Effect of Wet and Dry Greenhouse Conditions on the Development of Bisexual Flowers of Genus Dalechampia

Introduction

Dalechampia is a genus of plant species commonly found in tropical regions mostly in the Americas. It is characterized by their unisexual flowers and bisexual blossoms and play a vital role in the pollination cycle in these tropical regions. In this report we are analysing the different proportions between two species of Dalechampia (Dalechampia S and Dalechampia L) and the effects of growing in a dry and wet Greenhouse on Gland Area(GA) and Upper Bract Width(UBW).

Analysis Methods

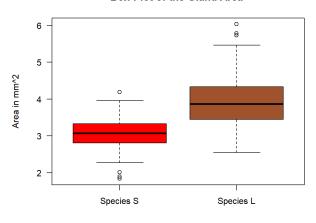
The dataset given contains 13 columns out of which 8 columns were measurements of the Blossoms of both the species. Log transformations were used to normalize the collected data. We first analyse the given dataset to find the differences in proportions in the two species of Dalechamplia for this we find the mean difference between GA and UBW of both the species. We use an ANOVA model to analyse the differences in dimensions between the two species and difference caused by the treatment conditions .For this we consider GAD (Gland-anther distance in mm), GSD (Gland-stigma distance in mm), GA (Gland area -square root of gland width * gland height in mm), UBW(Upper bract width in mm), UBL(Upper bract length in mm), LBW(Lower bract length in mm) and LBL(Lower bract length in mm) to be affected.

Finally, we use a Two-way ANOVA to analyse the effects of species and the treatment on Gland Area(GA) and Upper Bract Width(UBW) these were chosen so as to compare an area factor and a dimension factor of the blossom.

Results

To analyse the fundamental differences in both the species we find the means of the Gland Area(GA) and Upper Bract Width(UBW).

Box-Plot of the Gland Area



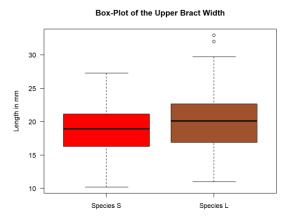


Fig 1:-Plot showing the difference in Gland Area

Fig 2:-Plot showing the difference in Lower Bract width

As shown in Fig 1 &Fig 2 the mean Gland Area(GA) and Upper Bract Width(UBW) of species S is smaller than species L by 25.27% and 8% respectively as calculated from their means.

ANOVA Analysis-Effect of Species

To analyse the difference in overall measurements of the two species an ANOVA analysis was performed.

Predictors	Df	Sum Sq	Mean Sq	F value	P value
Species	1	105.18	105.18	74.577	<2.2e-16
Residuals	362	510.53	1.41		

Table 1: -Results of the ANOVA analysis. Here the first row represents whether the difference in mean values in the species. F>3.95 and P<0.05 is considered significant.

Predictors	Estimates	Std.Error	t value	P value
Intercept	16.20980	0.08315	194.956	<2e -16
Species S	-1.08301	0.12541	-8.636	<2e-16

Table 2: -Summary of the ANOVA analysis here the first row represents the Species L and the second row represents Species S. t>+2|t<-2 and P<0.05 is considered significant.

The ANOVA results from Table 1 and Table 2 show that there is a significant difference between the dimensions of the Species and that the blossom of Dalechampia L is **larger** than Dalechampia S by **6.67%**.

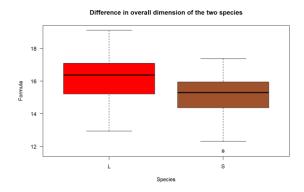


Fig3:-Boxplot of the ANOVA results

ANOVA Analysis-Effect of Treatment.

To analyse the difference in overall measurements of the two species caused because of the wet or dry Greenhouse conditions an ANOVA analysis was performed on each species.

Species S

Predictors	Df	Sum Sq	Mean Sq	F value	P value
Treatment(SpeciesS)	1	67.179	67.179	95.726	<2.2e-16
Residuals	158	110.881	0.702		

Table 3:- Results of the ANOVA analysis. Here the first row represents whether the difference in mean values in the treatments in Species S. F>3.95 and P<0.05 is considered significant.

