing  
## arguments to max; returning -Inf

## Warning in min(vLG.size.predict$sal\_tannin.PC1$y$fit): no non-missing  
## arguments to min; returning Inf

## [1] NaN

## Warning in max(vLG.size.predict$flavonOLES.PC1$y$fit): no non-missing  
## arguments to max; returning -Inf

## Warning in min(vLG.size.predict$flavonOLES.PC1$y$fit): no non-missing  
## arguments to min; returning Inf

## [1] NaN

Here, we evaluate the assumptions of mvabund and see which error distribution is appropriate. Specifically, we first look at a plot of the mean-variance relationship of our response variables. It is easy to see that the negative binomial model (black line) provides the best fit to this data, suggesting that we should specify this as the error distribution in our model

## START SECTION 2   
## Plotting if overlay is TRUE

## using grouping variable full.df$Genotype 232 mean values were 0 and could   
## not be included in the log-plot  
## using grouping variable full.df$Genotype 232 variance values were 0 and could not   
## be included in the log-plot

## FINISHED SECTION 2

We then fit a model and used residual plots to diagnose the model fit.

manyglm.full <- manyglm(full.mvabund ~ Genotype,  
 data = full.df,  
 family = "negative.binomial")  
plot(manyglm.full, which = 1:3) # residuals aren't quite normally distributed, but there doesn't seem to be any heteroscedasticity in the model fit. Note that replotting the residuals gives qualitatively the same picture (it's important to replot them because the residuals involve random number generation, see ?plot.manyglm)

Given that a negative binomial distribution seems to provide a good fit to the data, we tested whether the composition of gall-parasitoid interaction varied among willow genotypes. To further diagnose which interactions were driving this response, we conducted univariate analyses on each predictor, but adjusted for multiple comparisons. P-values were adjusted for multiple testing using a step-down resampling procedure. This methods provides strong control of family-wise error rates and makes use of resampling to ensure inferences take into account correlation between variables (Westfall & Young 1993).

From the table, it is clear to say that genotype has a strong effect on the composition of links in the network. Moreover, differences in community composition are driven primarily by 3 interactions: vLG\_Platy, vLG\_Tory, and vLG\_Mesopol.

anova.full <- anova.manyglm(manyglm.full, p.uni = "unadjusted") # Takes about 1 min and 30 sec to run.  
anova.full # vLG\_Platy, vLG\_Tory, and vLG\_Mesopol are driving the community response. rG\_Tory is marginally significant and vLG\_Eulo is close to marginal as well. aSG\_Tory is significant as well.

##   
## \* A B D E F G H I J K L M N O P Q R S T U V W X Y Z   
## 4 0 5 3 0 0 0 0 5 0 6 4 0 0 0 0 3 0 5 0 0 5 3 5 3 7

##   
## Call:  
## adonis(formula = bray.link.comm.sub ~ Genotype, data = link.comm.sub)   
##   
## Permutation: free  
## Number of permutations: 999  
##   
## Terms added sequentially (first to last)  
##   
## Df SumsOfSqs MeanSqs F.Model R2 Pr(>F)   
## Genotype 12 5.5719 0.46432 1.5739 0.29563 0.006 \*\*  
## Residuals 45 13.2760 0.29502 0.70437   
## Total 57 18.8479 1.00000   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table  
##   
## Response: Distances  
## Df Sum Sq Mean Sq F value Pr(>F)  
## Groups 12 0.2452 0.020432 0.2306 0.9957  
## Residuals 45 3.9879 0.088620

##   
## Mean distances:  
## Average  
## within groups 0.7041538  
## between groups 0.7794871  
## overall 0.7744740  
##   
## Summary statistics:  
## Statistic  
## MRPP A weights n 0.06649413  
## MRPP A weights n-1 0.07374668  
## MRPP A weights n(n-1) 0.09079738  
## Classification strength 0.05651108

Now we examine how variation in gall densities and gall size (for Iteomyia) affects the network.

First we created a dataset that contained complete observations of the network and predictor variables

## [1] 81

We then looked for evidence of variance inflation among the predictor variables. But found little evidence for it. CURRENTLY NOT WORKING

## log.1.aSG\_abund log.1.rG\_abund log.vLG\_abund vLG.height.mean   
## 1.058523 1.067443 1.009957 1.013748

We log transformed all predictor variables because it provided a much better fit to the data as determined by AIC. We then used AIC to compare our most complex model to our least complex. Instead of exploring all possible combinations, we started with the most complex model and used AIC to drop predictor variables with the lowest AIC values (i.e. least impact on removal). Using AIC, we identified 3 equivalenet models (difference in AIC < 2.1 amongst models).

