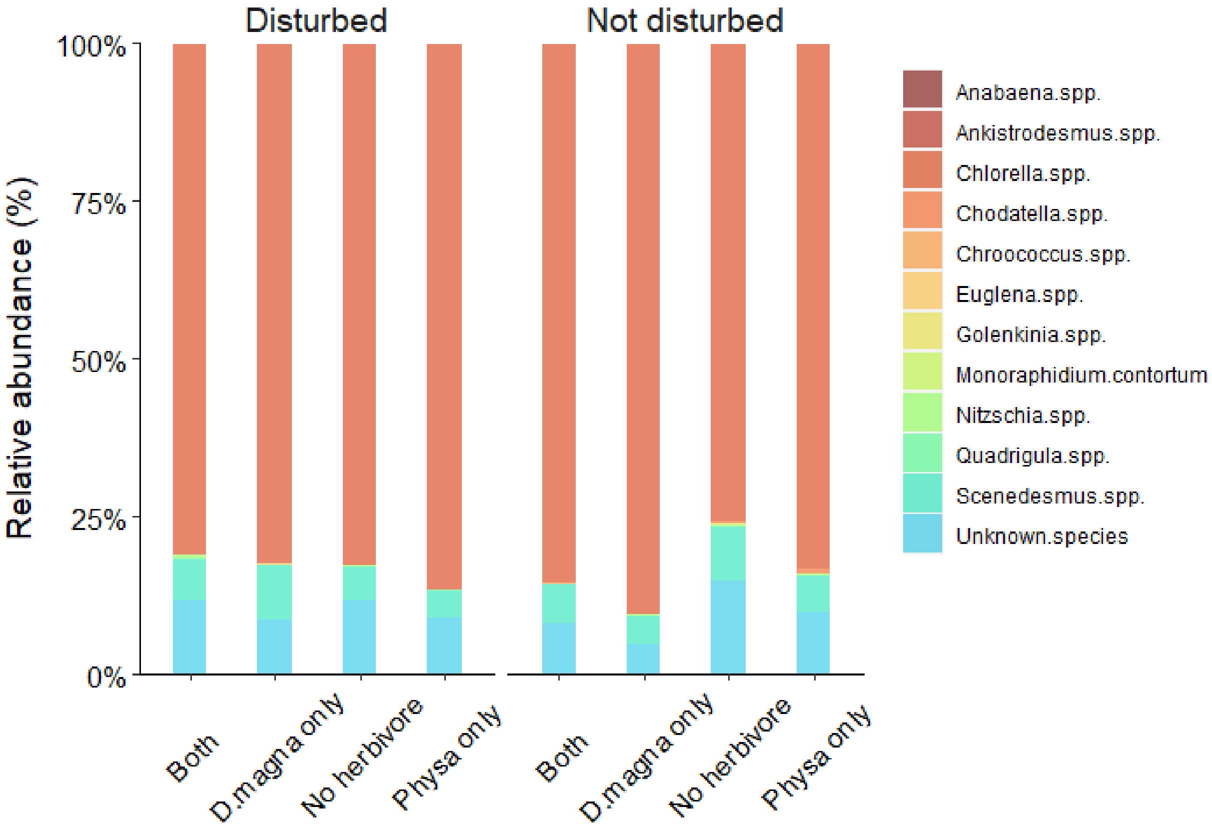

Fig 1: Algal community composition at the starting point.

