## pi\_curves\_nls

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### 3/18/2021

```
## install packages if you dont already have them in your library
if ("devtools" %in% rownames(installed.packages()) == 'FALSE') install.packages('devtools')
if ("segmented" %in% rownames(installed.packages()) == 'FALSE') install.packages('segmented')
if ("plotrix" %in% rownames(installed.packages()) == 'FALSE') install.packages('plotrix')
if ("gridExtra" %in% rownames(installed.packages()) == 'FALSE') install.packages('gridExtra')
if ("LoLinR" %in% rownames(installed.packages()) == 'FALSE') install_github('colin-olito/LoLinR')
if ("lubridate" %in% rownames(installed.packages()) == 'FALSE') install.packages('lubridate')
if ("chron" %in% rownames(installed.packages()) == 'FALSE') install.packages('chron')
if ("plyr" %in% rownames(installed.packages()) == 'FALSE') install.packages('plyr')
if ("dplyr" %in% rownames(installed.packages()) == 'FALSE') install.packages('dplyr')
if ("phytotools" %in% rownames(installed.packages()) == 'FALSE') install.packages('phytotools')
if ("tidyverse" %in% rownames(installed.packages()) == 'FALSE') install.packages('tidyverse')
if ("broom" %in% rownames(installed.packages()) == 'FALSE') install.packages('broom')
#Read in required libraries
library("devtools")
library("ggplot2")
library("segmented")
library("plotrix")
library("gridExtra")
library("LoLinR")
library("lubridate")
library("chron")
library('plyr')
library('dplyr')
library('phytotools')
library("tidyverse")
library("broom")
```

## Import data

```
Data <- read.csv(file = 'output/2_pi_curve_rates.csv')
#Data <- Data[1:40,]</pre>
```

#### Define data

Run models

```
#specify data
Data$PAR <- as.numeric(Data$Light_Value)
Data$Pc <- as.numeric(Data$micromol.cm2.h)
Data<-Data%>%
  filter(Pc>-2)
```

# Define PI curve function as a nonlinear Least Squares regression of a quadratic fit, test nls fit

```
Aquatic Photosynthesis, Falkowski  \begin{array}{l} Pmax = max \ photosynthesis \ (AKA\ Am\ from\ Bayesian\ script) \\ alpha = quantum\ yeild \ (AKA\ AQY\ from\ Bayesian\ script) \\ I/E = irradiance \ (AKA\ PAR\ from\ Bayesian\ script) \\ Rd = dark\ respiration \\ \end{array}
```

Using fixed initial values (not used, kept for reference):

```
#nls_data <- Data %>%

#filter(Pc>-2)%>% #remove low outliers

#group_by(colony_id) %>%

#nest(-colony_id) %>%

#mutate(model1 = map(data, ~

#nls(Pc ~ (Am*((AQY*PAR)/(sqrt(Am^2 + (AQY*PAR)^2)))-Rd), data=., start=list(Am

#tidy %>%

#dplyr::select(term, estimate) %>%

#spread(term, estimate))) %>%

#unnest(model1) %>%

#unnest(data) %>%

#group_by(colony_id)%>%

#summarise(Am=mean(Am), AQY=mean(AQY), Rd=mean(Rd))%>%

#mutate(timepoint="timepoint2")%>%

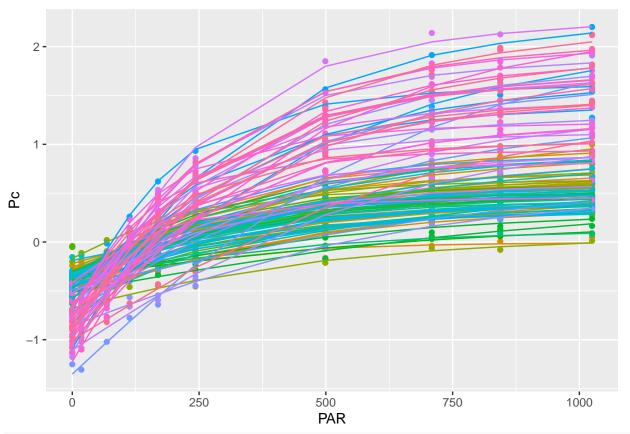
#write_csv(., "output/2_pi_curve_pars_NLS.csv")
```

Using flexible initial values based on input data:

Plot curve over data points.

```
augmented <- Data %>%
  filter(Pc>-2)%>%
  nest(-colony_id) %>%
  mutate(
    fit = map(data, ~ nls(Pc ~ (Am*((AQY*PAR)/(sqrt(Am^2 + (AQY*PAR)^2)))-Rd), data=., start=list(Am=0.*
        augmented = map(fit, augment),
    ) %>%
  unnest(augmented)

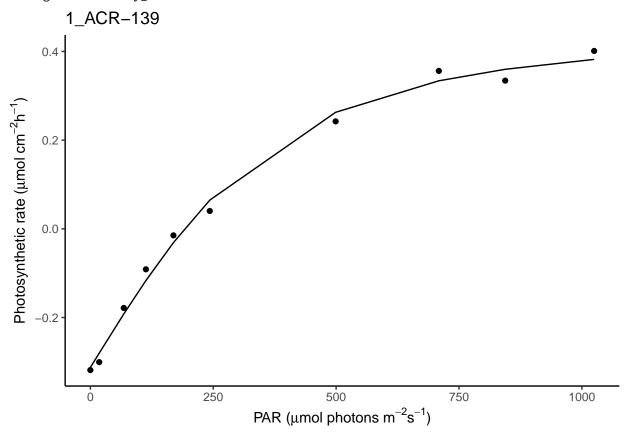
#all colonies together
augmented %>%
  group_by(colony_id)%>%
  qplot(PAR, Pc, data = ., geom = 'point', colour = colony_id) +
  geom_line(aes(y=.fitted))+
  theme(legend.position="none")
```



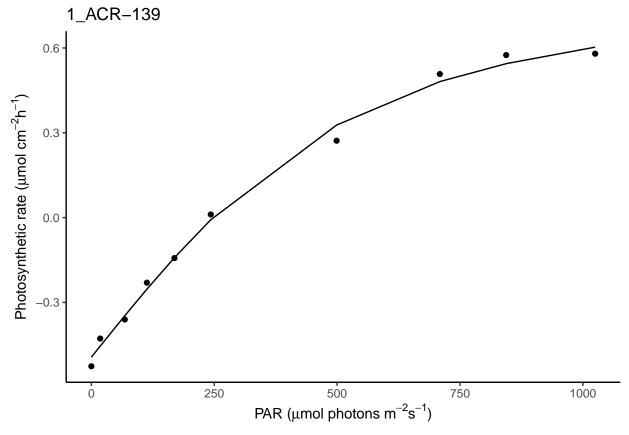
```
#view individual plots
by(augmented,augmented$colony_id, function(i) {
    ggplot(i) +
        geom_point(aes(PAR, Pc, group=colony_id)) +
        geom_line(aes(y=.fitted, x=PAR)) +
        theme_classic()+
        labs(x = expression(paste('PAR (', mu, "mol photons m"^-2, 's'^-1,")")),
            y = expression(paste('Photosynthetic rate (', mu, "mol cm"^-2, 'h'^-1,")")),
            title = paste0("1_", augmented$colony_id))
```

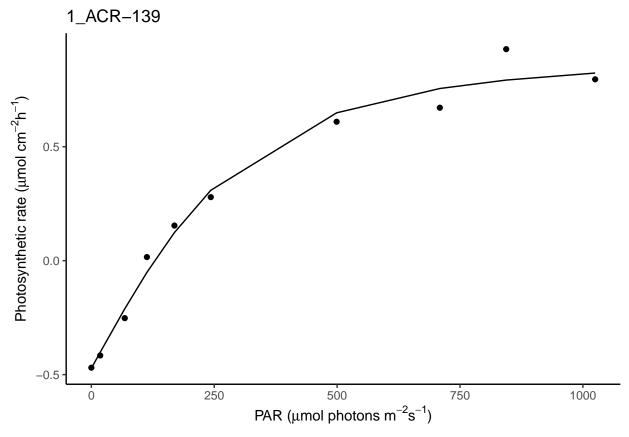
})

