Supplementary table 1. Chemical composition of 40% Long Ashton Solution (Hewitt, 1966), amended to provide 1mM NH_4NO_3.

Compound	Formula	Stock solution gdm^{-3}	Final conc. of nutrient solution fed rhizotrons
Macronutrients			
Potassium sulphate	K_2SO_4	21.75	0.8 mM
Calcium chloride 2 hydrate	$CaCl_2.2H_2O$	73.47	1.6 mM
Magnesium sulphate 7 hydrate	$MgSO_4.7H_2O$	46.0	0.6 mM
Disodium hydrogen orthophosphate 7 hydrate	$Na_2HPO_4.7H_2O$	22.28	0.53 mM
Ammonium nitrate	NH_4NO_3	50.25	1.0 mM
Micronutrients			
Ethylenediaminetetra-acetic acid ferric monosodium salt	$C_{10}H_{12}N_2O_8FeNa$	8.23	0.04 mM
Manganese II sulphate 1 hydrate	$MnSO_4.1H_2O$	1.69	4.0 nM
Zinc sulphate 7 hydrate	$ZnSO_4.7H_2O$	0.29	0.4 nM
Copper II sulphate 5 hydrate	$CuSO_4.5H_2O$	0.25	0.4 nM
Boric acid	HBO_3	3.1	0.02 mM
Disodium molybdate 2 hydrate	$Na_2MoO_4.2H_2O$	0.12	0.2 nM
Cobalt sulphate 7 hydrate	$CoSO_4.7H_2O$	0.053	0.08 nM
Sodium chloride	NaCl	5.85	0.04 mM

Supplementary file 1(File S1)

Assembly of rhizotron

A rhizotron is a transparent bioassay growth chamber that allows for real-time monitoring of plant roots without destroying the plant. Two type of rhizotrons were used to investigate the attachment and growth of *Striga hermonthica* throughout the study.

1. Materials

Black and clear Sheets of perspex glass, (30 cm x 40 cm x 2 mm)

Glass rods (40 cm x 1 cm x 1 cm)

Sheet of black cotton fabric (30cm x 40 cm)

A sheet of black polyethylene plastic material

Felt

Fold back clips

Silver sand

Procedure

2. Washing and sterilizing of river sand

River sand obtained from the Lagos bar beach was washed by running water through a pipe continuously into a drum containing the sand. The running water removes all organic matter from the sand. The sand was sterilized by pouring boiling water into the drum with the washed river sand until the water level is just above the level of the sand. This was left to stand for about one hour, after which the water was drained, and the sand allowed to dry.

3. Construction of rhizotron

The rhizotron was constructed by gluing 1 cm thick glass rods to both sides of a black Perspex glass sheet and a felt strip to the bottom of the glass sheet. Washed, sterilized and dry river sand was poured unto the black Perspex glass and a sheet of black cotton fabric placed on the surface of the river sand, a clear sheet Perspex glass was then placed upon the fabric. The entire setup was wrapped with a black polyethylene plastic material to shield the root zone from light and five fold-back clips were used to firmly hold the rhizotron set up together (figure 3.2).

4. Introduction of plant material into the rhizotrons

One surface-sterilized maize seed was placed per rhizotron, on the black cotton fabric, at a depth of about 2 cm. The maize lines, in the rhizotrons, were infested with *Striga hermonthica* seeds, by using a brush to carefully spread 2 g of *Striga hermonthica* seeds all over the rhizotron surface and especially on the exposed roots of the maize plants. The rhizotrons were fed two times (morning and evening) daily, with nutrient solution (40% Long Ashton solution containing $1 mol m^{-1}$ ammonium nitrate), to provide a total volume of 250 ml of nutrient solution per rhizotron per day.

Supplementary file 2 (File S2)

Preparation of 1mg/L GR24 solution

GR24 [(±)-(3aR*,8bS*,E)-3-(((R*)-4-methyl-5-oxo-2,5-dihydrofuran-2-yloxy) methylene)-3,3a,4,8b-tetrahydro-2H-indeno[1,2-b]furan-2-one)] is a synthetic strigolactone that is used to mimic the effects of strigolactones. It was prepared by dissolving 1 μg of GR24 in 1 ml of acetone and the mixture swirled slowly until the GR24 powder is completely dissolved. The solution was then made up to 1 L with double distilled water, stored at -20 ℃ and used as required.

