

coding challenge 4

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Contents

Plot 2: Boxplot for MassperSeed_mg with Fg + 70 added 7

###The link of manuscript is here: #### Noel, Z.A., Roze, L.V., Breunig, M., Trail, F. 2022. Endophytic fungi as promising biocontrol agent to protect wheat from Fusarium graminearum head blight. Plant Disease. manuscript where these data are published

Code for Question 5

```
##### Question 1
```

```
# Load 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(ggplot2)
```

```
library(readr)
```

```
# Read data
```

```
don_data <- read.csv("DON_data.csv", na.strings = "na")
```

```
colnames(don_data) <- gsub("\\.", " ", colnames(don_data))
```

```
##ambassador
```

```
ambassador_ntc <- don_data %>% filter(`Code on vial` %in% c("Glyc #11", "Glyc #12", "Glyc #13", "Glyc #14", "Glyc #15", "Glyc #16", "Glyc #17", "Glyc #18", "Glyc #19", "Glyc #20", "Glyc #21", "Glyc #22", "Glyc #23", "Glyc #24", "Glyc #25", "Glyc #26", "Glyc #27", "Glyc #28", "Glyc #29", "Glyc #30", "Glyc #31", "Glyc #32", "Glyc #33", "Glyc #34", "Glyc #35", "Glyc #36", "Glyc #37", "Glyc #38", "Glyc #39", "Glyc #40", "Glyc #41", "Glyc #42", "Glyc #43", "Glyc #44", "Glyc #45", "Glyc #46", "Glyc #47", "Glyc #48", "Glyc #49", "Glyc #50", "Glyc #51", "Glyc #52", "Glyc #53", "Glyc #54", "Glyc #55", "Glyc #56", "Glyc #57", "Glyc #58", "Glyc #59", "Glyc #60", "Glyc #61", "Glyc #62", "Glyc #63", "Glyc #64", "Glyc #65", "Glyc #66", "Glyc #67", "Glyc #68", "Glyc #69", "Glyc #70", "Glyc #71", "Glyc #72", "Glyc #73", "Glyc #74", "Glyc #75", "Glyc #76", "Glyc #77", "Glyc #78", "Glyc #79", "Glyc #80", "Glyc #81", "Glyc #82", "Glyc #83", "Glyc #84", "Glyc #85", "Glyc #86", "Glyc #87", "Glyc #88", "Glyc #89", "Glyc #90", "Glyc #91", "Glyc #92", "Glyc #93", "Glyc #94", "Glyc #95", "Glyc #96", "Glyc #97", "Glyc #98", "Glyc #99", "Glyc #100"))
```

```
ambassador_fg <- don_data %>% filter(`Code on vial` %in% c("Glyc + Fg #1", "Glyc + Fg #2", "Glyc + Fg #3", "Glyc + Fg #4", "Glyc + Fg #5", "Glyc + Fg #6", "Glyc + Fg #7", "Glyc + Fg #8", "Glyc + Fg #9", "Glyc + Fg #10", "Glyc + Fg #11", "Glyc + Fg #12", "Glyc + Fg #13", "Glyc + Fg #14", "Glyc + Fg #15", "Glyc + Fg #16", "Glyc + Fg #17", "Glyc + Fg #18", "Glyc + Fg #19", "Glyc + Fg #20", "Glyc + Fg #21", "Glyc + Fg #22", "Glyc + Fg #23", "Glyc + Fg #24", "Glyc + Fg #25", "Glyc + Fg #26", "Glyc + Fg #27", "Glyc + Fg #28", "Glyc + Fg #29", "Glyc + Fg #30", "Glyc + Fg #31", "Glyc + Fg #32", "Glyc + Fg #33", "Glyc + Fg #34", "Glyc + Fg #35", "Glyc + Fg #36", "Glyc + Fg #37", "Glyc + Fg #38", "Glyc + Fg #39", "Glyc + Fg #40", "Glyc + Fg #41", "Glyc + Fg #42", "Glyc + Fg #43", "Glyc + Fg #44", "Glyc + Fg #45", "Glyc + Fg #46", "Glyc + Fg #47", "Glyc + Fg #48", "Glyc + Fg #49", "Glyc + Fg #50", "Glyc + Fg #51", "Glyc + Fg #52", "Glyc + Fg #53", "Glyc + Fg #54", "Glyc + Fg #55", "Glyc + Fg #56", "Glyc + Fg #57", "Glyc + Fg #58", "Glyc + Fg #59", "Glyc + Fg #60", "Glyc + Fg #61", "Glyc + Fg #62", "Glyc + Fg #63", "Glyc + Fg #64", "Glyc + Fg #65", "Glyc + Fg #66", "Glyc + Fg #67", "Glyc + Fg #68", "Glyc + Fg #69", "Glyc + Fg #70", "Glyc + Fg #71", "Glyc + Fg #72", "Glyc + Fg #73", "Glyc + Fg #74", "Glyc + Fg #75", "Glyc + Fg #76", "Glyc + Fg #77", "Glyc + Fg #78", "Glyc + Fg #79", "Glyc + Fg #80", "Glyc + Fg #81", "Glyc + Fg #82", "Glyc + Fg #83", "Glyc + Fg #84", "Glyc + Fg #85", "Glyc + Fg #86", "Glyc + Fg #87", "Glyc + Fg #88", "Glyc + Fg #89", "Glyc + Fg #90", "Glyc + Fg #91", "Glyc + Fg #92", "Glyc + Fg #93", "Glyc + Fg #94", "Glyc + Fg #95", "Glyc + Fg #96", "Glyc + Fg #97", "Glyc + Fg #98", "Glyc + Fg #99", "Glyc + Fg #100"))