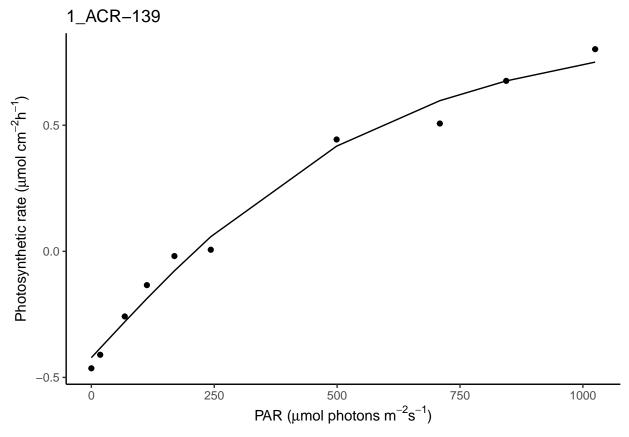
## augmented\$colony\_id: ACR-139

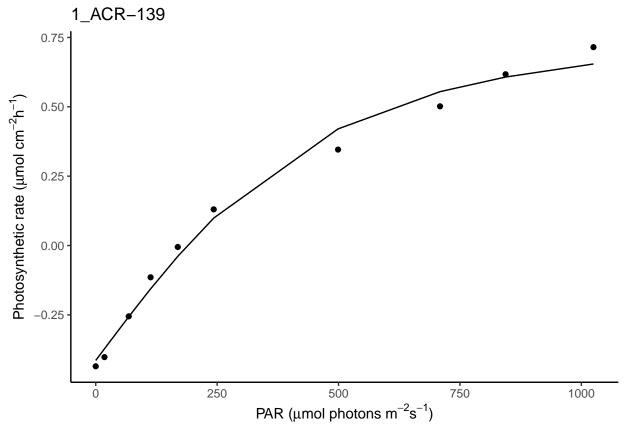


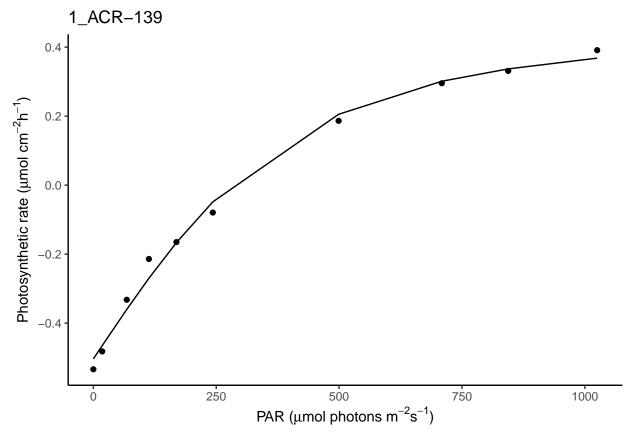
## -----

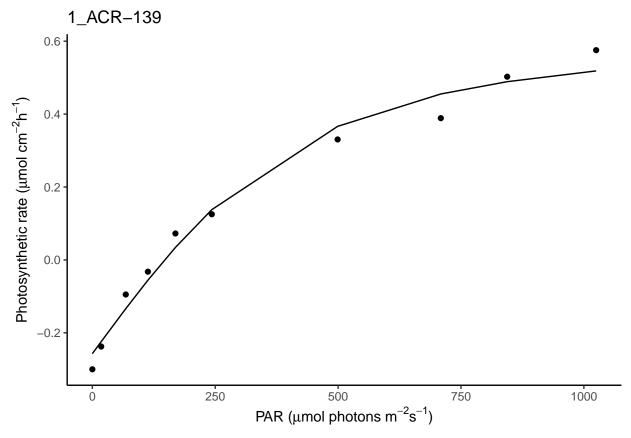


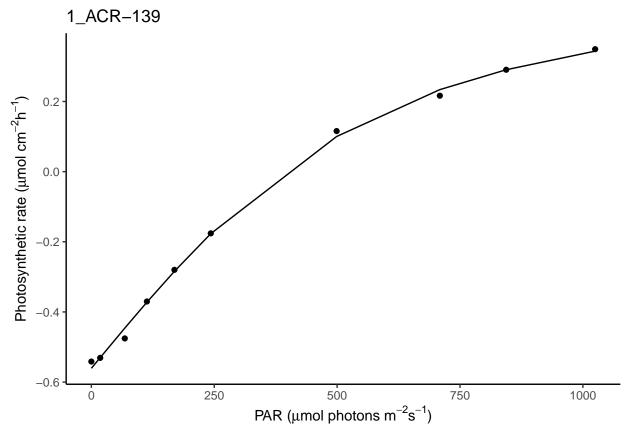


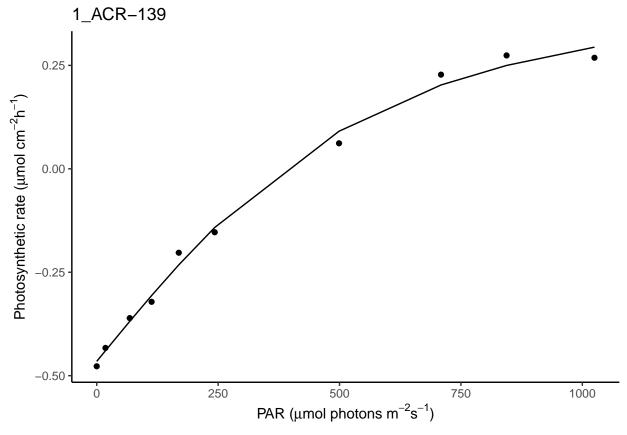


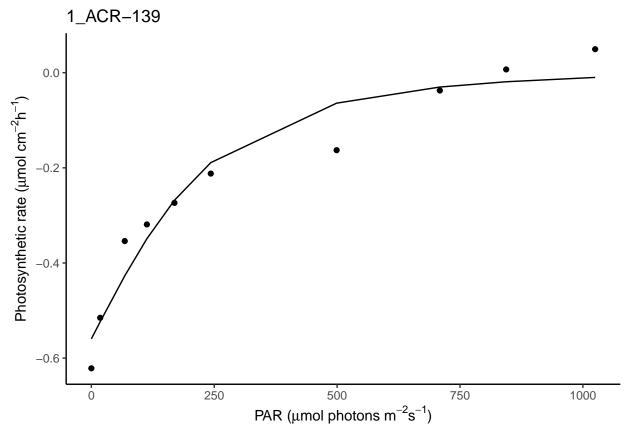


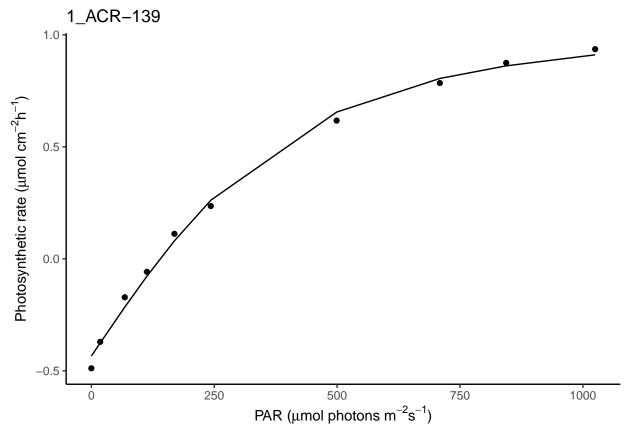


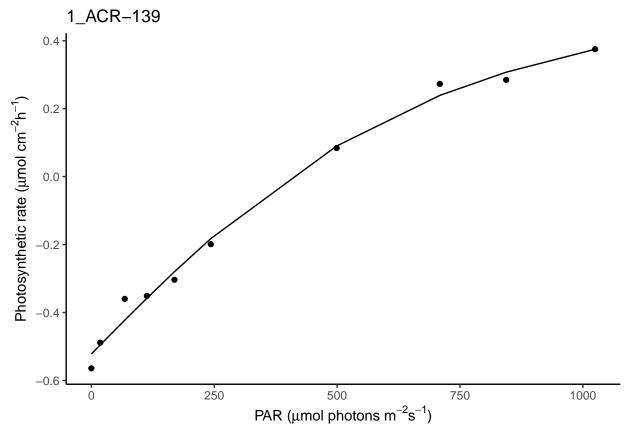


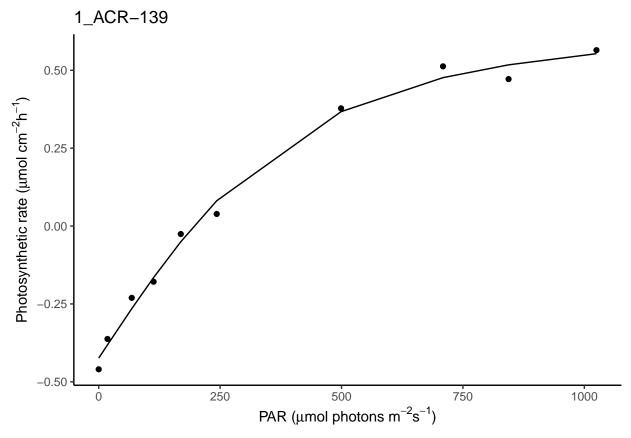


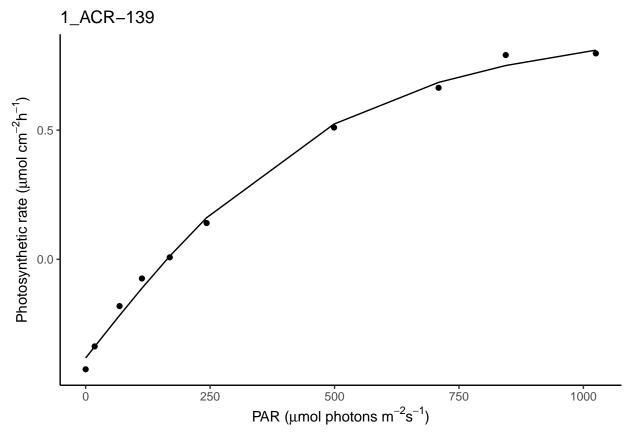


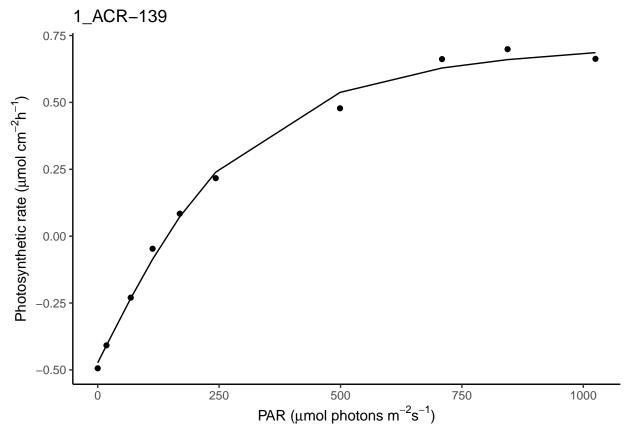


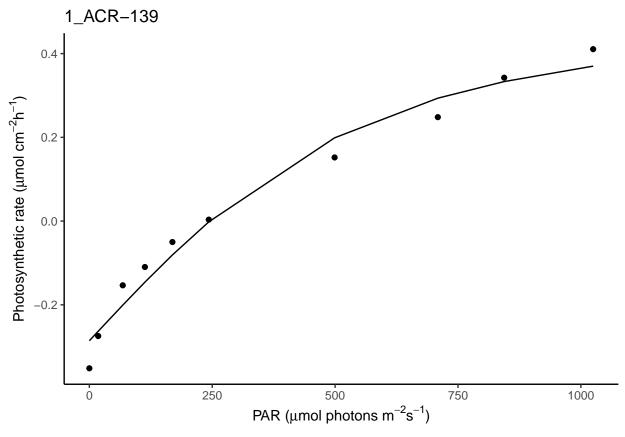


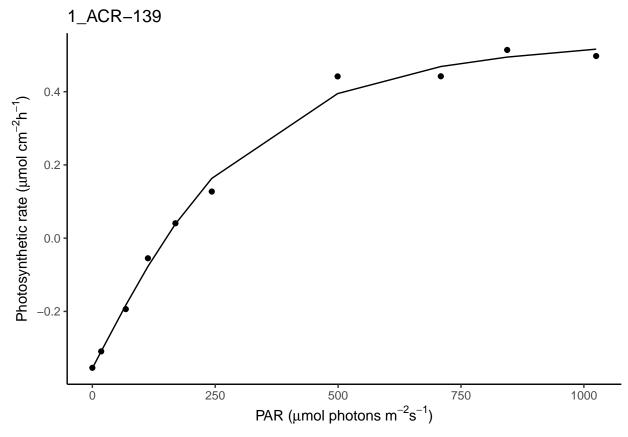


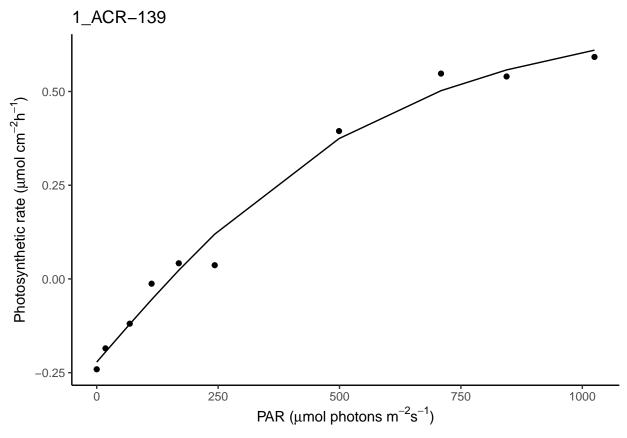


