

pi_curves_nls

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```
## 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/1_pi_curve_rates.csv')
#Data <- Data[1:40,]
```

Define data

```
#PAR <- as.numeric(Data$Light_Value)
#Pc <- as.numeric(Data$micromol.cm2.h)
#plot(PAR,Pc,xlab="", ylab="", xlim=c(0,max(PAR)), ylim=c(-2, 2), cex.lab=0.8,cex.axis=0.8,cex=1, main=
#mtext(expression("Irradiance ("*mu*"mol photons "*m^-2*s^-1*")"),side=1,line=3.3,cex=1) #add labels
#mtext(expression(Rate*" ("*mu*"mol "*O[2]*" "*cm^-2*h^-1*")"),side=2,line=2,cex=1) #add labels
```

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

```
#Aquatic Photosynthesis, Falkowski
#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

#df <- data.frame(PAR, Pc)
#curve.nls <- nls(Pc ~ (Am*((AQY*PAR)/(sqrt(Am^2 + (AQY*PAR)^2)))-Rd), data=df, start=list(Am=1, AQY=0.
#my.fit <- summary(curve.nls)
#my.fit
```

Run models - NOTE: Need to look at starting values, the starts make a difference in the outcome right?

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

#use tidy to group by colony, then map data using nls curve and pull out coefficients to generate a new d

#Script version 1
#nls_data <- Data %>%
  #filter(colony_id==c("ACR-140"))%>%
  #group_by(colony_id) %>% #group by colony
  #nest(-colony_id) %>% #nest data by colony
  #mutate(
    # fit = map(data, ~ nls(Pc ~ (Am*((AQY*PAR)/(sqrt(Am^2 + (AQY*PAR)^2)))-Rd), data=.), #fit nls curv
    # tidied = map(fit, tidy), #pull out coefficients from model
  # ) %>%
  # unnest(tidied) %>% #unnest data
  # select(colony_id, term, estimate) %>% #keep columns we want
  # spread(term, estimate) #spread columns by coefficient for each colony

#Script version 2 - adjusted starting values to reflect values we are getting from models on single col