```

```
ambassador_37fg <- don_data %>% filter(`Code on vial` %in% c("37 + Fg #7", "37 + Fg #8", "37 + Fg #9", "37 + Fg #10", "37 + Fg #11", "37 + Fg #12", "37 + Fg #13", "37 + Fg #14", "37 + Fg #15", "37 + Fg #16", "37 + Fg #17", "37 + Fg #18", "37 + Fg #19", "37 + Fg #20", "37 + Fg #21", "37 + Fg #22", "37 + Fg #23", "37 + Fg #24", "37 + Fg #25", "37 + Fg #26", "37 + Fg #27", "37 + Fg #28", "37 + Fg #29", "37 + Fg #30", "37 + Fg #31", "37 + Fg #32", "37 + Fg #33", "37 + Fg #34", "37 + Fg #35", "37 + Fg #36", "37 + Fg #37", "37 + Fg #38", "37 + Fg #39", "37 + Fg #40", "37 + Fg #41", "37 + Fg #42", "37 + Fg #43", "37 + Fg #44", "37 + Fg #45", "37 + Fg #46", "37 + Fg #47", "37 + Fg #48", "37 + Fg #49", "37 + Fg #50", "37 + Fg #51", "37 + Fg #52", "37 + Fg #53", "37 + Fg #54", "37 + Fg #55", "37 + Fg #56", "37 + Fg #57", "37 + Fg #58", "37 + Fg #59", "37 + Fg #60", "37 + Fg #61", "37 + Fg #62", "37 + Fg #63", "37 + Fg #64", "37 + Fg #65", "37 + Fg #66", "37 + Fg #67", "37 + Fg #68", "37 + Fg #69", "37 + Fg #70", "37 + Fg #71", "37 + Fg #72", "37 + Fg #73", "37 + Fg #74", "37 + Fg #75", "37 + Fg #76", "37 + Fg #77", "37 + Fg #78", "37 + Fg #79", "37 + Fg #80", "37 + Fg #81", "37 + Fg #82", "37 + Fg #83", "37 + Fg #84", "37 + Fg #85", "37 + Fg #86", "37 + Fg #87", "37 + Fg #88", "37 + Fg #89", "37 + Fg #90", "37 + Fg #91", "37 + Fg #92", "37 + Fg #93", "37 + Fg #94", "37 + Fg #95", "37 + Fg #96", "37 + Fg #97", "37 + Fg #98", "37 + Fg #99", "37 + Fg #100"))
```

```
ambassador_40fg <- don_data %>% filter(`Code on vial` %in% c("40 + Fg #1", "40 + Fg #2", "40 + Fg #3", "40 + Fg #4", "40 + Fg #5", "40 + Fg #6", "40 + Fg #7", "40 + Fg #8", "40 + Fg #9", "40 + Fg #10", "40 + Fg #11", "40 + Fg #12", "40 + Fg #13", "40 + Fg #14", "40 + Fg #15", "40 + Fg #16", "40 + Fg #17", "40 + Fg #18", "40 + Fg #19", "40 + Fg #20", "40 + Fg #21", "40 + Fg #22", "40 + Fg #23", "40 + Fg #24", "40 + Fg #25", "40 + Fg #26", "40 + Fg #27", "40 + Fg #28", "40 + Fg #29", "40 + Fg #30", "40 + Fg #31", "40 + Fg #32", "40 + Fg #33", "40 + Fg #34", "40 + Fg #35", "40 + Fg #36", "40 + Fg #37", "40 + Fg #38", "40 + Fg #39", "40 + Fg #40", "40 + Fg #41", "40 + Fg #42", "40 + Fg #43", "40 + Fg #44", "40 + Fg #45", "40 + Fg #46", "40 + Fg #47", "40 + Fg #48", "40 + Fg #49", "40 + Fg #50", "40 + Fg #51", "40 + Fg #52", "40 + Fg #53", "40 + Fg #54", "40 + Fg #55", "40 + Fg #56", "40 + Fg #57", "40 + Fg #58", "40 + Fg #59", "40 + Fg #60", "40 + Fg #61", "40 + Fg #62", "40 + Fg #63", "40 + Fg #64", "40 + Fg #65", "40 + Fg #66", "40 + Fg #67", "40 + Fg #68", "40 + Fg #69", "40 + Fg #70", "40 + Fg #71", "40 + Fg #72", "40 + Fg #73", "40 + Fg #74", "40 + Fg #75", "40 + Fg #76", "40 + Fg #77", "40 + Fg #78", "40 + Fg #79", "40 + Fg #80", "40 + Fg #81", "40 + Fg #82", "40 + Fg #83", "40 + Fg #84", "40 + Fg #85", "40 + Fg #86", "40 + Fg #87", "40 + Fg #88", "40 + Fg #89", "40 + Fg #90", "40 + Fg #91", "40 + Fg #92", "40 + Fg #93", "40 + Fg #94", "40 + Fg #95", "40 + Fg #96", "40 + Fg #97", "40 + Fg #98", "40 + Fg #99", "40 + Fg #100"))
```

```