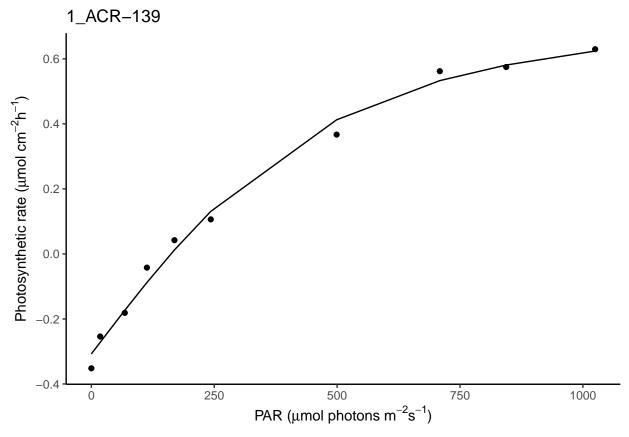


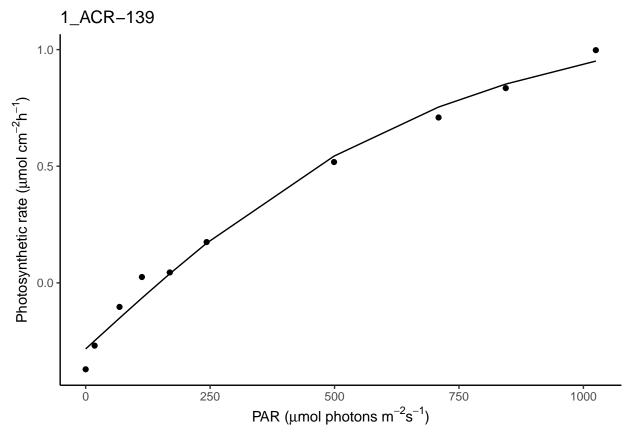


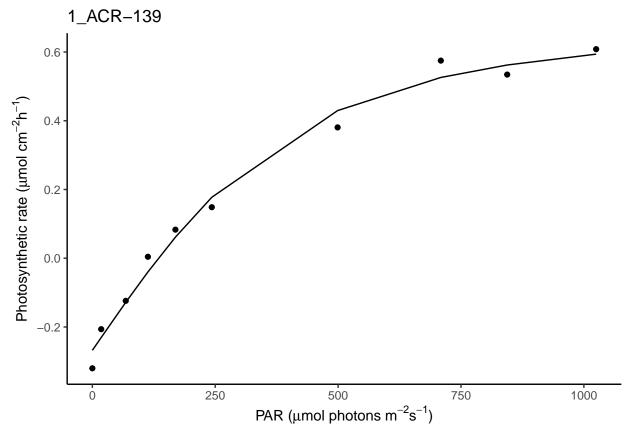


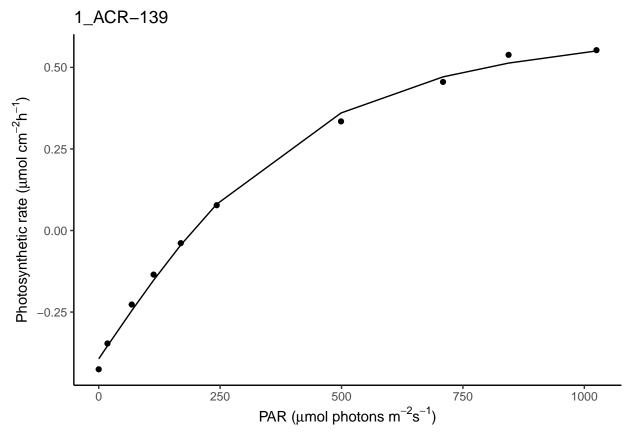


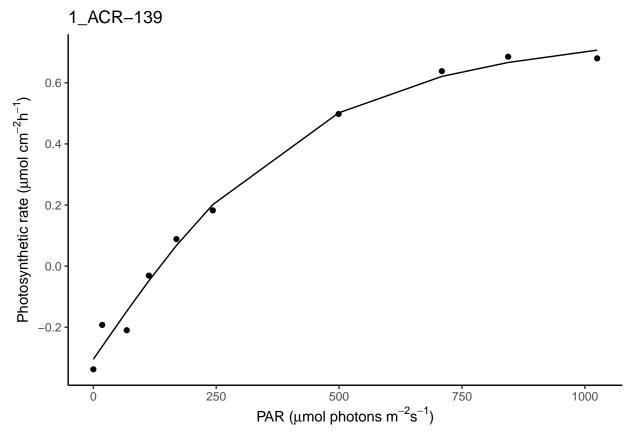


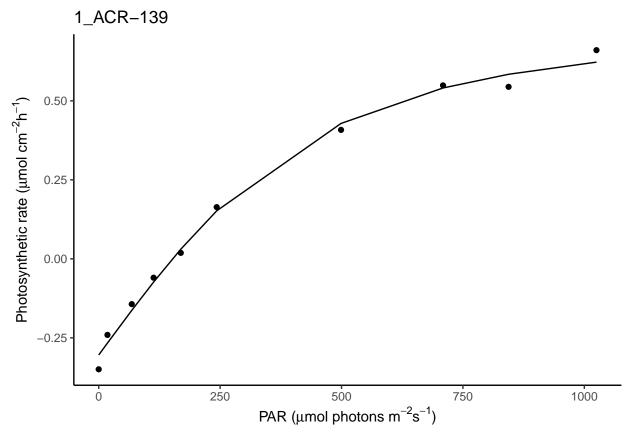


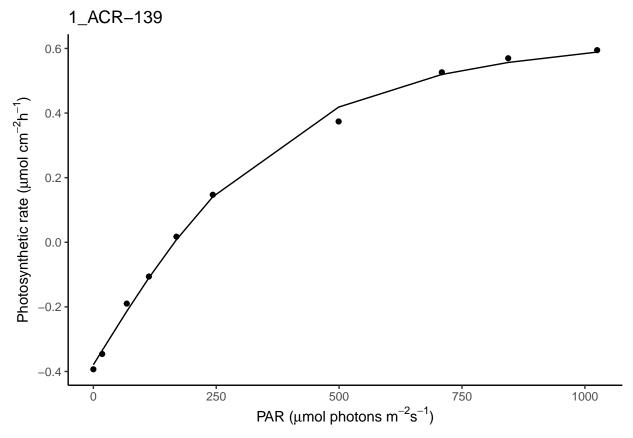


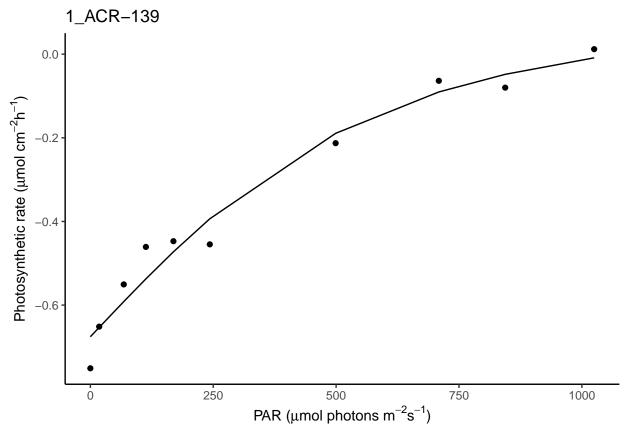


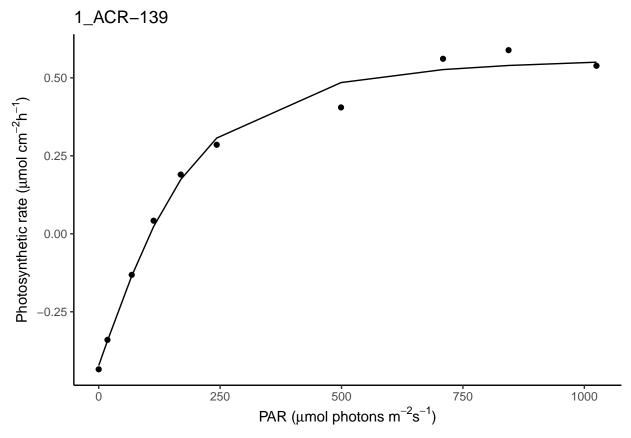


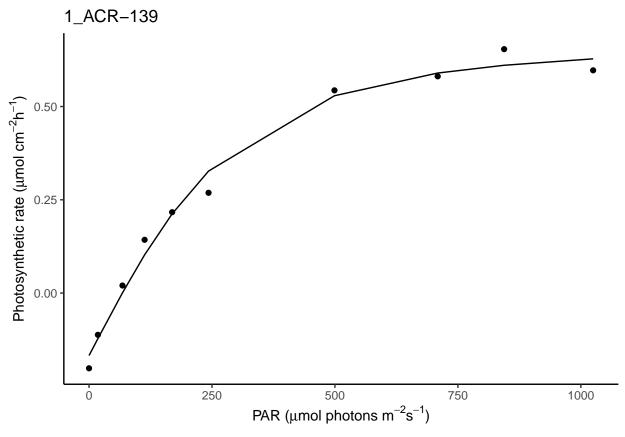


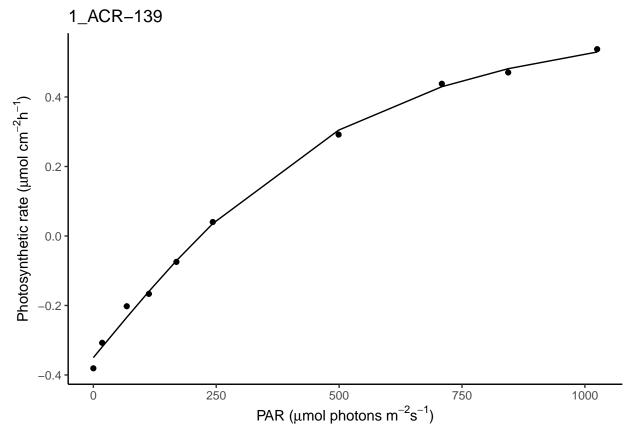


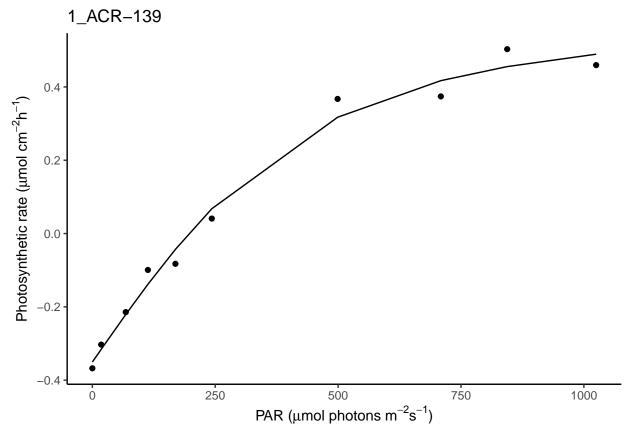


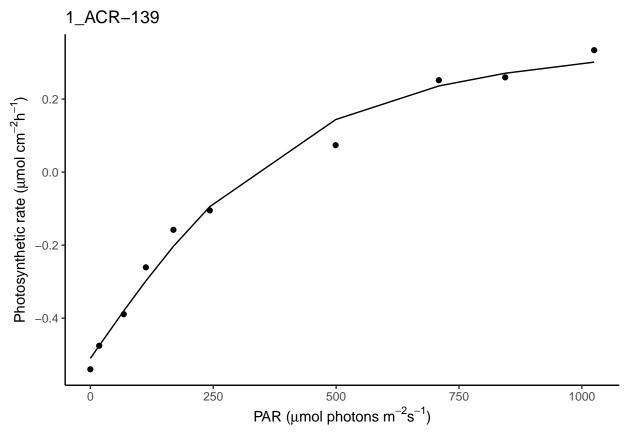


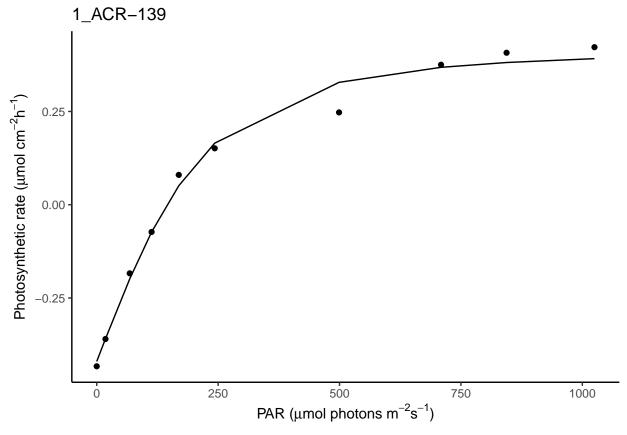


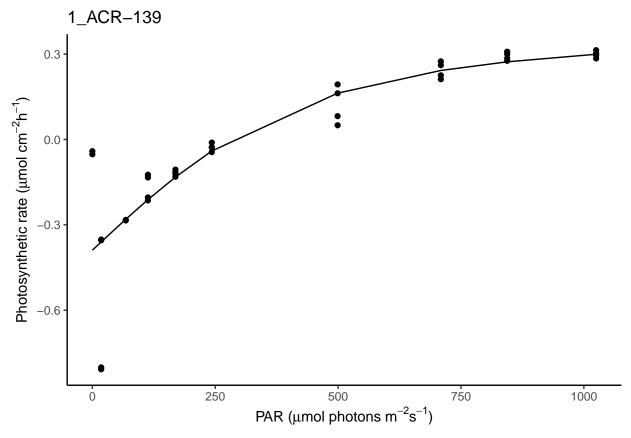


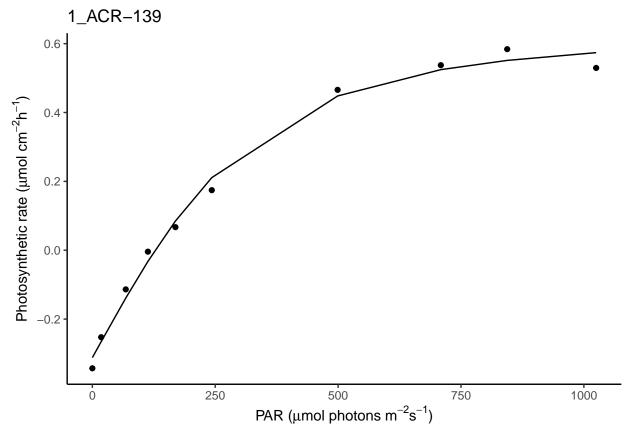


