Effect of treatments on leaves

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## 1 Effect of Treatments on leaves to produce roots

An experiment was conducted to find the rooting potential of the leaves mainly angiosperms to root when treated with different phyto-hormones.



* In the experiment, 4 treatments were applied on 8 different species, and the observations included:
	+ Number of roots (num\_roots\_n).
	+ Length of the longest root in centimeters (lng\_long\_root\_cm).
	+ Diameter of the longest root in millimeters (dia\_long\_root\_mm).

#### Loading Required packages

library(tidyverse)
library(gt)

#### Loading the data and formatting

The data is loaded as a dataframe thesisdata and columns such as treatments(Treatment) and species(Species) are changes to factors as they are not suitable as strings.

# Loading data
thesisdata <- read\_csv("thesisdata.csv",
 show\_col\_types = FALSE)
# formating data
ths\_data <- thesisdata
ths\_data$Treatment <- as.factor(ths\_data$Treatment)
ths\_data$Treatment <-
 factor(ths\_data$Treatment,levels = c("Control",
 "Coconut water",
 "IBA 1000ppm",
 "IBA 100ppm + Coconut water"))
ths\_data$Species <- factor(ths\_data$Species)

ths\_data %>% head()

# A tibble: 6 × 5
 Species Treatment num\_roots\_n lng\_long\_root\_cm dia\_long\_root\_mm
 <fct> <fct> <dbl> <dbl> <dbl>
1 Conidium verigatum Control 0 0 0
2 Conidium verigatum Control 0 0 0
3 Conidium verigatum Control 0 0 0
4 Conidium verigatum Control 0 0 0
5 Conidium verigatum Control 0 0 0
6 Conidium verigatum Control 0 0 0

* Confirming that only 8 species and 4 treatments are used in the experiment.

treatments\_and\_species <- list(unique(ths\_data$Treatment), unique(ths\_data$Species))

names(treatments\_and\_species) <- c("Treatment", "Species")
treatments\_and\_species

$Treatment
[1] Control Coconut water
[3] IBA 1000ppm IBA 100ppm + Coconut water
Levels: Control Coconut water IBA 1000ppm IBA 100ppm + Coconut water

$Species
[1] Conidium verigatum Rawolfia tetraphylla Justicia Sps
[4] Zizupus rugosa Jasminum Sps Cyclea pelteta
[7] Bredelia scandens Hemigraphis alternata
8 Levels: Bredelia scandens Conidium verigatum ... Zizupus rugosa

### 1.1 Aggregating data and formatting the results into a table.

The data is aggregated in [Table 1](#tbl-aggregate-summary) by the average of root lengths with standard deviation(SD)

ths\_data\_1 <- ths\_data %>% group\_by(Species, Treatment) %>%
 summarise(avg\_n\_roots = mean(num\_roots\_n),
 SD\_n\_roots = sd(num\_roots\_n),
 avg\_lng\_root = mean(lng\_long\_root\_cm),
 SD\_lng\_root = sd(lng\_long\_root\_cm),
 avg\_dia\_root = mean(dia\_long\_root\_mm),
 SD\_dia\_root = sd(dia\_long\_root\_mm)) %>%
 # rounding of to 2 digits
 mutate(across(where(is.double), ~round(., digits = 2))) %>%
 # combining means and SD into a single column
 unite(avg\_n\_roots\_SD, avg\_n\_roots, SD\_n\_roots, sep = " \u00b1 ") %>%
 unite(avg\_lng\_root\_SD, avg\_lng\_root, SD\_lng\_root, sep = " \u00b1 ") %>%
 unite(avg\_dia\_root\_SD, avg\_dia\_root, SD\_dia\_root, sep = " \u00b1 ") %>%
 # using 'gt' package to get a table
 gt(rowname\_col = "Treatment") %>%
 tab\_header(
 title = "Thesis Data of the Species",
 subtitle = "Influence of growth regulators on the root generation"
 ) %>%
 opt\_align\_table\_header(align = "center") %>%
 cols\_label( # renaming columns
 avg\_n\_roots\_SD = md("Mean number of roots \u00b1 SD"), #md is markdown language
 avg\_lng\_root\_SD = md("Mean length of longest roots \u00b1 SD (cm)"),
 avg\_dia\_root\_SD = md("Mean diameter of longest roots \u00b1 SD (mm)")
 ) %>% # fixing columns width
 cols\_width(Treatment ~ px(150),
 avg\_n\_roots\_SD ~ px(150),
 avg\_lng\_root\_SD ~ px(150),
 avg\_dia\_root\_SD ~ px(150),
 ) %>%
 cols\_align(align = "center")