Supplementary file 3 (File S3)

R scripts for statistical analysis

A. Script for Mann-Whitney u test

```
setwd("C:/Users/nunachukwu/Desktop/mech")
data <- read.table("exudateg.txt",header=TRUE)
hist(data$nogerm)

library(FSA)
Summarize(nogerm ~ Maizeline,data = data)
library(lattice)
histogram(~ nogerm | Maizeline, data=data,layout=c(1,3))

##Simple boxplots of values across groups##
boxplot(nogerm ~ Maizeline, data = data, ylab="nogerm",  xlab="Maizeline")
```

B. Kruskal–Wallis test

```
data <- read.table("exudateelong.txt",header=TRUE)

hist(data$nogerm)

### Specify the order of factor levels###

library(dplyr)

data =mutate(data, Maizeline = factor(Maizeline, levels=unique(Maizeline)))

library(FSA)

Summarize(nogerm ~ Maizeline,data = data)

library(lattice)

histogram(~ nogerm | Maizeline, data=data,layout=c(1,3))

##Simple boxplots of values across groups##

boxplot(nogerm ~ Maizeline, data = data, ylab="nogerm", xlab="Maizeline")
```

```
###Kruskal–Wallis test##

kruskal.test(nogerm ~ Maizeline, data = data)

data$Maizeline = factor(data$Maizeline, levels=c( "TZISTR1108" , "5057"))

### Dunn test###

library(FSA)

PT = dunnTest(nogerm ~Maizeline, data=data,  method="bh")

PT

PT = PT$res

PT

library(rcompanion)

cldList(comparison = PT$Comparison, p.value   = PT$P.adj, threshold = 0.05)
```