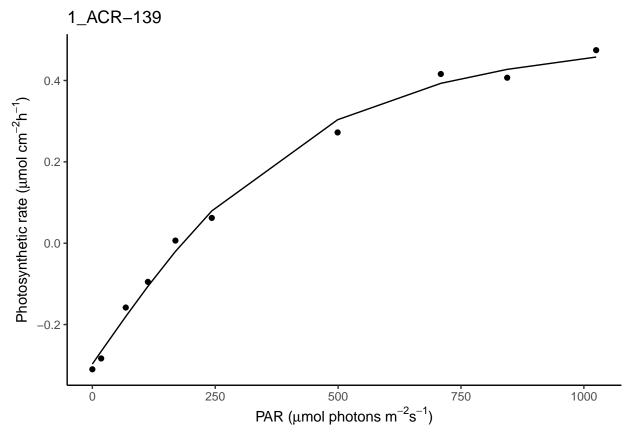


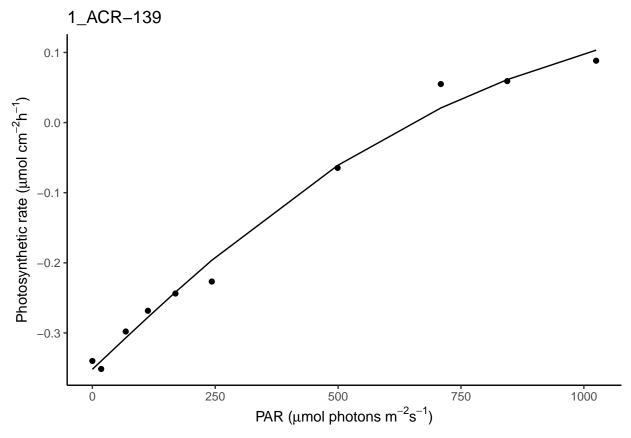


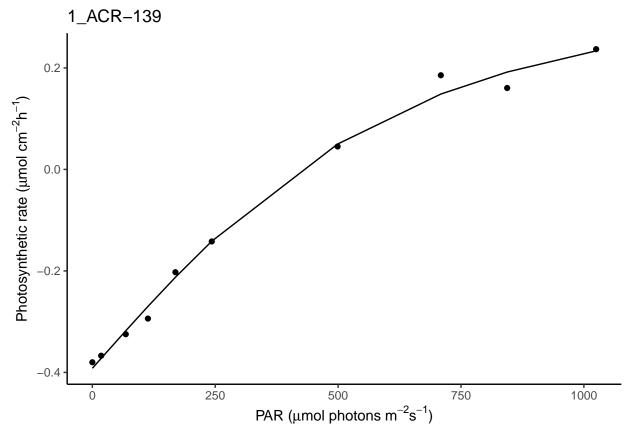


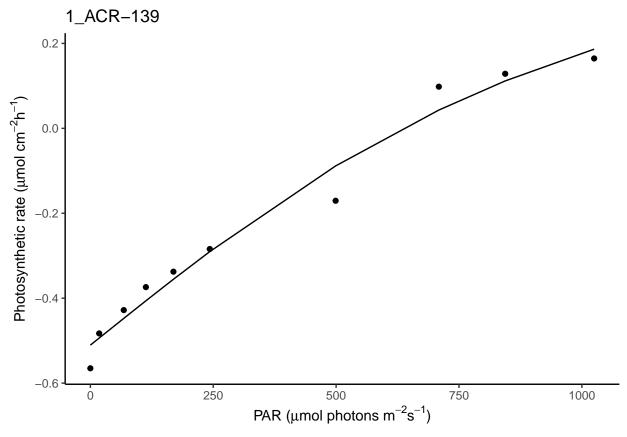


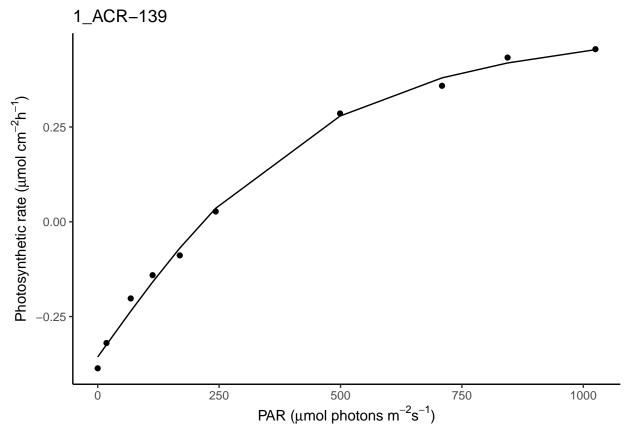


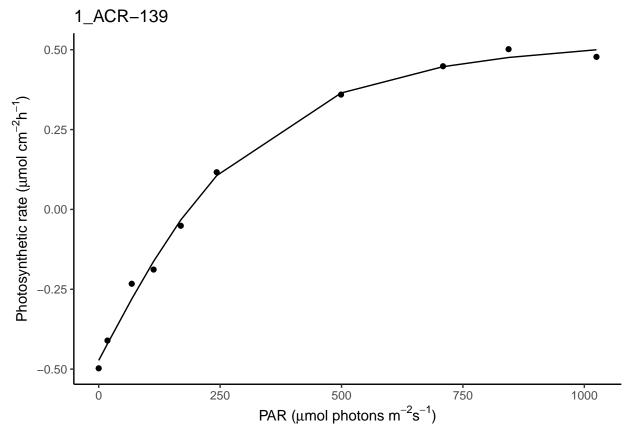


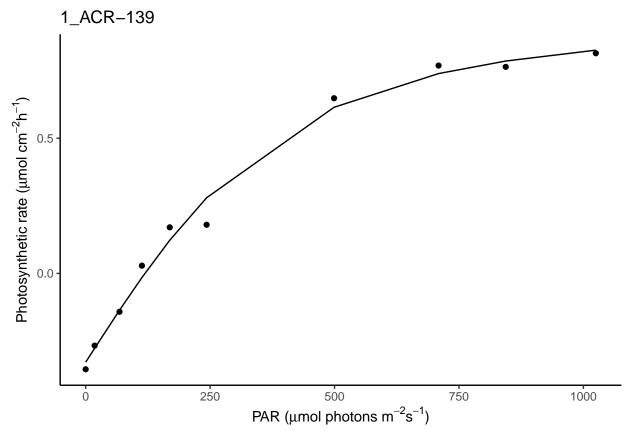


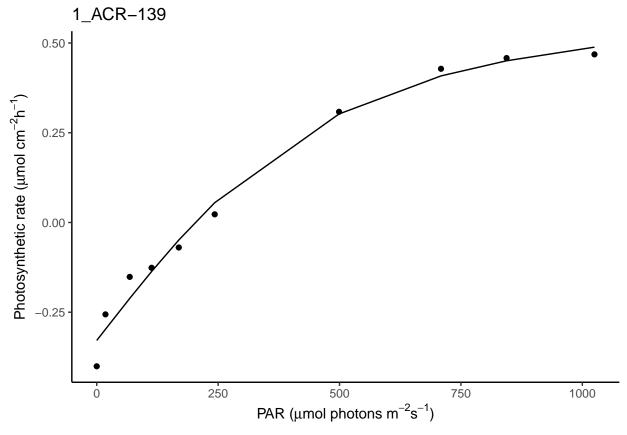


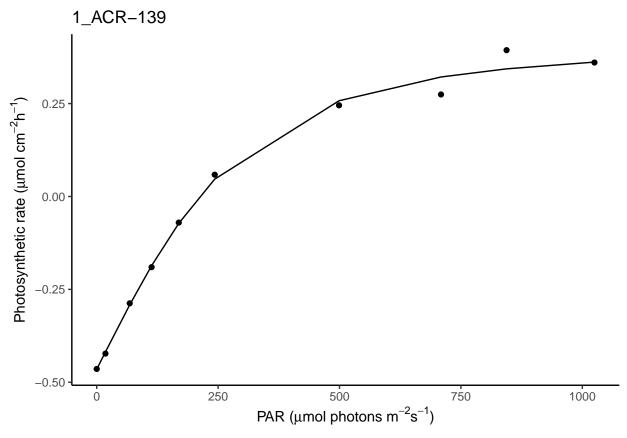


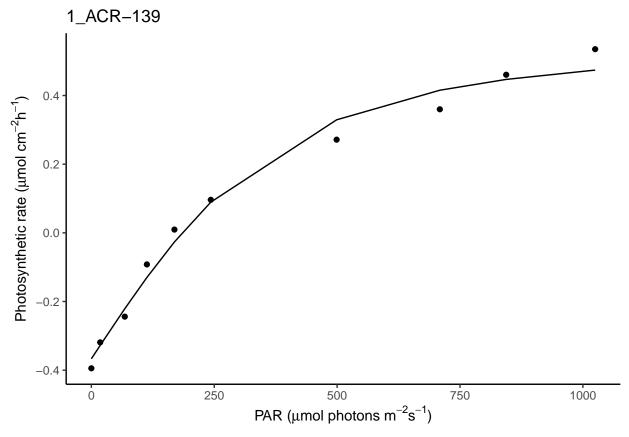


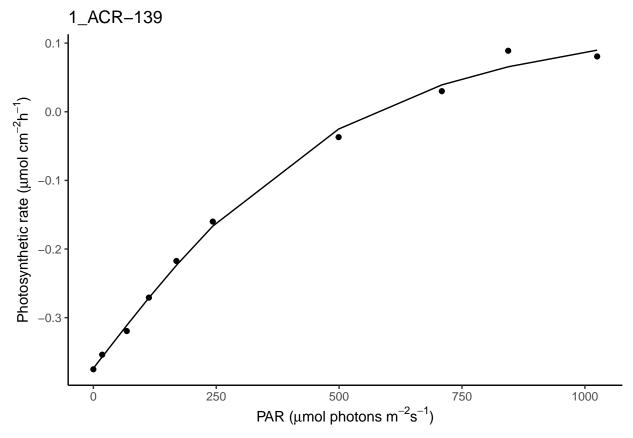


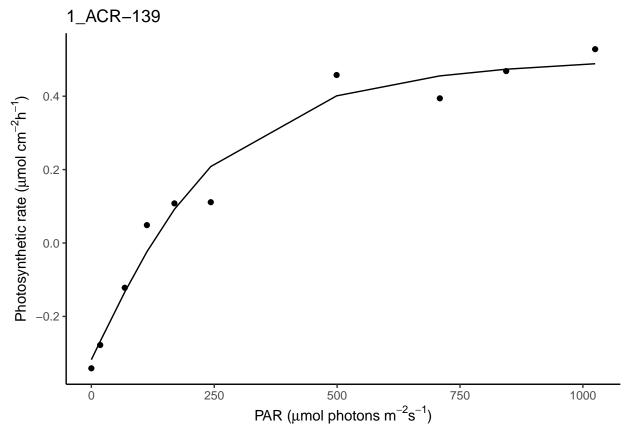


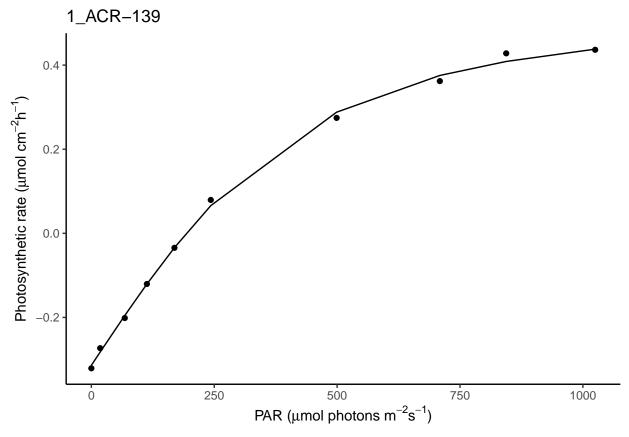


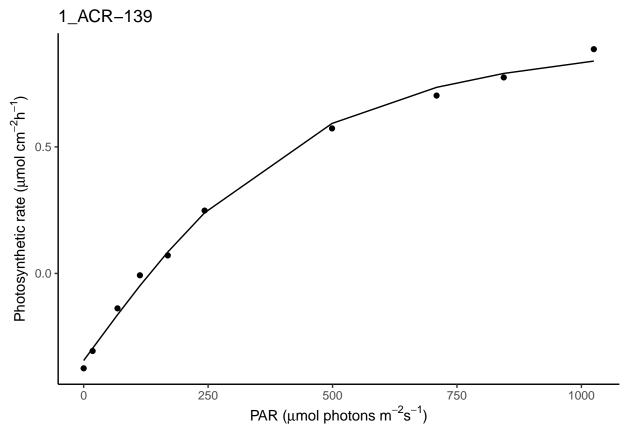


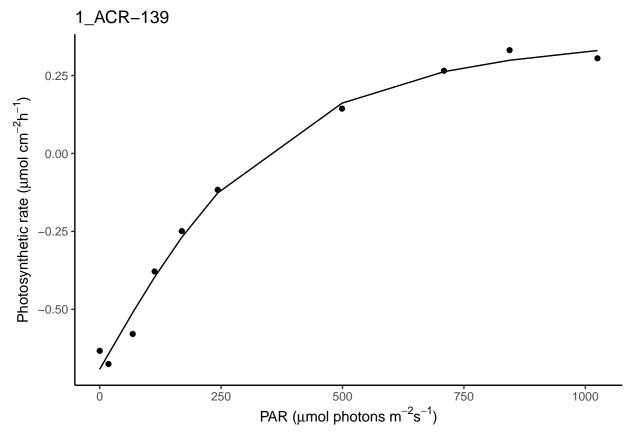


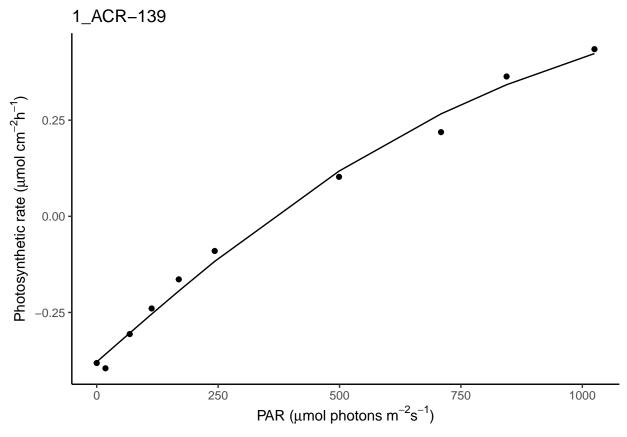


