Figure S2

```r
library(readxl)
library(lubridate)
```

```
##
## Attaching package: 'lubridate'

## The following objects are masked from 'package:base':
##
##     date, intersect, setdiff, union
```

```r
library(mgcv)
```

```
## Loading required package: nlme

## This is mgcv 1.8-34. For overview type 'help("mgcv-package")'.
```

```r
library(ggplot2)
library(ggsignif)
library(readr)
library(emmeans)
library(tidyr)
library(plyr)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:plyr':
##
##     arrange, count, desc, failwith, id, mutate, rename, summarise,
##     summarize

## The following object is masked from 'package:nlme':
##
##     collapse

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
#load in raw data
dat <- data.frame(read_csv("S2_data.csv"))
```

```
##
## -- Column specification ---------------------------------------------------
## cols(
##   `Repeat(Date)` = col_datetime(format = ""),
##   Algae = col_character(),
```

```
##    Treatment = col_character(),
##    Well_ID = col_character(),
##    Larvae = col_character(),
##    Time_to_first_expulsion = col_double(),
##    `Well_ID (#1)` = col_character()
## )
```
```r
head(dat)
```
```
##    Repeat.Date.         Algae Treatment Well_ID Larvae Time_to_first_expulsion
## 1    2020-10-22 M. gaditana      DMSO     MD1      1                     720
## 2    2020-10-22 M. gaditana      DMSO     MD1      2                     720
## 3    2020-10-22 M. gaditana      DMSO     MD1      3                      70
## 4    2020-10-22 M. gaditana      DMSO     MD1      4                     165
## 5    2020-10-22 M. gaditana      DMSO     MD1      5                      70
## 6    2020-10-22 M. gaditana      DMSO     MD1      6                      70
##      Well_ID...1.
## 1 M_D_2020-10-22
## 2 M_D_2020-10-22
## 3 M_D_2020-10-22
## 4 M_D_2020-10-22
## 5 M_D_2020-10-22
## 6 M_D_2020-10-22
```
```r
#clean up raw data
dat$Algae <- factor(dat$Algae, levels= c("SSB01", "M. gaditana", "N. oculata", "C. velia"))
dat$Treatment <- factor(dat$Treatment)
dat$Repeat.Date. <- factor(as.character(dat$Repeat.Date.))
dat$Well_ID <- factor(dat$Well_ID)
head(dat)
```
```
##    Repeat.Date.         Algae Treatment Well_ID Larvae Time_to_first_expulsion
## 1    2020-10-22 M. gaditana      DMSO     MD1      1                     720
## 2    2020-10-22 M. gaditana      DMSO     MD1      2                     720
## 3    2020-10-22 M. gaditana      DMSO     MD1      3                      70
## 4    2020-10-22 M. gaditana      DMSO     MD1      4                     165
## 5    2020-10-22 M. gaditana      DMSO     MD1      5                      70
## 6    2020-10-22 M. gaditana      DMSO     MD1      6                      70
##      Well_ID...1.
## 1 M_D_2020-10-22
## 2 M_D_2020-10-22
## 3 M_D_2020-10-22
## 4 M_D_2020-10-22
## 5 M_D_2020-10-22
## 6 M_D_2020-10-22
```