nls_data <- Data %>%
  #filter(colony_id==c("ACR-140"))%>%
  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="timepoint1")%>%
write_csv(., "output/1_pi_curve_pars_NLS.csv")

```

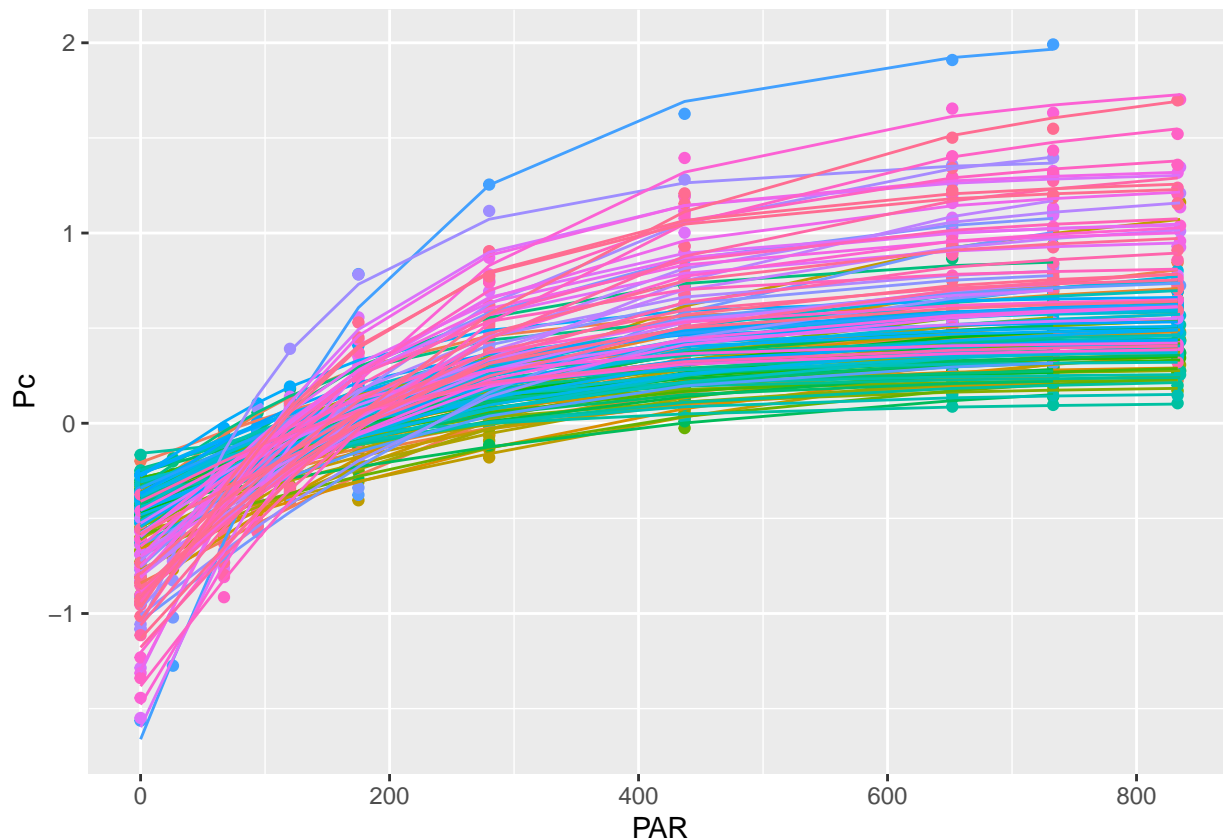
Plot curve over data points.

```

augmented <- Data %>%
  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")

```

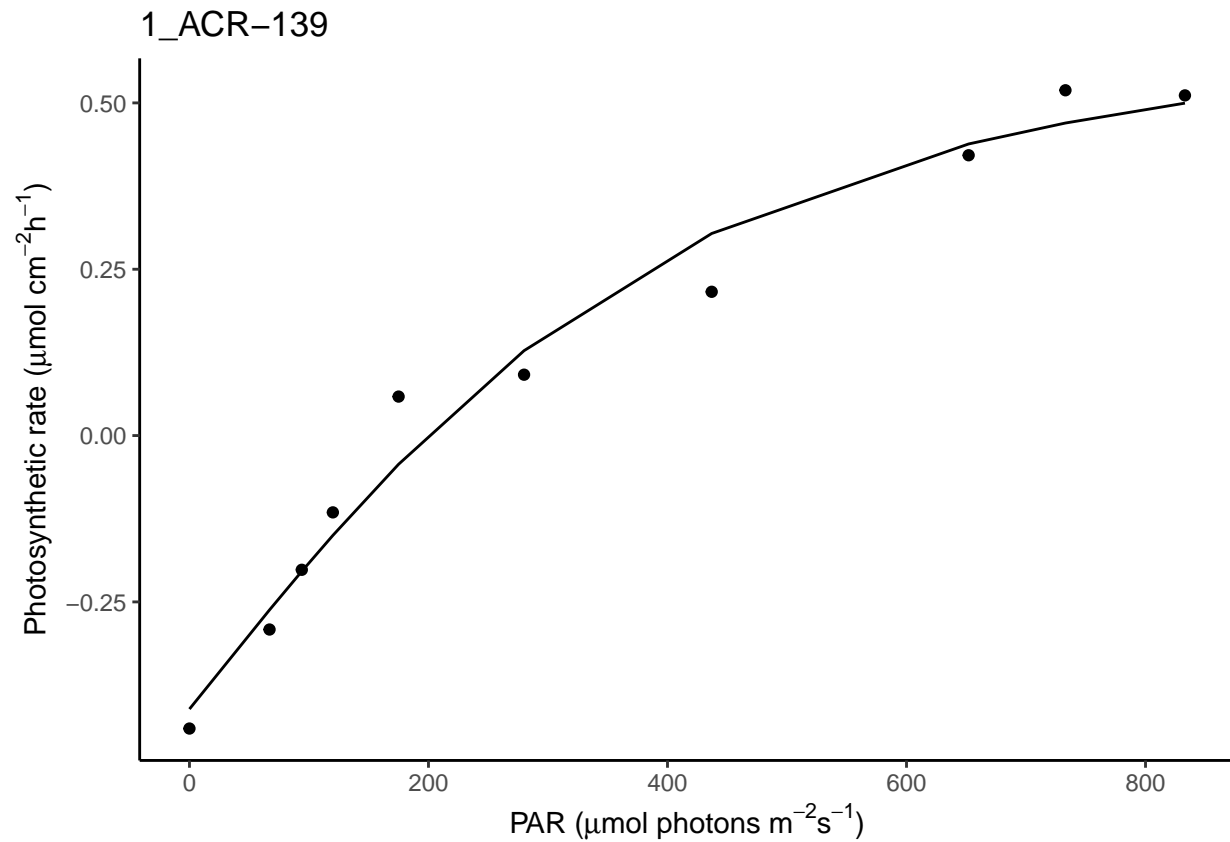


```

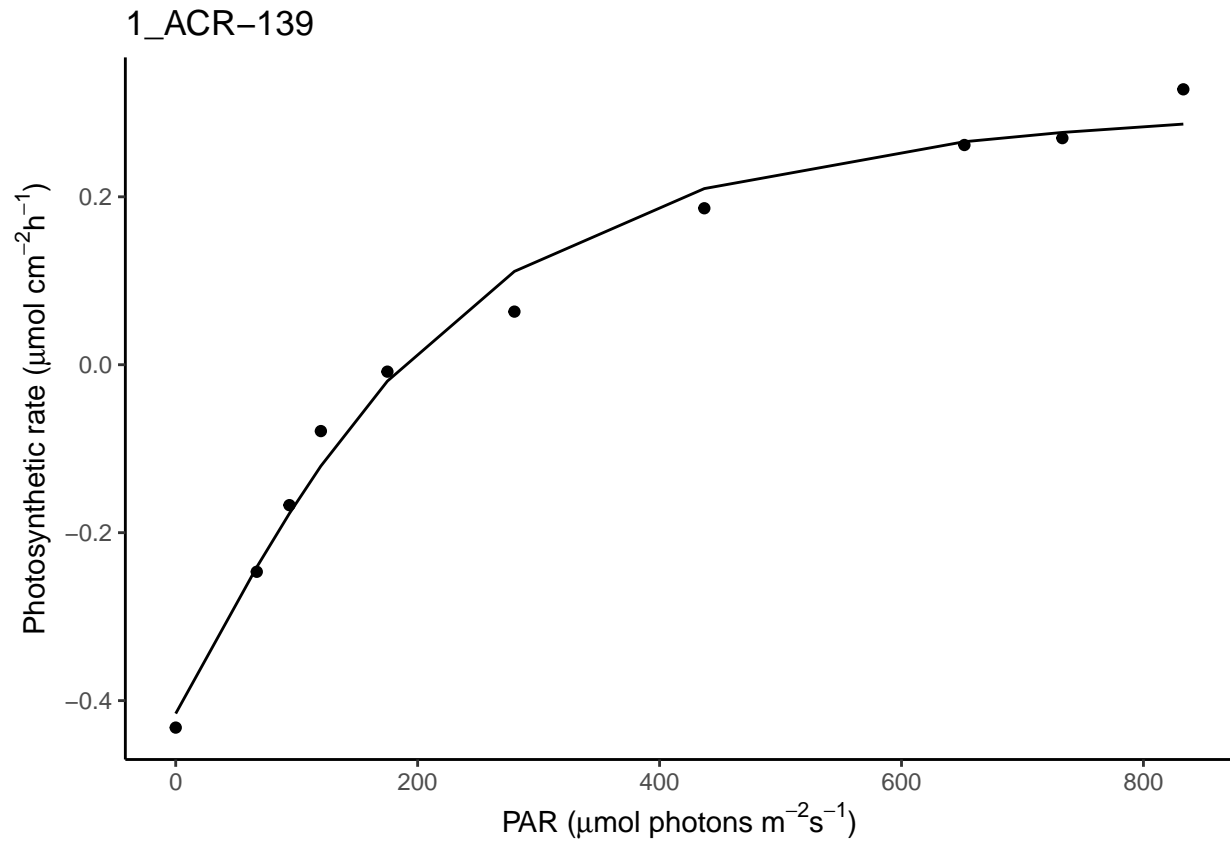
#view individual plots
by(augmented, augmented$colony_id, function(i) {
  ggplot(i) +
    geom_point(aes(PAR, Pc, group=colony_id)) +
    geom_line(aes(y=.fitted, x=PAR)) +
    theme_classic()+
    labs(x = expression(paste('PAR (', mu, "mol photons m"^-2, 's'^-1,")')),
         y = expression(paste('Photosynthetic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

```

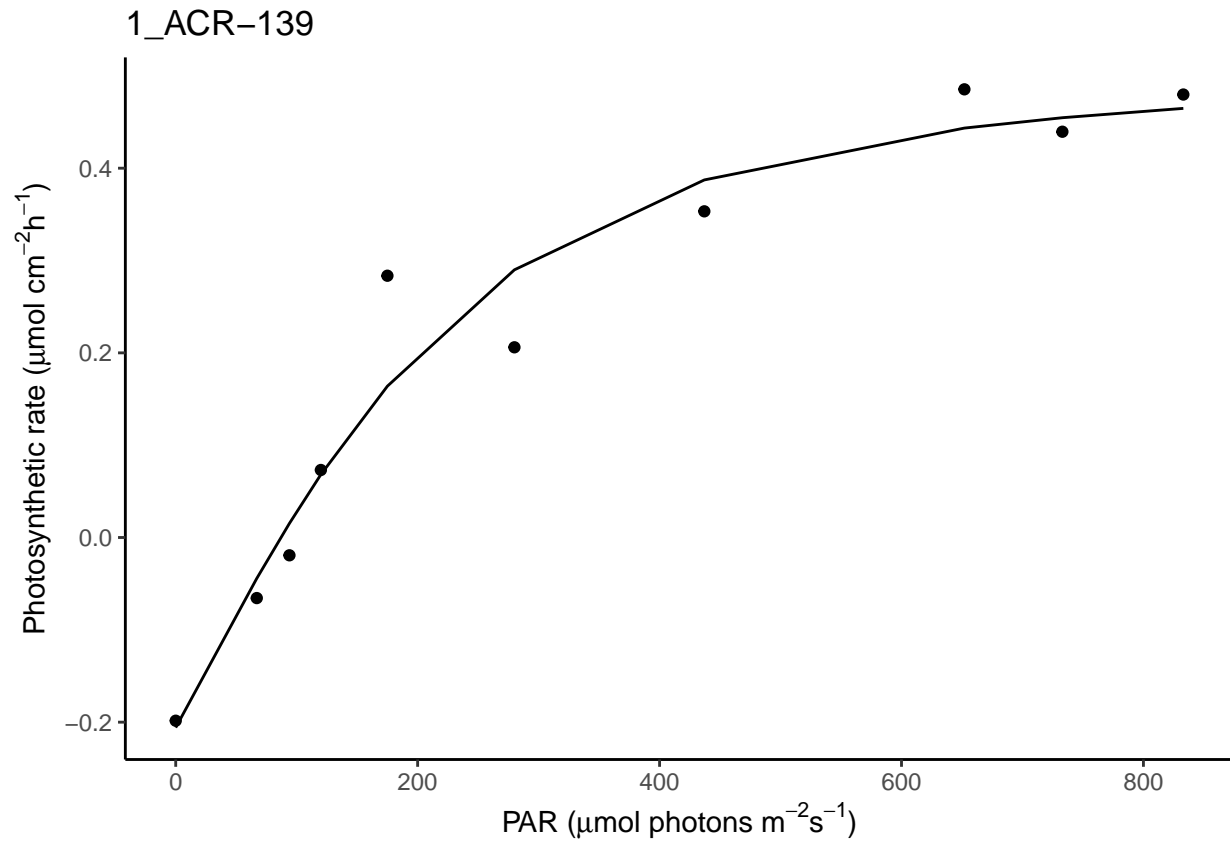
```
## augmented$colony_id: ACR-139
```



