Mycotoxin Analysis

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1. 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. <https://doi.org/10.1094/PDIS-06-21-1253-RE>

# Load necessary libraries (only once at top)

library(ggplot2) library(ggpubr) library(dplyr) library(rstatix) library(magrittr)

install.packages(c(“ggplot2”, “ggpubr”, “dplyr”, “rstatix”, “magrittr”))

library(ggplot2)  
library(ggpubr)  
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

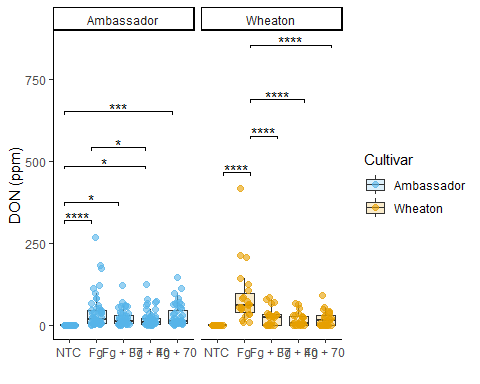
library(rstatix)

##   
## Attaching package: 'rstatix'

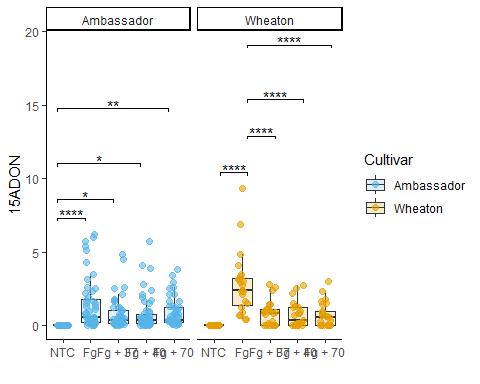
## The following object is masked from 'package:stats':  
##   
## filter

library(magrittr) # Still needed for compatibility  
  
  
# Load the dataset with proper NA handling  
df <- read.csv("C:/Users/Blake/Downloads/MycotoxinData.csv", na.strings = c("na", "nd", "")) # Added empty string as NA  
  
# Convert and clean data  
df$Treatment <- factor(df$Treatment, levels = c("NTC", "Fg", "Fg + 37", "Fg + 40", "Fg + 70"))  
df$Cultivar <- factor(df$Cultivar)  
  
# Drop NA rows explicitly  
df <- df[complete.cases(df$DON, df$X15ADON, df$MassperSeed\_mg), ]  
  
# Define consistent visual parameters  
cbbPalette <- c("#56B4E9", "#E69F00")  
jitter\_width <- 0.2  
point\_alpha <- 0.6  
  
# Function to perform pairwise tests within cultivars (keeping %>% here for clarity)  
perform\_pairwise <- function(data, var) {  
 data <- group\_by(data, Cultivar)  
 results <- pairwise\_t\_test(data, reformulate("Treatment", response = var), p.adjust.method = "bonferroni")  
 results <- add\_xy\_position(results, x = "Treatment", group = "Cultivar")  
 return(results)  
}

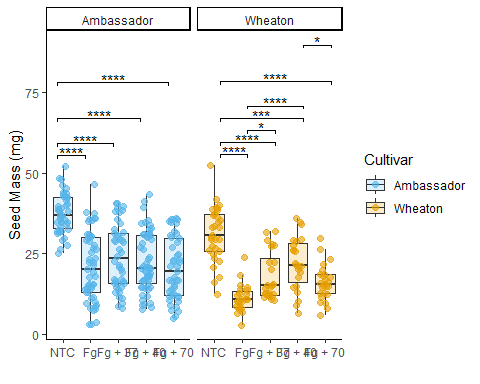
# DON Plot ----------------------------------------------------------------  
don\_stats <- perform\_pairwise(df, "DON")  
  
p1 <- ggplot(df, aes(x = Treatment, y = DON, fill = Cultivar)) +  
 geom\_boxplot(alpha = 0.2, width = 0.7, outlier.shape = NA) +  
 geom\_jitter(  
 aes(color = Cultivar),  
 width = jitter\_width,  
 height = 0,  
 alpha = point\_alpha,  
 size = 2  
 ) +  
 scale\_fill\_manual(values = cbbPalette) +  
 scale\_color\_manual(values = cbbPalette) +  
 labs(y = "DON (ppm)", x = "") +  
 theme\_classic() +  
 facet\_wrap(~Cultivar) +  
 stat\_pvalue\_manual(  
 don\_stats,  
 label = "p.adj.signif",  
 tip.length = 0.01,  
 hide.ns = TRUE  
 )  
p1



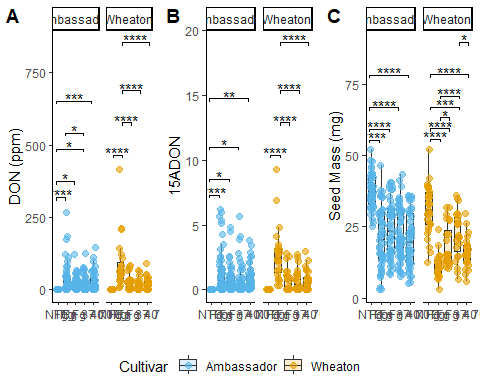
# 15ADON Plot -------------------------------------------------------------  
x15adon\_stats <- perform\_pairwise(df, "X15ADON")  
  
p2 <- ggplot(df, aes(x = Treatment, y = X15ADON, fill = Cultivar)) +  
 geom\_boxplot(alpha = 0.2, width = 0.7, outlier.shape = NA) +  
 geom\_jitter(  
 aes(color = Cultivar),  
 width = jitter\_width,  
 height = 0,  
 alpha = point\_alpha,  
 size = 2  
 ) +  
 scale\_fill\_manual(values = cbbPalette) +  
 scale\_color\_manual(values = cbbPalette) +  
 labs(y = "15ADON", x = "") +  
 theme\_classic() +  
 facet\_wrap(~Cultivar) +  
 stat\_pvalue\_manual(  
 x15adon\_stats,  
 label = "p.adj.signif",  
 tip.length = 0.01,  
 hide.ns = TRUE  
 )  
p2



# Seed Mass Plot ----------------------------------------------------------  
mass\_stats <- perform\_pairwise(df, "MassperSeed\_mg")  
  
p3 <- ggplot(df, aes(x = Treatment, y = MassperSeed\_mg, fill = Cultivar)) +  
 geom\_boxplot(alpha = 0.2, width = 0.7, outlier.shape = NA) +  
 geom\_jitter(  
 aes(color = Cultivar),  
 width = jitter\_width,  
 height = 0,  
 alpha = point\_alpha,  
 size = 2  
 ) +  
 scale\_fill\_manual(values = cbbPalette) +  
 scale\_color\_manual(values = cbbPalette) +  
 labs(y = "Seed Mass (mg)", x = "") +  
 theme\_classic() +  
 facet\_wrap(~Cultivar) +  
 stat\_pvalue\_manual(  
 mass\_stats,  
 label = "p.adj.signif",  
 tip.length = 0.01,  
 hide.ns = TRUE  
 )  
p3



# Combine plots -----------------------------------------------------------  
final\_plot <- ggarrange(  
 p1, p2, p3,  
 ncol = 3,  
 labels = c("A", "B", "C"),  
 common.legend = TRUE,  
 legend = "bottom"  
)  
  
# Display and save  
print(final\_plot)



# ggsave("mycotoxin\_analysis.png", final\_plot, width = 16, height = 6, dpi = 300)