```r
#model data with generalised linear mixed modes
summary <- data.frame()

for(i in unique(dat$Algae))
{
#i <- unique(dat$Algae)[1]
  Dat <- droplevels(dat[dat$Algae==i,])
  ##Regression model:
  mod <- gam(Time_to_first_expulsion ~ Treatment + s(Well_ID,bs='re'),data=Dat,family=nb())
  S <- summary(mod)$p.table
```

```r
if(S[2,4]>0.1)
  {
    p <- ""
  }
if(S[2,4]<0.1)
  {
    p  <- ""
  }
if(S[2,4]<0.05)
  {
    p  <- "*"
  }
if(S[2,4]<0.01)
  {
    p  <- "**"
  }
if(S[2,4]<0.001)
  {
    p  <- "***"
  }
newline <- data.frame(Algae=i,outcome=S[1,1],SE=S[1,2],type="DMSO",p=NA,pvalue=NA)
  summary <- rbind(summary,newline)
newline <- data.frame(Algae=i,outcome=S[1,1] + S[2,1],SE=S[2,2],type="LatB",p=p, pvalue=S[2,4])
  summary <- rbind(summary,newline)
}

summary$up <- exp(summary$outcome + 1.96*summary$SE)
summary$down <- exp(summary$outcome - 1.96*summary$SE)
summary$outcome <- exp(summary$outcome)

summary
```

```
##        Algae  outcome        SE type    p   pvalue       up     down
## 1 M. gaditana 416.9101 0.1620987 DMSO <NA>       NA 572.8272 303.4319
## 2 M. gaditana 375.8582 0.2276165 LatB      0.6488149 587.1852 240.5875
```

```r
write_csv(summary, "S2_summary.csv")
```

```r
summary$Algae <- factor(summary$Algae, levels= c("SSB01", "M. gaditana", "N. oculata", "C. velia"))
formatter60 <- function(x){
x/60
}
#Plot graph
P1 <- ggplot() +
  geom_dotplot(data = Dat, aes(x=Algae, y=Time_to_first_expulsion, group=Treatment, color = Treatment,
  scale_color_manual(values=c("#E0D532",alpha("#E0D532",0.6))) +
  scale_fill_manual(values=c("#E0D532",alpha("#E0D532",0.6))) +
  theme_classic() +
  labs(x = "", y = "Time to first expulsion") +
  geom_text(data = summary, aes(x=Algae,y=4790),label=summary$p,size=6) +
  scale_y_continuous(expand = c(0, 0), limits = c(0,800), labels = formatter60, breaks=c(120,240,360,48
```
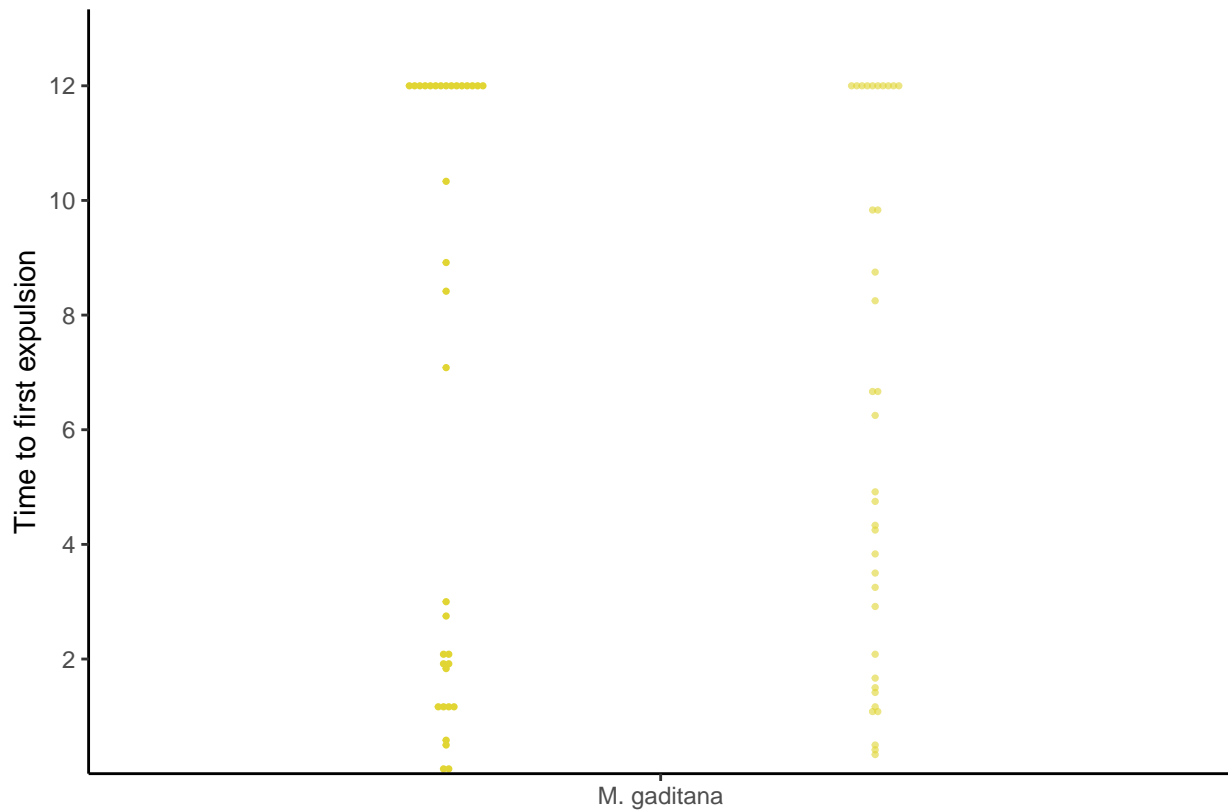
```
## Warning: Ignoring unknown parameters: size
```

```
plot(P1)
```

Warning: Removed 2 rows containing missing values (geom_text).


```
ggsave("Figure_S2.pdf",width=16,height=11,units="cm")
```

Warning: Removed 2 rows containing missing values (geom_text).

```
# get n count per treatment
ndat <- ddply(dat, c("Algae", "Treatment", "Repeat.Date."), summarise,
              N    = length(Larvae))
n_Figure <-  ddply(ndat, c("Algae", "Treatment"), summarise,
              N    = length(Repeat.Date.))
n_Figure
```

```
##         Algae Treatment N
## 1 M. gaditana      DMSO 3
## 2 M. gaditana      LatB 3
```

```
write_csv(n_Figure, "S2_n.csv")
```