Terhonen E., Kujala S., Pyhäjärvi T., Sutela S. (2025). Genetic variation of resistance in Scots pine as possible solution against *Diplodia sapinea*. Fennica vol. 59 no. 2 article id 25028.
https://doi.org/10.14214/sf.25028

## Supplementary file S1

R syntax and codes used in analyses:
A linear model (LM) was fitted using the lme4 package (Bates et al. 2015) to analyze necrosis length (cm) across factors (lm(NecrosisLength ~ Treatment + Growth + SideShoots + MotherID)). Fixed effects included Mother ID, seedling length (cm), inoculation treatment (fungi grown at +20 °C, +35 °C, or mock control), 2023 growth in cm, and number of side shoots. Population was not included due to low number of Mother IDs within populations.

```
# Install necessary packages
install.packages(c("lme4", "lmerTest", "readxl"))
# Load libraries
library(lme4)
library(lmerTest)
library("readxl")
# Replace "data.xlsx" with your real filename, use file: https://doi.org/10.23729/fd-f7666f35-f2d9-3b9e-a0f9-68c06775879a
your_data <- read_excel("data.xlsx")
# Set factors correctly
your_data$MotherID <- as.factor(your_data$MotherID)
your_data$Treatment <- as.factor(your_data$Treatment)
#Build the model
lm_model <- lm(NecrosisLength ~ Treatment + Growth + SideShoots + MotherID, data = your_data)
summary(lm_model)
```

The necrosis data between mother IDs was assessed for each inoculation methods (+20 °C and +35 °C), separately and combined, after 2 weeks and 2 months using the Shapiro–Wilk test (shapiro.test()). If the data were not normally distributed, the analysis was performed with the Kruskal–Wallis test (kruskal.test()), followed by post hoc analyses pairwise comparison using the Dunn–Bonferroni method (dunn.test()). For normally distributed data, an analysis of variance (ANOVA) (aov()) was conducted, followed by Tukey’s post hoc test (TukeyHSD()).

```
install.packages("dplyr", “rstatix”)
library("dplyr")
library(rstatix)
#prepare excel file with your “necrosis” data plus variable factor (group), replace data.xlsx with your file name
my_data <- read_excel("data.xlsx")
shapiro.test(my_data$necrosis)
```

```
#if p-value is lower than 0.05 data is non-normally distributed
#kruskall wallis test
kruskal.test(necrosis ~ group, data = my_data)
# Install the package
install.packages("dunn.test")
# Load the package
library(dunn.test)
dunn.test(weight ~ group, data = my_data, method = "bonferroni")

#ANOVA
necrosis.df <- read_excel("data.xlsx")
necrosis.df$group=factor(necrosis.df$group)
anovafit=aov(necrosis~ group,data=necrosis.df)
summary(anovafit)
tukey.test <- TukeyHSD(anovafit)
tukey.test
```

## Reference

Bates D, Mächler M, Bolker B, Walker S (2015) Fitting linear mixed-effects models using lme4. J Stat Softw 67(1): 1–48. https://doi.org/10.18637/jss.v067.i01