ambassador_70fg <- don_data %>% filter(`Code on vial` %in% c("70 + Fg #1", "70 + Fg #2", "70 + Fg #3", "70 + Fg #4", "70 + Fg #5", "70 + Fg #6", "70 + Fg #7", "70 + Fg #8", "70 + Fg #9", "70 + Fg #10", "70 + Fg #11", "70 + Fg #12", "70 + Fg #13", "70 + Fg #14", "70 + Fg #15", "70 + Fg #16", "70 + Fg #17", "70 + Fg #18", "70 + Fg #19", "70 + Fg #20", "70 + Fg #21", "70 + Fg #22", "70 + Fg #23", "70 + Fg #24", "70 + Fg #25", "70 + Fg #26", "70 + Fg #27", "70 + Fg #28", "70 + Fg #29", "70 + Fg #30", "70 + Fg #31", "70 + Fg #32", "70 + Fg #33", "70 + Fg #34", "70 + Fg #35", "70 + Fg #36", "70 + Fg #37", "70 + Fg #38", "70 + Fg #39", "70 + Fg #40", "70 + Fg #41", "70 + Fg #42", "70 + Fg #43", "70 + Fg #44", "70 + Fg #45", "70 + Fg #46", "70 + Fg #47", "70 + Fg #48", "70 + Fg #49", "70 + Fg #50", "70 + Fg #51", "70 + Fg #52", "70 + Fg #53", "70 + Fg #54", "70 + Fg #55", "70 + Fg #56", "70 + Fg #57", "70 + Fg #58", "70 + Fg #59", "70 + Fg #60", "70 + Fg #61", "70 + Fg #62", "70 + Fg #63", "70 + Fg #64", "70 + Fg #65", "70 + Fg #66", "70 + Fg #67", "70 + Fg #68", "70 + Fg #69", "70 + Fg #70", "70 + Fg #71", "70 + Fg #72", "70 + Fg #73", "70 + Fg #74", "70 + Fg #75", "70 + Fg #76", "70 + Fg #77", "70 + Fg #78", "70 + Fg #79", "70 + Fg #80", "70 + Fg #81", "70 + Fg #82", "70 + Fg #83", "70 + Fg #84", "70 + Fg #85", "70 + Fg #86", "70 + Fg #87", "70 + Fg #88", "70 + Fg #89", "70 + Fg #90", "70 + Fg #91", "70 + Fg #92", "70 + Fg #93", "70 + Fg #94", "70 + Fg #95", "70 + Fg #96", "70 + Fg #97", "70 + Fg #98", "70 + Fg #99", "70 + Fg #100"))
```

```
# Extract WHEATON group data
```

```

wheaton_ntc <- don_data %>% filter(`Code on vial` %in% c("Glyc #1", "Glyc #2", "Glyc #3", "Glyc #4")
wheaton_fg <- don_data %>% filter(`Code on vial` %in% c("Fg #1", "Fg #2", "Fg #3", "Fg #4", "Fg #5", "Fg #6")
wheaton_37fg <- don_data %>% filter(`Code on vial` %in% c("37 + Fg #1", "37 + Fg #2", "37 + Fg #3", "37 + Fg #4", "37 + Fg #5", "37 + Fg #6")
wheaton_40fg <- don_data %>% filter(`Code on vial` %in% c("40 + Fg #1", "40 + Fg #2", "40 + Fg #3", "40 + Fg #4", "40 + Fg #5", "40 + Fg #6")
wheaton_70fg <- don_data %>% filter(`Code on vial` %in% c("70 + Fg #1", "70 + Fg #2", "70 + Fg #3", "70 + Fg #4", "70 + Fg #5", "70 + Fg #6")

# Merge data and add Cultivar labels
ambassador_ntc$Cultivar <- "AMBASSADOR"
ambassador_fg$Cultivar <- "AMBASSADOR"
ambassador_37fg$Cultivar <- "AMBASSADOR"
ambassador_40fg$Cultivar <- "AMBASSADOR"
ambassador_70fg$Cultivar <- "AMBASSADOR"

wheaton_ntc$Cultivar <- "WHEATON"

wheaton_fg$Cultivar <- "WHEATON"
wheaton_37fg$Cultivar <- "WHEATON"
wheaton_40fg$Cultivar <- "WHEATON"
wheaton_70fg$Cultivar <- "WHEATON"

# Combine all data
combined_data <- bind_rows(ambassador_ntc, ambassador_fg, ambassador_37fg, ambassador_40fg, ambassador_70fg,
                           wheaton_ntc, wheaton_fg, wheaton_37fg, wheaton_40fg, wheaton_70fg)

# Replace "na" with NA and convert DON column to numeric(to adjust y vale)
combined_data$DON[combined_data$DON == "na"] <- NA
combined_data$DON <- as.numeric(combined_data$DON)

# Remove rows with missing DON values
combined_data <- combined_data %>% filter(!is.na(DON))

# Change Treatment column's name
combined_data <- combined_data %>%
  mutate(Treatment = case_when(
    Treatment == "Glycerol" ~ "NTC", # Change Glycerol to NTC
    Treatment == "Glycerol + Fg" ~ "Fg", # Change Glycerol + Fg to Fg
    TRUE ~ Treatment # Keep other values unchanged
  ))

# Define blue and green colors
custom_colors <- c("#0072B2", "#009E73") # Blue and green

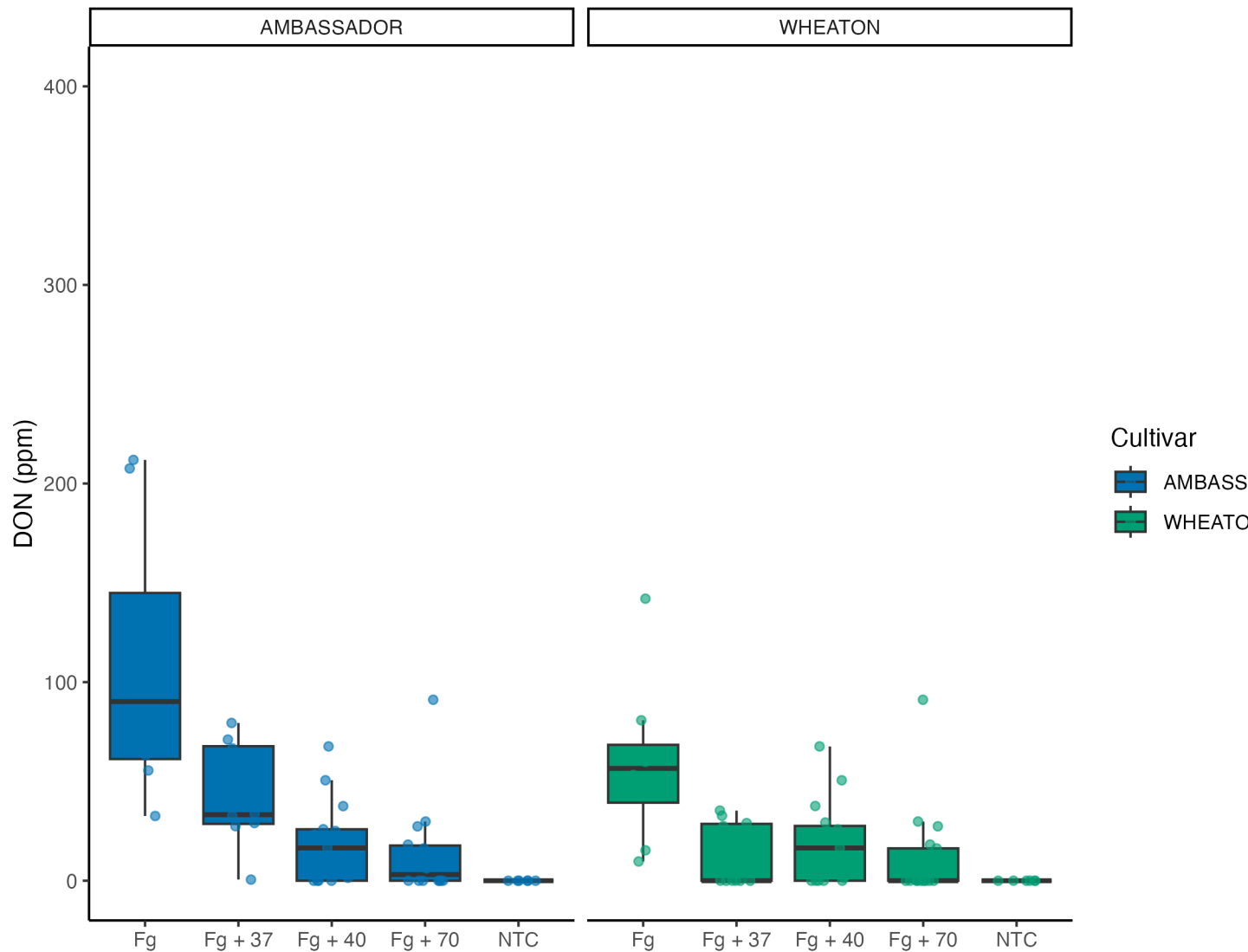
# Create the boxplot
DON_plot <- ggplot(combined_data, aes(x=Treatment, y=DON, fill=Cultivar)) +
  geom_boxplot(outlier.shape = NA) + # Boxplot
  geom_jitter(aes(color=Cultivar), width=0.2, alpha=0.6) + # Jitter points with transparency 0.6
  scale_fill_manual(values=custom_colors) + # Fill colors
  scale_color_manual(values=custom_colors) + # Point colors
  labs(y="DON (ppm)", x="") + # Axis labels
  theme_classic() + # Classic theme
  facet_wrap(~Cultivar) + # Facet by Cultivar
  coord_cartesian(ylim = c(0, 400)) # Set y-axis range from 0 to 400
# Plot 1: save DON figure