## Single term deletions  
##   
## Model:  
## net.trait ~ log.vLG\_abund + vLG.height.mean + log.1.rG\_abund +   
## log.1.aSG\_abund  
## Df AIC  
## <none> 844.19  
## log.vLG\_abund 12 889.86  
## vLG.height.mean 12 841.79  
## log.1.rG\_abund 12 892.25  
## log.1.aSG\_abund 12 845.04

## Single term deletions  
##   
## Model:  
## net.trait ~ log.vLG\_abund + log.1.rG\_abund + log.1.aSG\_abund  
## Df AIC  
## <none> 841.79  
## log.vLG\_abund 12 880.19  
## log.1.rG\_abund 12 890.48  
## log.1.aSG\_abund 12 843.10

## Single term deletions  
##   
## Model:  
## net.trait ~ log.vLG\_abund + log.1.rG\_abund  
## Df AIC  
## <none> 843.10  
## log.vLG\_abund 12 880.87  
## log.1.rG\_abund 12 887.84

## Single term deletions  
##   
## Model:  
## net.trait ~ log.1.rG\_abund  
## Df AIC  
## <none> 880.87  
## log.1.rG\_abund 12 927.98

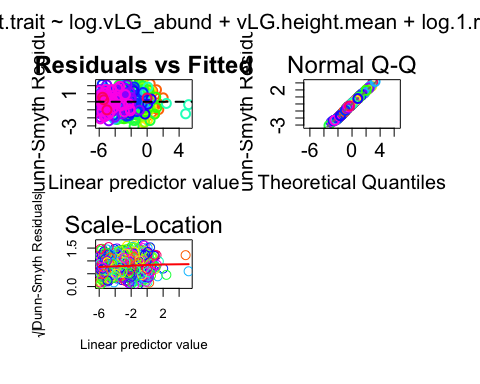
## Model Formula  
## 1 3 log.vLG\_abund + log.1.rG\_abund + log.1.aSG\_abund  
## 2 4 log.vLG\_abund + log.1.rG\_abund  
## 3 2 log.vLG\_abund + vLG.height.mean + log.1.rG\_abund + log.1.aSG\_abund  
## 4 1 log.vLG\_abund \* vLG.height.mean + log.1.rG\_abund + log.1.aSG\_abund  
## 5 5 log.1.rG\_abund  
## 6 6 1  
## AIC  
## 1 841.7936  
## 2 843.0978  
## 3 844.1923  
## 4 862.6600  
## 5 880.8745  
## 6 927.9810

## Time elapsed: 0 hr 3 min 4 sec

## Analysis of Deviance Table  
##   
## net.mvabund.6.null: net.trait ~ 1  
## net.mvabund.5: net.trait ~ log.1.rG\_abund  
## net.mvabund.4: net.trait ~ log.vLG\_abund + log.1.rG\_abund  
## net.mvabund.3: net.trait ~ log.vLG\_abund + log.1.rG\_abund + log.1.aSG\_abund  
## net.mvabund.2: net.trait ~ log.vLG\_abund + vLG.height.mean + log.1.rG\_abund + log.1.aSG\_abund  
## net.mvabund.1.full: net.trait ~ log.vLG\_abund \* vLG.height.mean + log.1.rG\_abund + log.1.aSG\_abund  
##   
## Multivariate test:  
## Res.Df Df.diff Dev Pr(>Dev)   
## net.mvabund.6.null 80   
## net.mvabund.5 79 1 64.14 0.001 \*\*\*  
## net.mvabund.4 78 1 22.90 0.049 \*   
## net.mvabund.3 77 1 67.91 0.001 \*\*\*  
## net.mvabund.2 76 1 24.85 0.023 \*   
## net.mvabund.1.full 75 1 5.53 0.683   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
## Arguments:  
## Test statistics calculated assuming uncorrelated response (for faster computation)   
## P-value calculated using 999 resampling iterations via resampling (to account for correlation in testing).

After deciding on the model with all main effects and no interactions, we examined the residuals and everything looked pretty good.

plot(net.mvabund.2, which = 1:3) # residuals look pretty good.



We then examined the which processes underlied variation in the gall-parasitoid interactions.

anova.net <- anova.manyglm(net.mvabund.2, p.uni = "unadjusted") # takes about 2.5 min to run.  
anova.net # not that since the P-values are determined by a resampling procedure, they may differ slightly between runs. Therefore, we retain all P-values < 0.10 (during at least one run) for the coefficient summary below.  
  