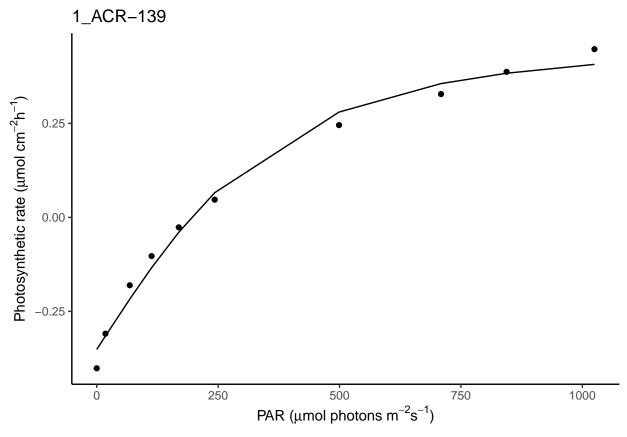


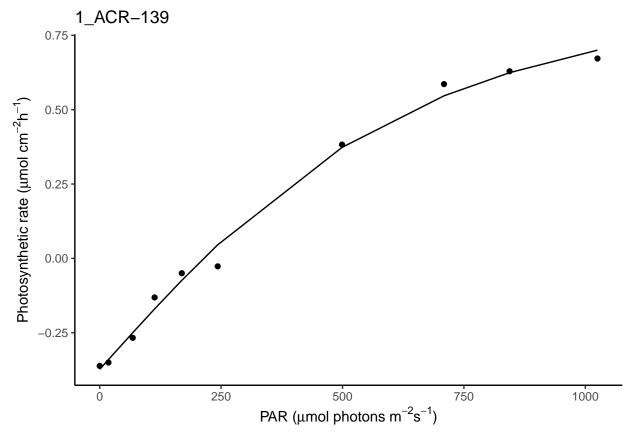


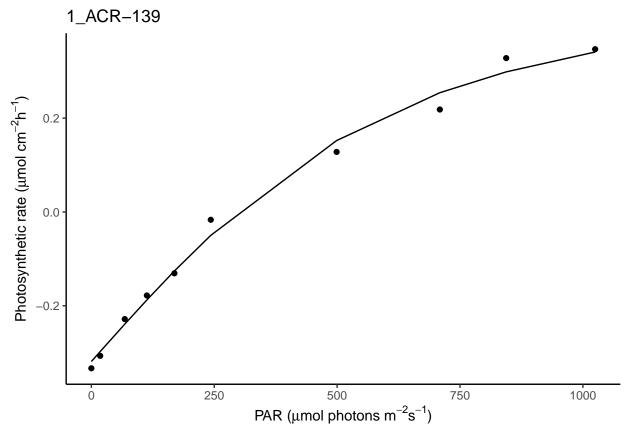


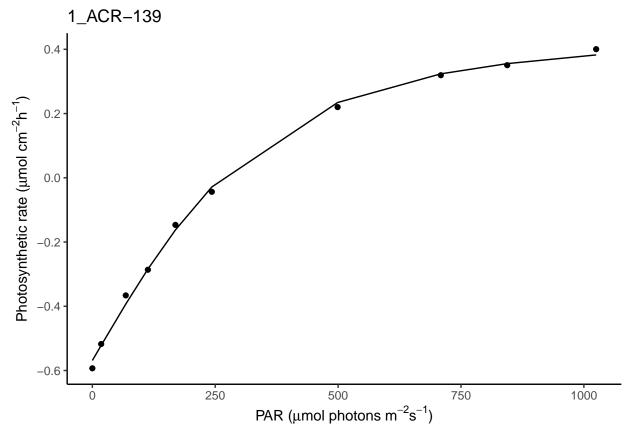


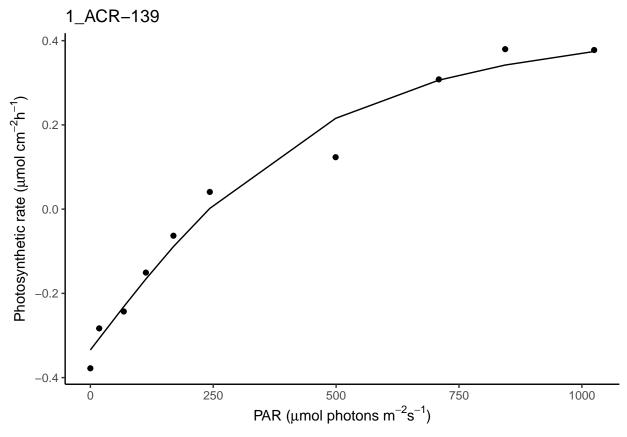


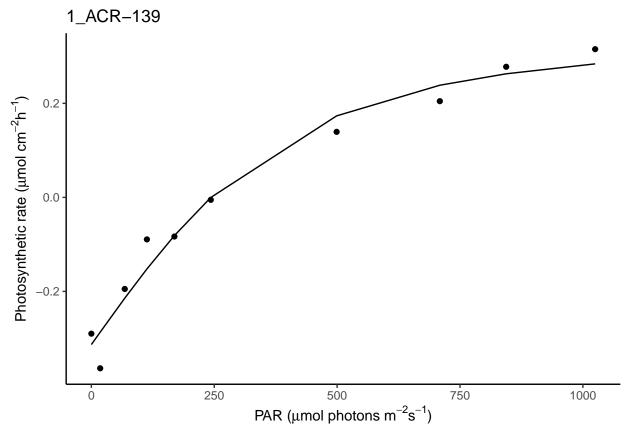


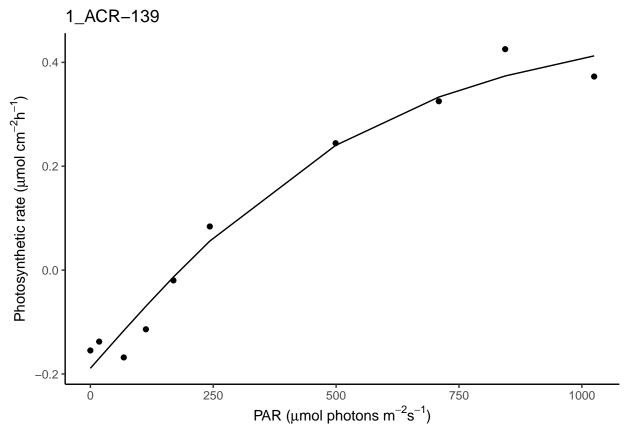


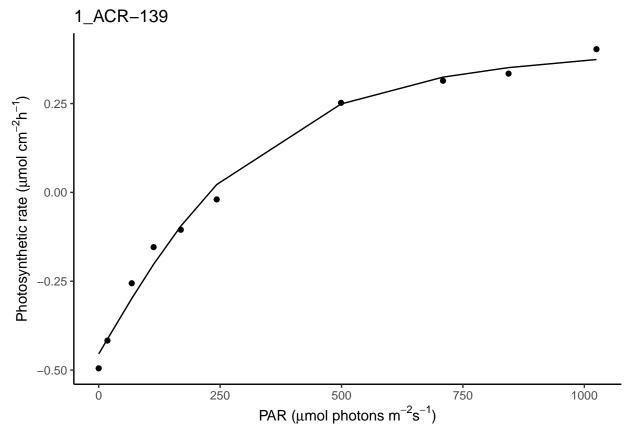


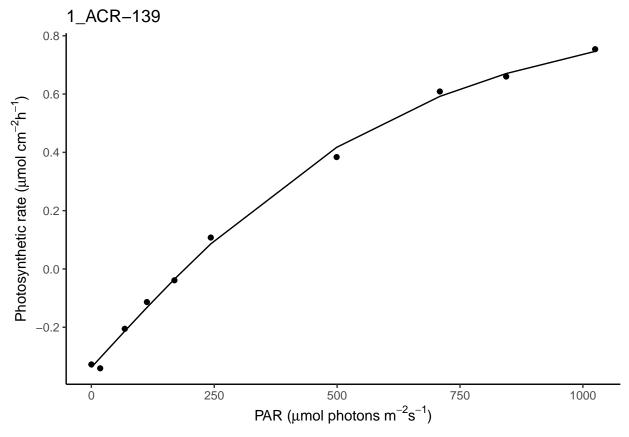


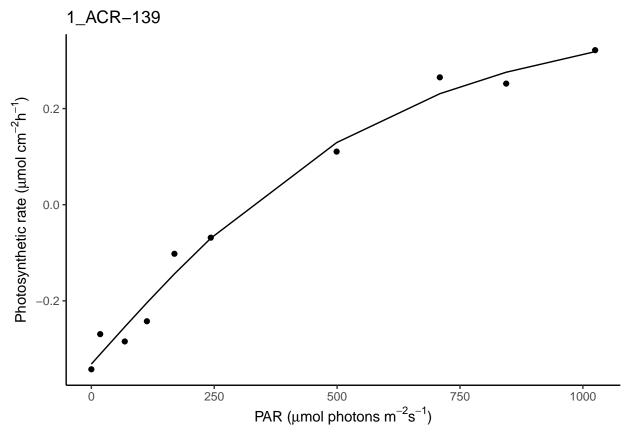


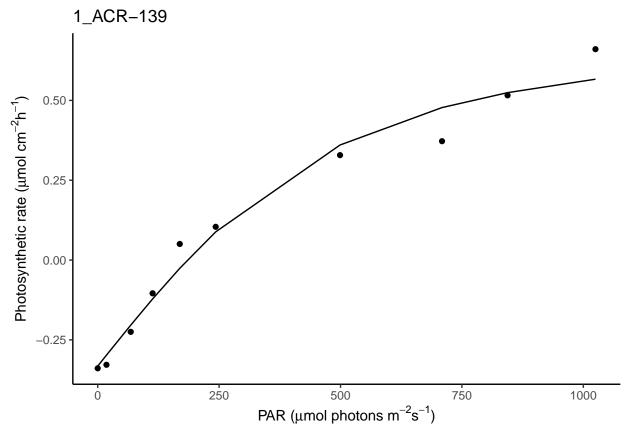


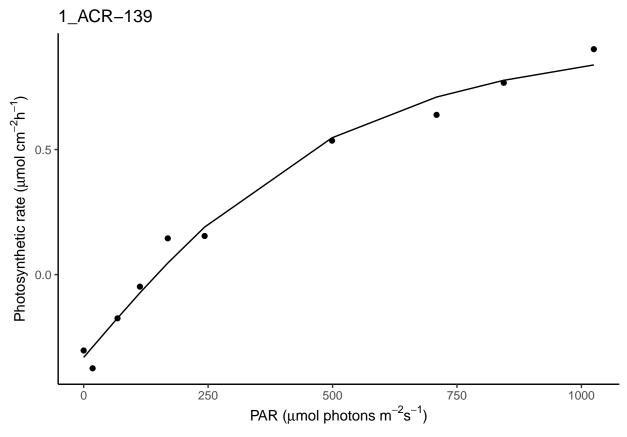


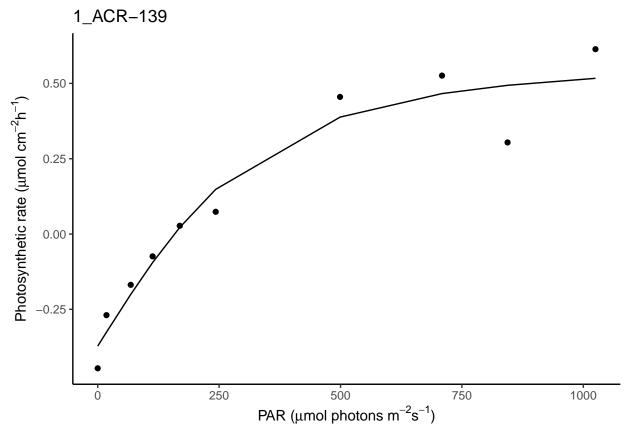


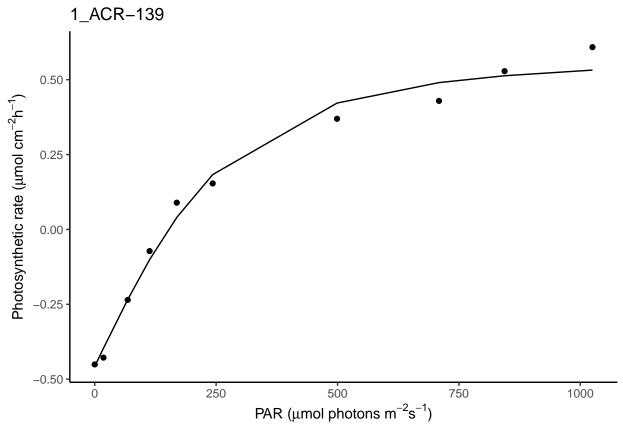


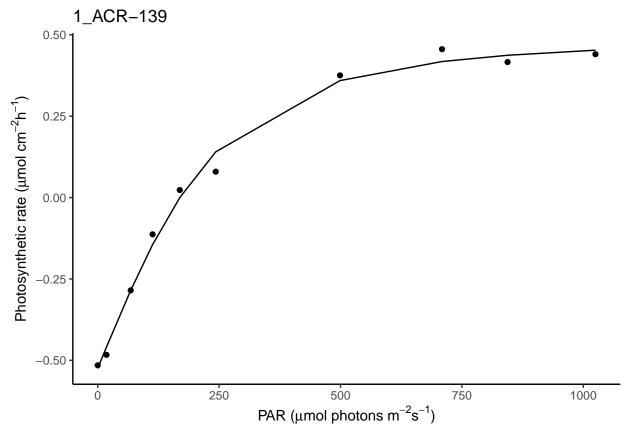


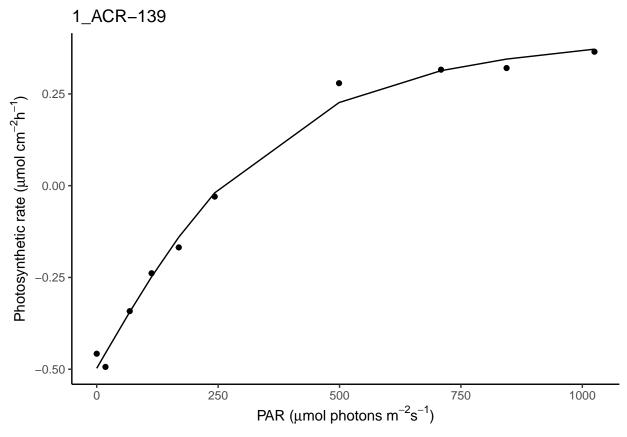