```

```
ggsave("DON_plot.png", width = 8, height = 6, dpi = 300)
```

```
####a separate code chunk for the figures plotting the DON data
```

```
knitr::include_graphics("DON_plot.png")
```



```
#####Question 2
# Load libraries
library(dplyr)
library(ggplot2)
library(readr) # For read_csv function

# Read data
don_data <- read_csv("DON_data.csv", na.strings = "na")
colnames(don_data) <- gsub("\\.", " ", colnames(don_data))
# Extract AMBASSADOR group data
```

```
ambassador_ntc <- don_data %>% filter(`Code on vial` %in% c("Glyc #11", "Glyc #12", "Glyc #13", "Glyc #14"))
ambassador_fg <- don_data %>% filter(`Code on vial` %in% c("Glyc + Fg #1", "Glyc + Fg #2", "Glyc + Fg #3", "Glyc + Fg #4"))
ambassador_37fg <- don_data %>% filter(`Code on vial` %in% c("37 + Fg #7", "37 + Fg #8", "37 + Fg #9", "37 + Fg #10"))
ambassador_40fg <- don_data %>% filter(`Code on vial` %in% c("40 + Fg #1", "40 + Fg #2", "40 + Fg #3", "40 + Fg #4"))
ambassador_70fg <- don_data %>% filter(`Code on vial` %in% c("70 + Fg #1", "70 + Fg #2", "70 + Fg #3", "70 + Fg #4"))

# Extract WHEATON group data
wheaton_ntc <- don_data %>% filter(`Code on vial` %in% c("Glyc #1", "Glyc #2", "Glyc #3", "Glyc #4"))
wheaton_fg <- don_data %>% filter(`Code on vial` %in% c("Fg #1", "Fg #2", "Fg #3", "Fg #4", "Fg #5", "Fg #6"))
wheaton_37fg <- don_data %>% filter(`Code on vial` %in% c("37 + Fg #1", "37 + Fg #2", "37 + Fg #3", "37 + Fg #4"))
wheaton_40fg <- don_data %>% filter(`Code on vial` %in% c("40 + Fg #1", "40 + Fg #2", "40 + Fg #3", "40 + Fg #4"))
wheaton_70fg <- don_data %>% filter(`Code on vial` %in% c("70 + Fg #1", "70 + Fg #2", "70 + Fg #3", "70 + Fg #4"))

# Merge data and add Cultivar labels
ambassador_ntc$Cultivar <- "AMBASSADOR"
ambassador_fg$Cultivar <- "AMBASSADOR"
ambassador_37fg$Cultivar <- "AMBASSADOR"
ambassador_40fg$Cultivar <- "AMBASSADOR"
ambassador_70fg$Cultivar <- "AMBASSADOR"

wheaton_ntc$Cultivar <- "WHEATON"
wheaton_fg$Cultivar <- "WHEATON"
wheaton_37fg$Cultivar <- "WHEATON"
wheaton_40fg$Cultivar <- "WHEATON"
wheaton_70fg$Cultivar <- "WHEATON"

# Combine all data
combined_data <- bind_rows(ambassador_ntc, ambassador_fg, ambassador_37fg, ambassador_40fg, ambassador_70fg,
                           wheaton_ntc, wheaton_fg, wheaton_37fg, wheaton_40fg, wheaton_70fg)

# Replace "na" with NA and convert DON column to numeric
combined_data$DON[combined_data$DON == "na"] <- NA
combined_data$DON <- as.numeric(combined_data$DON)

# Remove rows with missing DON values
combined_data <- combined_data %>% filter(!is.na(DON))

# Modify Treatment column values
combined_data <- combined_data %>%
  mutate(Treatment = case_when(
    Treatment == "Glycerol" ~ "NTC", # Change Glycerol to NTC
    Treatment == "Glycerol + Fg" ~ "Fg", # Change Glycerol + Fg to fg
    TRUE ~ Treatment # Keep other values unchanged
  ))

# Change the factor order of Treatment
combined_data$Treatment <- factor(combined_data$Treatment,
                                levels = c("NTC", "Fg", "Fg + 37", "Fg + 40", "Fg + 70"))

# Define blue and green colors
custom_colors <- c("#0072B2", "#009E73") # Blue and green

# Create the boxplot
```

```
# Extract WHEATON group data
```

```
# Merge data and add Cultivar labels
```

```
wheaton_ntc$Cultivar <- "WHEATON"
wheaton_fg$Cultivar <- "WHEATON"
wheaton_37fg$Cultivar <- "WHEATON"
wheaton_40fg$Cultivar <- "WHEATON"
wheaton_70fg$Cultivar <- "WHEATON"
```

```
# Combine all data
```

```
# Replace "na" with NA and convert DON column to numeric
```

```
# Remove rows with missing DON values
```