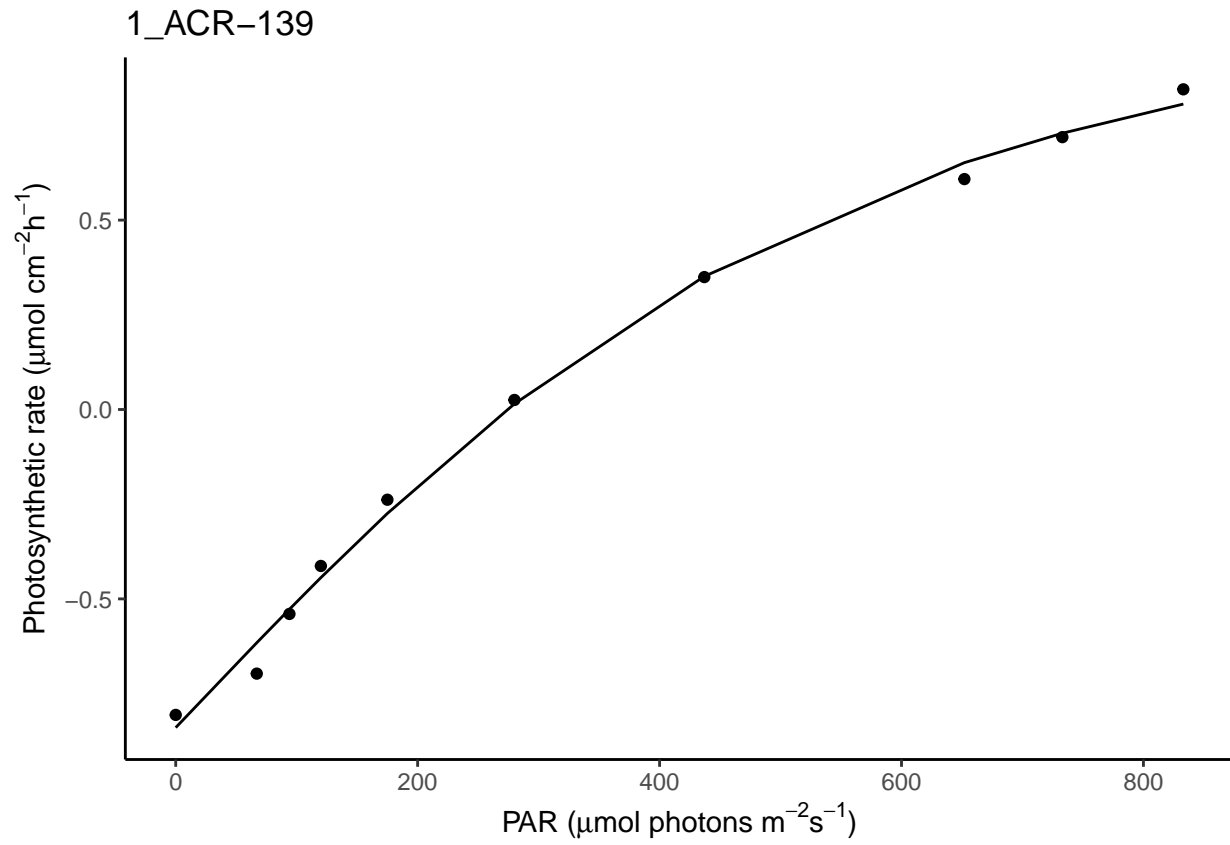
```
## -----
## augmented$colony_id: ACR-140
```



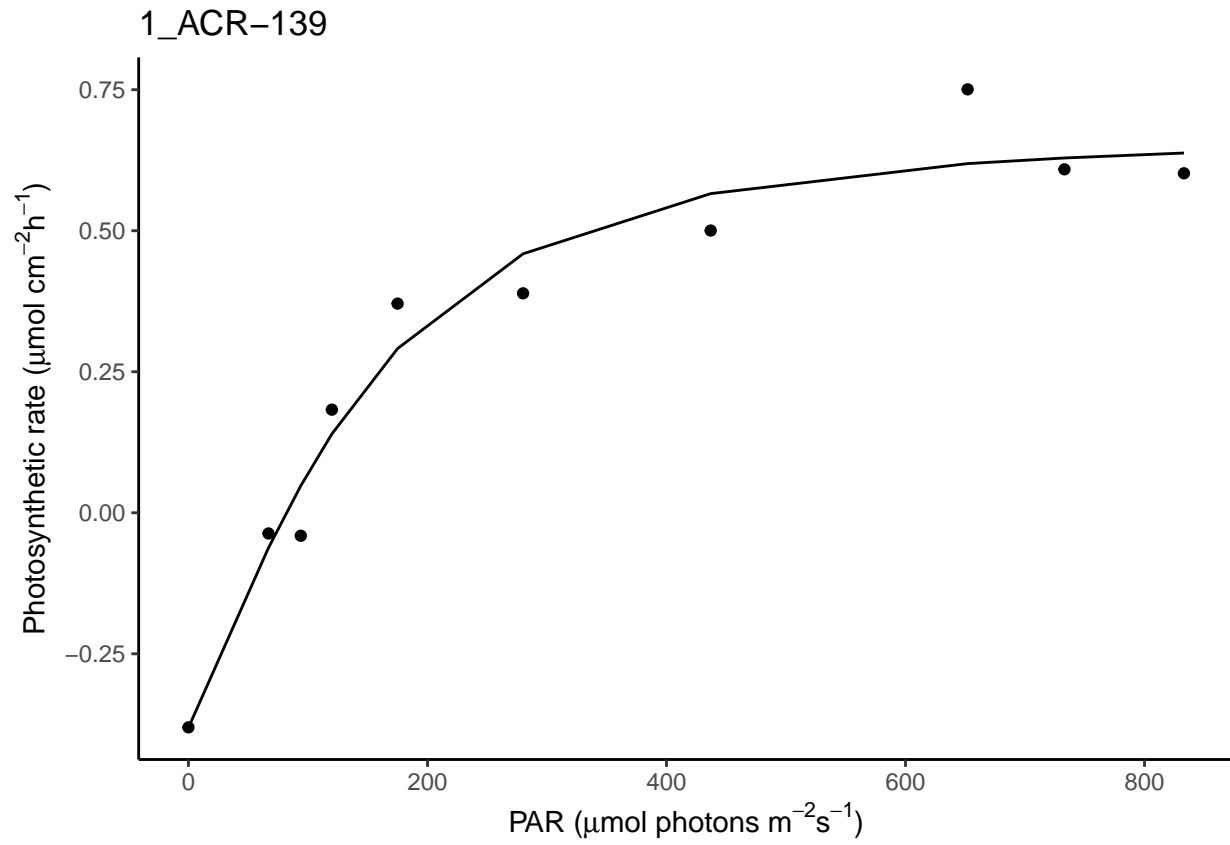
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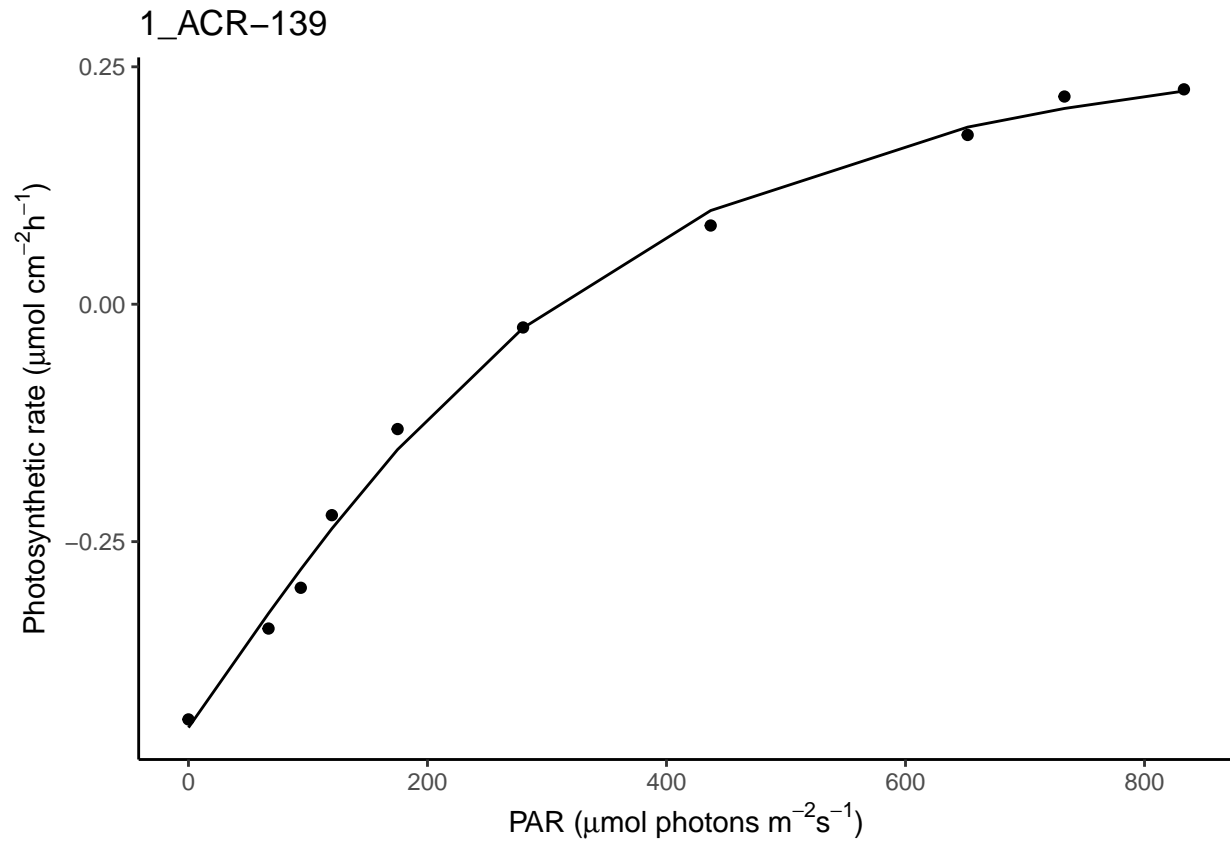
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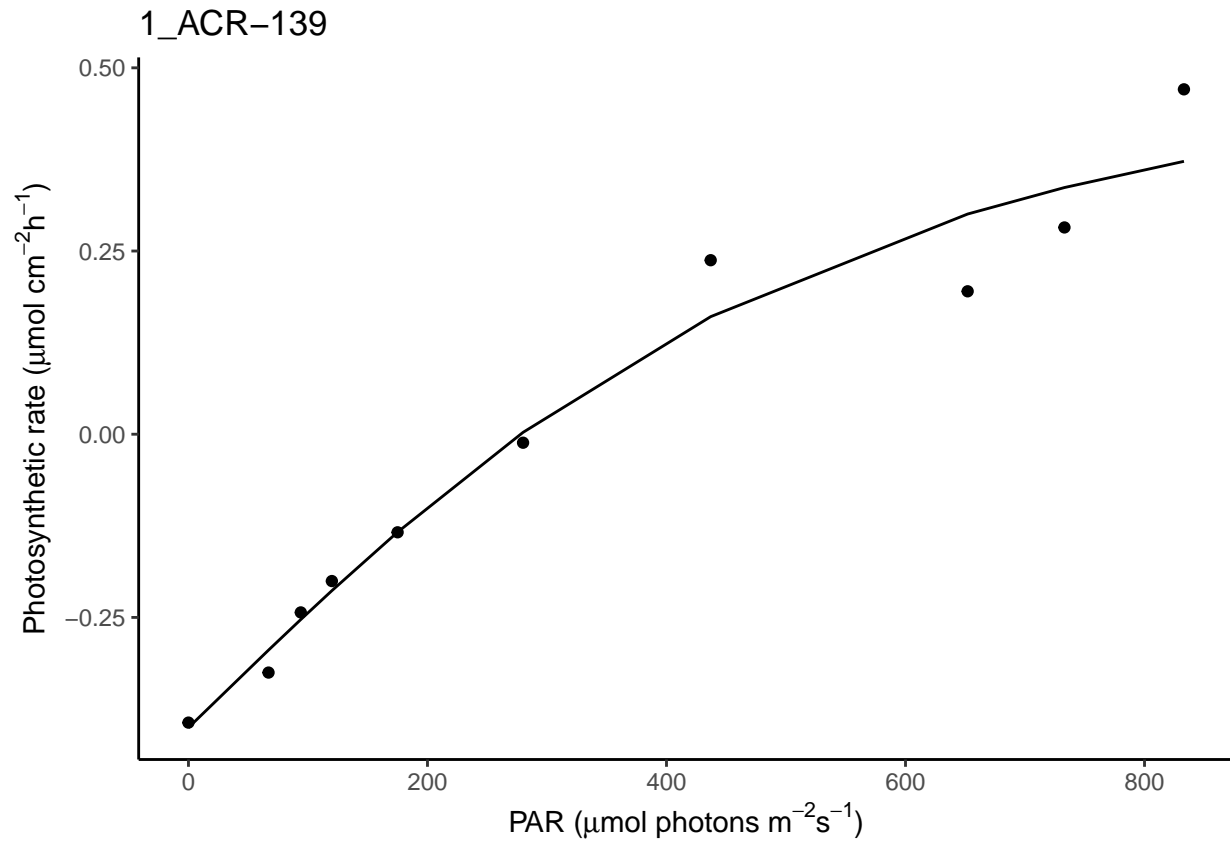
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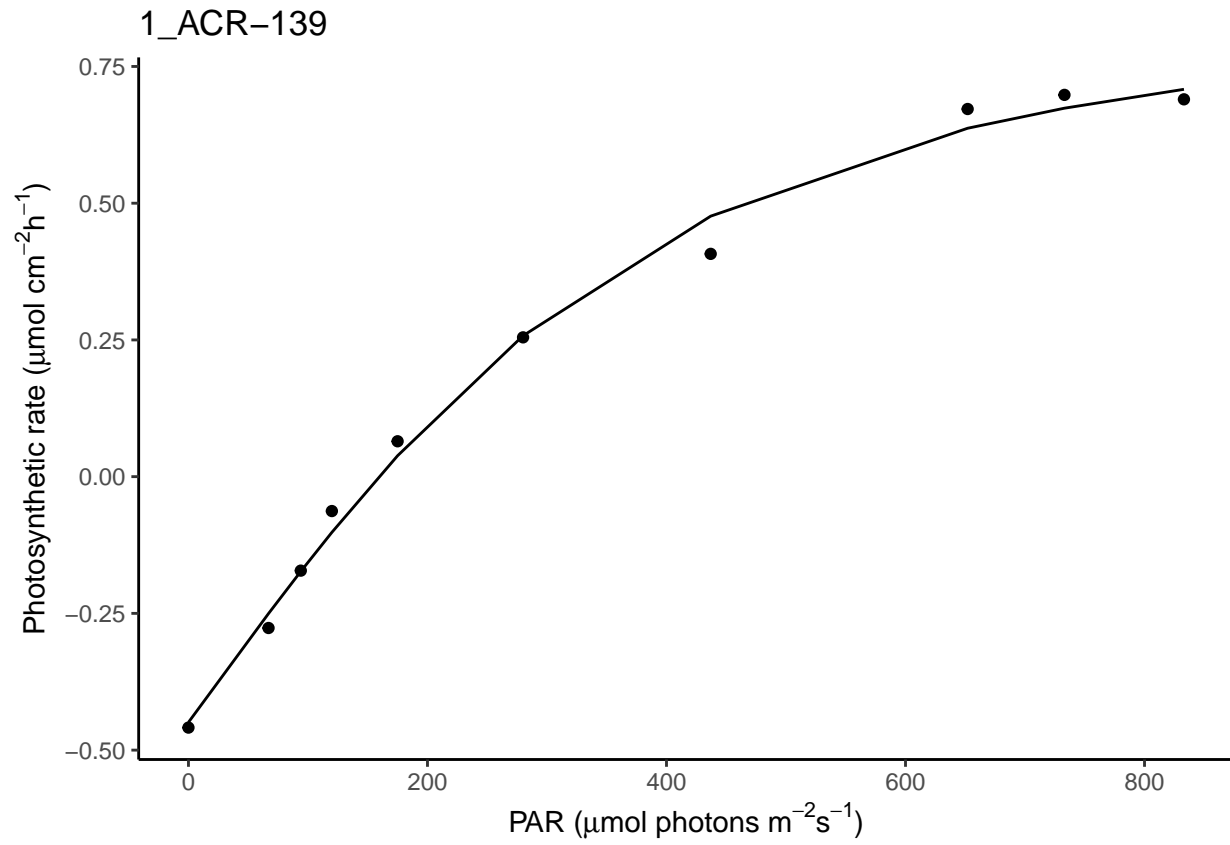
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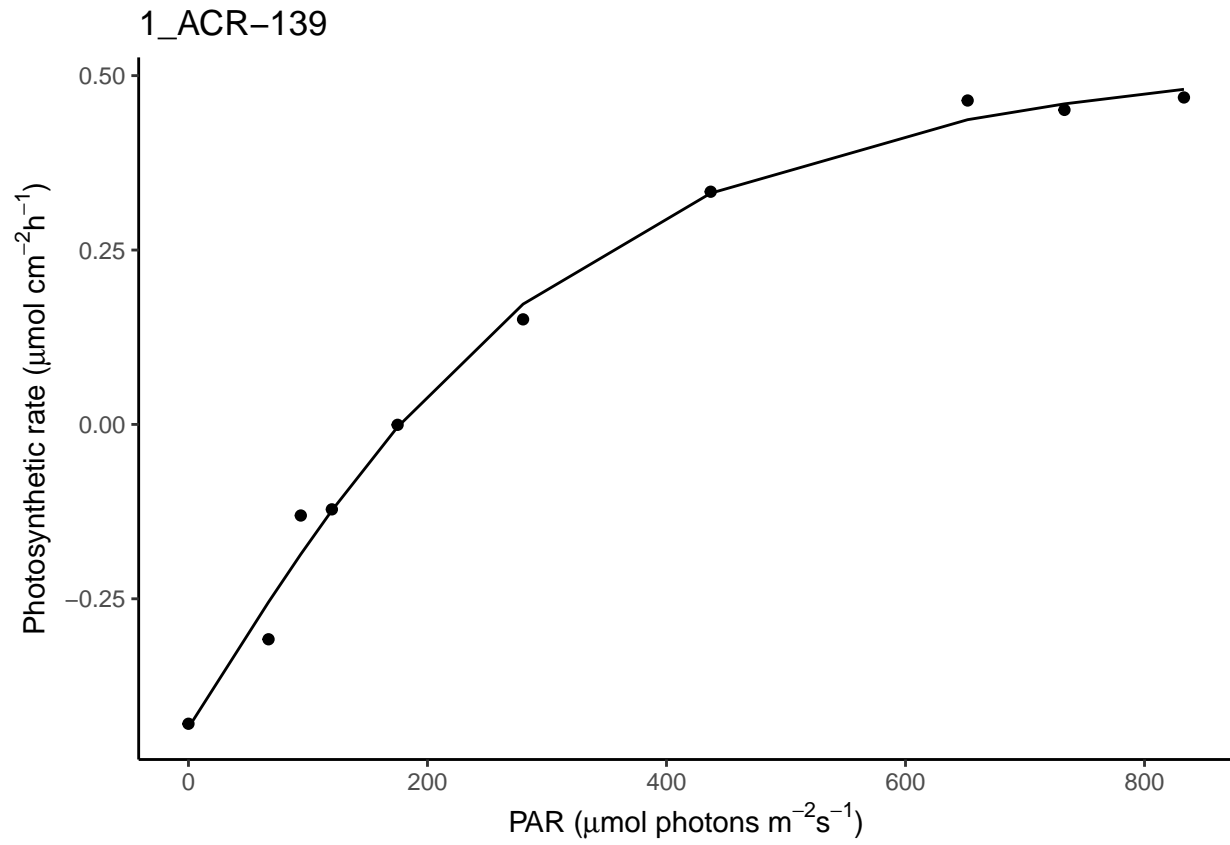
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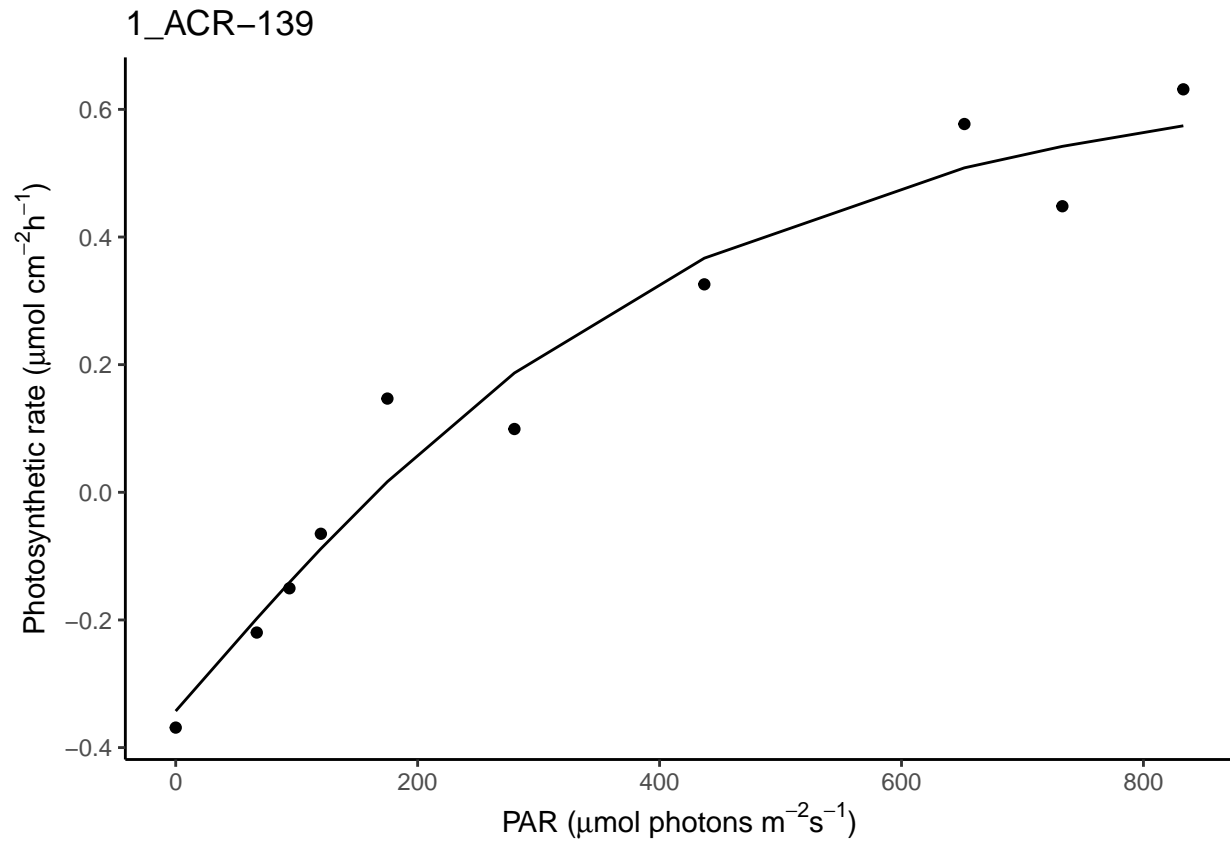
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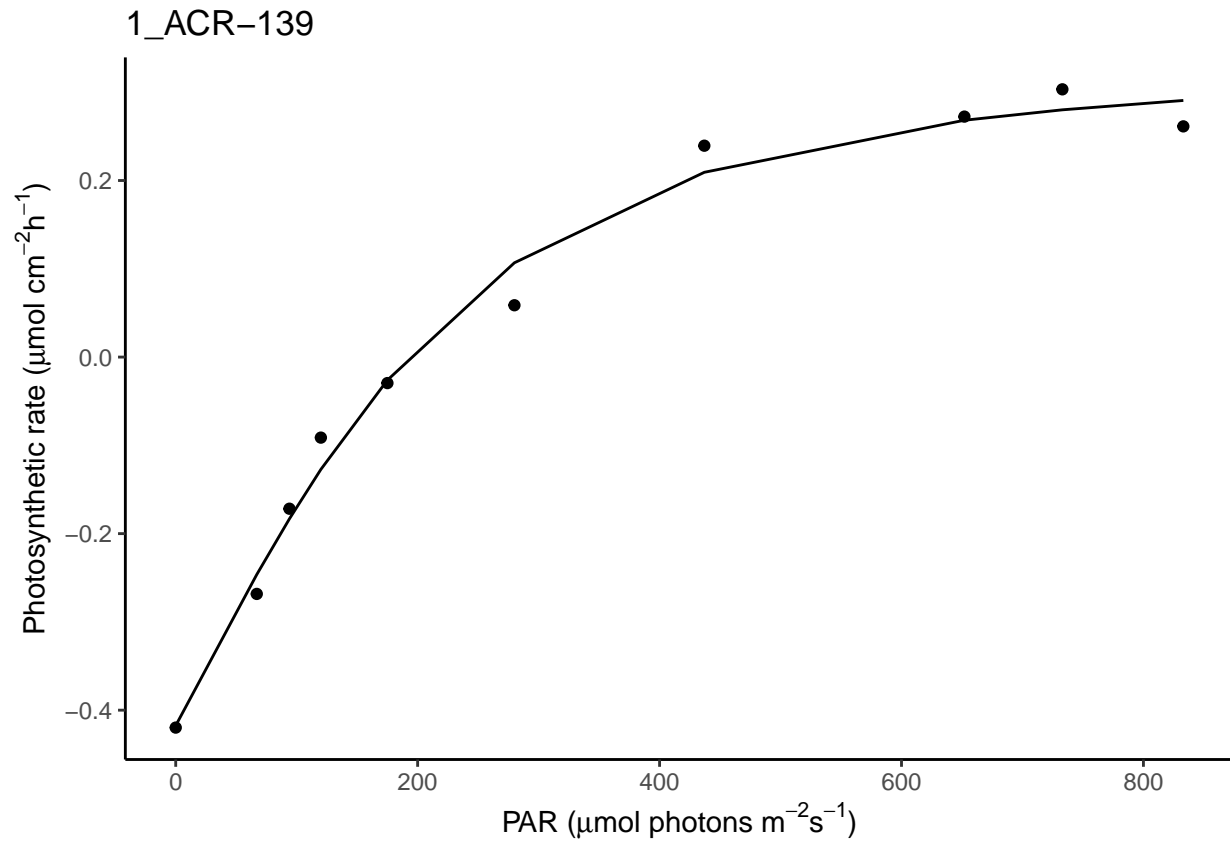
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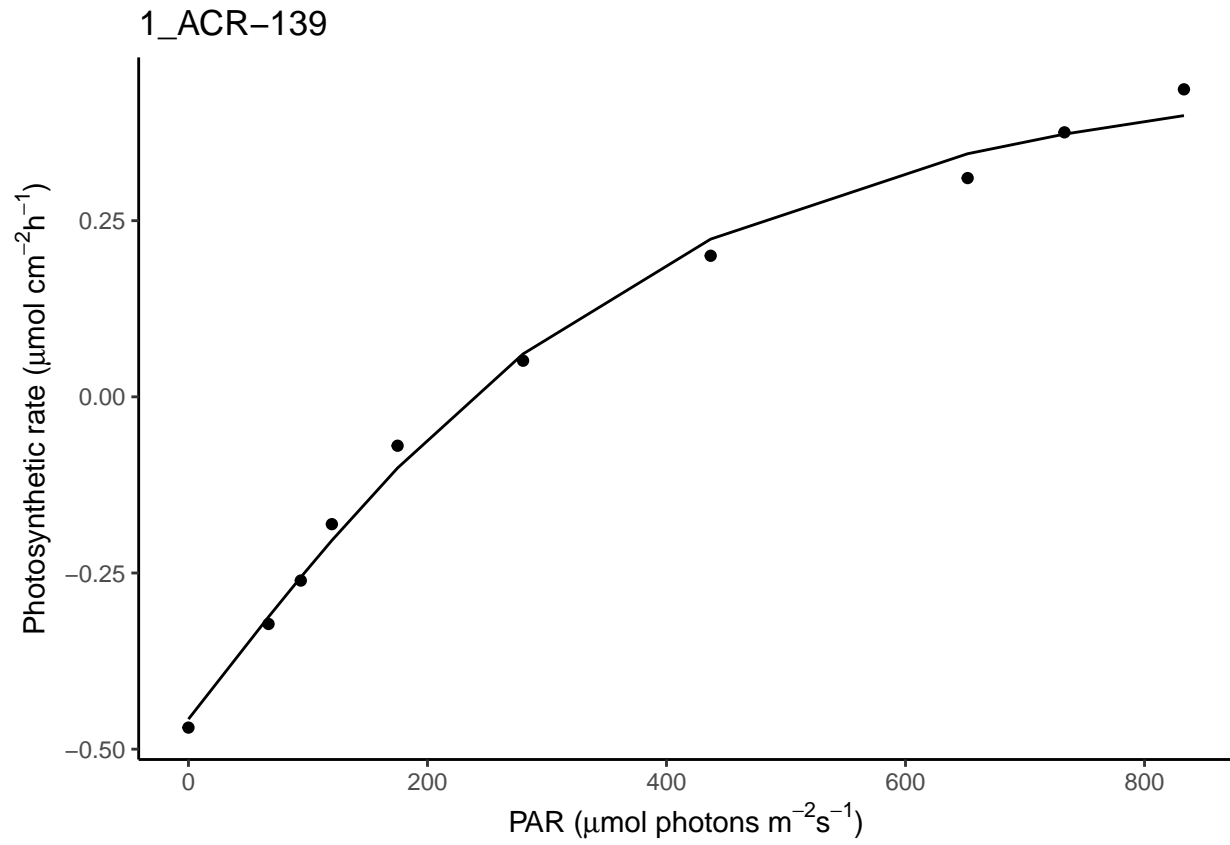
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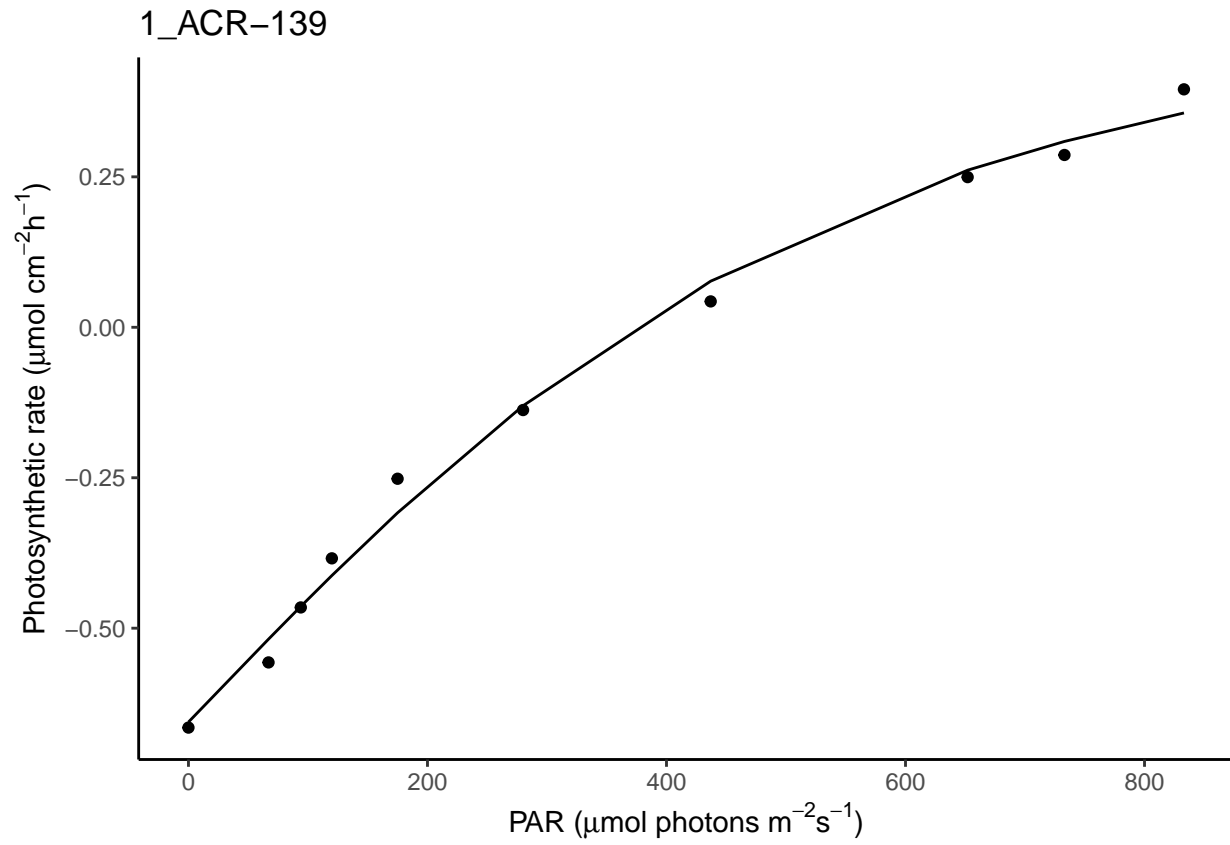