Predictors	Estimates	Std.Error	t value	P value
Intercept(Dry)	14.41043	0.09873	145.963	<2e -16
Wet (Species S)	1.30247	0.13312	9.784	<2e-16

Table 4: -Summary of the ANOVA analysis here the first row represents the effect of dry treatment in Species S and the second row represents the wet treatment. t > +2|t < -2 and P < 0.05 is considered significant.

Tables 3 and 4 show that the there is significant difference between the means of the dimension of the blossoms of Dalechampia Species S caused by the treatment. The blosoms that were measured after wet treatment are in average 9.03% larger than the blossoms measured after dry treatment in the greenhouse.

Species L

Predictors	Df	Sum Sq	Mean Sq	F value	P value
Treatment(SpeciesL)	1	168.79	67.179	208.31	<2.2e-16
Residuals	202	163.68	0.81		

Table 3:- Results of the ANOVA analysis. Here the first row represents whether the difference in mean values in the treatments in Species L. F>3.95 and P<0.05 is considered significant.

Predictors	Estimates	Std.Error	t value	P value
Intercept(Dry)	15.32656	0.08785	174.47	<2e -16
Wet (SpeciesL)	1.82001	0.12610	14.43	<2e-16

Table 4: -Summary of the ANOVA analysis here the first row represents the effect of dry treatment in Species L and the second row represents the wet treatment. t > +2|t < -2 and P < 0.05 is considered significant.

Tables 3 and 4 show that the there is significant difference between the means of the dimension of the blossoms of Dalechampia Species S caused by the treatment. The blosoms that were measured after wet treatment are in average 11.87% larger than the blossoms measured after dry treatment in the greenhouse.

II-Way ANOVA-Effect of Species and Treatment on GA and UBW

To analyse the effects of species and treatment on the Gland Area(GA) and Upper Bract Width(UBW) we perform a two way ANOVA Analysis.

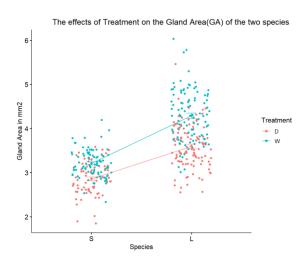


Fig4: - Relationship between Gland Area(GA) the species and the treatment at the greenhouse.

Predictors	Df	Sum Sq	Mean Sq	F value	P value
Species	1	70.099	70.099	326.573	<2.2e-16
Treatment	1	27.133	27.133	126.406	<2.2e-16
Species:Treatment	1	2.607	2.607	12.148	0.0005519
Residuals	362	77.704	0.215		

Table 5: -Summary of the ANOVA analysis for GA here the first row represents the effect of Species, the second row represents treatment(Wet or Dry) and the third row represents the interaction effect between the two.

From Table 5 and Fig 4 we can see a significant effect of treatment and species and their interaction on Gland Area determined by the F-value and P values. The Gland area of Species S is on average **0.739mm**² lesser than Species L when grown in dry greenhouse conditions whereas it is on average **1.080mm**² smaller than Species L when grown in wet conditions. The Gland Area of Species L is on average **0.694mm**² larger when grown in wet conditions than in dry conditions this is compared to the **0.352mm**² of Species S in the same conditions.

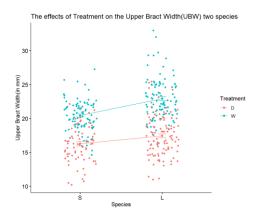


Fig5: - Relationship between Upper Bract Width (UBW) the species and the treatment at the greenhouse.

Predictors	Df	Sum Sq	Mean Sq	F value	P value
Species	1	215.4	215.4	28.032	2.07e-07
Treatment	1	2205.5	2205.5	287.049	<2e-16
Species:Treatment	1	38.6	38.6	5.023	0.0256
Residuals	362	2781.4	7.7		

Table 6: -Summary of the ANOVA analysis for UBW here the first row represents the effect of Species, the second row represents treatment(Wet or Dry) and the third row represents the interaction effect between the two.