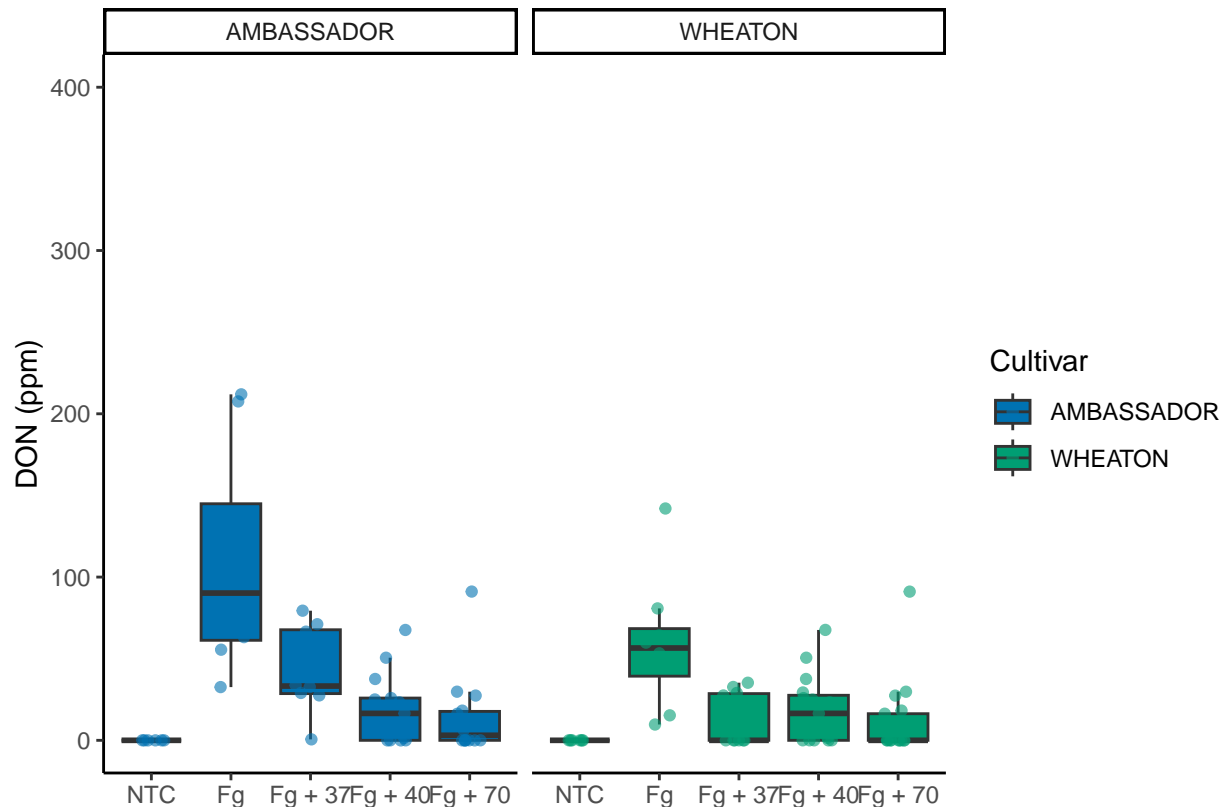
Modify Treatment column values

Change the factor order of Treatment

```
# Define blue and green colors
```

```
# Create the boxplot
```

```
ggplot(combined_data, aes(x=Treatment, y=DON, fill=Cultivar)) +
  geom_boxplot(outlier.shape = NA) + # Boxplot
  geom_jitter(aes(color=Cultivar), width=0.2, alpha=0.6) + # Jitter points with transparency 0.6
  scale_fill_manual(values=custom_colors) + # Fill colors
  scale_color_manual(values=custom_colors) + # Point colors
  labs(y="DON (ppm)", x="") + # Axis labels
  theme_classic() + # Classic theme
  facet_wrap(~Cultivar) + # Facet by Cultivar
  coord_cartesian(ylim = c(0, 400)) # Set y-axis range from 0 to 400
```



####Question 3

Load required libraries

```
library(dplyr)
```

```
library(ggplot2)
```

```
library(readr) # For read_csv function
```

Read data

```
mycotoxin_data <- read_csv("MycotoxinData.csv", na.strings = "na")
```