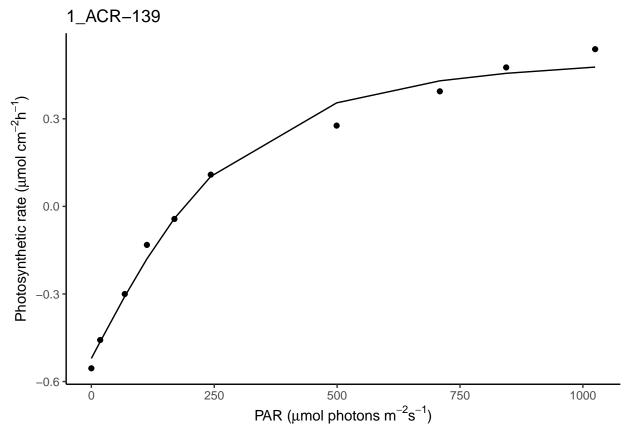


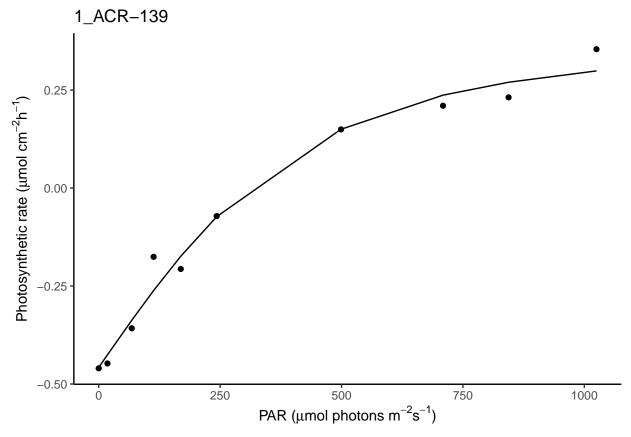


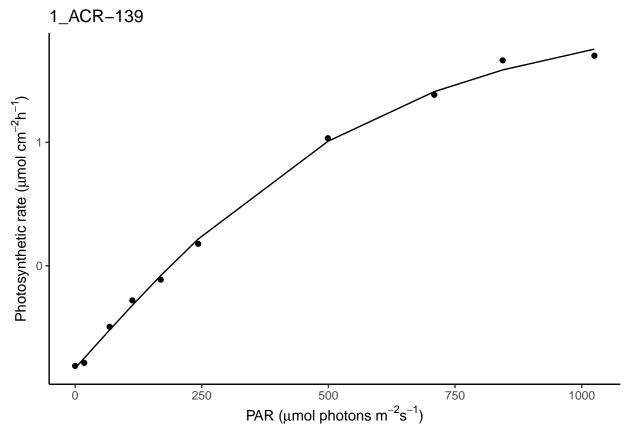


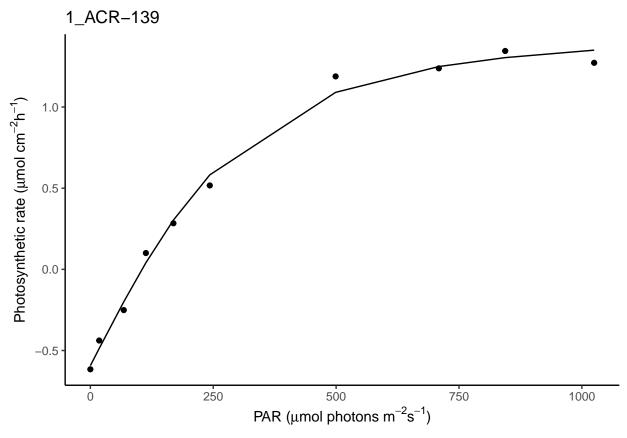


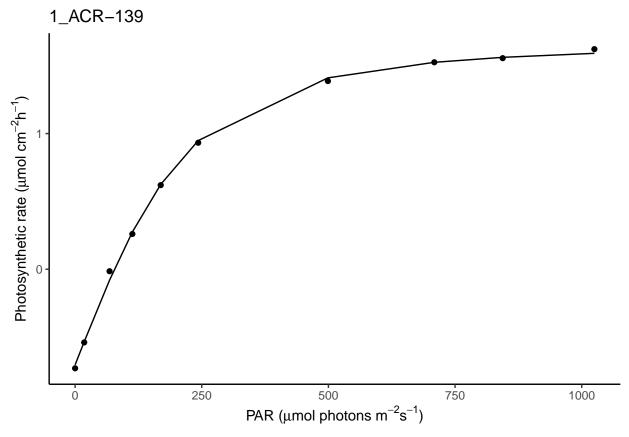


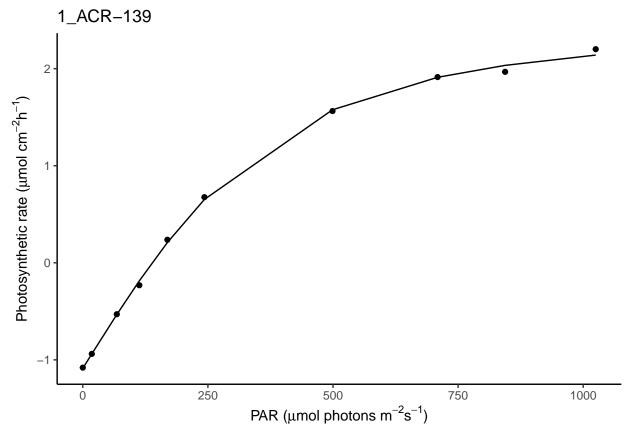


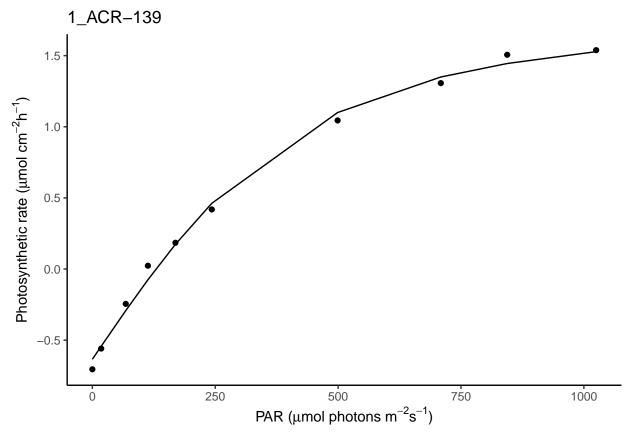


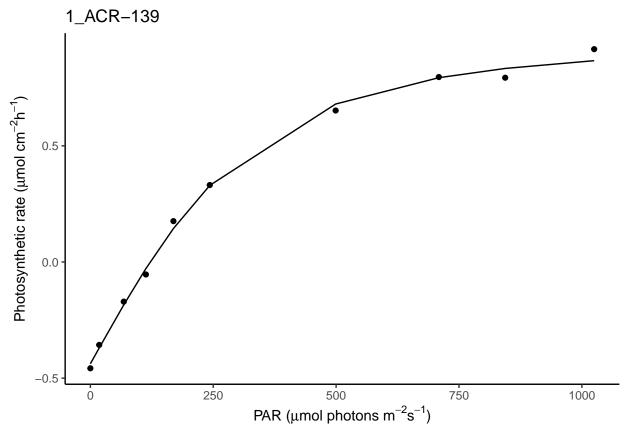


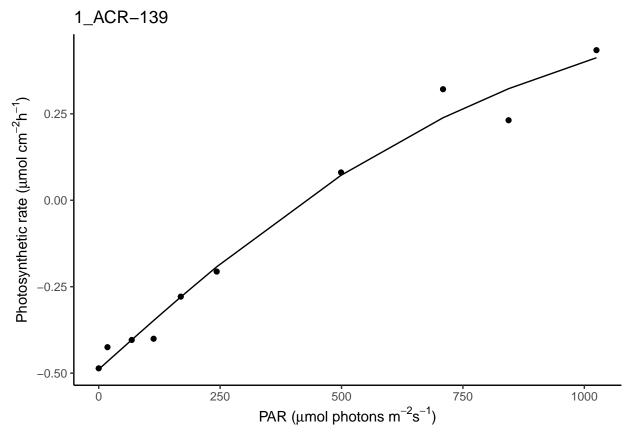


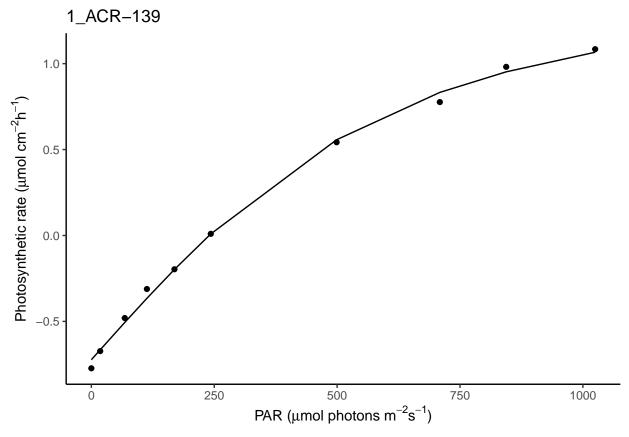


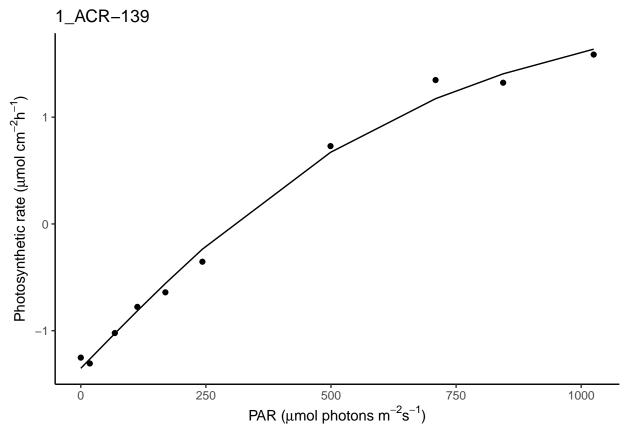


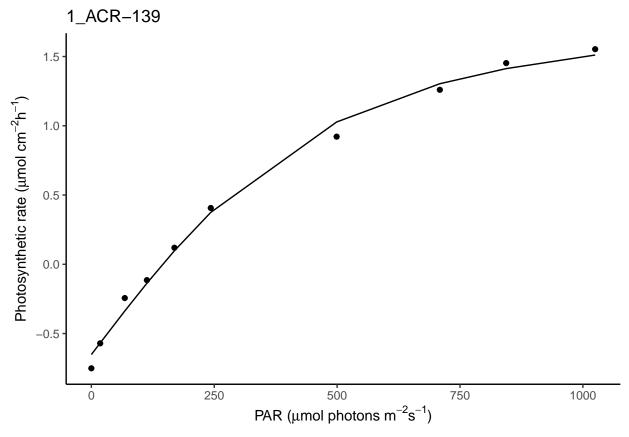


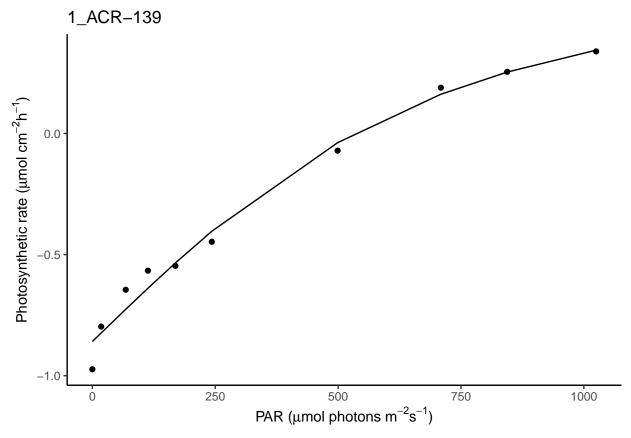


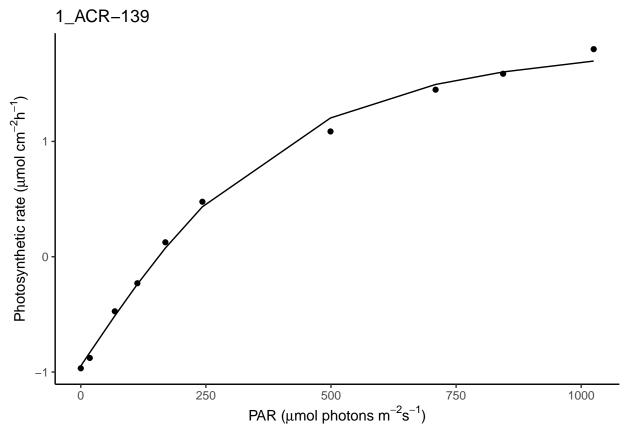


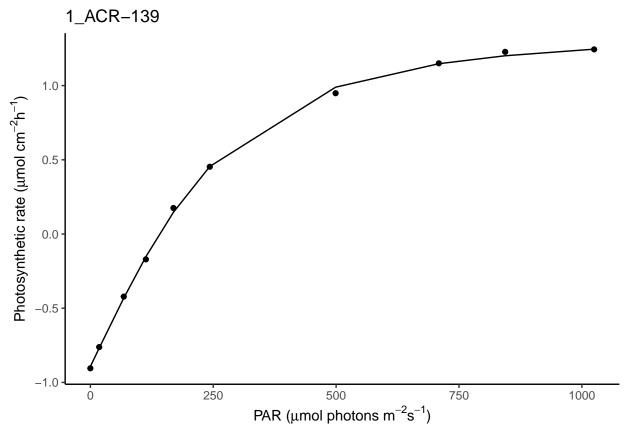


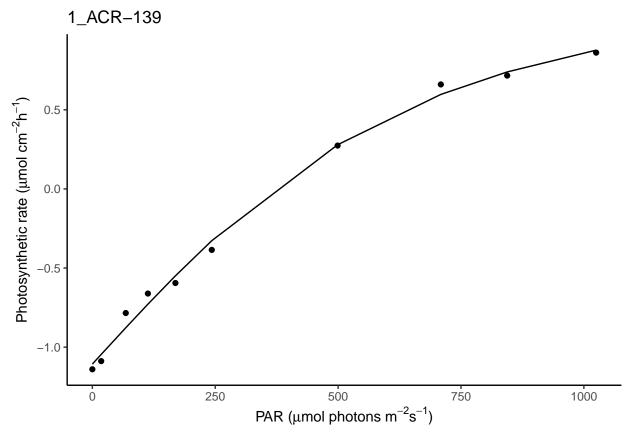