C. Script for ANCOVA

```
setwd("C:/Users/nunachukwu/Desktop/mech")
data <- read.table("devrate.txt",header=TRUE)
library(dplyr)

#### Make mazeline a factor##
cols <- c("Maizeline", "DPI")
data[cols] <- lapply(data[cols], factor)
data$lcount <- as.numeric(data$lcount)

#### Separate lateral roots data from major roots##

lateralroots <- data %>% slice(1:60)
majorroots <- data %>% slice(61:120)

 #### Histogragh of both root types###
hist(lateralroots$lcount)
hist(majorroots$lcount)

### Scatter plot of both data to see the general trend##
```

```
library(lattice)
xyplot (lcount ~ DPI | Maizeline, data = lateralroots,
      ylab="No of leaves",xlab="days post infestation")
xyplot(lcount ~ DPI | Maizeline, data = majorroots,
      ylab="No of leaves",xlab="days post infestation")


###Lateral roots###
modl1<- aov(lcount~DPI+Maizeline, data= lateralroots)
summary(modl1)
modl2 <- aov(lcount~DPI*Maizeline, data= lateralroots)
summary(modl2)
### Compare both models##
anova(modl2,modl1)
 Anolate <- lm(lcount~Maizeline*DPI, data=lateralroots)
summary(Anolate)

#### View the residuals###

par(mfrow=c(2,2))
plot(Anolate)
par(mfrow=c(1,1))

#### Plot the regression lines###
resl <- subset(lateralroots, Maizeline=="ZD05l")
susl <- subset(lateralroots, Maizeline=="5057l")
reg1l <- lm(lcount~DPI, data=resl)
summary(reg1l)
reg2l <- lm(lcount~DPI, data=susl)
summary(reg2l)
plot(lcount~DPI, data=lateralroots, type='n')
points(resl$DPI,resl$lcount, pch=20)
points(susl$DPI,susl$lcount, pch=10)
abline(reg1l, lty=3)
abline(reg2l, lty=3)
legend("bottomright", c("TZISTR1108","5057"), lty=c(1,2), pch=c(20,10), cex= 0.65)
```

```
#### Major roots##
mod2m <- aov(lcount~DPI+Maizeline, data= majorroots)
summary(mod2m)
mod1m <- aov(lcount~DPI*Maizeline, data= majorroots)
summary(mod1m)
### Compare both models##
anova(mod2m,mod1m)
Anomaj <-lm(lcount~Maizeline*DPI, data=majorroots)
summary(Anomaj)

#### View the residuals###
par(mfrow=c(2,2))
plot(Anolate)
par(mfrow=c(1,1))

#### Plot the regression lines###

resm <- subset(majorroots, Maizeline=="ZD05m")
susm <- subset(majorroots, Maizeline=="5057m")
reg1m <- lm(lcount~DPI, data=resm)
summary(reg1m)
reg2m <- lm(lcount~DPI, data=susm)
summary(reg2m)
plot(lcount~DPI, data=majorroots, type='n')
points(resm$DPI,resm$lcount, pch=20)
points(susm$DPI,susm$lcount, pch=10)
abline(reg1m, lty=3)
abline(reg2m, lty=3)
legend("bottomright", c("TZISTR1108","5057"), lty=c(1,2), pch=c(20,10), cex= 0.65)
anova(Anomaj)
```
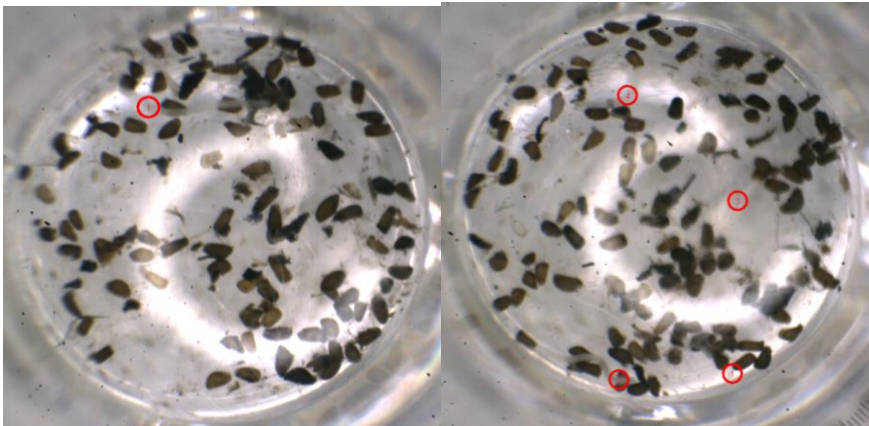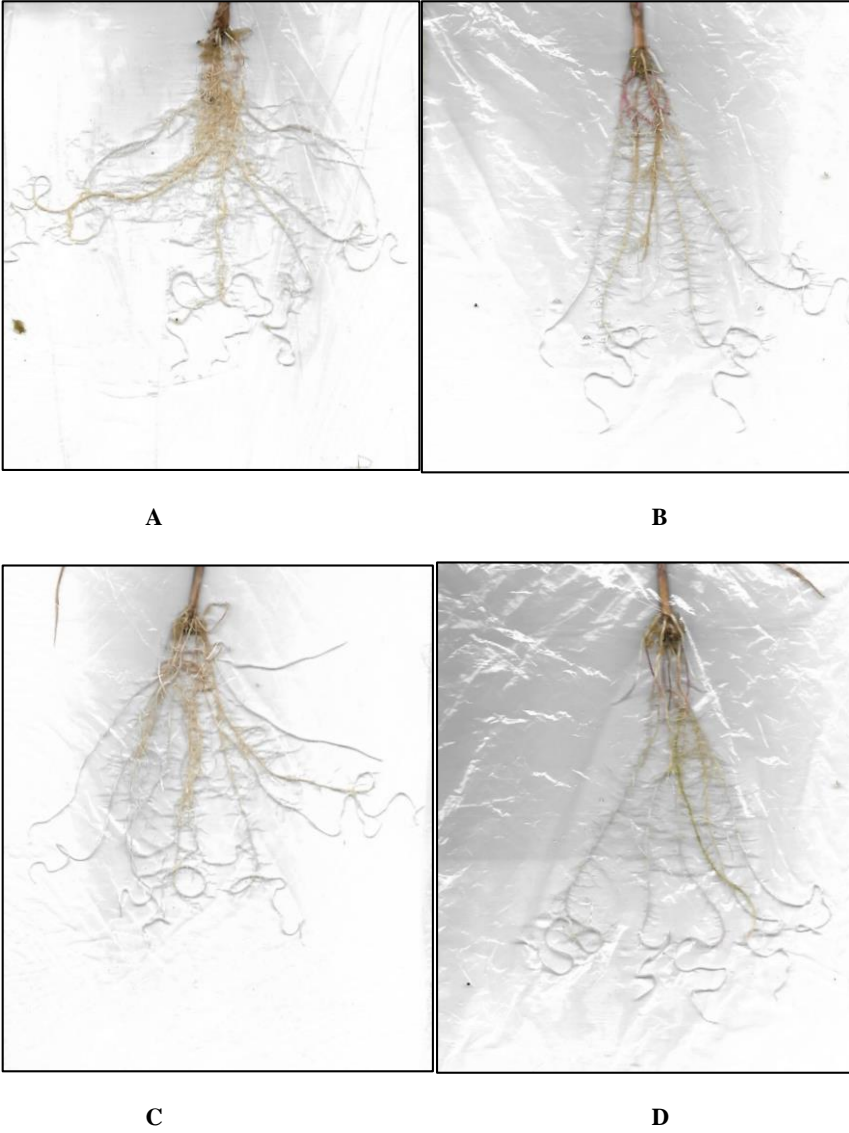
A