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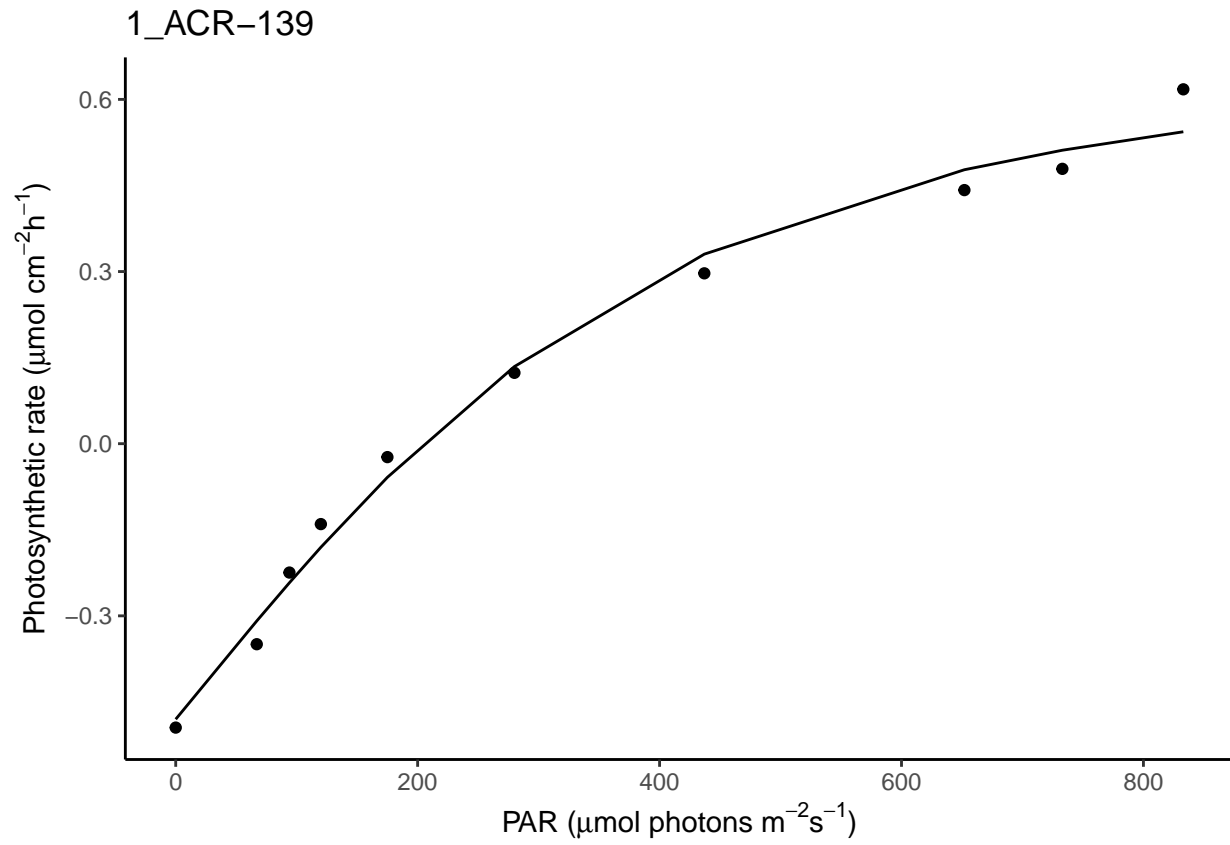
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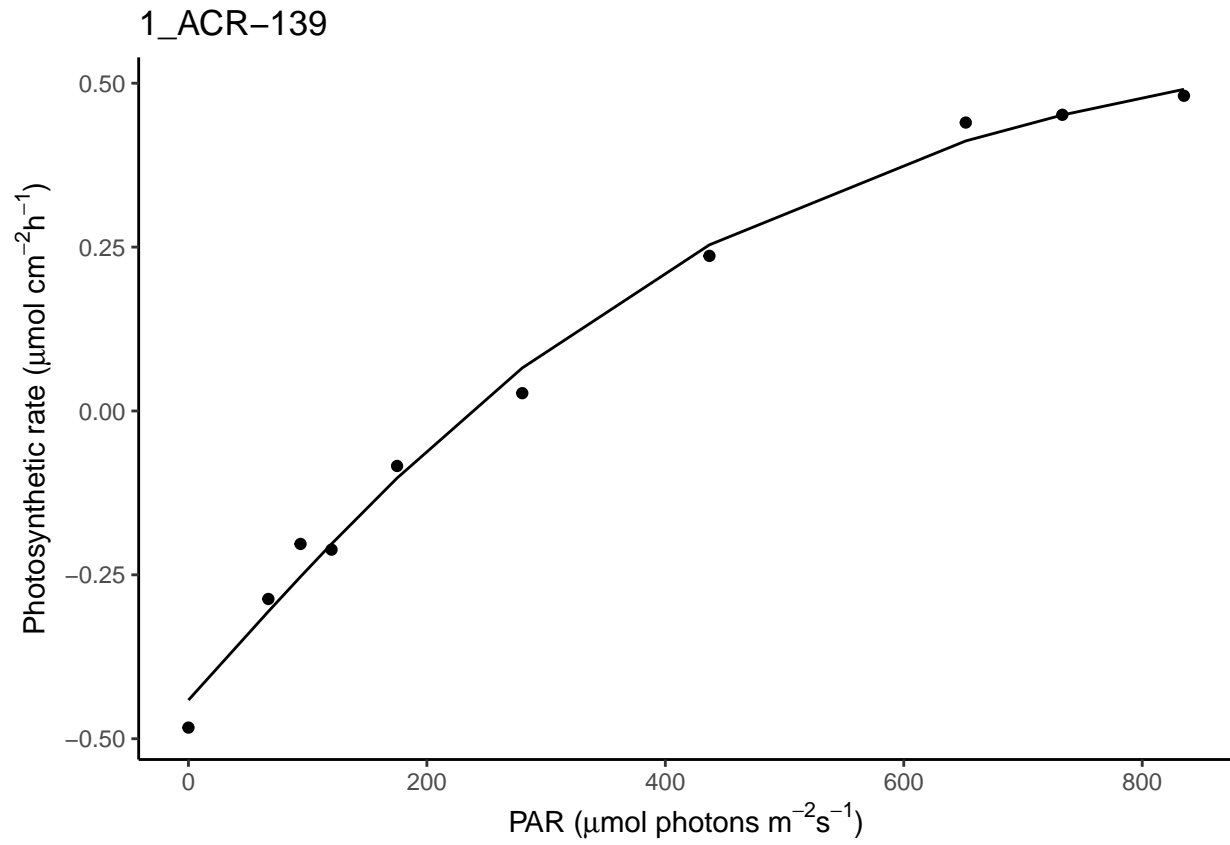
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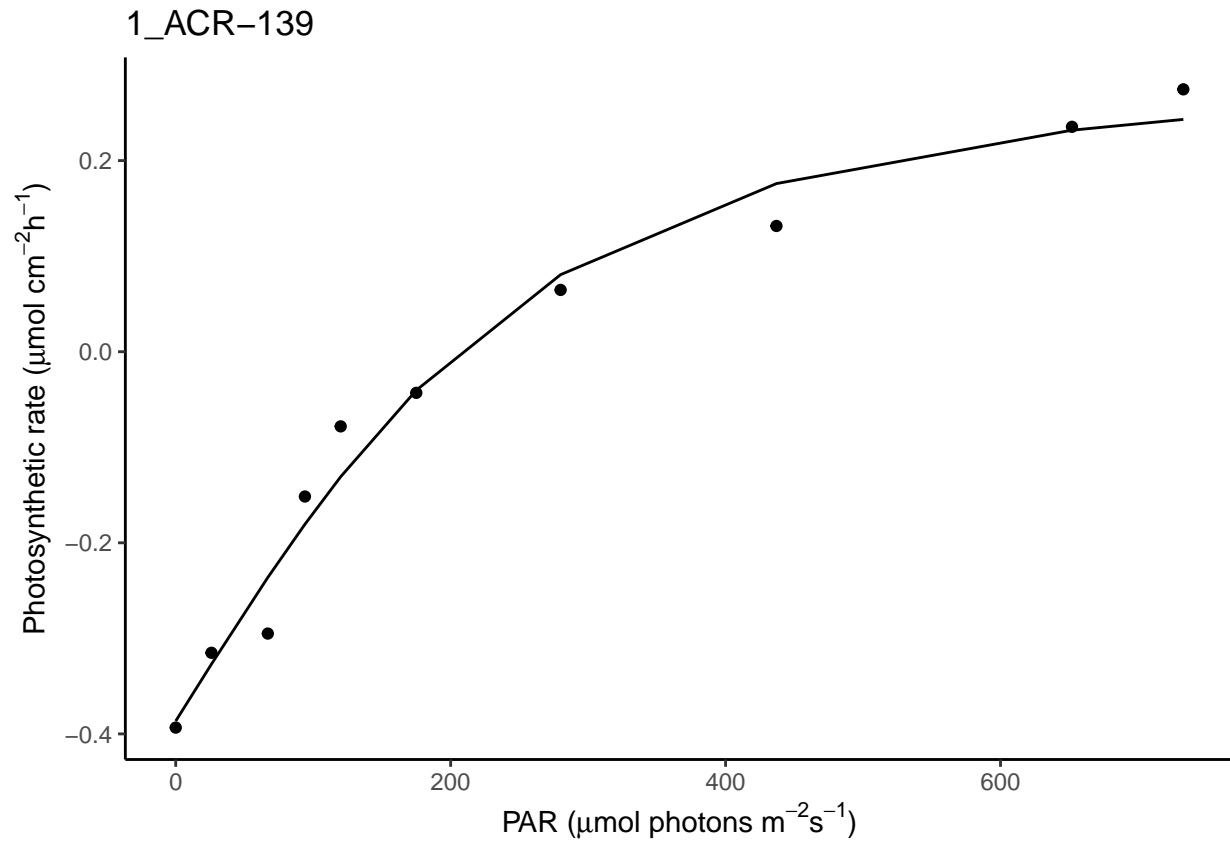
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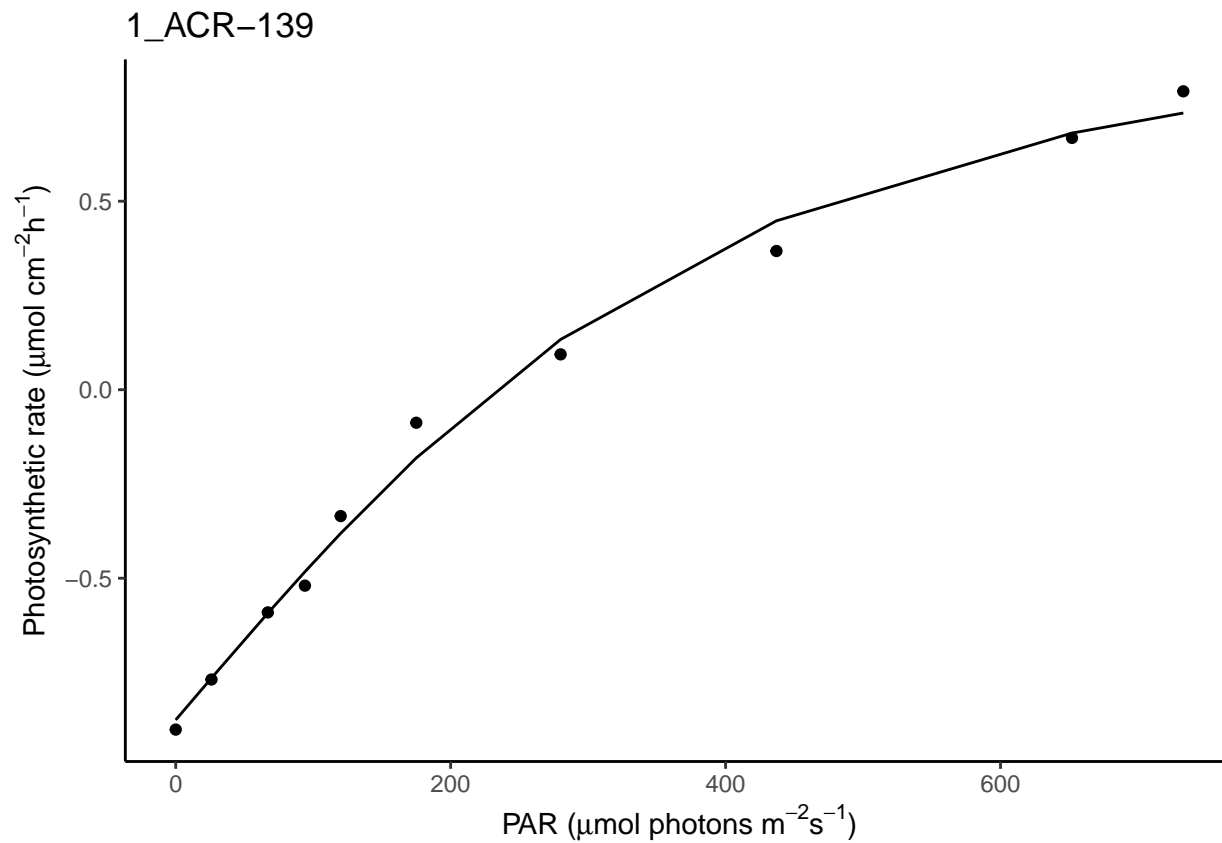
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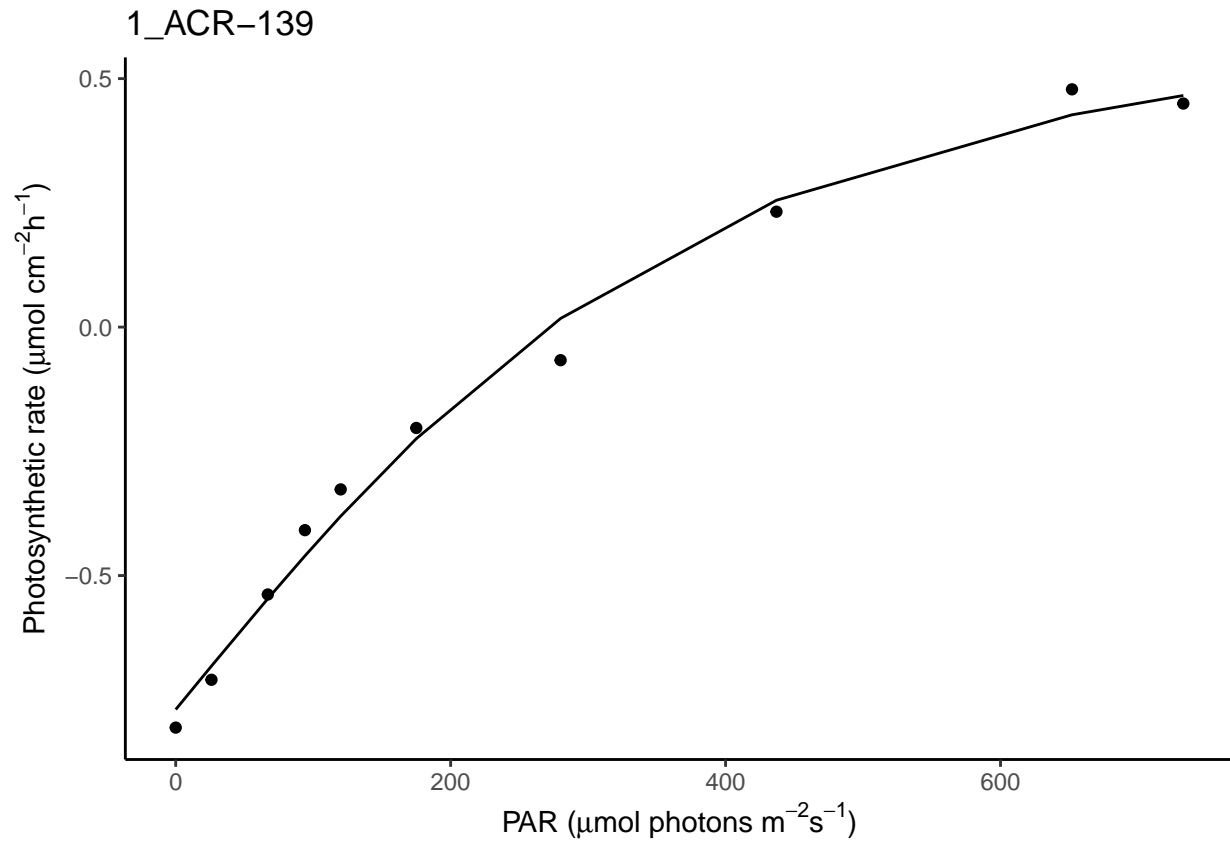
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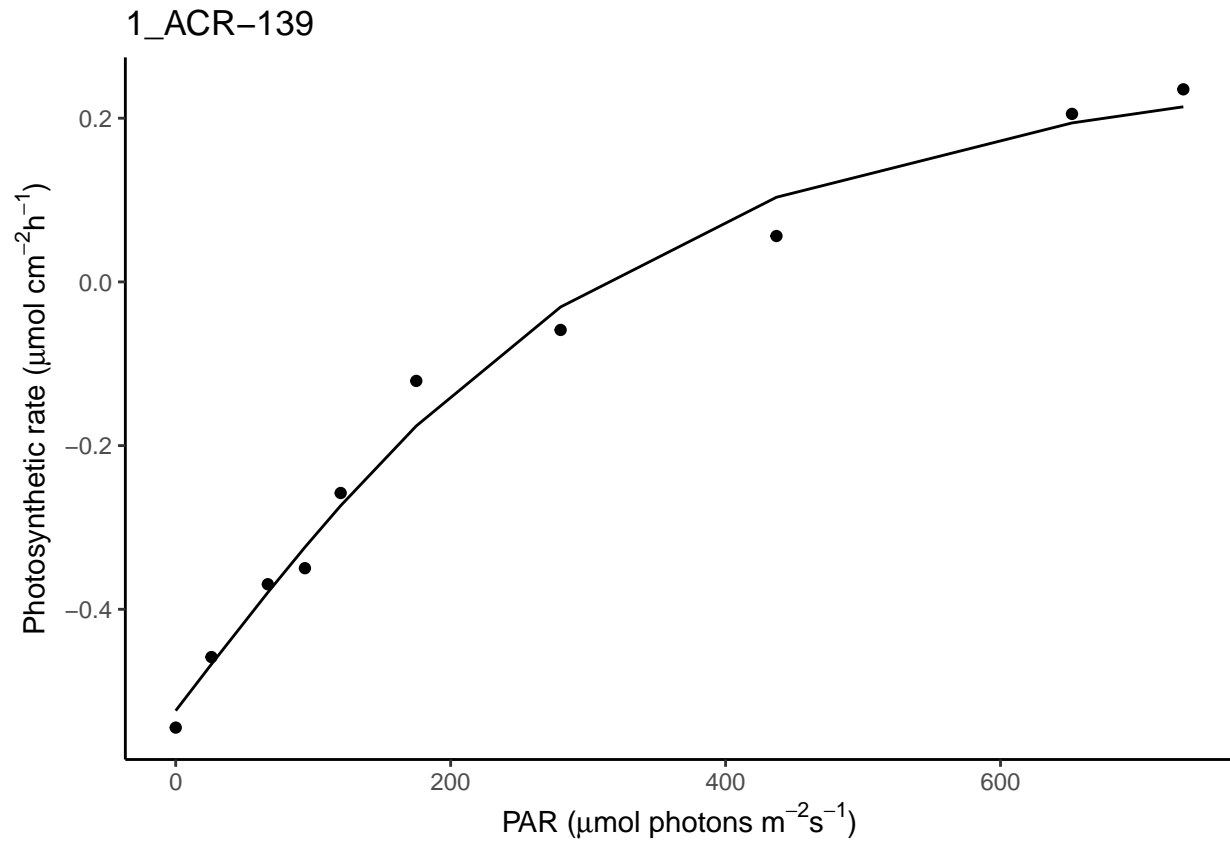
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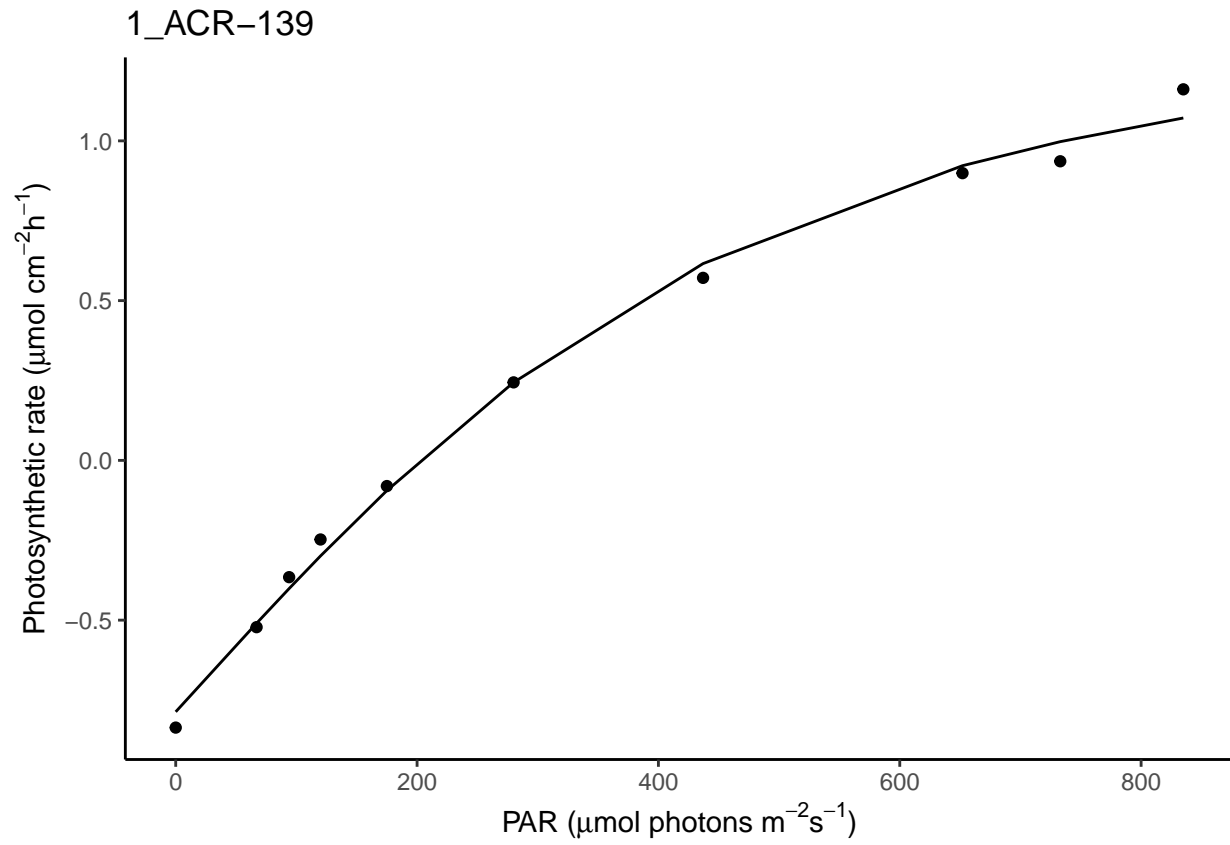
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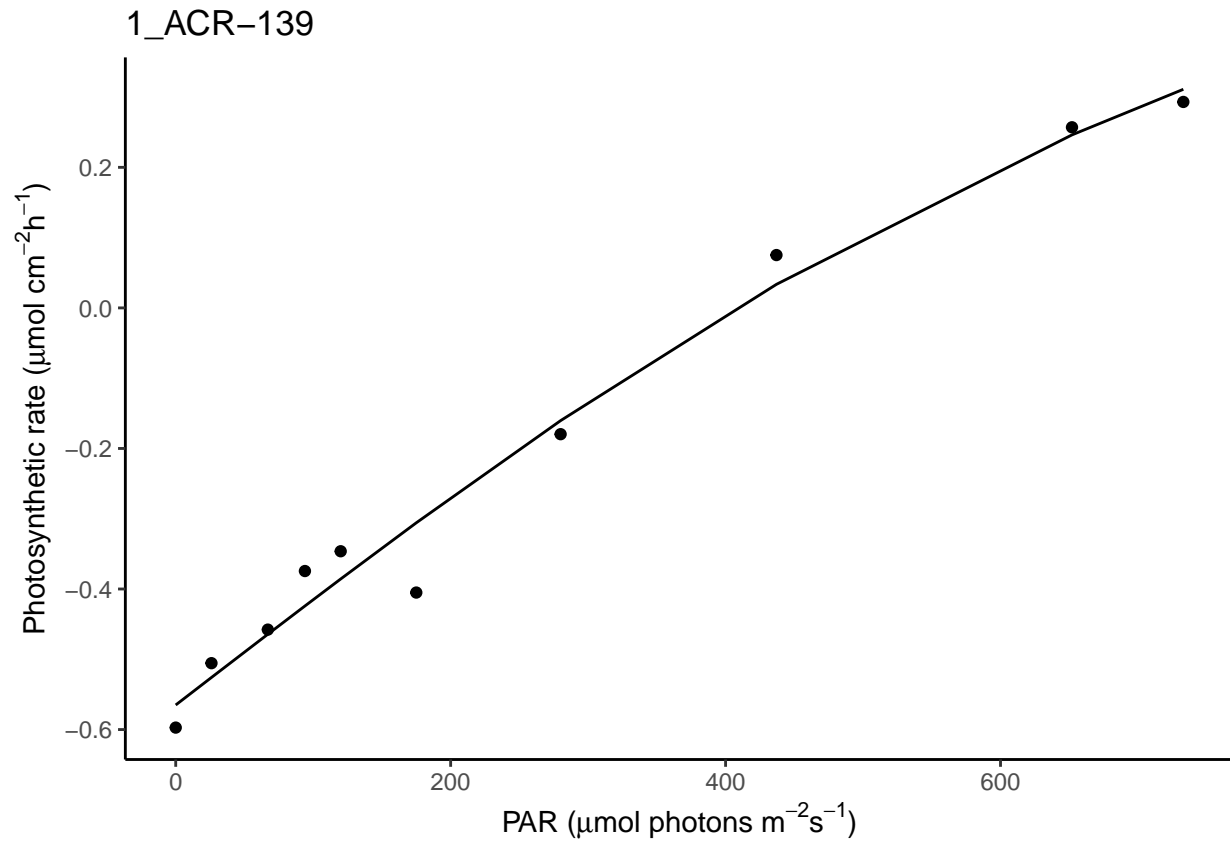
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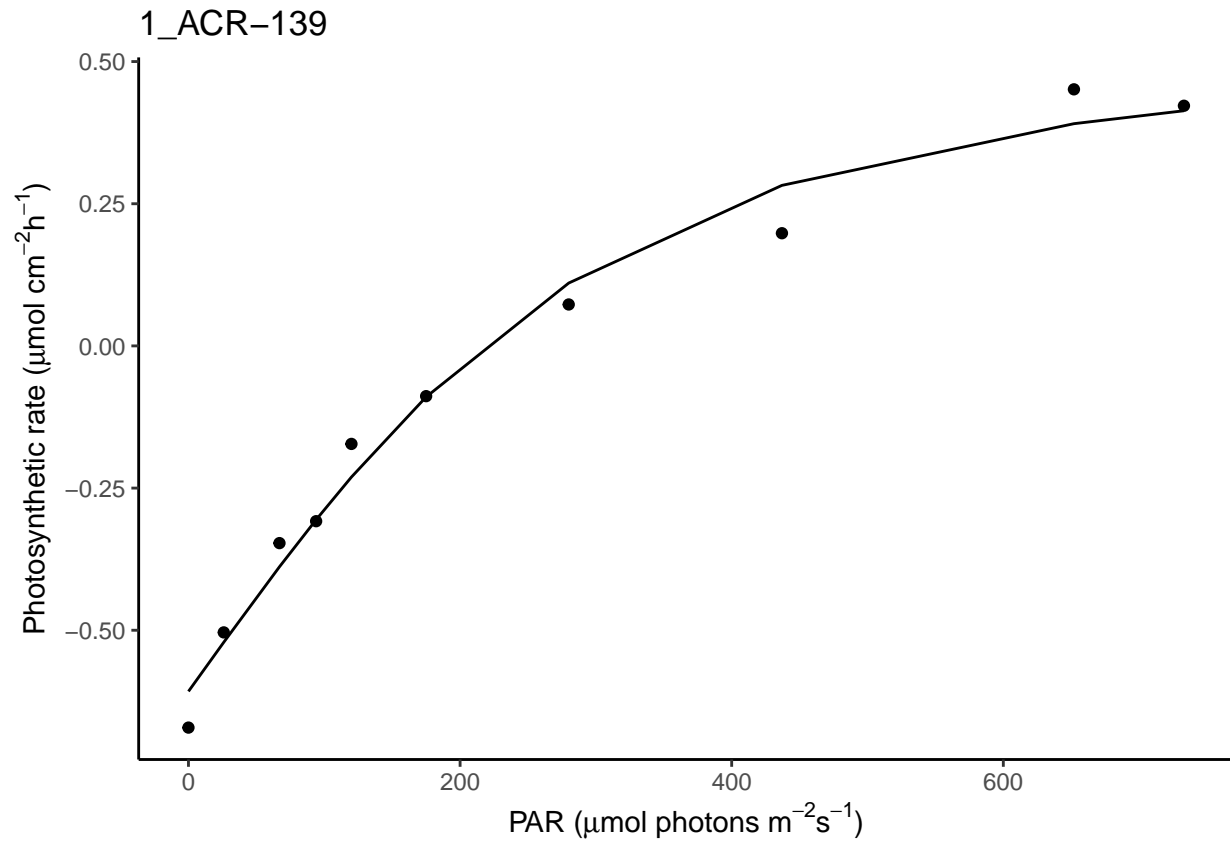
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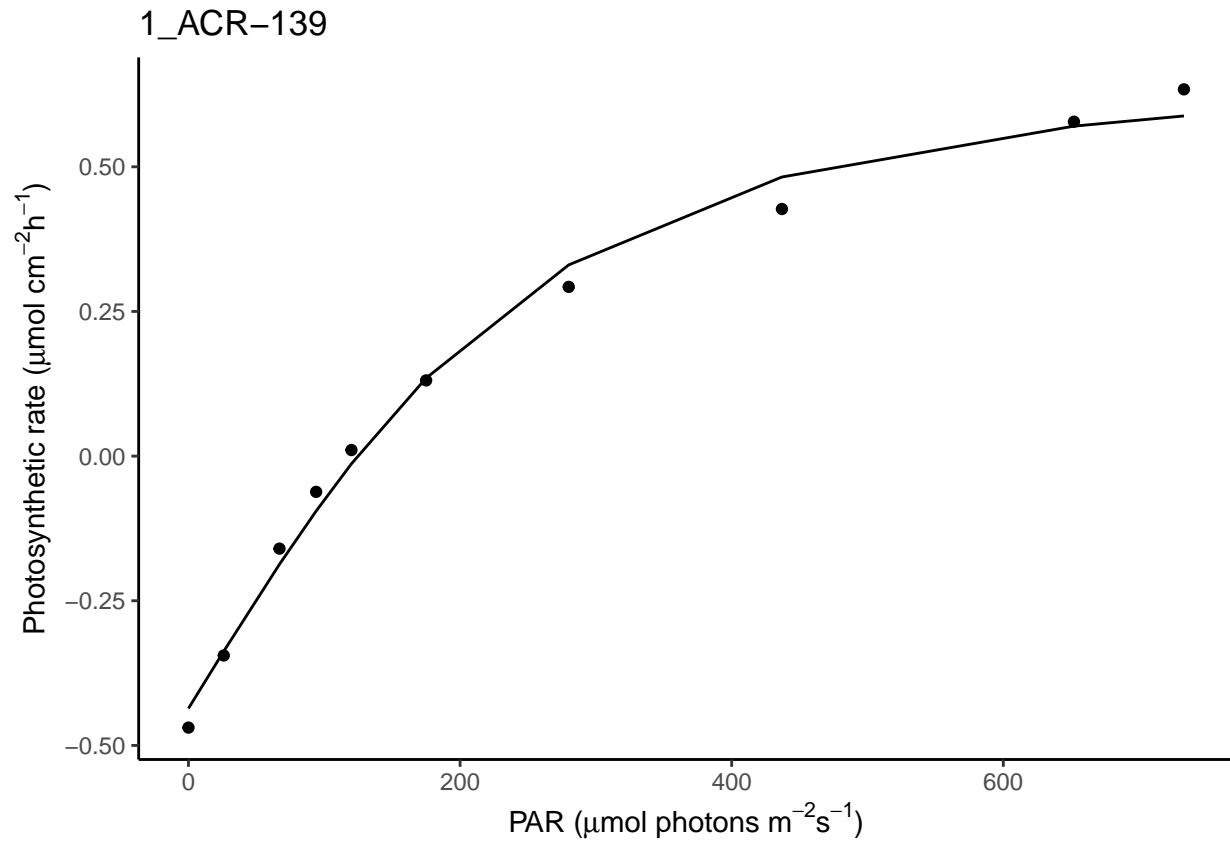