Check column names

```
print(colnames(mycotoxin_data))
```

```
## [1] "Treatment"      "Cultivar"      "BioRep"      "MassperSeed_mg"
## [5] "DON"            "X15ADON"
```

```
# Filter data for Cultivar Wheaton and Ambassador, and Treatment Fg, Fg + 37, Fg + 40, Fg + 70, NTC
filtered_data <- mycotoxin_data %>%
  filter(Cultivar %in% c("Wheaton", "Ambassador") &
    Treatment %in% c("Fg", "Fg + 37", "Fg + 40", "Fg + 70", "NTC"))

# Replace "na" with NA and convert 15ADON and MassperSeed_mg columns to numeric
filtered_data$`X15ADON`[filtered_data$`15ADON` == "na"] <- NA
filtered_data$`X15ADON` <- as.numeric(filtered_data$`X15ADON`)
```

```
## Warning: NAs introduced by coercion
```

```
filtered_data$MassperSeed_mg[filtered_data$MassperSeed_mg == "na"] <- NA
filtered_data$MassperSeed_mg <- as.numeric(filtered_data$MassperSeed_mg)

# Remove rows with missing values in 15ADON or MassperSeed_mg
filtered_data <- filtered_data %>%
  filter(!is.na(`X15ADON`)) %>%
  filter(!is.na(MassperSeed_mg))

# Ensure Treatment is a factor and set desired order
filtered_data$Treatment <- factor(filtered_data$Treatment,
  levels = c("NTC", "Fg", "Fg + 37", "Fg + 40", "Fg + 70"))

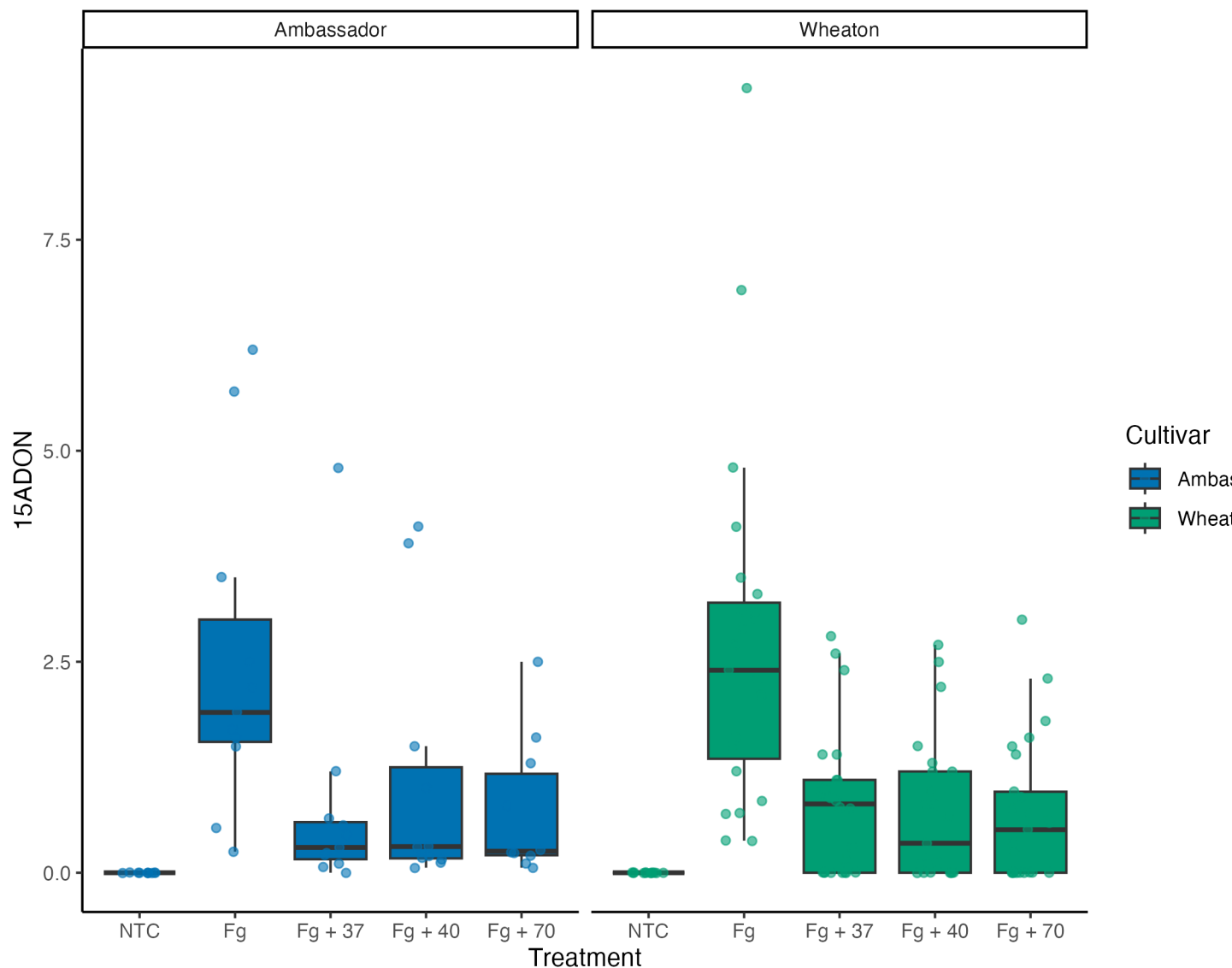
# Define blue and green colors
custom_colors <- c("#0072B2", "#009E73") # Blue and green

# Plot 1: Boxplot for 15ADON with Fg + 70 added
if ("X15ADON" %in% colnames(filtered_data)) {
  colnames(filtered_data)[colnames(filtered_data) == "X15ADON"] <- "15ADON"
}
plot_15adon <- ggplot(filtered_data, aes(x=Treatment, y=`15ADON`, fill=Cultivar)) +
  geom_boxplot(outlier.shape = NA) +
  geom_jitter(aes(color=Cultivar), width=0.2, alpha=0.6) +
  scale_fill_manual(values=custom_colors) +
  scale_color_manual(values=custom_colors) +
  labs(y="15ADON", x="Treatment") +
  theme_classic() +
  facet_wrap(~Cultivar) +
  coord_cartesian(ylim = c(0, max(filtered_data$`15ADON`, na.rm = TRUE)))

# Save updated 15ADON figure
ggsave("plot_15adon.png", plot = plot_15adon, width = 8, height = 6, dpi = 300)
```

```
###a separate code chunk for the figures plotting the 15adon data
```

```
knitr::include_graphics("plot_15adon.png")
```