B

C

Supplementary figure 1 (Figure S1). *Striga hermonthica* seeds treated with exudates from 5057 and TZISTR1108.
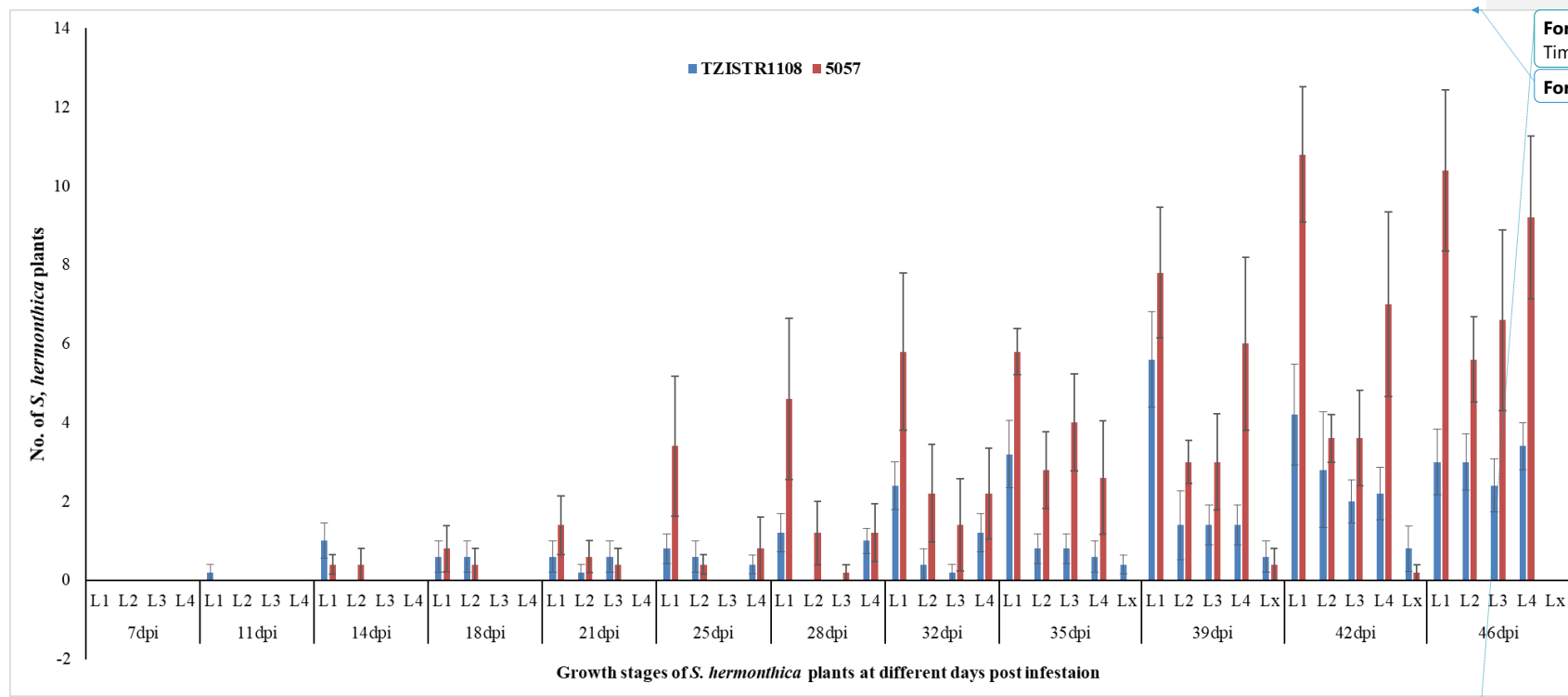
A. Seeds treated with exudates from TZISTR1108, B = Seeds treated with exudates from 5057.