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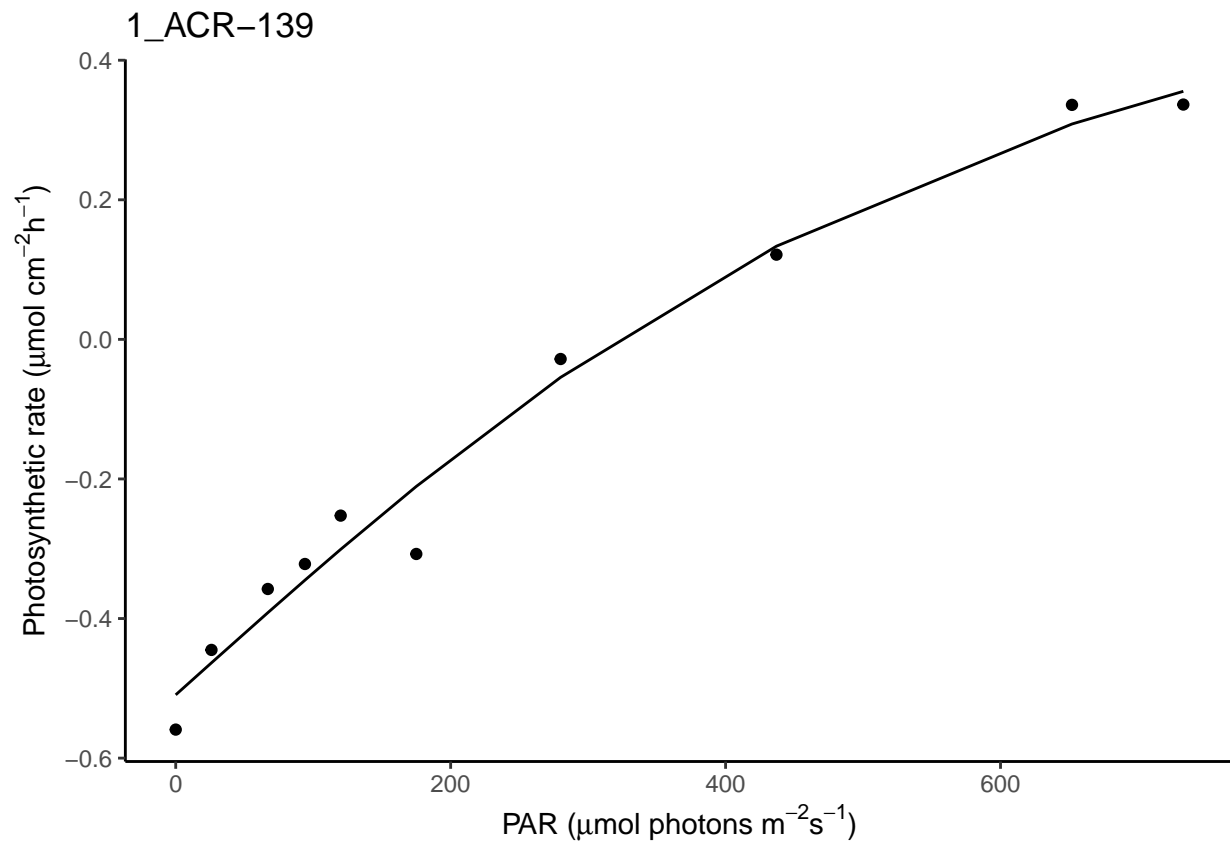
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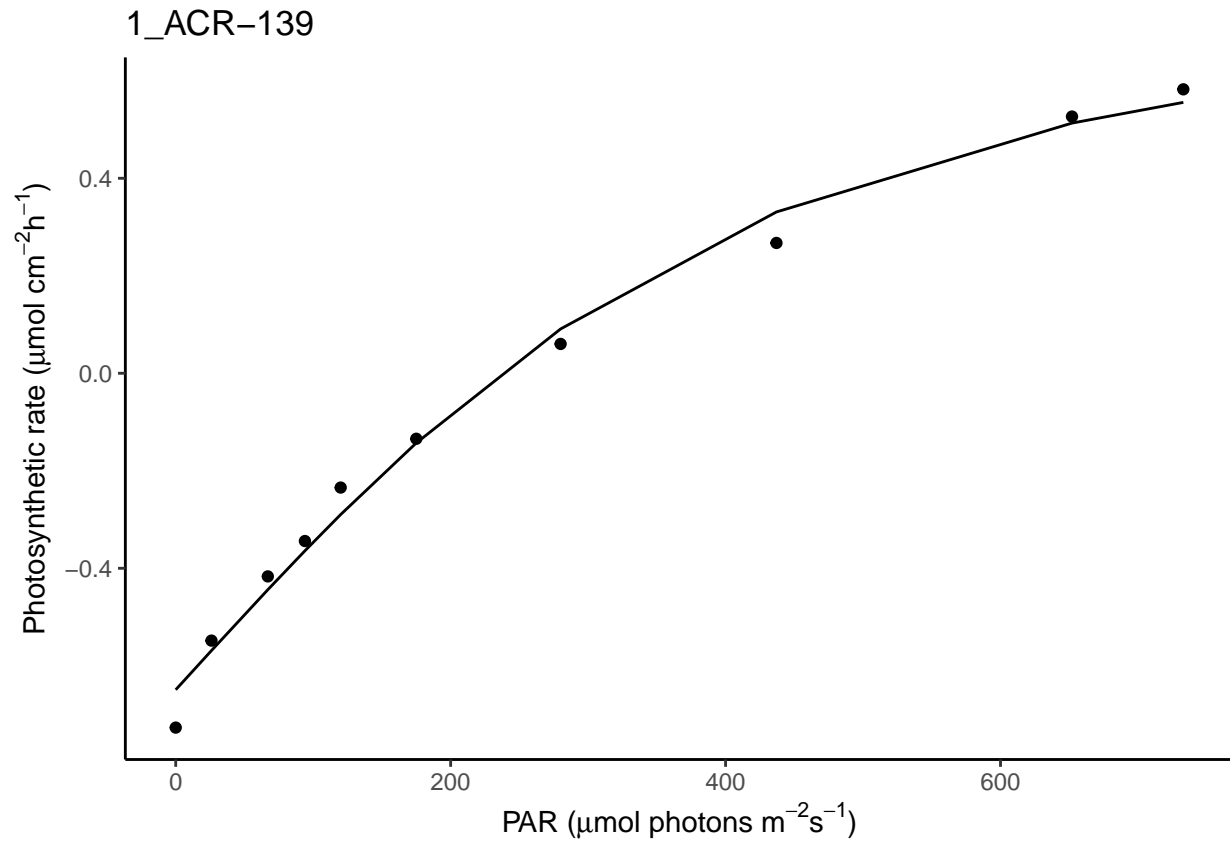
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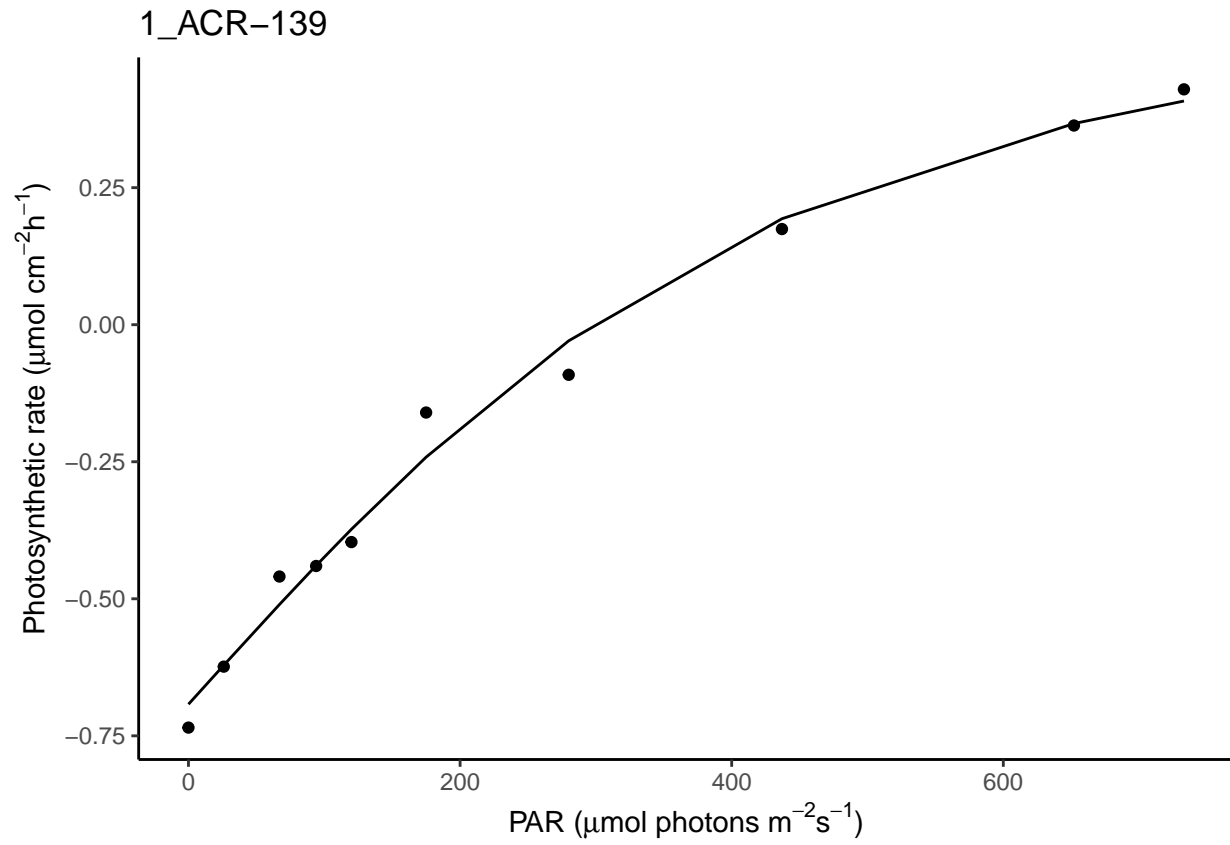
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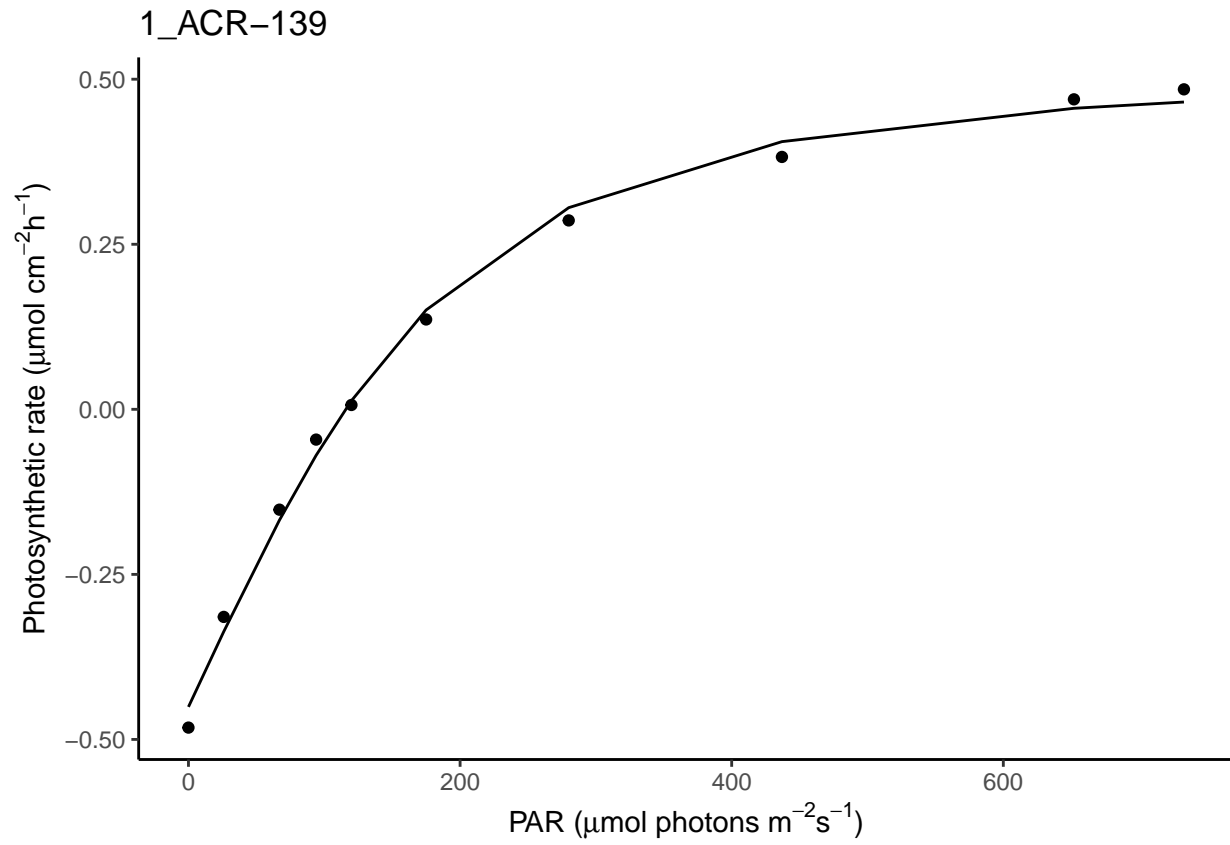
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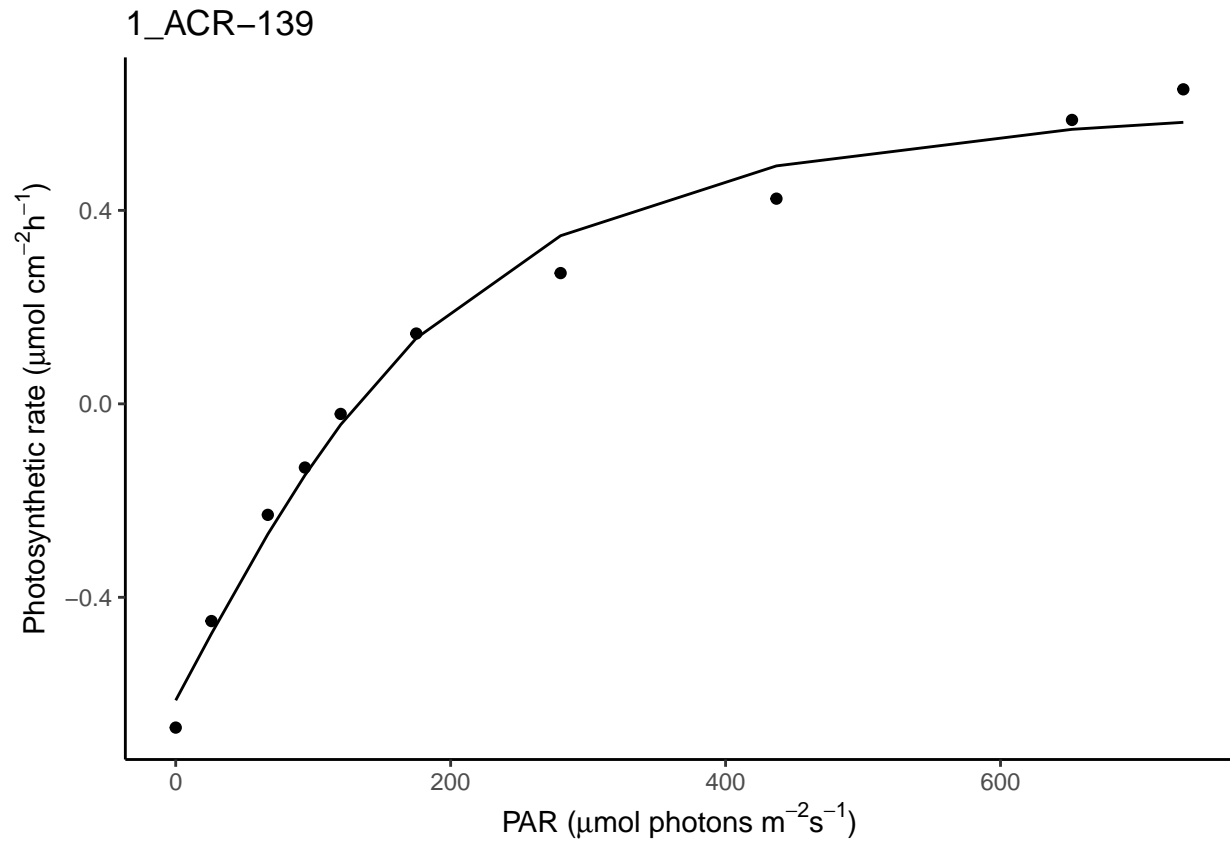
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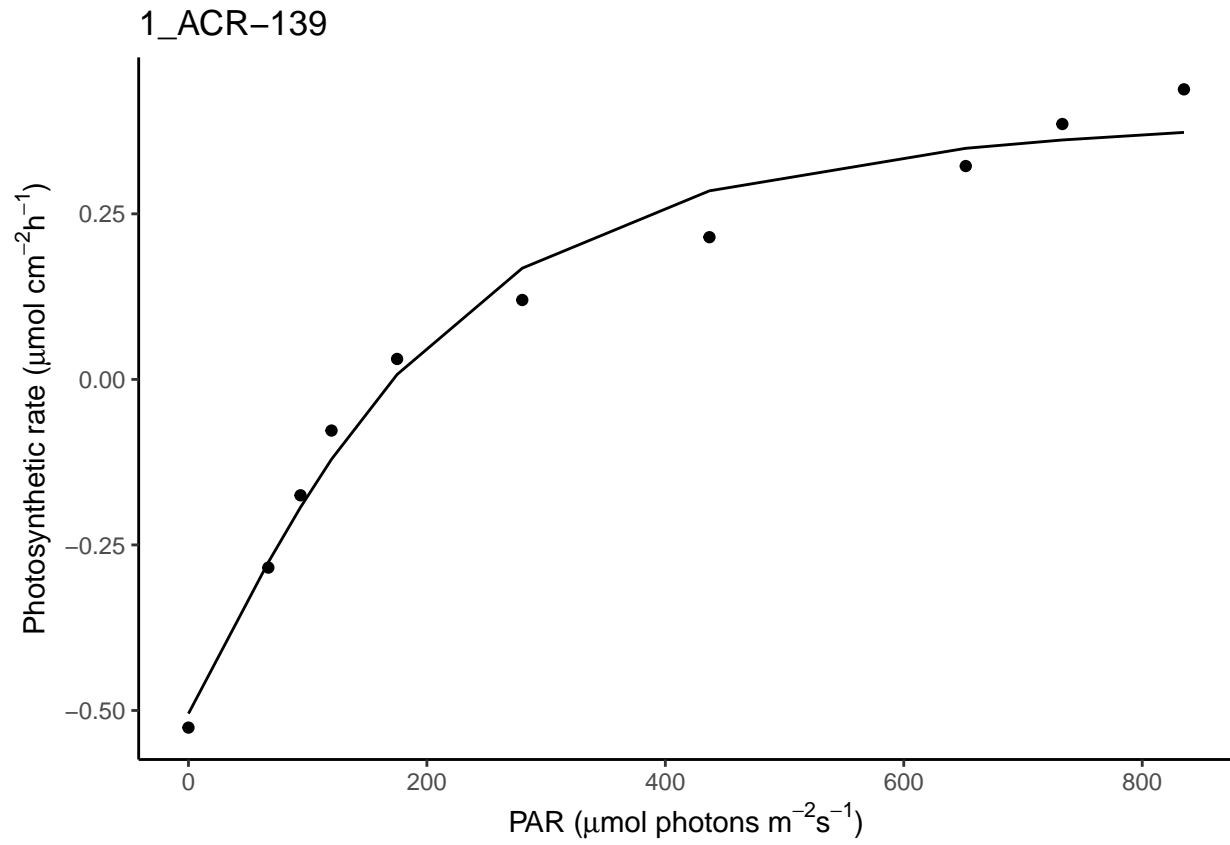
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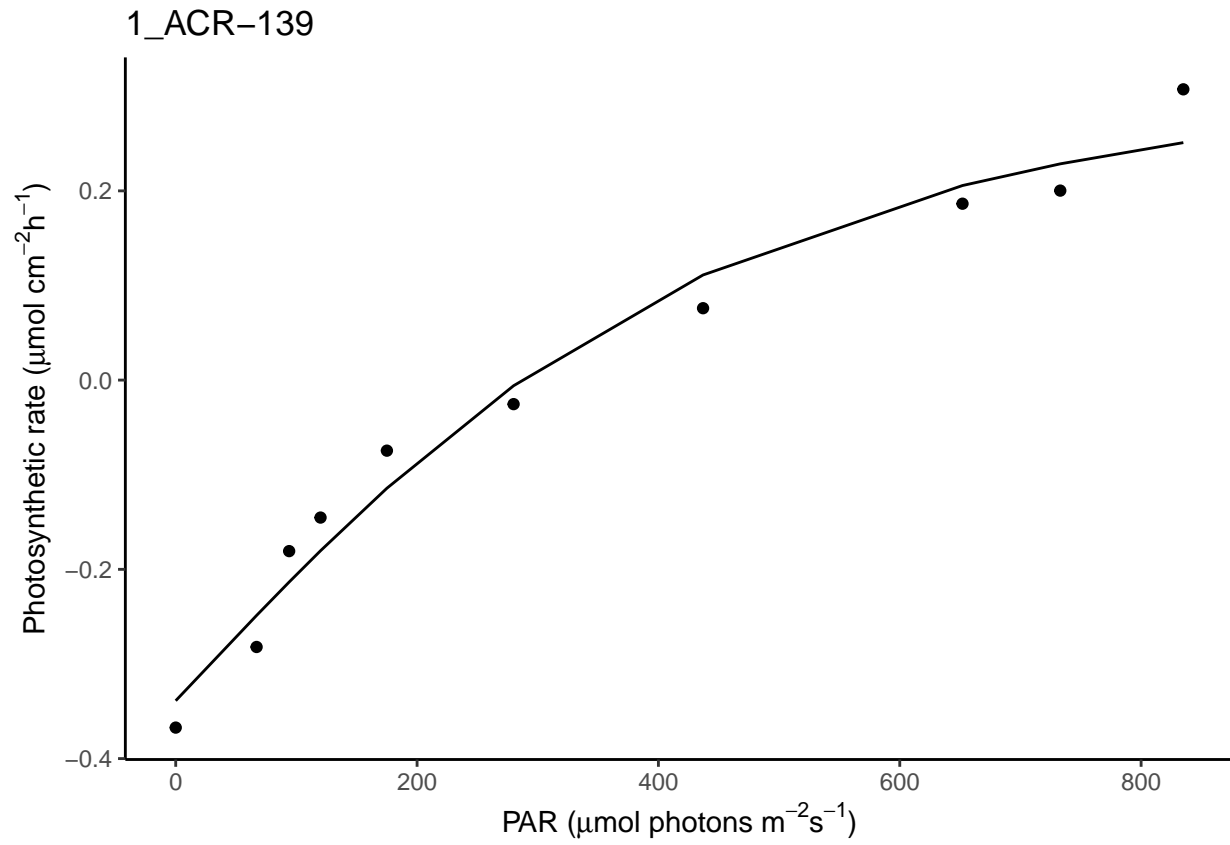
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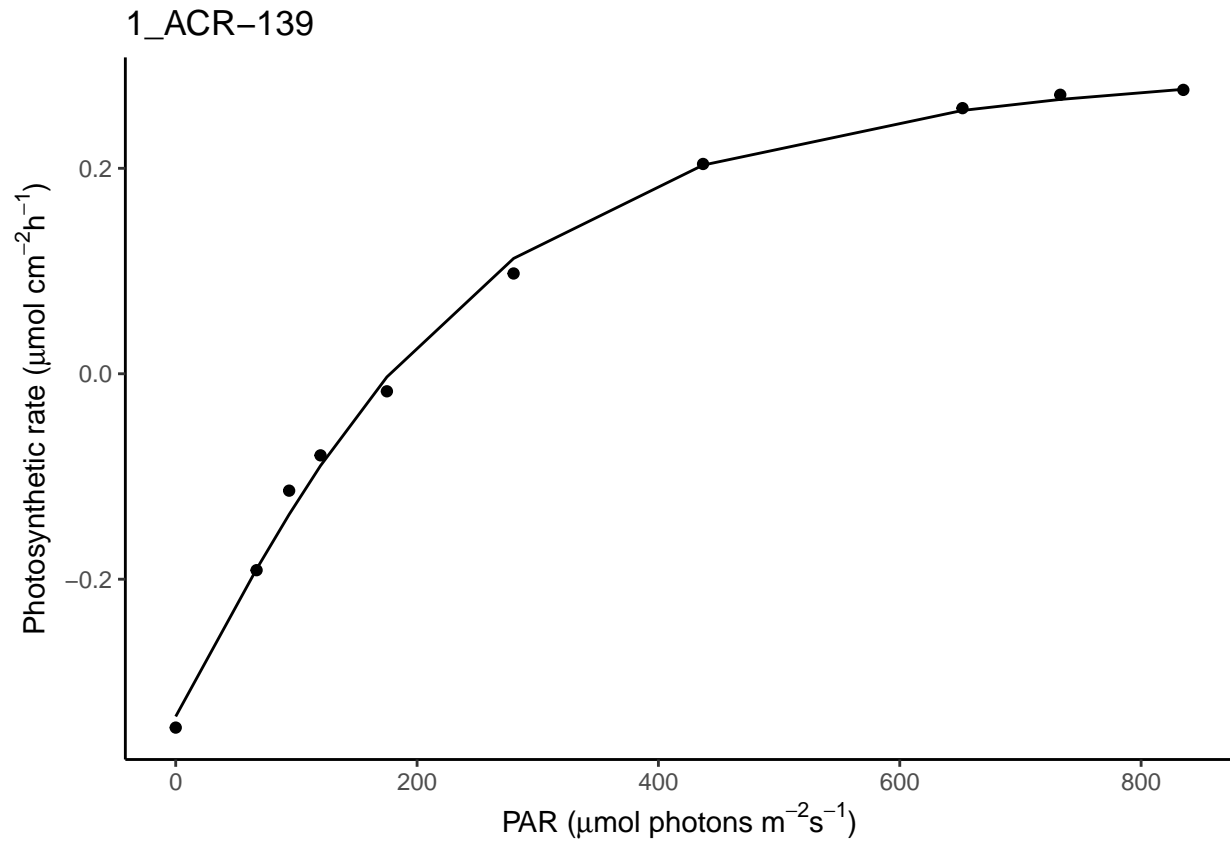
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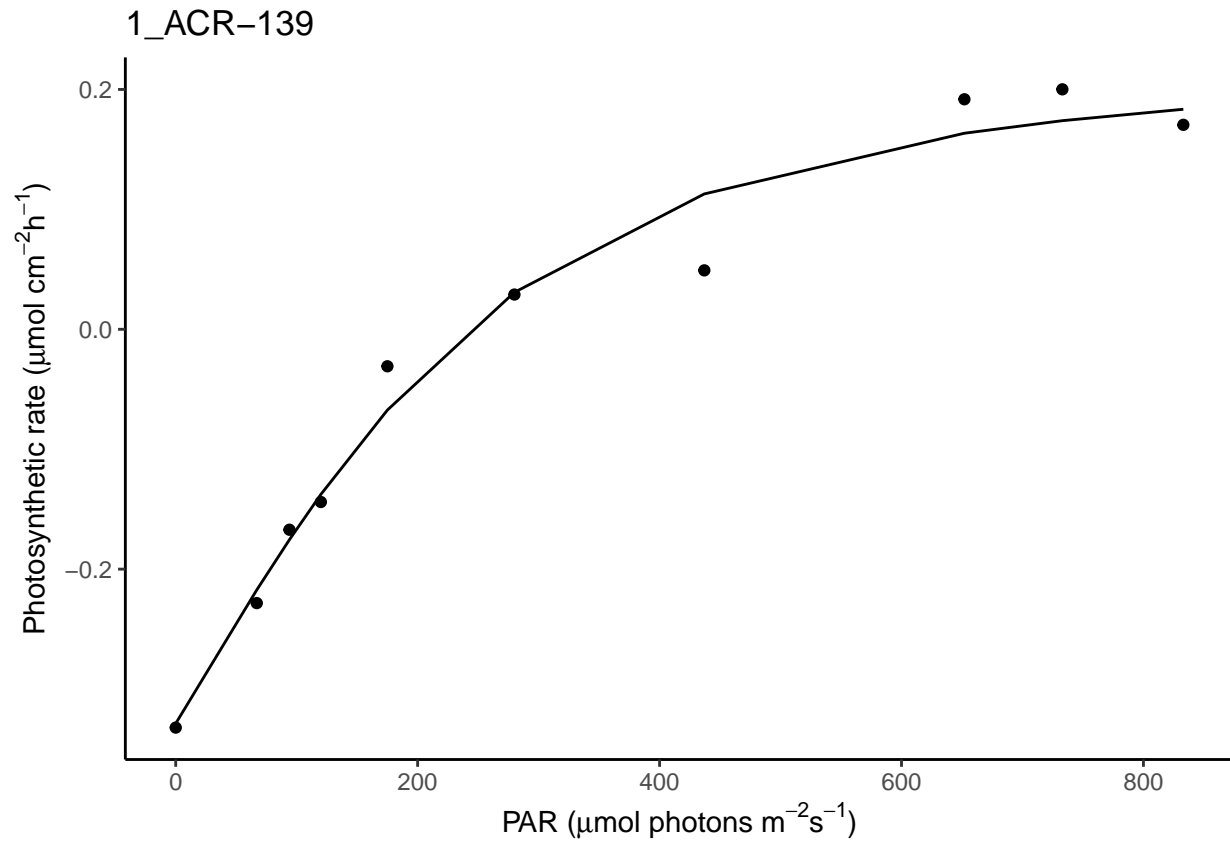