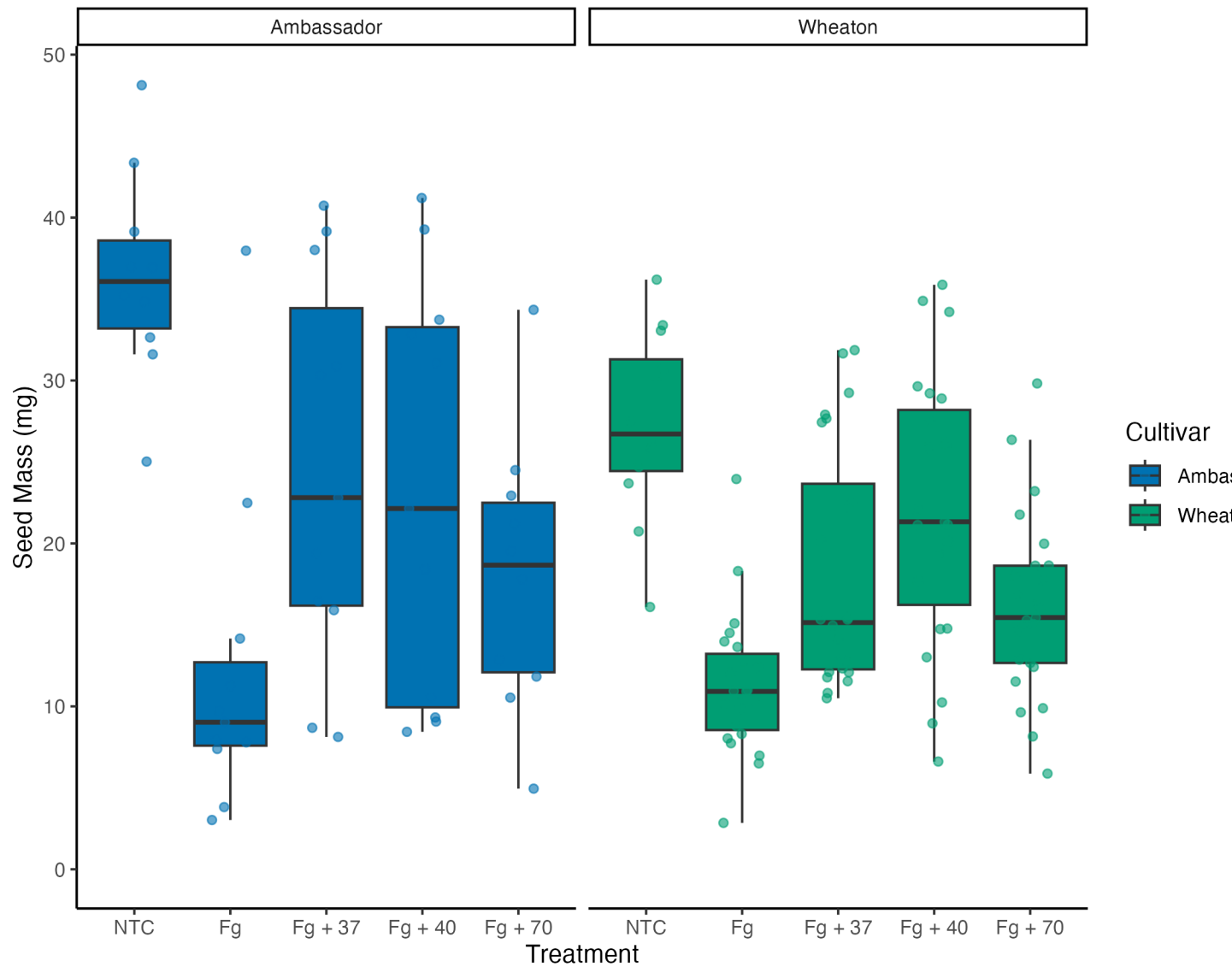
Plot 2: Boxplot for MassperSeed_mg with Fg + 70 added

```
mass_per_seed_plot <- ggplot(filtered_data, aes(x=Treatment, y=MassperSeed_mg, fill=Cultivar)) +
  geom_boxplot(outlier.shape = NA) +
  geom_jitter(aes(color=Cultivar), width=0.2, alpha=0.6) +
  scale_fill_manual(values=custom_colors) +
  scale_color_manual(values=custom_colors) +
  labs(y="Seed Mass (mg)", x="Treatment") +
  theme_classic() +
  facet_wrap(~Cultivar) +
  coord_cartesian(ylim = c(0, max(filtered_data$MassperSeed_mg, na.rm = TRUE)))

# Save updated MassperSeed_mg figure
ggsave("mass_per_seed_plot_updated.png", plot = mass_per_seed_plot, width = 8, height = 6, dpi = 300)
```

###a separate code chunk for the figures plotting the MassperSeed_mg figure

```
knitr::include_graphics("mass_per_seed_plot_updated.png")
```



###Question 4

```
''' r
library(ggpubr)

# Use ggarrange to combine the plots
combined_plot <- ggarrange(
  DON_plot,
  plot_15adon,
  mass_per_seed_plot,
  ncol = 3, nrow = 1,
```



```

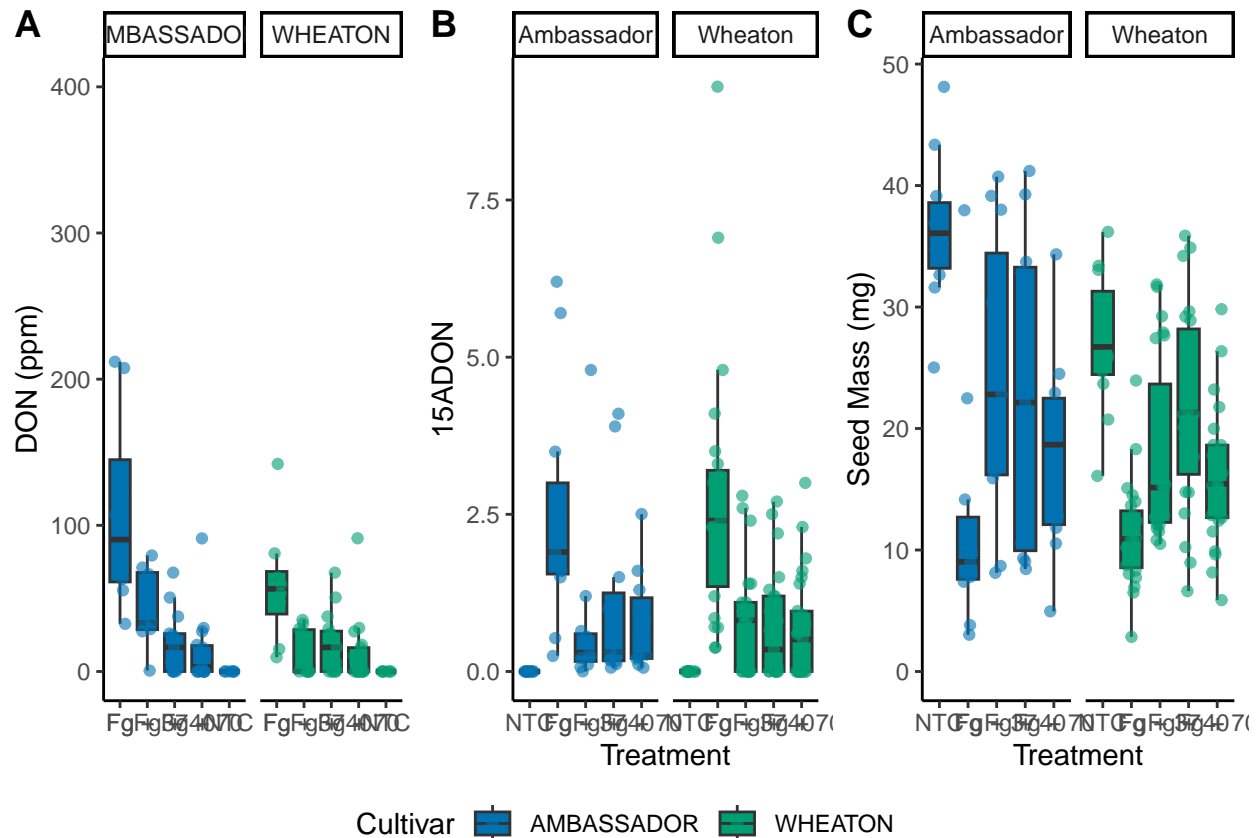
labels = c("A", "B", "C"),
common.legend = TRUE,
legend = "bottom"
)