(The red circles show germinating *Striga hermonthica* seeds)

C. Germinated *S. hermonthica* seeds with elongated radicles.

A

B

C

D

Supplementary figure 2 (**Figure S2**)

Scanned pictures of the roots of both genotypes. (A) and (C) are 5057 plants, while (B) and (D) are TZISTR1108 plants. The 5057 plants are seen to have more, slightly shorter major roots than the TZISTR1108 plants.
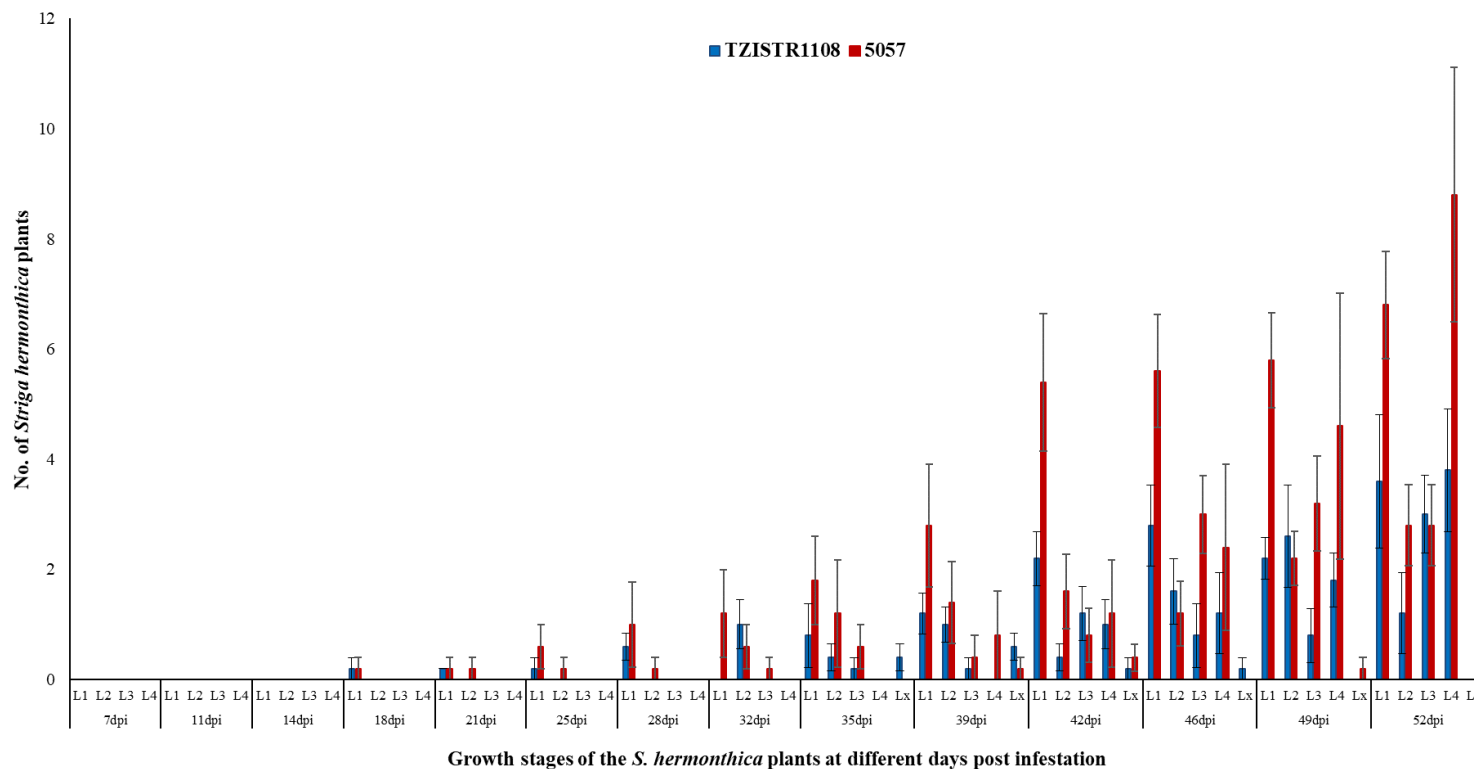
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Supplementary figure 3 (Figure S3). Histogram of Mean number of attached *Striga hermonthica* on resistant and susceptible maize lines in group A (No GR24 treatment).

L1= 2-4 partially horizontal opened leaves, L2= 6-8 partially horizontal opened leaves, L3 =10-12 partially horizontal opened leaves, L4 = *Striga* plants with 13 leaves and above, Lx= Discoloured dead or dying plants. Error bars show standard error.

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Supplementary figure 4 (Figure S4). Histogram of Mean number of attached *Striga hermonthica* on resistant and susceptible maize lines in group B (GR24 treatment).

L1= 2-4 partially horizontal opened leaves, L2= 6-8 partially horizontal opened leaves, L3 =10-12 partially horizontal opened leaves, L4 = *Striga* plants with 13 leaves and above, Lx= Discoloured dead or dying plant. Error bars show standard error.