anova.net.null <- anova.manyglm(net.mvabund.2, net.mvabund.6.null) # takes about 30 sec to run  
anova.net.null  
  
sig.coef.df.2 <- mutate(melt(coef(net.mvabund.2)),  
 predictor\_response = paste(X1, X2, sep = "\_")) %>%  
 # select(predictor = X1, response = X2, predictor\_response, value) %>%  
 subset(predictor\_response %in% c("log.1.aSG\_abund\_aSG\_Tory",   
 "log.1.rG\_abund\_rG\_Eulo",  
 "log.1.rG\_abund\_rG\_Platy",  
 "log.1.rG\_abund\_rG\_Lestodip", # marginal  
 "log.vLG\_abund\_SG\_Platy", # marginal  
 "log.vLG\_abund\_vLG\_Mymarid",  
 "vLG.height.mean\_vLG\_Eulo", # marginal  
 "vLG.height.mean\_rG\_Tory", "log.1.rG\_abund\_rG\_Tory",  
 "vLG\_abund\_vLG\_Mesopol", "vLG.height.mean\_vLG\_Mesopol",   
 "vLG.height.mean\_vLG\_Platy", "log.vLG\_abund\_vLG\_Platy",  
 "vLG.height.mean\_vLG\_Tory", "log.vLG\_abund\_vLG\_Tory")) %>% # vLG.height.mean is marginal for vLG\_Tory  
 select(predictor = X1, response = X2, coefficient = value)  
arrange(sig.coef.df.2, predictor, response)  
1 - exp(-0.2157298) # 19% decrease in vLG\_Platy interaction with every one unit increase in gall size.  
1 - exp(-0.2697011) # 24% decrease in vLG\_Mesopolobous interaction with every one unit increase in gall size.

The results from the link composition analysis suggest that increases in gall abundance lead to increasing food web complexity for those individual nodes, whereas differences in leaf gall size lead to fundamental differences in link composition.

Then we examined whether the proportion of galls parasitized varied among willow genotypes

vLG.ptized.glm <- glm(vLG\_parasitized/vLG\_abund ~ Genotype, data = full.df,   
 weights = vLG\_abund, family = "binomial")  
  
rG.ptized.glm <- glm(rG\_parasitized/rG\_abund ~ Genotype, data = full.df,   
 weights = rG\_abund, family = "binomial")  
  
aSG.ptized.glm <- glm(aSG\_parasitized/aSG\_abund ~ Genotype, data = full.df,  
 weights = aSG\_abund, family = "binomial")

Summary of results from parasitism models

## Analysis of Deviance Table  
##   
## Model: binomial, link: logit  
##   
## Response: vLG\_parasitized/vLG\_abund  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev Pr(>Chi)   
## NULL 81 173.310   
## Genotype 23 75.793 58 97.518 1.503e-07 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table  
##   
## Model: binomial, link: logit  
##   
## Response: rG\_parasitized/rG\_abund  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev Pr(>Chi)   
## NULL 67 80.965   
## Genotype 21 31.127 46 49.838 0.07157 .  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table  
##   
## Model: binomial, link: logit  
##   
## Response: aSG\_parasitized/aSG\_abund  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev Pr(>Chi)  
## NULL 30 21.2977   
## Genotype 18 15.694 12 5.6032 0.6139

Further explore the factors determining gall parasitism rates among willow genotypes. These were the best models as determined by AIC.

vLG\_total.ptism <- glm(vLG\_parasitized/vLG\_abund ~ vLG.height.mean,   
 data = full.df, weights = vLG\_abund, family = "binomial")  
  
vLG\_Platy.ptism <- glm(vLG\_Platy/vLG\_abund ~ vLG.height.mean\*vLG\_abund,   
 data = full.df, weights = vLG\_abund, family = "binomial")  
  
vLG\_Mesopol.ptism <- glm(vLG\_Mesopol/vLG\_abund ~ vLG.height.mean\*vLG\_abund,   
 data = full.df, weights = vLG\_abund, family = "binomial")  
  
vLG\_Tory.ptism <- glm(vLG\_Tory/vLG\_abund ~ vLG.height.mean + vLG\_abund,   
 data = full.df, weights = vLG\_abund, family = "binomial")

## Analysis of Deviance Table (Type II tests)  
##   
## Response: vLG\_parasitized/vLG\_abund  
## LR Chisq Df Pr(>Chisq)   
## vLG.height.mean 22.279 1 2.358e-06 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type II tests)  
##   
## Response: vLG\_Platy/vLG\_abund  
## LR Chisq Df Pr(>Chisq)   
## vLG.height.mean 17.5845 1 2.748e-05 \*\*\*  
## vLG\_abund 0.7253 1 0.394416   
## vLG.height.mean:vLG\_abund 8.7078 1 0.003168 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type II tests)  
##   
## Response: vLG\_Mesopol/vLG\_abund  
## LR Chisq Df Pr(>Chisq)   
## vLG.height.mean 7.2752 1 0.006991 \*\*  
## vLG\_abund 0.2943 1 0.587506   
## vLG.height.mean:vLG\_abund 4.2108 1 0.040167 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type II tests)  
##   
## Response: vLG\_Tory/vLG\_abund  
## LR Chisq Df Pr(>Chisq)   
## vLG.height.mean 3.8328 1 0.05026 .  
## vLG\_abund 5.2428 1 0.02204 \*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

The odds of a leaf gall being parasitized decreased by 25% with every one mm increase in gall size.

1-exp(coef(vLG\_total.ptism)[2]) # 25% reduction in the odds of vLG being parasitized with every one unit increase in gall size.