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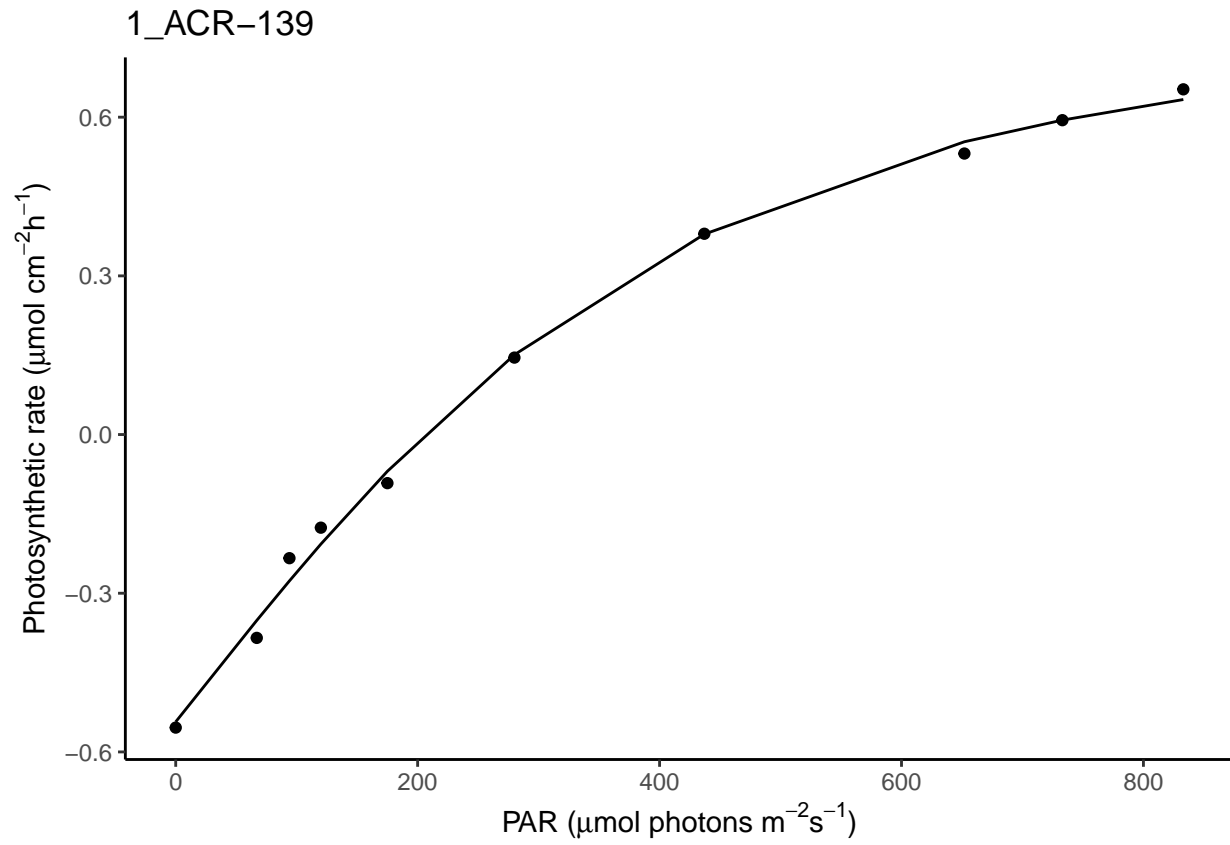
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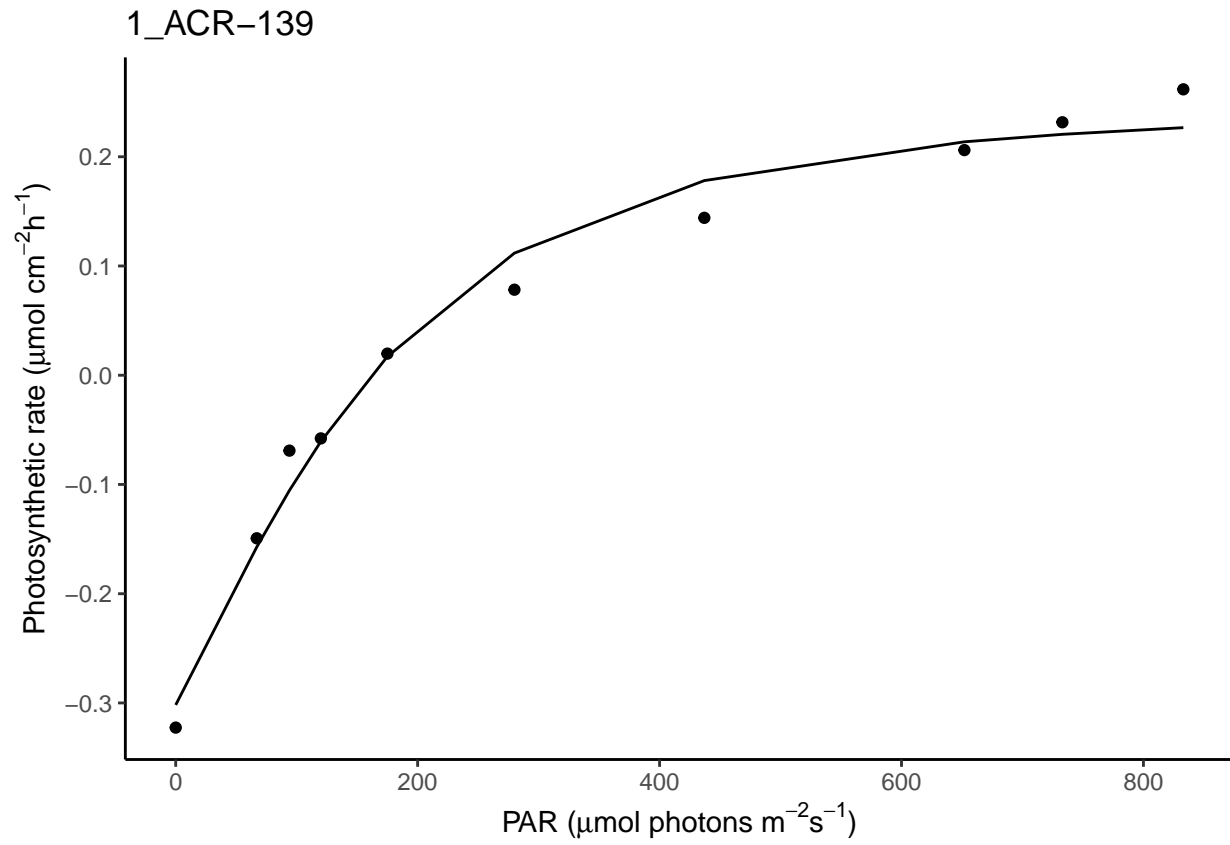
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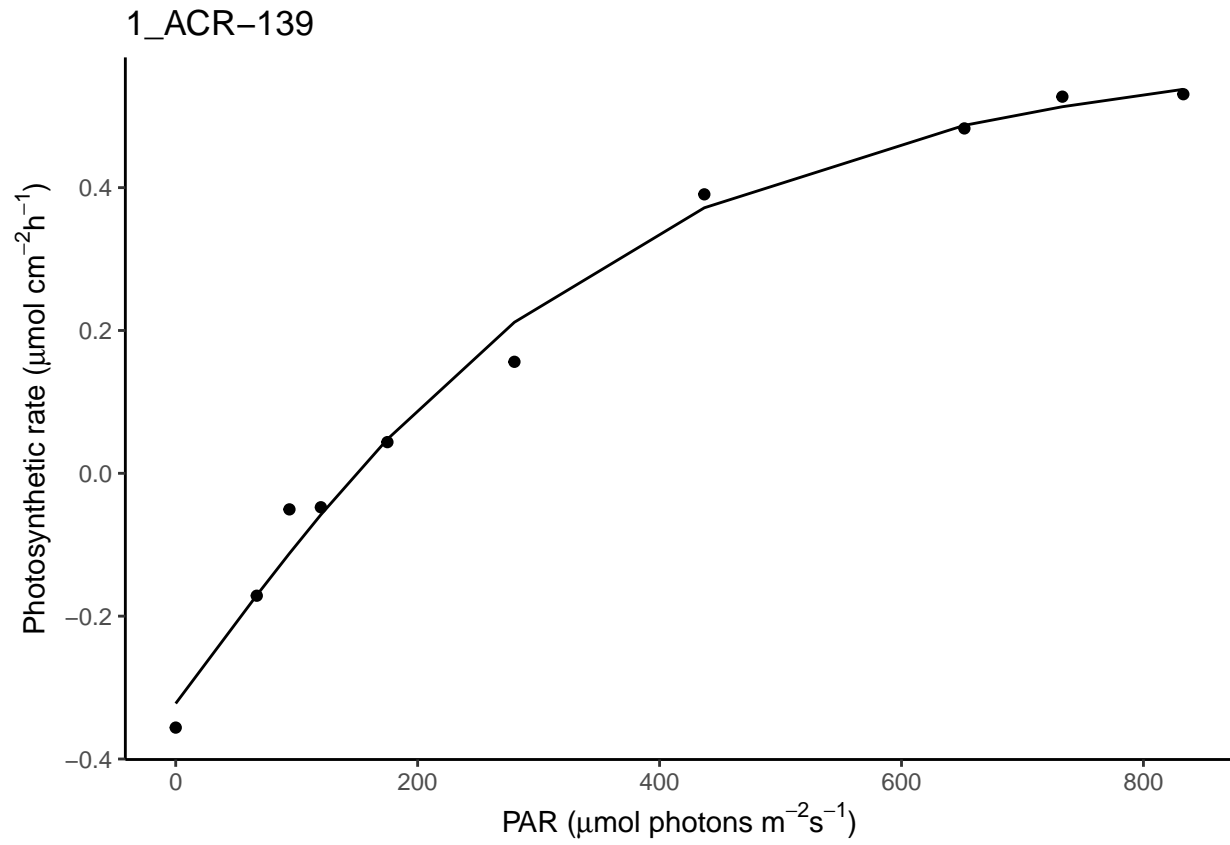
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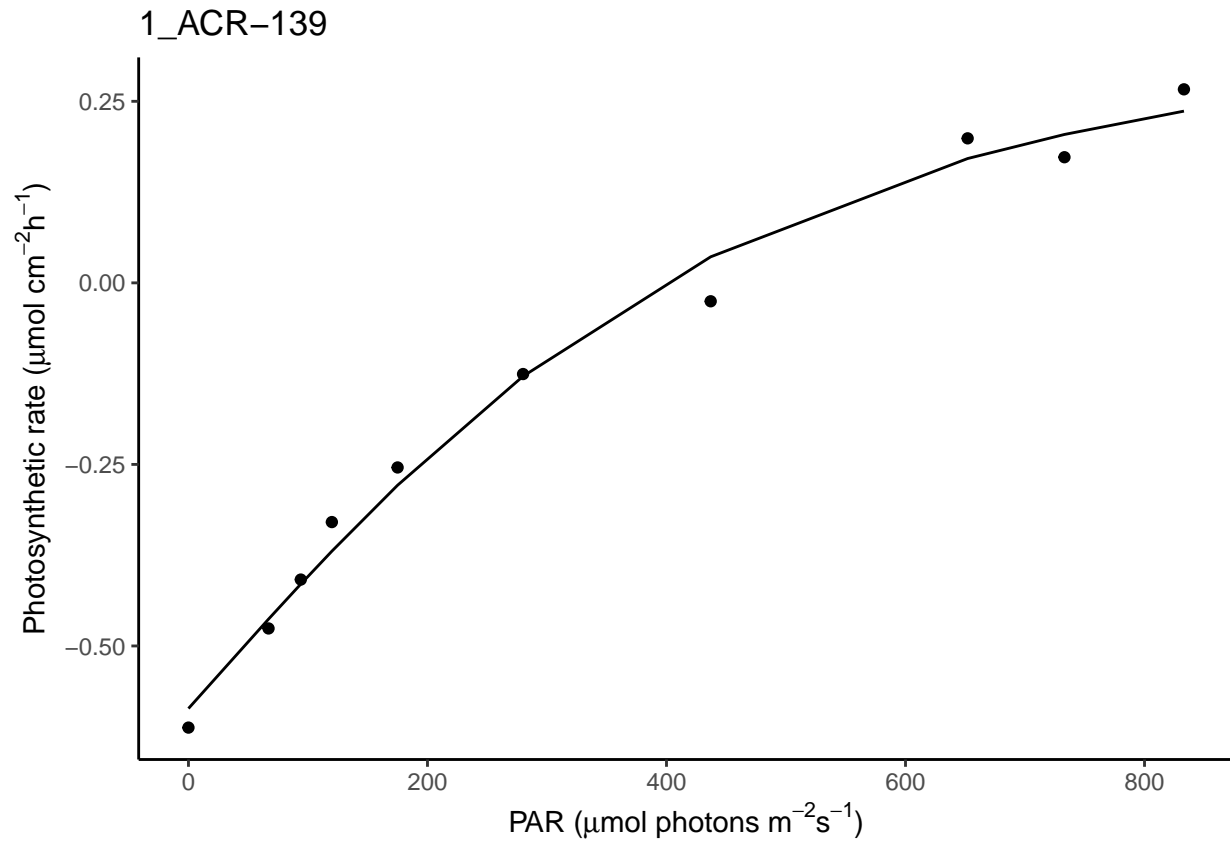
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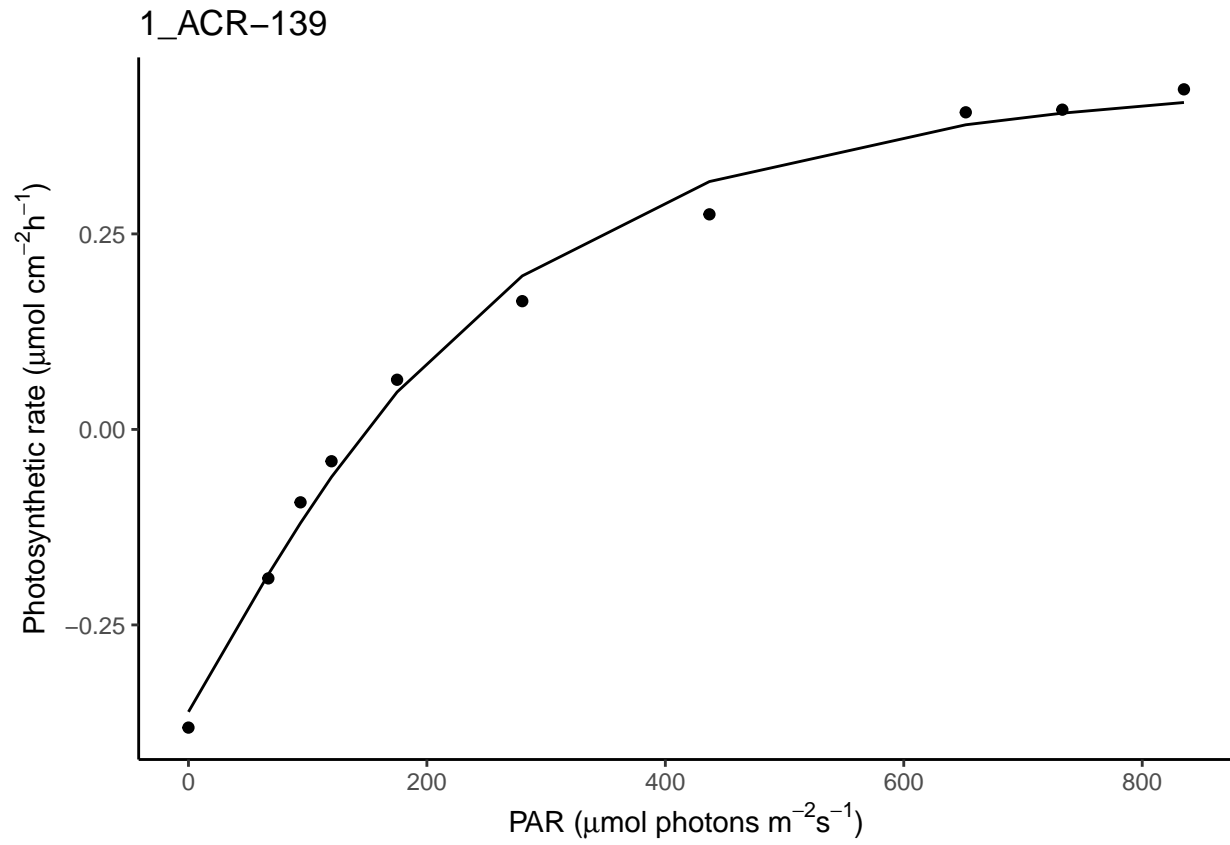
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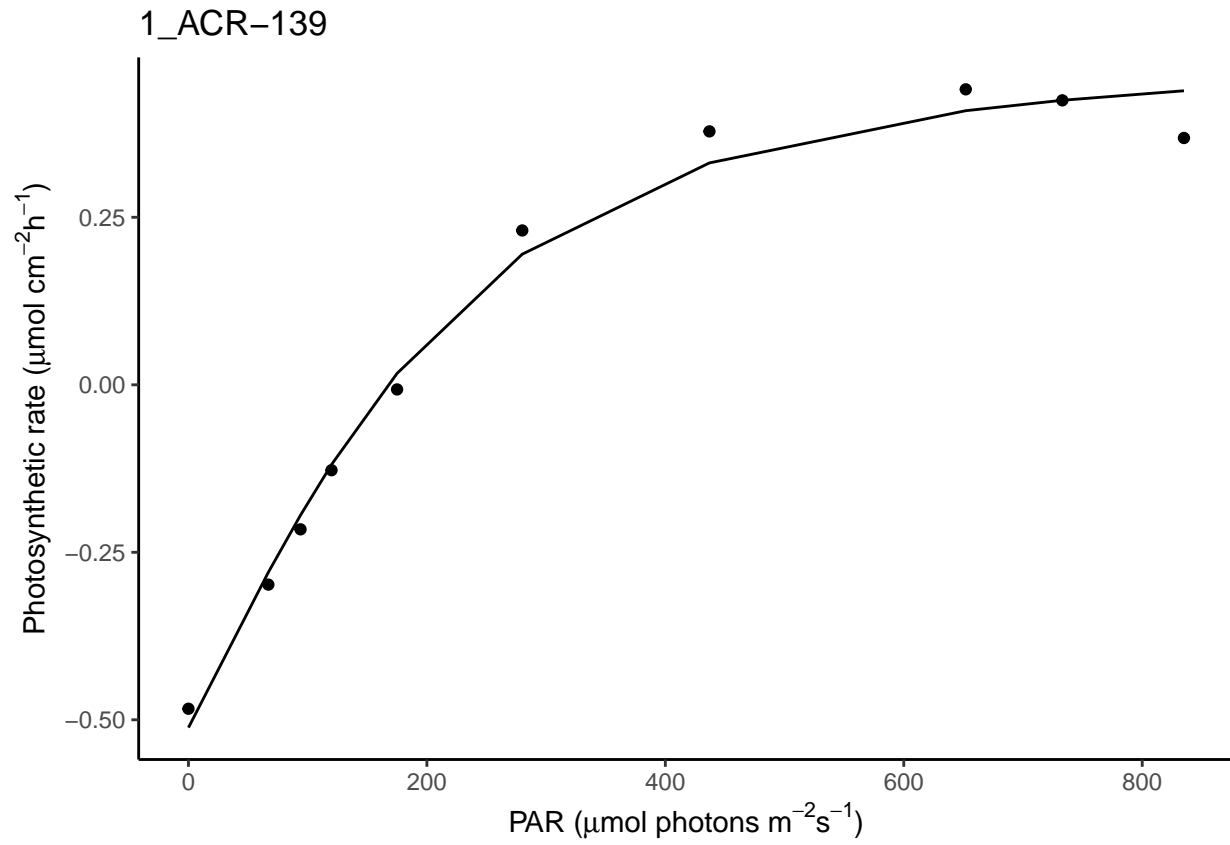
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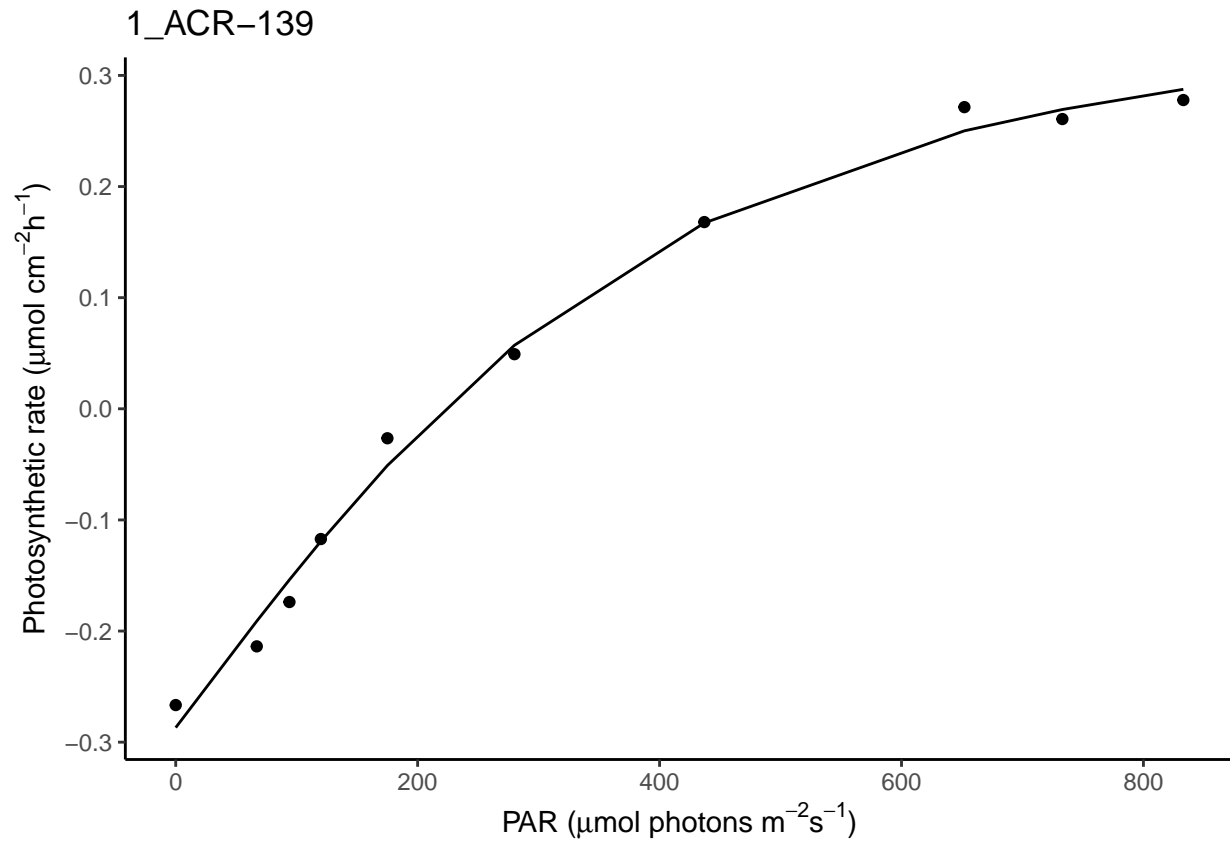
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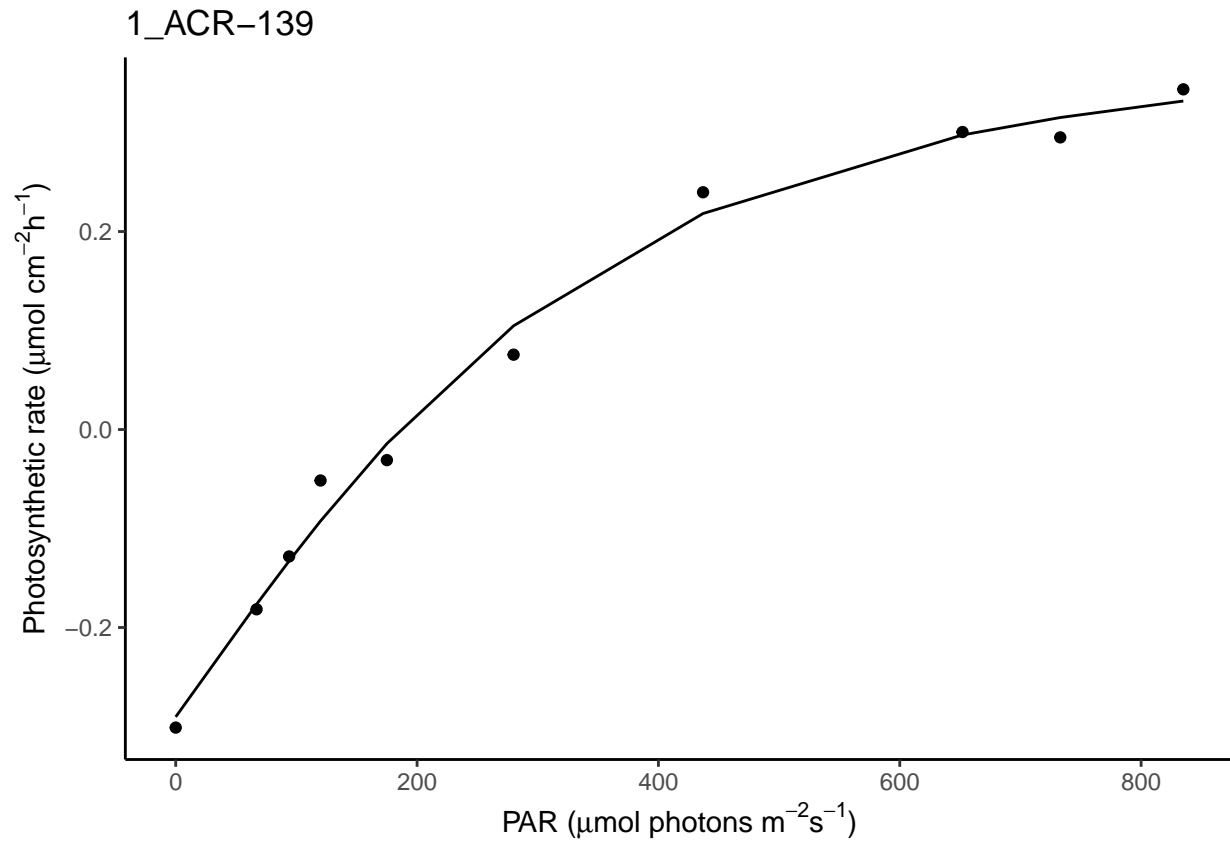
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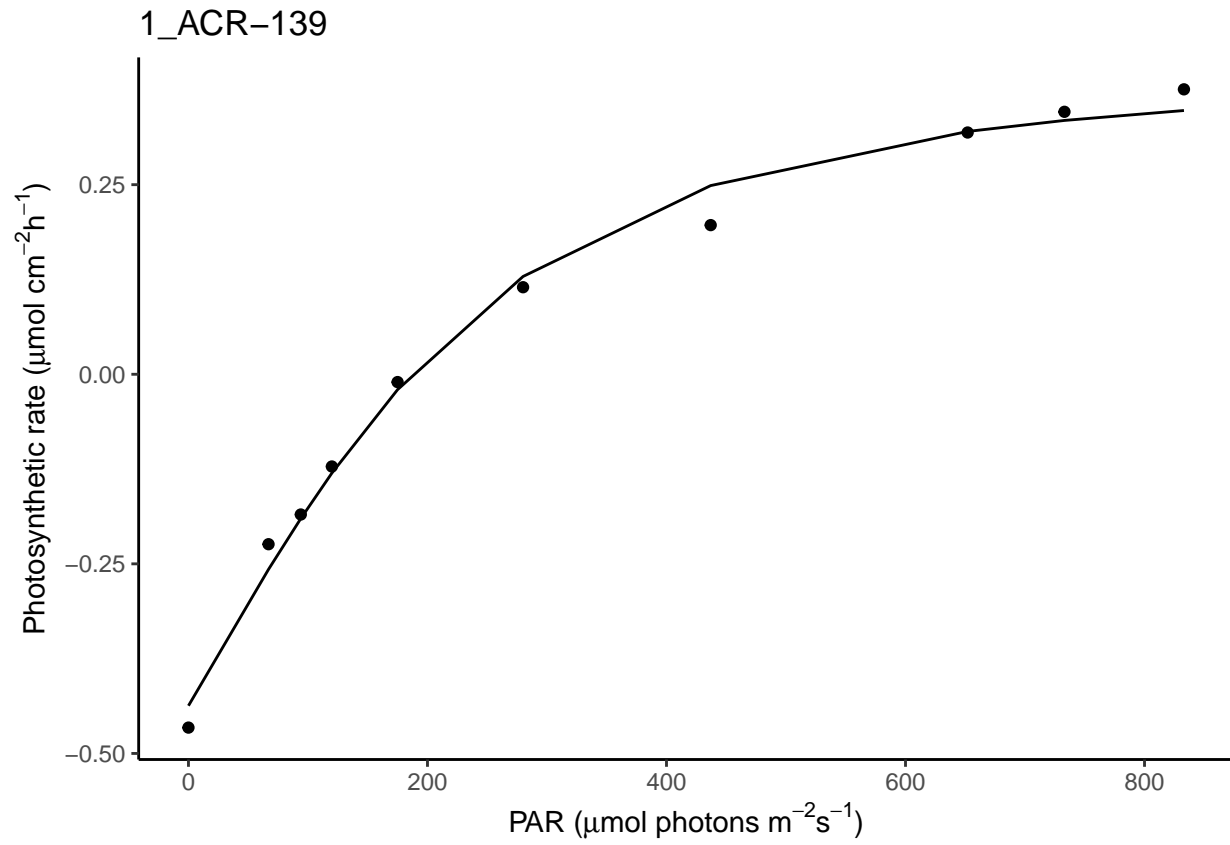
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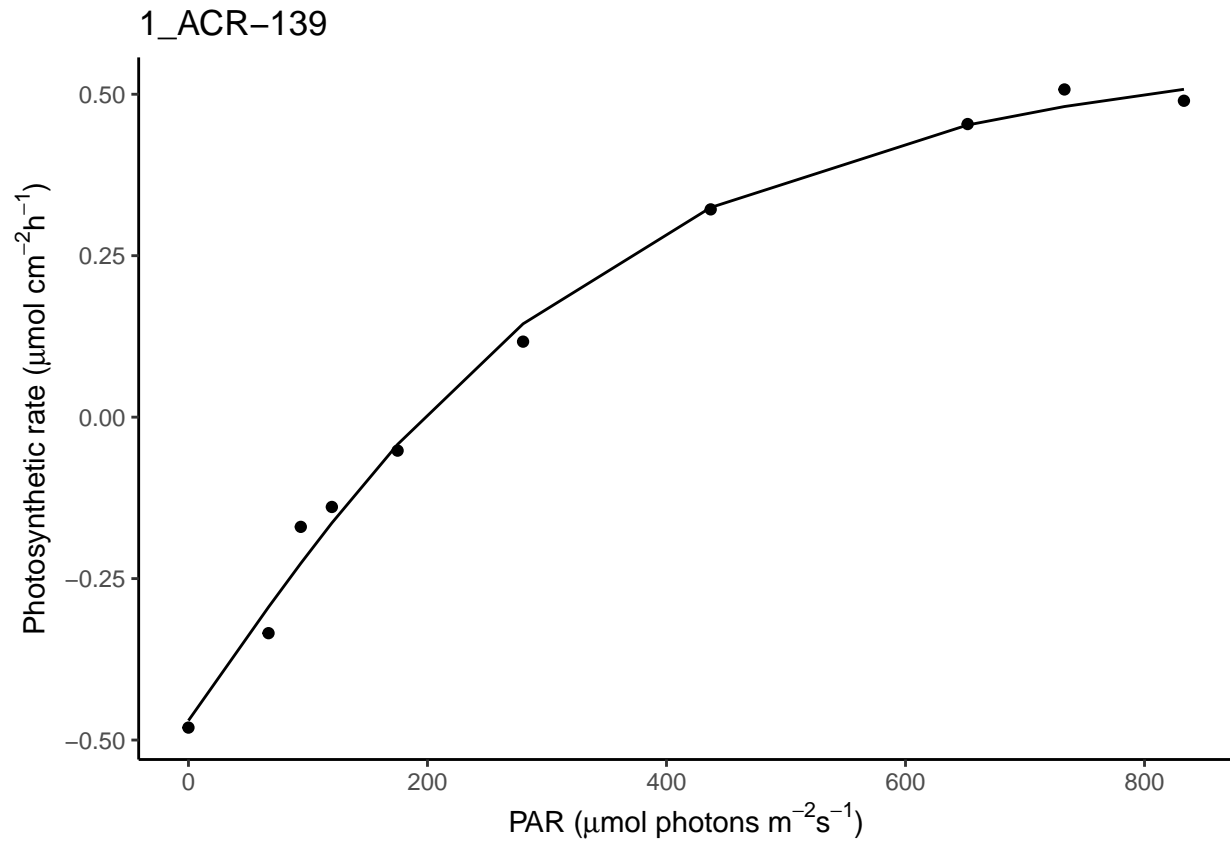