ths\_data\_1

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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| Table 1: Aggregating data and finding average of each parameter by species and treatmentTable 1: Thesis Data of the SpeciesInfluence of growth regulators on the root generation

|  | Mean number of roots ± SD | Mean length of longest roots ± SD (cm) | Mean diameter of longest roots ± SD (mm) |
| --- | --- | --- | --- |
| Bredelia scandens |
| Control | 0 ± 0 | 0 ± 0 | 0 ± 0 |
| Coconut water | 0 ± 0 | 0 ± 0 | 0 ± 0 |
| IBA 1000ppm | 3.22 ± 0.44 | 6.06 ± 2.02 | 0.89 ± 0.17 |
| IBA 100ppm + Coconut water | 3 ± 0.5 | 6.02 ± 1.26 | 0.77 ± 0.2 |
| Conidium verigatum |
| Control | 0 ± 0 | 0 ± 0 | 0 ± 0 |
| Coconut water | 2.89 ± 1.05 | 4.52 ± 1.1 | 0.62 ± 0.15 |
| IBA 1000ppm | 7.89 ± 3.62 | 7.52 ± 2.55 | 0.76 ± 0.15 |
| IBA 100ppm + Coconut water | 2.44 ± 0.88 | 4.74 ± 1.09 | 0.81 ± 0.18 |
| Cyclea pelteta |
| Control | 0 ± 0 | 0 ± 0 | 0 ± 0 |
| Coconut water | 3.33 ± 0.71 | 2.48 ± 0.37 | 0.18 ± 0.04 |
| IBA 1000ppm | 5.22 ± 1.39 | 4.89 ± 1.17 | 0.28 ± 0.07 |
| IBA 100ppm + Coconut water | 8.89 ± 2.03 | 12.64 ± 3.23 | 0.45 ± 0.1 |
| Hemigraphis alternata |
| Control | 0 ± 0 | 0 ± 0 | 0 ± 0 |
| Coconut water | 1.11 ± 0.33 | 5.89 ± 0.84 | 0.65 ± 0.11 |
| IBA 1000ppm | 2.22 ± 0.83 | 8.06 ± 1.58 | 0.77 ± 0.11 |
| IBA 100ppm + Coconut water | 1.11 ± 0.33 | 5.33 ± 1.93 | 0.57 ± 0.09 |
| Jasminum Sps |
| Control | 0 ± 0 | 0 ± 0 | 0 ± 0 |
| Coconut water | 1.89 ± 0.6 | 8.06 ± 0.88 | 0.5 ± 0.05 |
| IBA 1000ppm | 5.11 ± 1.17 | 14.82 ± 1.59 | 0.88 ± 0.19 |
| IBA 100ppm + Coconut water | 2.67 ± 1.22 | 12.12 ± 2.27 | 1.71 ± 0.25 |
| Justicia Sps |
| Control | 0 ± 0 | 0 ± 0 | 0 ± 0 |
| Coconut water | 1.22 ± 0.44 | 3.28 ± 1.24 | 0.35 ± 0.21 |
| IBA 1000ppm | 1.89 ± 0.78 | 8.64 ± 2.41 | 1.08 ± 0.26 |
| IBA 100ppm + Coconut water | 1.22 ± 0.44 | 5.47 ± 1.84 | 1.35 ± 0.23 |
| Rawolfia tetraphylla |
| Control | 0.56 ± 1.13 | 0.26 ± 0.51 | 0.04 ± 0.09 |
| Coconut water | 1.78 ± 0.97 | 5.4 ± 2.64 | 0.36 ± 0.1 |
| IBA 1000ppm | 4.78 ± 2.17 | 11.59 ± 4.79 | 0.4 ± 0.12 |
| IBA 100ppm + Coconut water | 2.67 ± 1.41 | 10.09 ± 2.34 | 0.61 ± 0.19 |
| Zizupus rugosa |
| Control | 0 ± 0 | 0 ± 0 | 0 ± 0 |
| Coconut water | 1.22 ± 0.83 | 2.94 ± 1.34 | 0.38 ± 0.18 |
| IBA 1000ppm | 4.44 ± 1.59 | 5.56 ± 2.08 | 0.53 ± 0.15 |
| IBA 100ppm + Coconut water | 2.22 ± 0.67 | 4.26 ± 1.11 | 0.63 ± 0.17 |

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### 1.2 Plotting the data for better understanding.