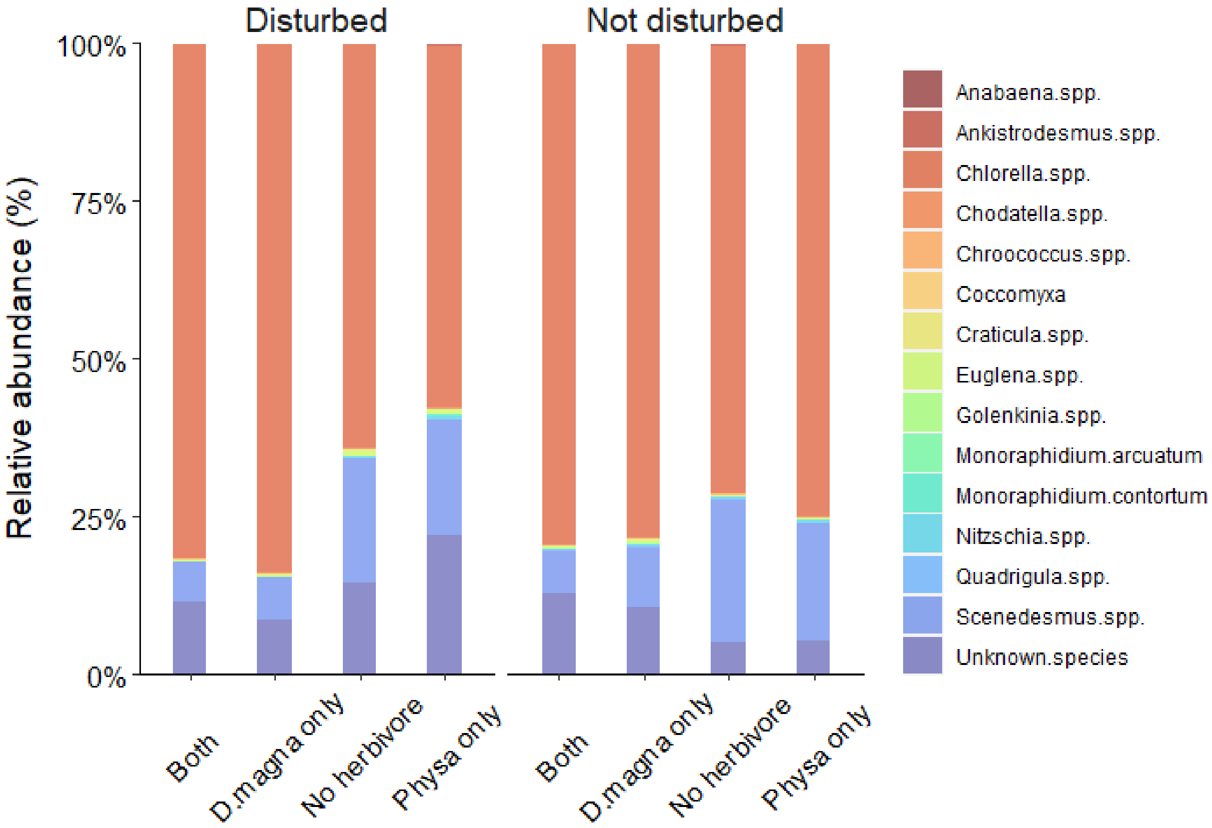

Fig 2: Algal community composition at the mid-point.

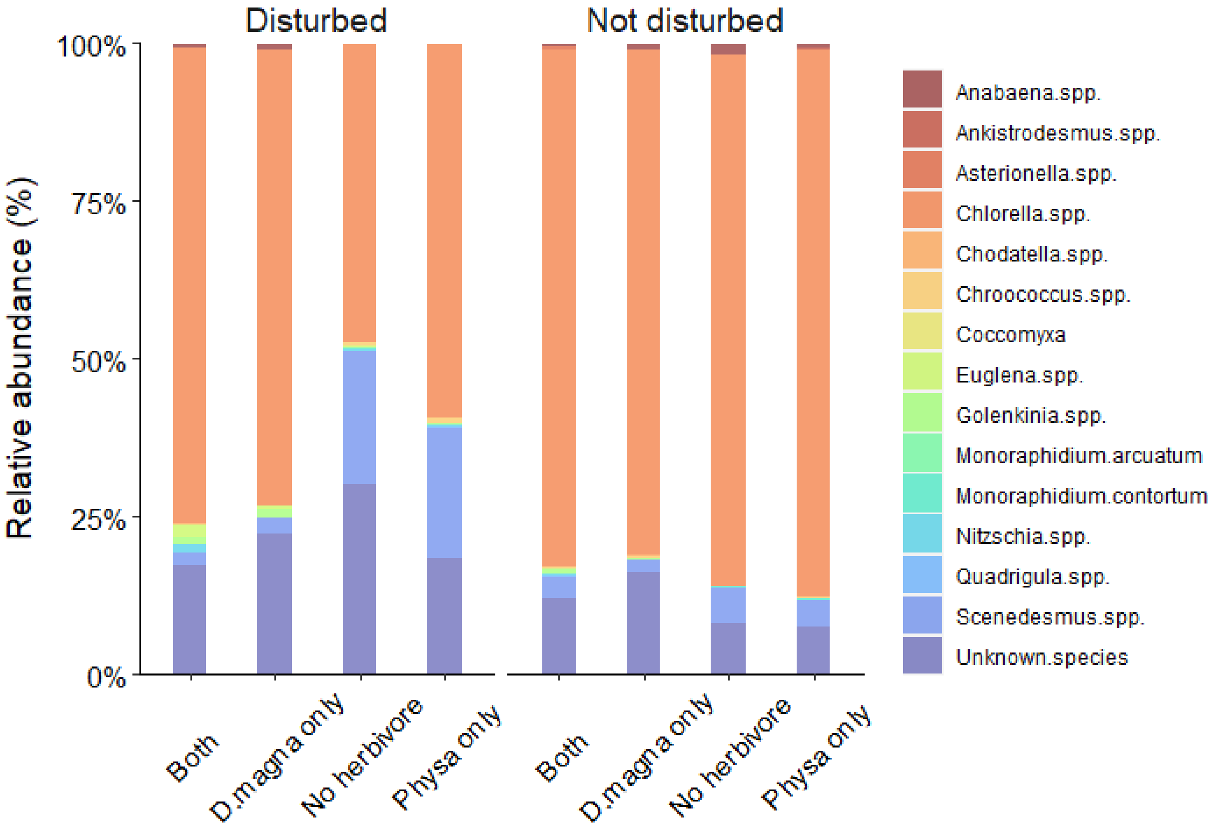

Fig 3: Algal community composition at the end of the experiment.