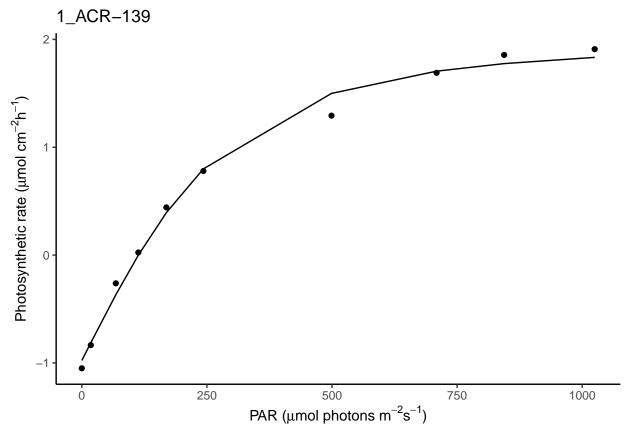


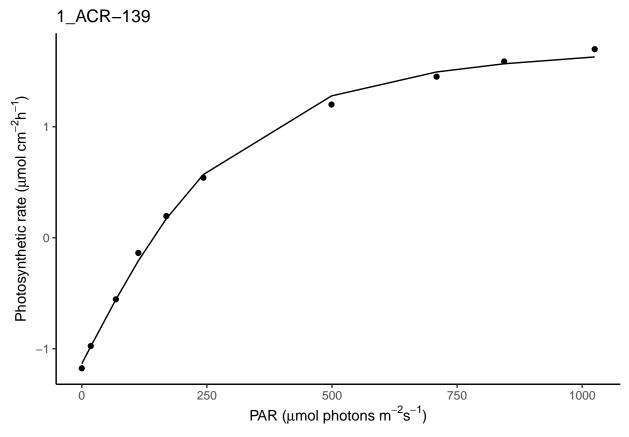


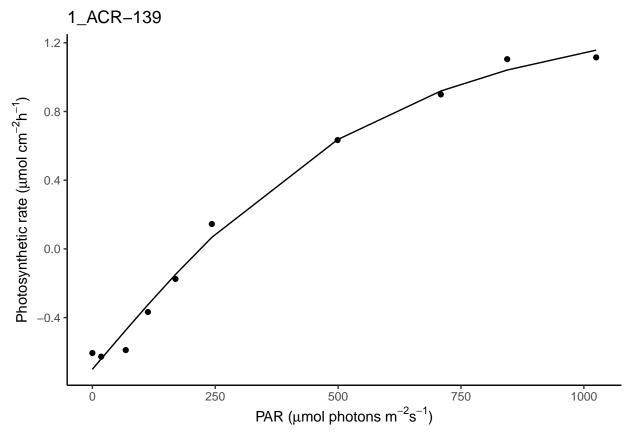


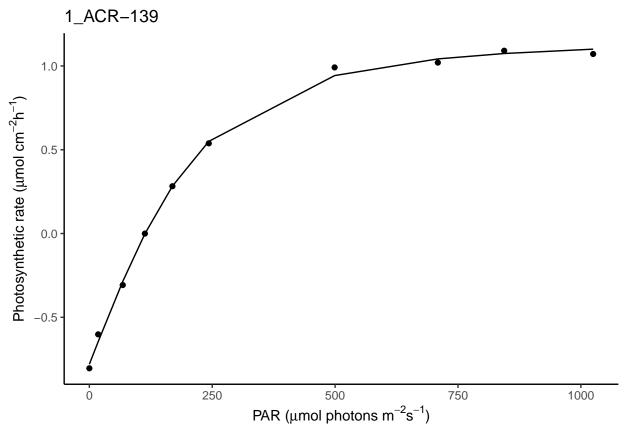


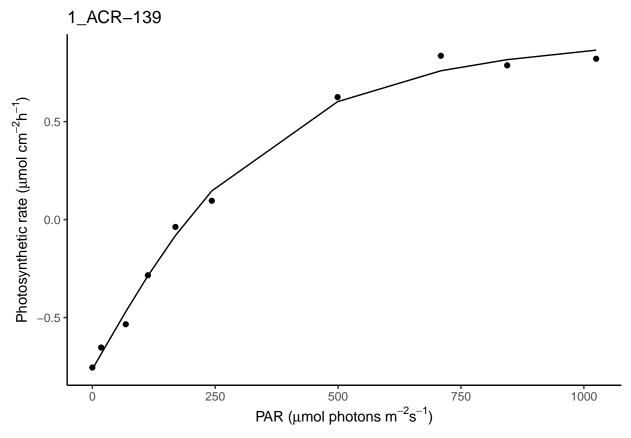


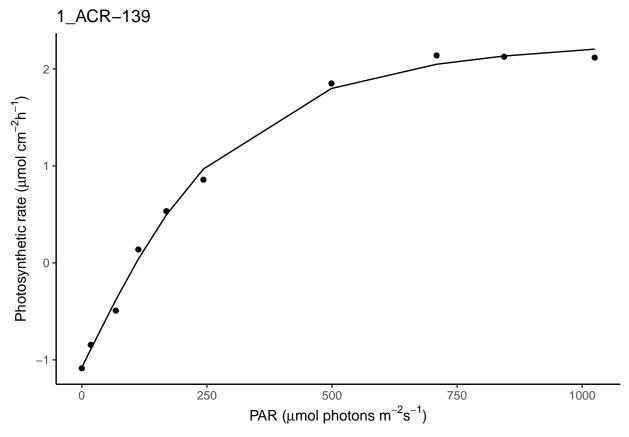


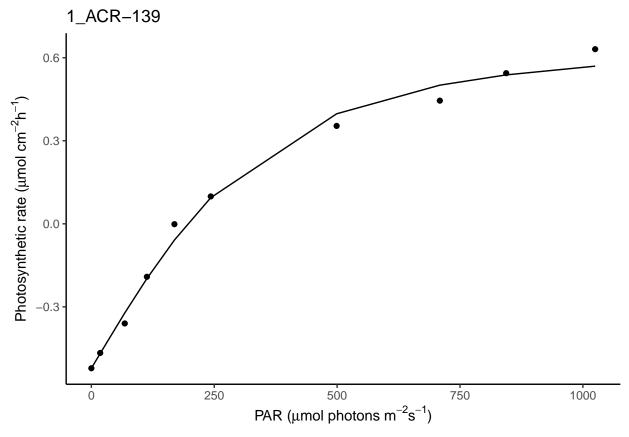


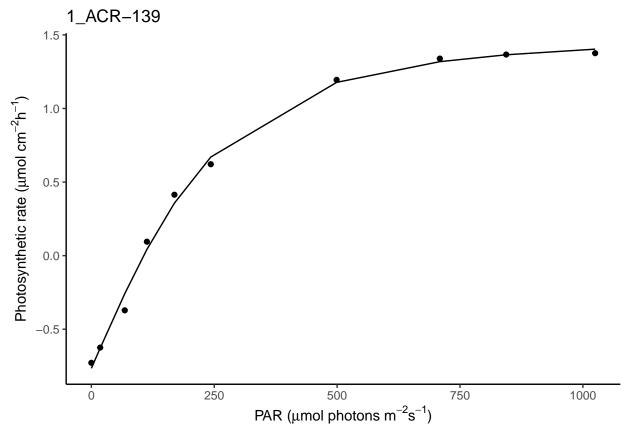


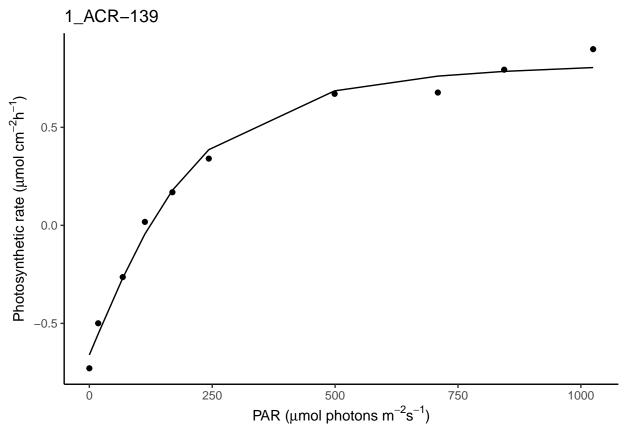


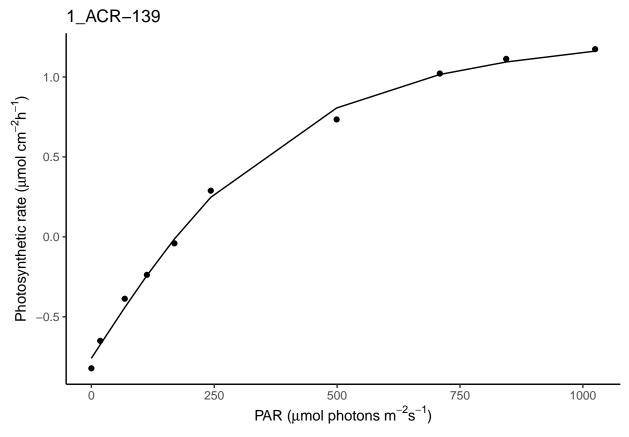


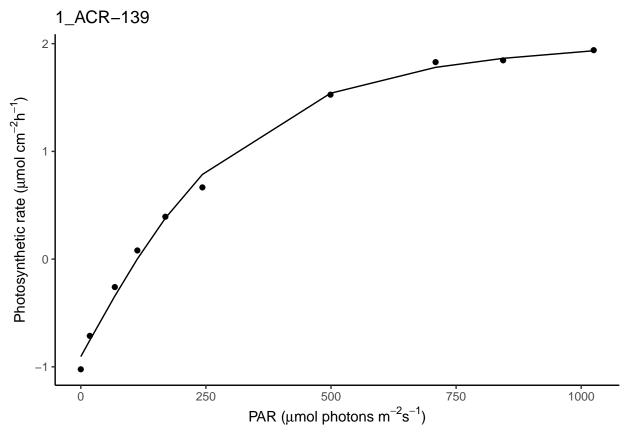


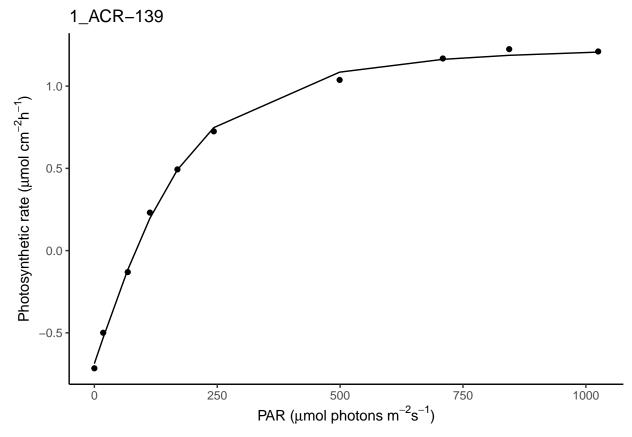


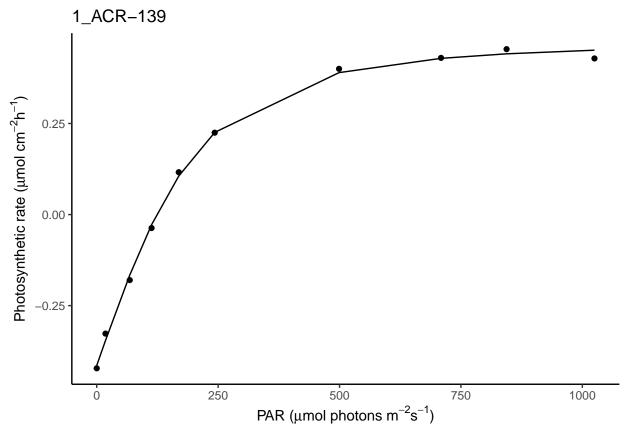


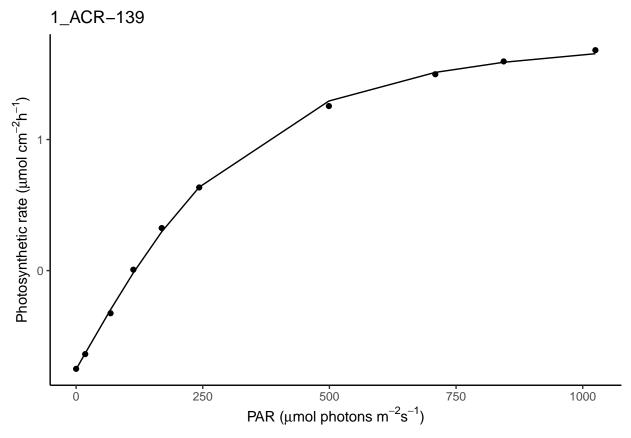


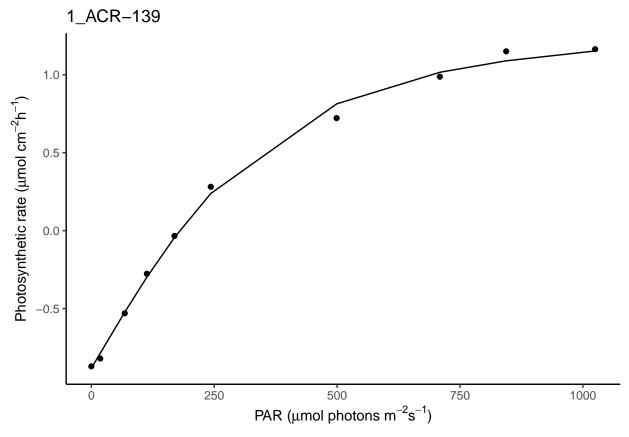


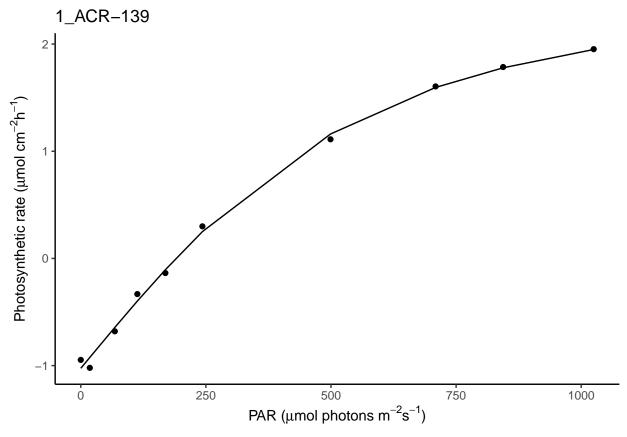