* Plotting a bar graph [Figure 1](#fig-treatment-effect) to see how each treatment performed on each species.

ths\_data |> summarise(avg\_n\_roots = mean(num\_roots\_n),
 avg\_lng\_root = mean(lng\_long\_root\_cm),
 avg\_dia\_root = mean(dia\_long\_root\_mm),
 .by = c(Species, Treatment)) %>%
 rename("Mean number of Roots" = avg\_n\_roots,
 "Mean length of Longest root(cm)" = avg\_lng\_root,
 "Mean diameter of Longest roots(mm)" = avg\_dia\_root) %>%
 tidyr::pivot\_longer(c("Mean number of Roots", "Mean length of Longest root(cm)",
 "Mean diameter of Longest roots(mm)")) |>
 ggplot(aes(x = Species, y = value, fill = name)) +
 geom\_col(alpha = 0.7, position = "dodge") +
 facet\_wrap(~Treatment, ncol = 2) +
 theme\_bw() + labs(y = " ", fill = "Parameters",
 title = "Effect of treatments on rooting") +
 theme(legend.position = "bottom",
 axis.text.x = element\_text(angle = 45, hjust = 1),
 plot.title = element\_text(size = 18))

|  |
| --- |
| Figure 1: Influence of pytohormone treatments on leaves of different species |

* We can clearly see that *Control* treatment is not producing any roots in majority of the species.
* **IBA 1000ppm** is clearly showing most promising results in most of the species in the graph.

### 1.3 Finding correlation

We are going to filter out the control treatment as it is not significant at producing roots at all and plot [Figure 2](#fig-root_length_vs_root_dia-scatterplot) to find which treatment has better correlation at producing roots with higher diameters.

ths\_data |> filter(Treatment!= "Control") |>
 ggplot(aes(x = lng\_long\_root\_cm, y = dia\_long\_root\_mm)) +
 geom\_point(aes(color = Treatment)) +
 geom\_smooth(method = "lm", aes(group = Treatment, color = Treatment)) +
 labs(title = "Plotting Root length Vs Root Diameter",
 x = "Length of the longest root",
 y = "Diameter of the longest root") +
 theme(legend.position = "bottom",
 plot.title = element\_text(size = 18))

`geom\_smooth()` using formula = 'y ~ x'

|  |
| --- |
| Figure 2: Plotting a scatter plot to find correlation between root lengths and diameters |

* The graph clearly shows that the Coconut Water treatment has the highest slope but other treatments which produced higher root lengths did not have a correlation as that of Coconut Water treatment.

### 1.4 Statistical Analysis

Let’s conduct a anova test on the data after filtering Control as it has not given any roots.

Let *H0* be Null hypothesis *H1* be Alternate hypothesis

# ANOVA Model
model\_anova <- ths\_data %>%
 filter(Treatment != "Control") %>%
 aov(num\_roots\_n ~ Treatment, data = .)

# Summary
model\_anova %>% summary()

 Df Sum Sq Mean Sq F value Pr(>F)
Treatment 2 256.0 128.00 27.43 2.51e-11 \*\*\*
Residuals 213 993.9 4.67
---
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# TukeyHSD
model\_anova %>% TukeyHSD(conf.level = 0.95)

 Tukey multiple comparisons of means
 95% family-wise confidence level

Fit: aov(formula = num\_roots\_n ~ Treatment, data = .)

$Treatment
 diff lwr upr
IBA 1000ppm-Coconut water 2.666667 1.8169277 3.5164057
IBA 100ppm + Coconut water-Coconut water 1.347222 0.4974832 2.1969612
IBA 100ppm + Coconut water-IBA 1000ppm -1.319444 -2.1691835 -0.4697054
 p adj
IBA 1000ppm-Coconut water 0.0000000
IBA 100ppm + Coconut water-Coconut water 0.0006848
IBA 100ppm + Coconut water-IBA 1000ppm 0.0009086

We can see from p adj that all the treatments means are different and we can reject the *H0* hypothesis. *H1* holds at 95% confidence interval.