From Table 6 and Figure 5 we can see a significant effect of species and treatment and their interaction on UBW. The upper bract with of species S is on average 1.178 mm shorter than species L in dry greenhouse conditions and 2.492mm shorter in wet conditions . Also, UBW of species L on average is 5.492mm longer in wet conditions as compared to 4.179mm in species S. Finally, UBW of species S is on average 3mm longer than when grown in wet conditions when species L is grown in dry conditions. On the contrary UBW in species L in wet condition is on average 6.67mm longer compared to species S in dry condition.

Conclusion:

The dimensions of the Dalechampia Species S is generally smaller compared to Species L by almost 6.67%. Dalechampia Species S grows around 9.3% larger in wet conditions compared to 11.87% of Dalechampia Species L.From the ANOVA tests we can conclude that there is a statistically significant effect of Species, Treatment and their interaction on Gland Area(GA) and Upper Bract Width(UBW) by varying degrees.

Appendix

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#R-code Q1.R
#Code used for analyzing blossom data of two species of Dalechampia S and L
#13-01-2022 BIOS-14
library(dplyr)#Used to filter data.
library(car)#Used for TukeyHSD.
library(ggpubr) #Used to plot II-dimensional Anova Plots.
data=read.csv("exam2022_part1.csv")
#Filtering given Dataset by species.
S=filter(data,data\$sp == 'S')
L=filter(data,data$sp =='L')
#Boxplots used to identify differences of GA and UBW in between species
boxplot(S\$GA,L\$GA,names = c("Species S","Species L"), ylab = "Area in line to the context of t
mm^2",las=1,col=c("red","sienna"),main="Box-Plot of the Gland Area ")
boxplot(S$UBW,L$UBW,names=c("Species S","Species L"),ylab="Length in
mm",las=1,col=c("red","sienna"),main="Box-Plot of the Upper Bract Width")
#Modelling starts
species=as.factor(data$sp)#Selecting the species as factors.
#Model-Difference in dimensions between Species.
m5 = lm(log(UBW) + log(UBL) + log(LBU) + log(LBW) + log(GA) + log(GSD) + log(GAD) \sim species, data = data) + log(UBW) + log(UBU) + 
#Boxplot for the model
boxplot(log(UBW) + log(UBL) + log(LBL) + log(LBW) + log(GA) + log(GSD) + log(GAD) \sim species, data = data, las = 1, constant = 
ol=c("red", "sienna"), xlab="Species", ylab="Formula", main="Difference in overall dimension of the two
species")
#Check the effects of wet and dry greenhouse
#Initializing them as factors
conditionS=as.factor(S$treat)
conditionL=as.factor(L$treat)
#Model 2-Effect of Treatment on dimension
#For Species S
m6 = lm(log(UBW) + log(UBL) + log(LBW) + log(CAW) + l
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#For Species L
m7 = lm(log(UBW) + log(UBL) + log(LBL) + log(LBW) + log(GA) + log(GSD) + log(GAD) \sim conditionL, data = L)
#2Way ANOVA to find the effects of treatment and species on GA and LBW
m8=aov(GA~sp*treat,data=data) #Model for GA
summary(m8)
TukeyHSD(m8)
#Plot for Model
ggline(data,x="sp",y="GA",col="treat",
    add=c("mean_se","jitter"),
    ylab="Gland Area in mm2",xlab="Species",
    legend.title="Treatment",legend="right",
    main="
                The effects of Treatment on the Gland Area(GA) of the two species")
m9=aov(UBW~sp*treat,data=data)#Model for UBW
summary(m9)
TukeyHSD(m9)
#plot for the Model
ggline(data,x="sp",y="UBW",col="treat",
    add=c("mean_se","jitter"),
    ylab="Upper Bract Width(in mm)",xlab="Species",
    legend.title="Treatment",legend="right",
    main="The effects of Treatment on the Upper Bract Width(UBW) two species")
```