```

```

# Display the combined plot
print(combined_plot)

```



```

# Save the combined plot as a PNG file
ggsave("combined_plot.png", plot = combined_plot, width = 16, height = 6, dpi = 300)

###quuestion 5
## #Add t-test significance markers to plot 1
DON_plot_ttest <- DON_plot +
  geom_pwc(
    aes(group = Treatment),           # Grouping variable for pairwise comparison
    method = "t_test",                # Perform t-test
    label = "{p.adj.format}{p.adj.signif}", # Display adjusted p-value and significance stars
    p.adjust.method = "bonferroni"    # Adjust p-values using Bonferroni correction
  )

```

```

# Save the updated plot with t-test results
ggsave("DON_plot_with_geom_pwc.png", plot = DON_plot_ttest, width = 8, height = 6, dpi = 300)

#Add t-test significance markers to plot 2
plot_15adon_ttest <- plot_15adon +
  geom_pwc(
    aes(group = Treatment),          # Grouping variable for pairwise comparison
    method = "t_test",               # Perform t-test
    label = "{p.adj.format}{p.adj.signif}", # Display adjusted p-value and significance stars
    p.adjust.method = "bonferroni"    # Adjust p-values using Bonferroni correction
  )

# Save the updated plot with t-test results
ggsave("plot_15adon_with_ttest.png", plot = plot_15adon_ttest, width = 8, height = 6, dpi = 300)

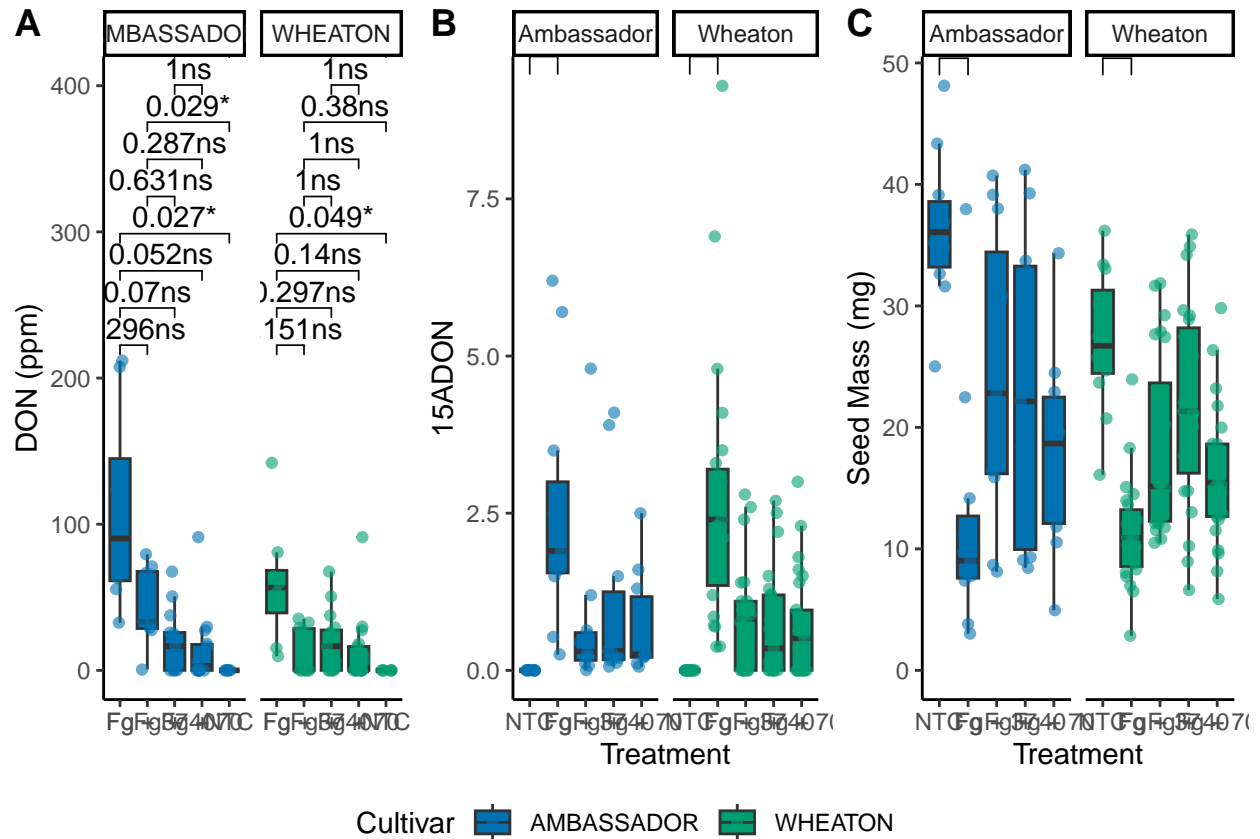
#Add t-test significance markers to plot 3
mass_per_seed_plot_ttest <- mass_per_seed_plot +
  geom_pwc(
    aes(group = Treatment),          # Grouping variable for pairwise comparison
    method = "t_test",               # Perform t-test
    label = "{p.adj.format}{p.adj.signif}", # Display adjusted p-value and significance stars
    p.adjust.method = "bonferroni"    # Adjust p-values using Bonferroni correction
  )

#Save the updated plot with t-test results
ggsave("mass_per_seed_plot_with_ttest.png", plot = mass_per_seed_plot_ttest, width = 8, height = 6, dpi = 300)

# Use ggarrange to combine the plots
combined__with_ttestplot <- ggarrange(
  DON_plot_ttest,
  plot_15adon_ttest,
  mass_per_seed_plot_ttest,
  ncol = 3, nrow = 1,
  labels = c("A", "B", "C"),
  common.legend = TRUE,
  legend = "bottom"
)

# Display the combined plot
print(combined__with_ttestplot)

```



```
# Save the combined plot as a PNG file
```

```
ggsave("combined__with_ttestplot.png", plot = combined__with_ttestplot, width = 8, height = 6, dpi = 300)
```

```
### a separate code chunk for three combined figure
```

```
knitr::include_graphics("combined__with_ttestplot.png")
```