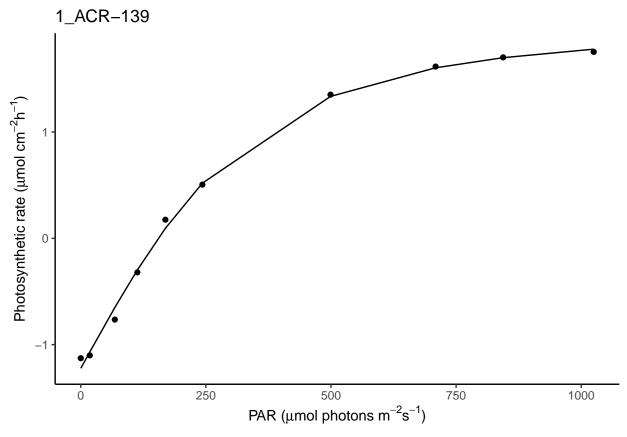


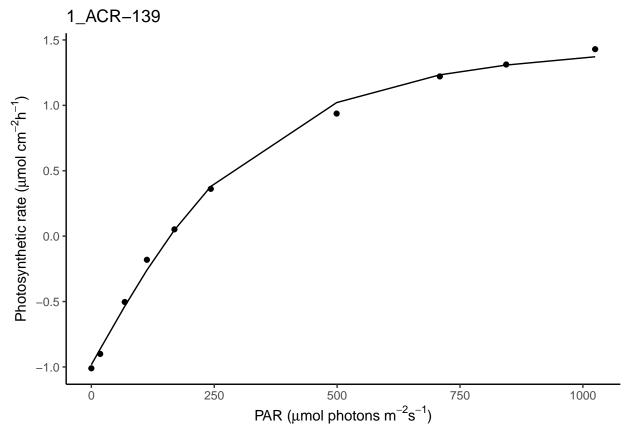


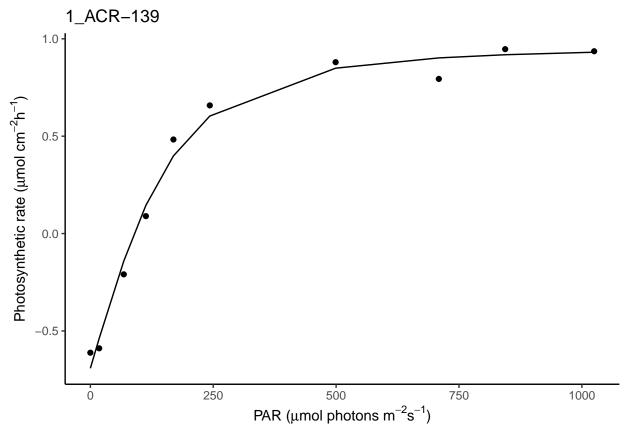


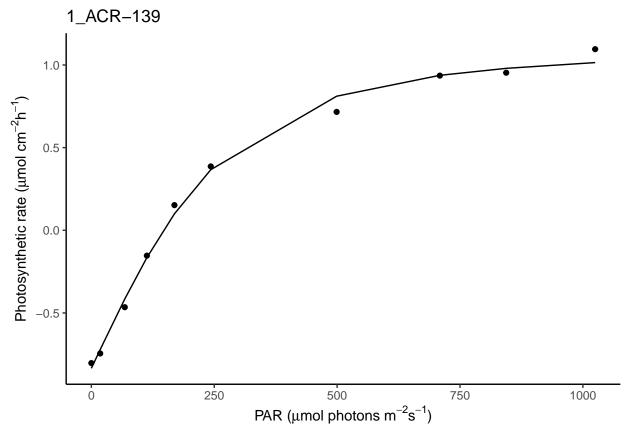


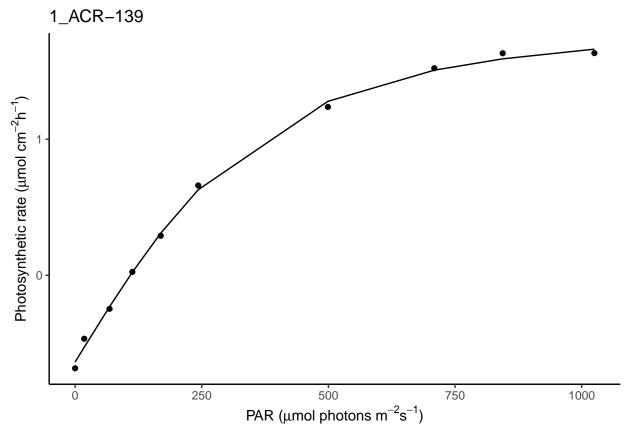


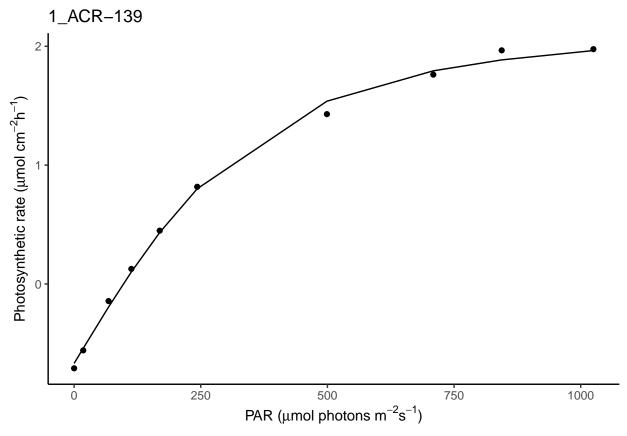


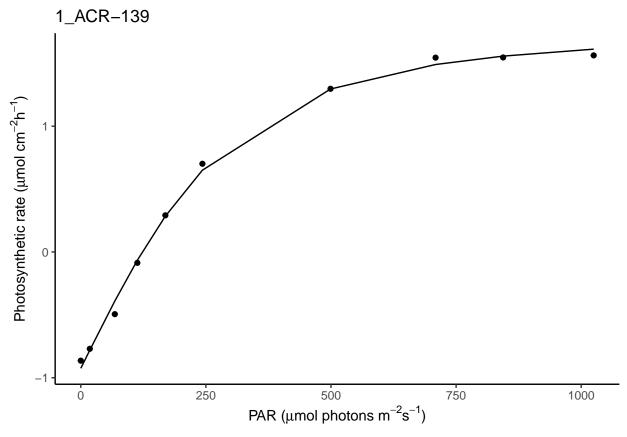


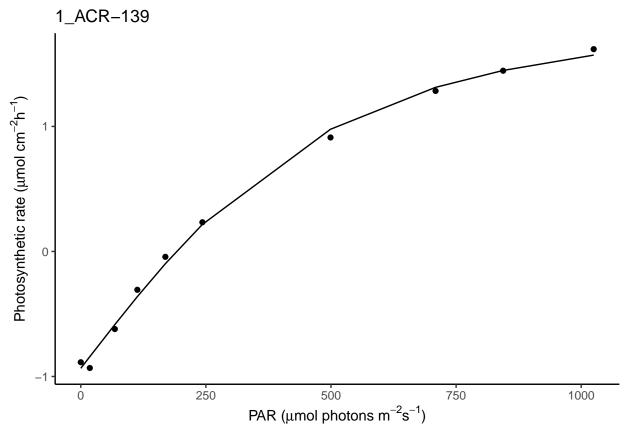


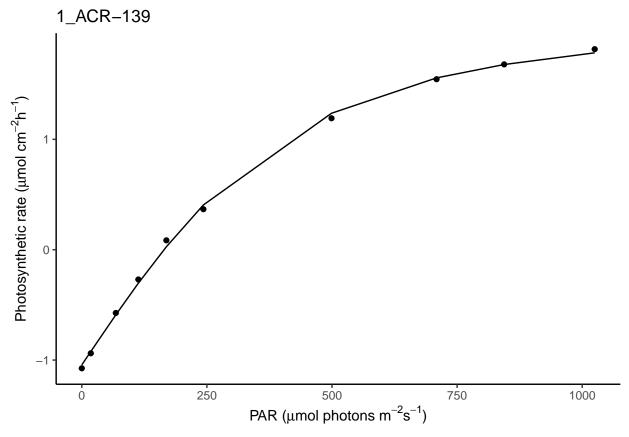


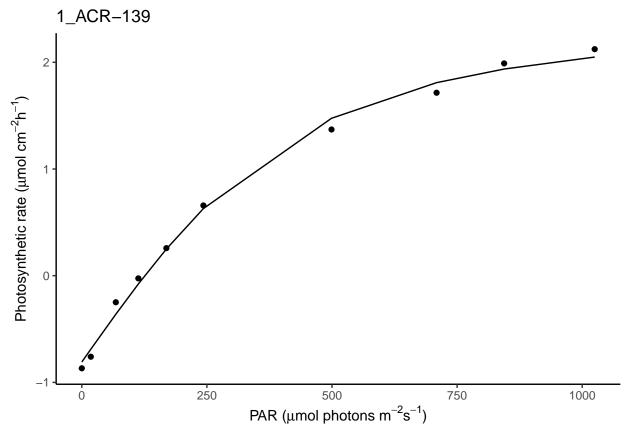


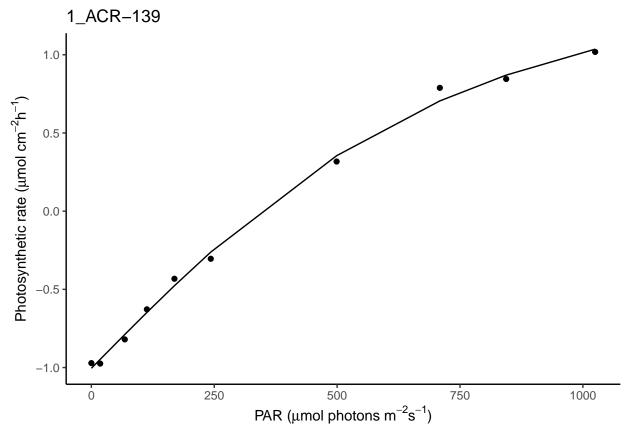


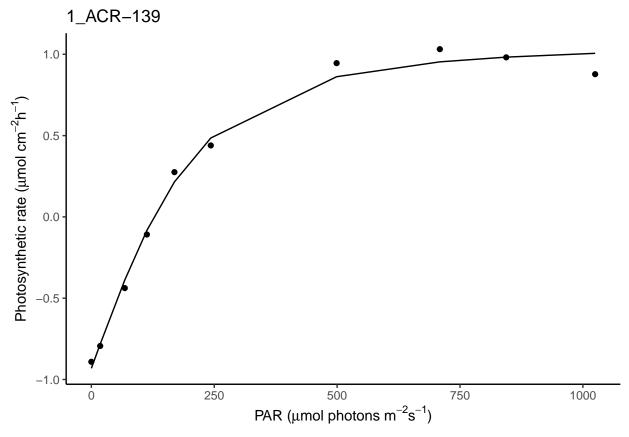


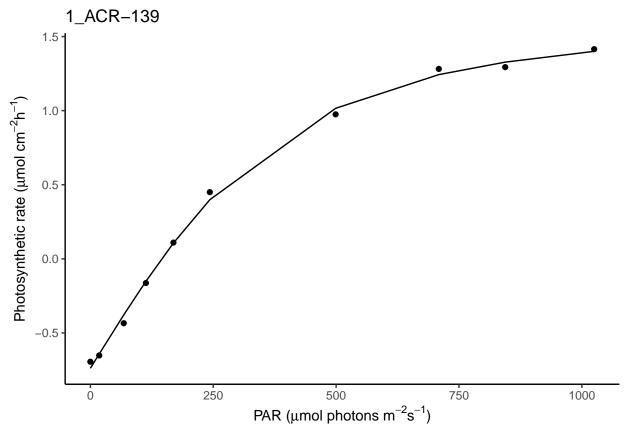


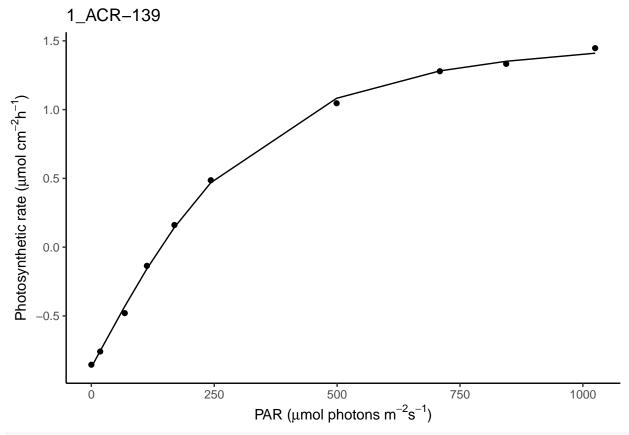












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