Script in R

```r
## Loading packages

library(ggplot2)

library(data.table)

library(dplyr)

library(viridis)

## Importing dataset

data = fread("data.csv", sep = ",")

## See data

DT::datatable(data)

## Checking the structure

str(data)

## Converting factors

data[, Herbivore_treatment := factor(Herbivore_treatment)]

data[, Eutrophication_treatment := factor(Eutrophication_treatment)]

data[, Collection_point := factor(Collection_point)]

data[, Species := factor(Species)]

## Converting to numeric

names(data)

data[, (5:ncol(data)) := lapply(.SD, as.numeric), .SDcols =
5:ncol(data)]

## Checking the structure again

str(data)

## Subseting the data

time1 <- subset(data, Collection_point=="1")

time2 <- subset(data, Collection_point=="2")

time3 <- subset(data, Collection_point=="3")
```

```
## Plotting: stacked bars

# Define the number of colors you want

nb.cols <- 16

mycolors <- viridis_pal(option = "turbo", direction = -1)(nb.cols)


# Starting

ggplot(time1, aes(fill=Species, y=Count, x=Herbivore_treatment)) +

  geom_bar( stat="identity", position="fill", width=0.4, alpha = 0.6)+

  scale_fill_manual(values = mycolors) +

  scale_y_continuous(expand = c(0, 0), labels = scales::percent)+

  facet_wrap(.~Eutrophication_treatment, ncol=2)+

  theme(panel.grid.major = element_blank(),

        panel.grid.minor = element_blank(),

        panel.border = element_blank(),

        panel.background = element_blank(),

        strip.background = element_rect(colour="white", fill="white"),

        strip.text.x = element_text(angle = 0, size=14),

        plot.title = element_blank(),

        axis.text.x = element_text(colour="black", size = 12, angle = 45, vjus = 0.5),

        axis.text.y = element_text(colour="black", size = 12, angle = 0),

        axis.title.x = element_text(angle = 0, vjus = - 0.5, size = 14, margin = margin(t = 0, r = 10, b = 0, l = 0)),

        axis.title.y = element_text(angle = 90, vjus = .5, size = 14, margin = margin(t = 0, r = 10, b = 0, l = 0)),

        axis.line = element_line(size=0.5, colour = "black"),

        legend.background = element_blank(),

        legend.justification=c(0,1),

        legend.position = "right",

        legend.title = element_blank())+
```

```
  labs(title = "", x = "", y = "Relative abundance (%)")
```

```
# Mid-point
ggplot(time2, aes(fill=Species, y=Count, x=Herbivore_treatment)) +
  geom_bar( stat="identity", position="fill", width=0.4, alpha = 0.6)+
  scale_fill_manual(values = mycolors) +
  scale_y_continuous(expand = c(0, 0), labels = scales::percent)+
  facet_wrap(.~Eutrophication_treatment, ncol=2)+
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.border = element_blank(),
        panel.background = element_blank(),
        strip.background = element_rect(colour="white", fill="white"),
        strip.text.x = element_text(angle = 0, size=14),
        plot.title = element_blank(),
        axis.text.x = element_text(colour="black", size = 12, angle = 45, vjus = 0.5),
        axis.text.y = element_text(colour="black", size = 12, angle = 0),
        axis.title.x = element_text(angle = 0, vjus = - 0.5, size = 14, margin = margin(t = 0, r = 10, b = 0, l = 0)),
        axis.title.y = element_text(angle = 90, vjus = .5, size = 14, margin = margin(t = 0, r = 10, b = 0, l = 0)),
        axis.line = element_line(size=0.5, colour = "black"),
        legend.background = element_blank(),
        legend.justification=c(0,1),
        legend.position = "right",
        legend.title = element_blank())+
  labs(title = "", x = "", y = "Relative abundance (%)")
```

End of the experiment

```
ggplot(time3, aes(fill=Species, y=Count, x=Herbivore_treatment)) +
  geom_bar( stat="identity", position="fill", width=0.4, alpha = 0.6)+
  scale_fill_manual(values = mycolors) +
  scale_y_continuous(expand = c(0, 0), labels = scales::percent)+
  facet_wrap(.~Eutrophication_treatment, ncol=2)+
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.border = element_blank(),
        panel.background = element_blank(),
        strip.background = element_rect(colour="white", fill="white"),
        strip.text.x = element_text(angle = 0, size=14),
        plot.title = element_blank(),
        axis.text.x = element_text(colour="black", size = 12, angle = 
45, vjus = 0.5),
        axis.text.y = element_text(colour="black", size = 12, angle = 
0),
        axis.title.x = element_text(angle = 0, vjus = - 0.5, size = 
14, margin = margin(t = 0, r = 10, b = 0, l = 0)),
        axis.title.y = element_text(angle = 90, vjus = .5, size = 14, 
margin = margin(t = 0, r = 10, b = 0, l = 0)),
        axis.line = element_line(size=0.5, colour = "black"),
        legend.background = element_blank(),
        legend.justification=c(0,1),
        legend.position = "right",
        legend.title = element_blank())+
  labs(title = "", x = "", y = "Relative abundance (%)")
```