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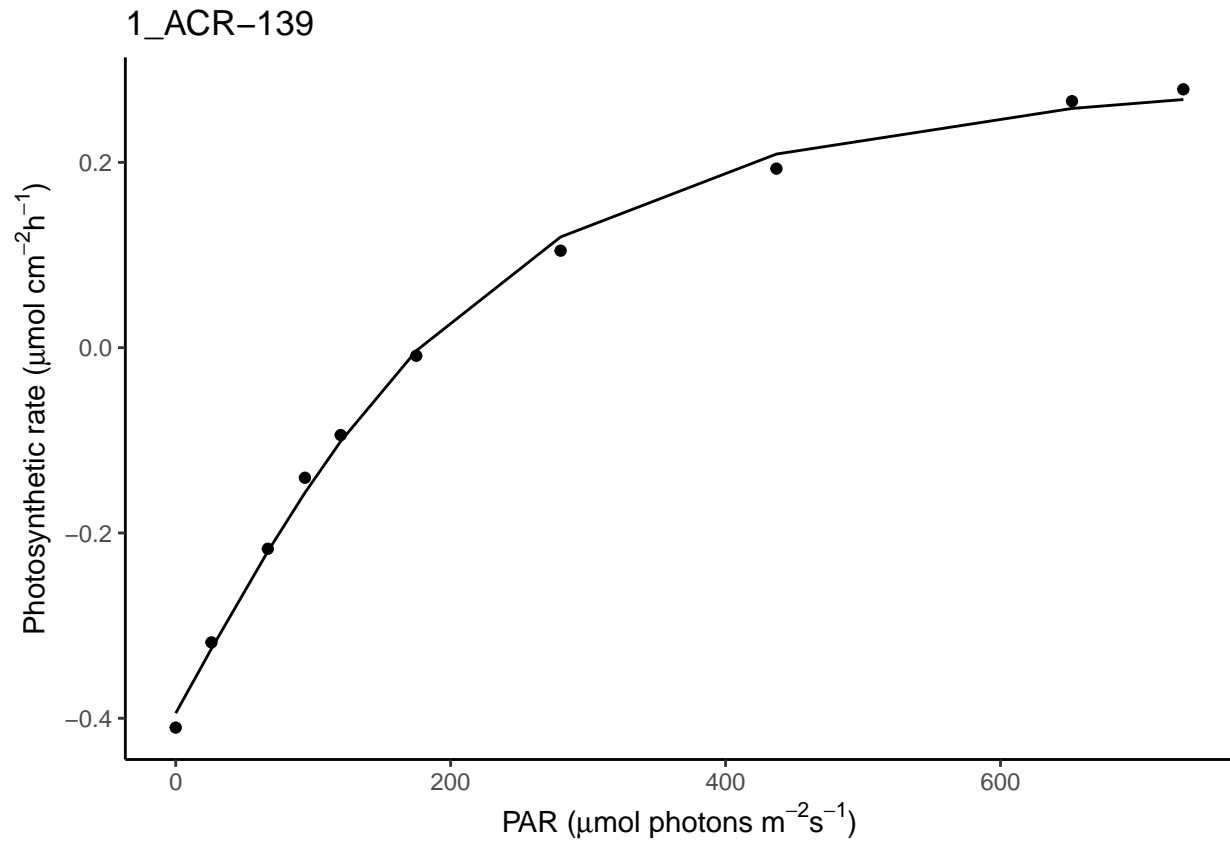
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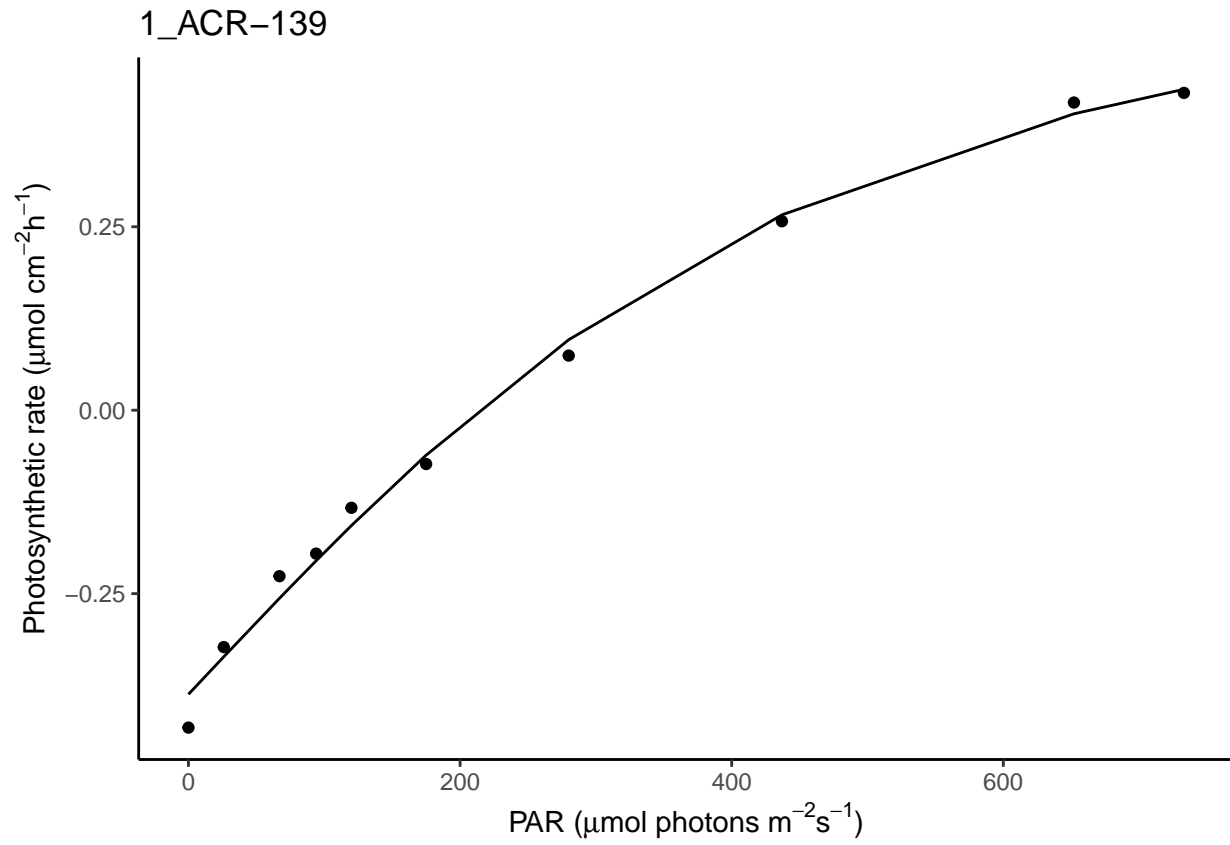
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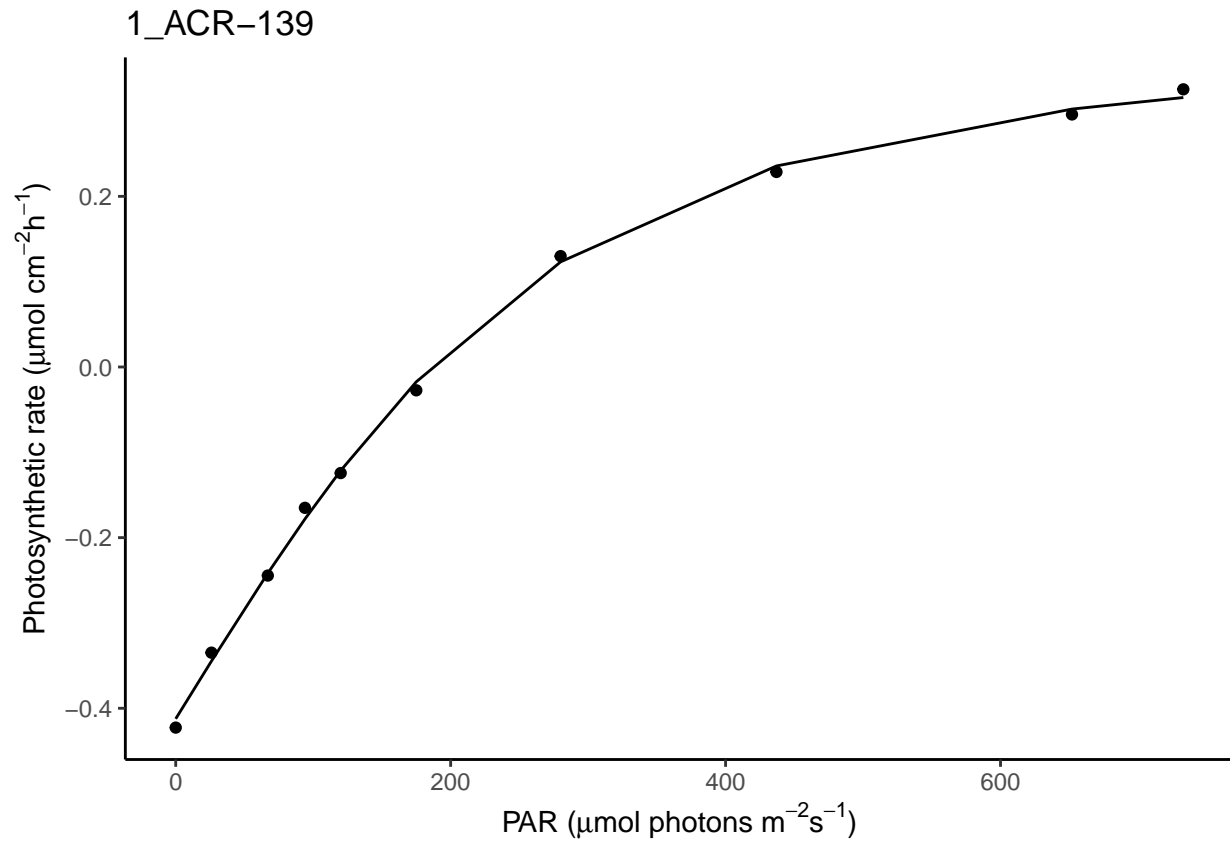
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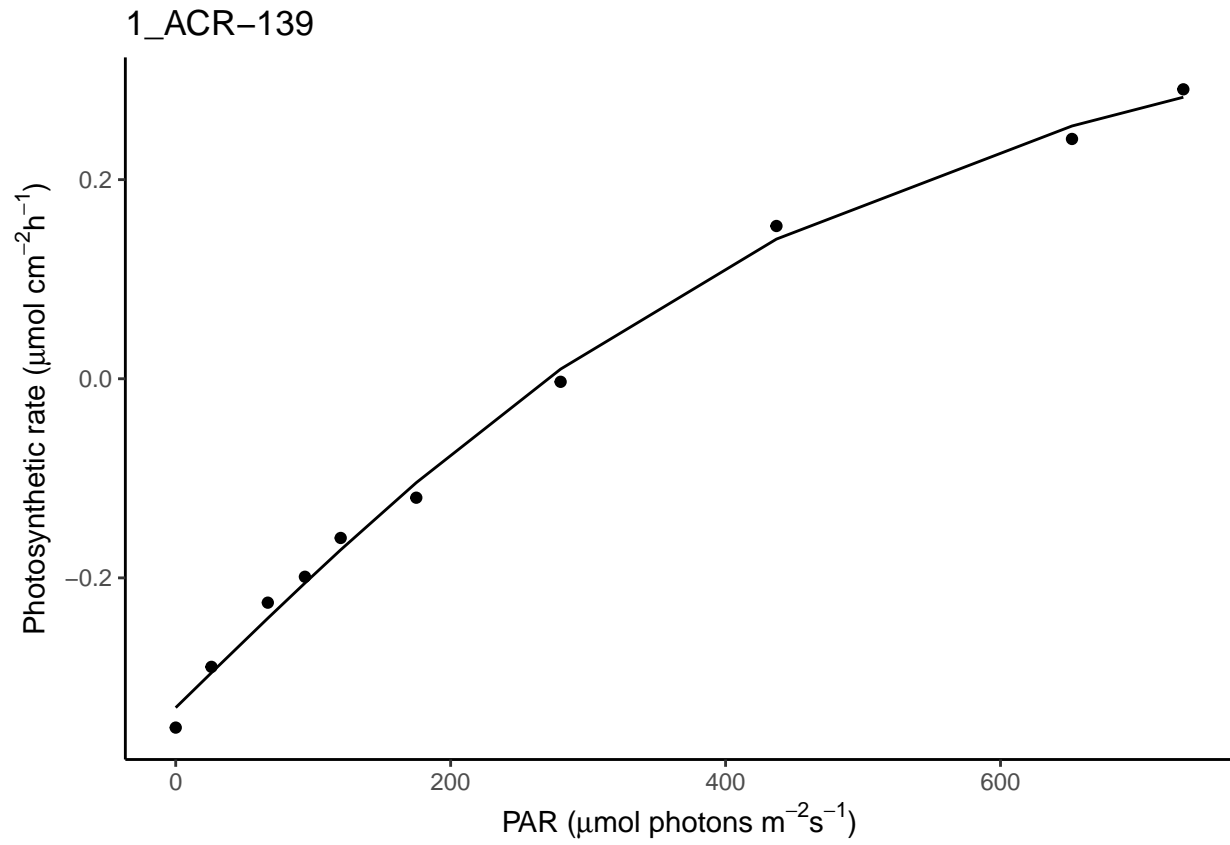
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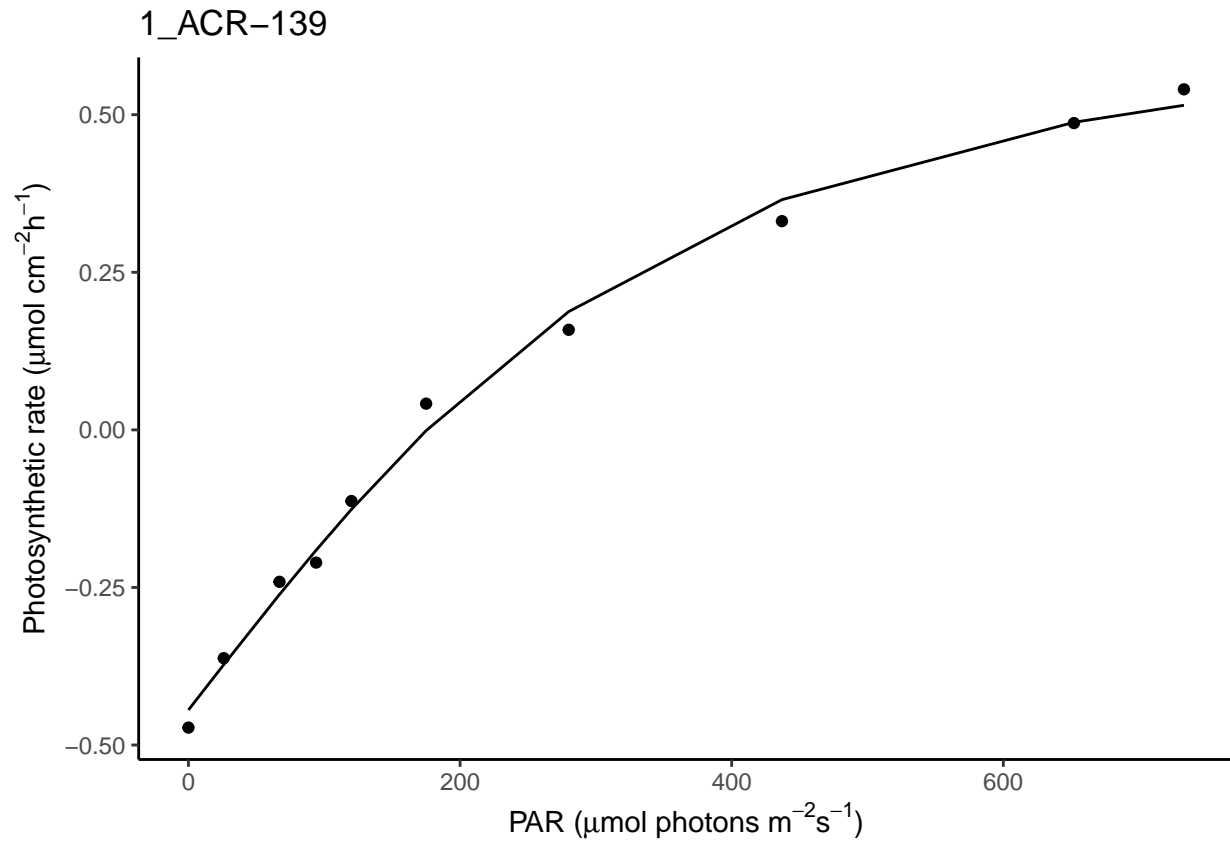
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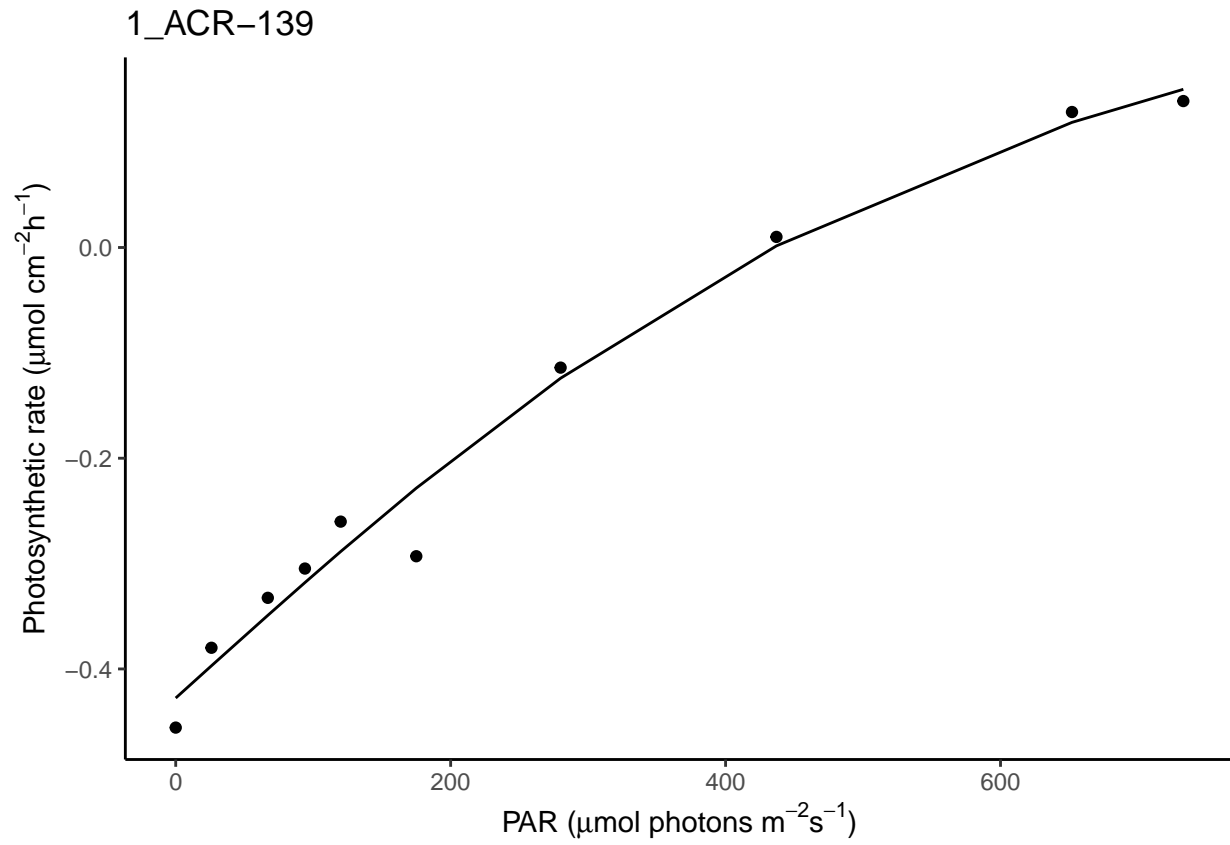
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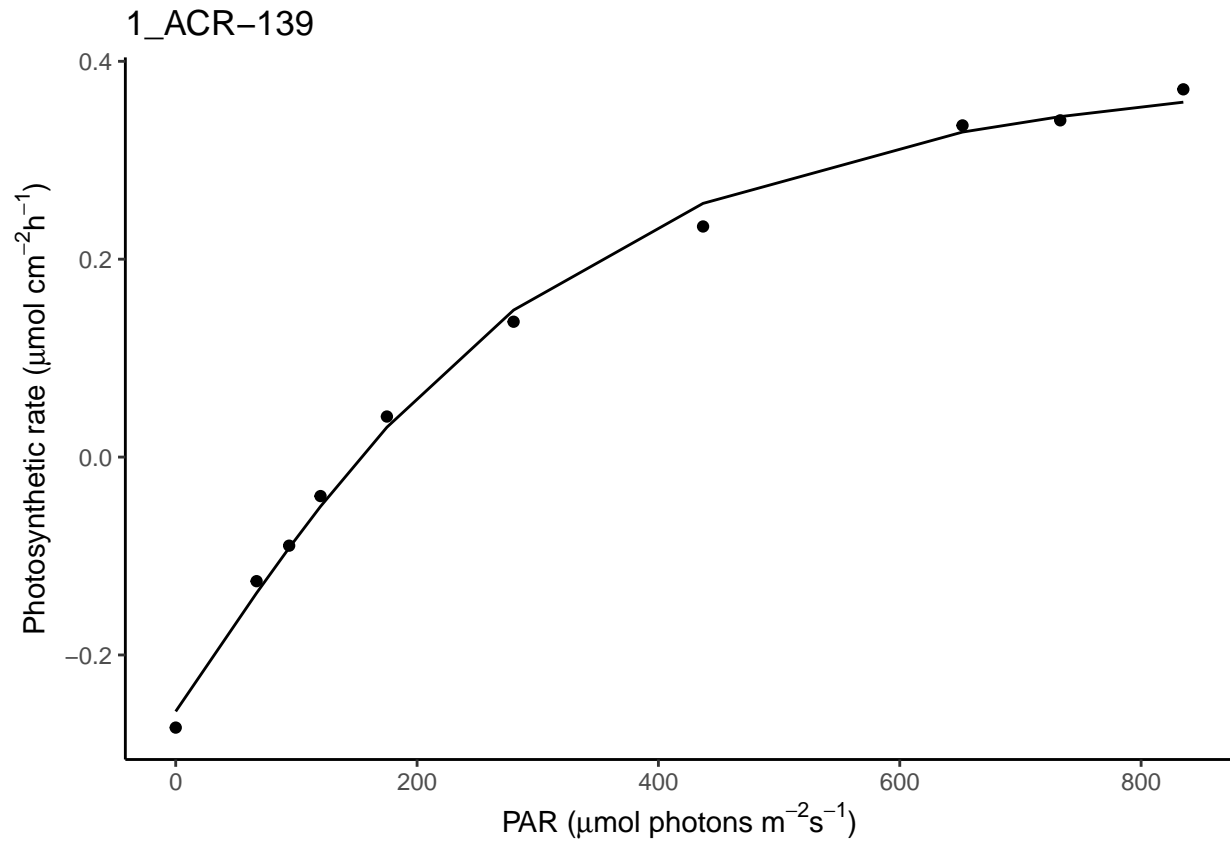
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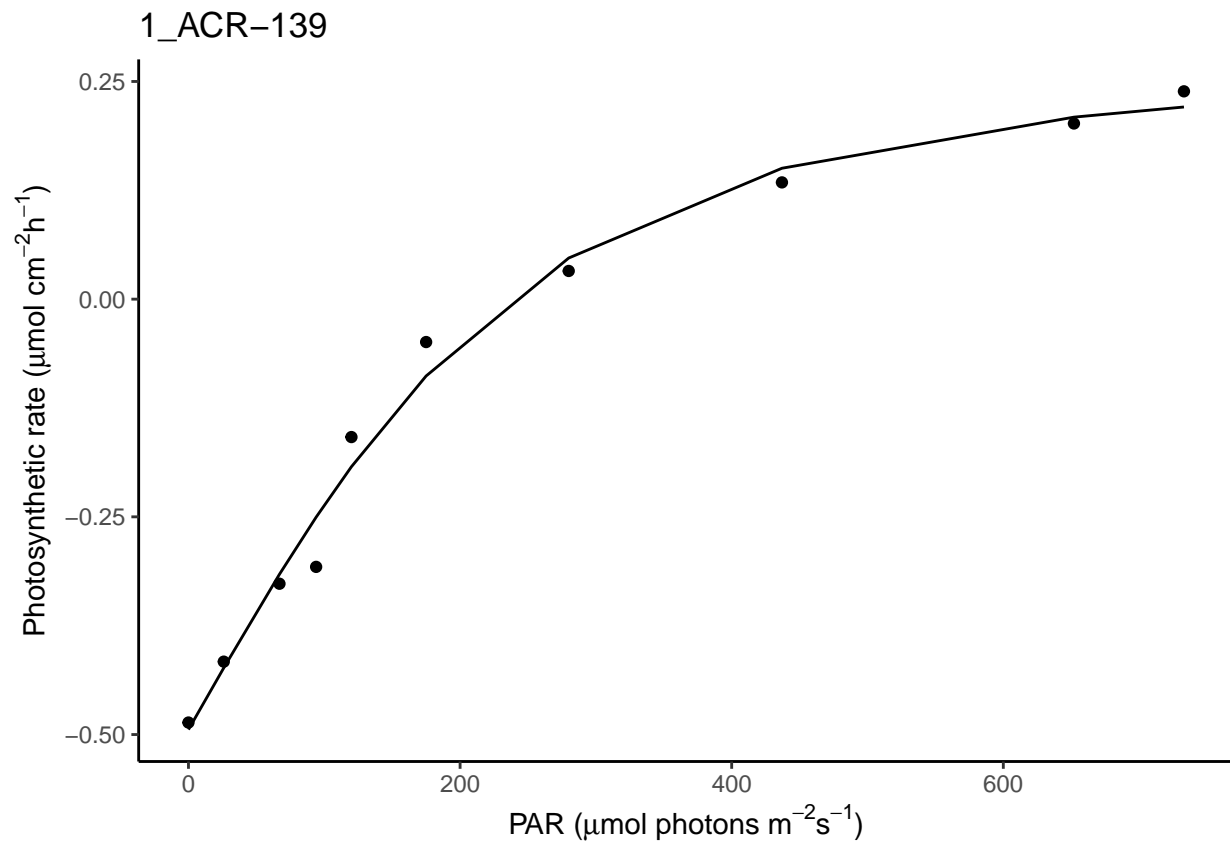
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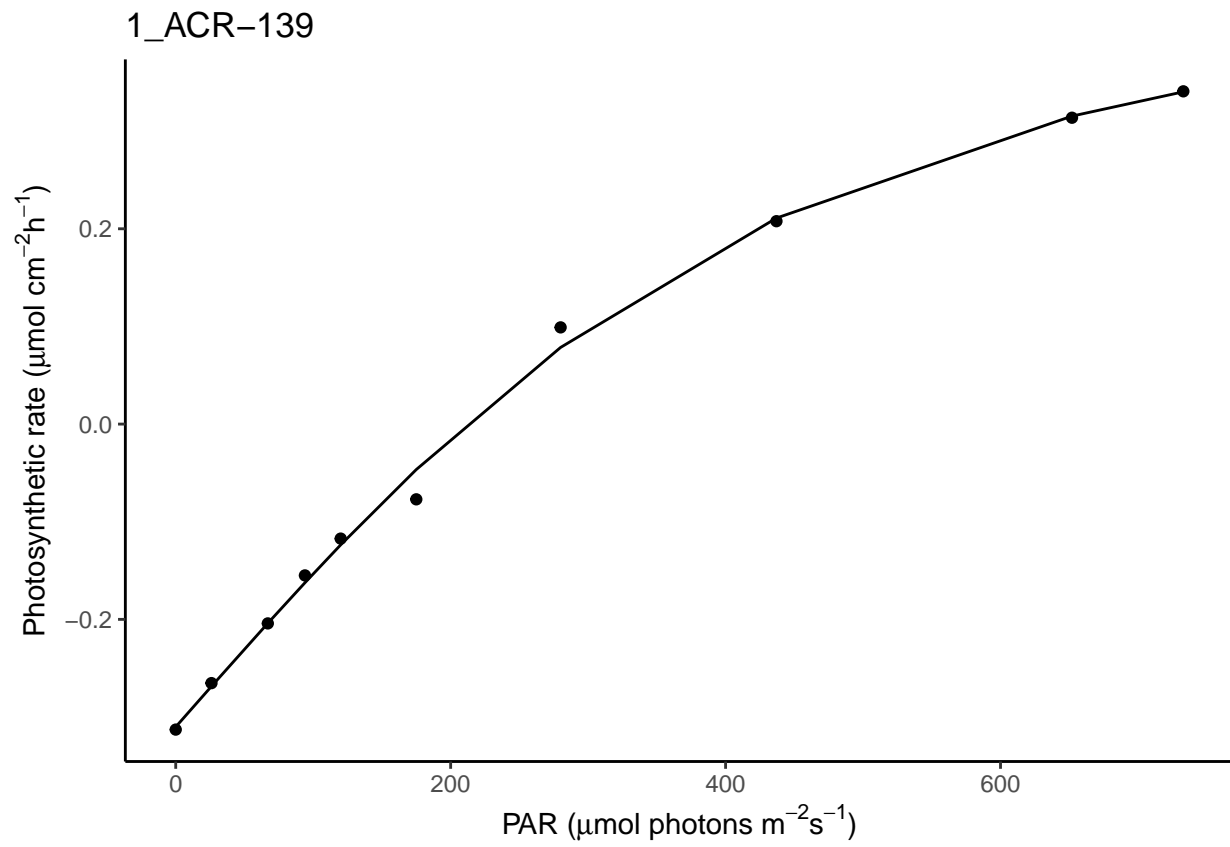
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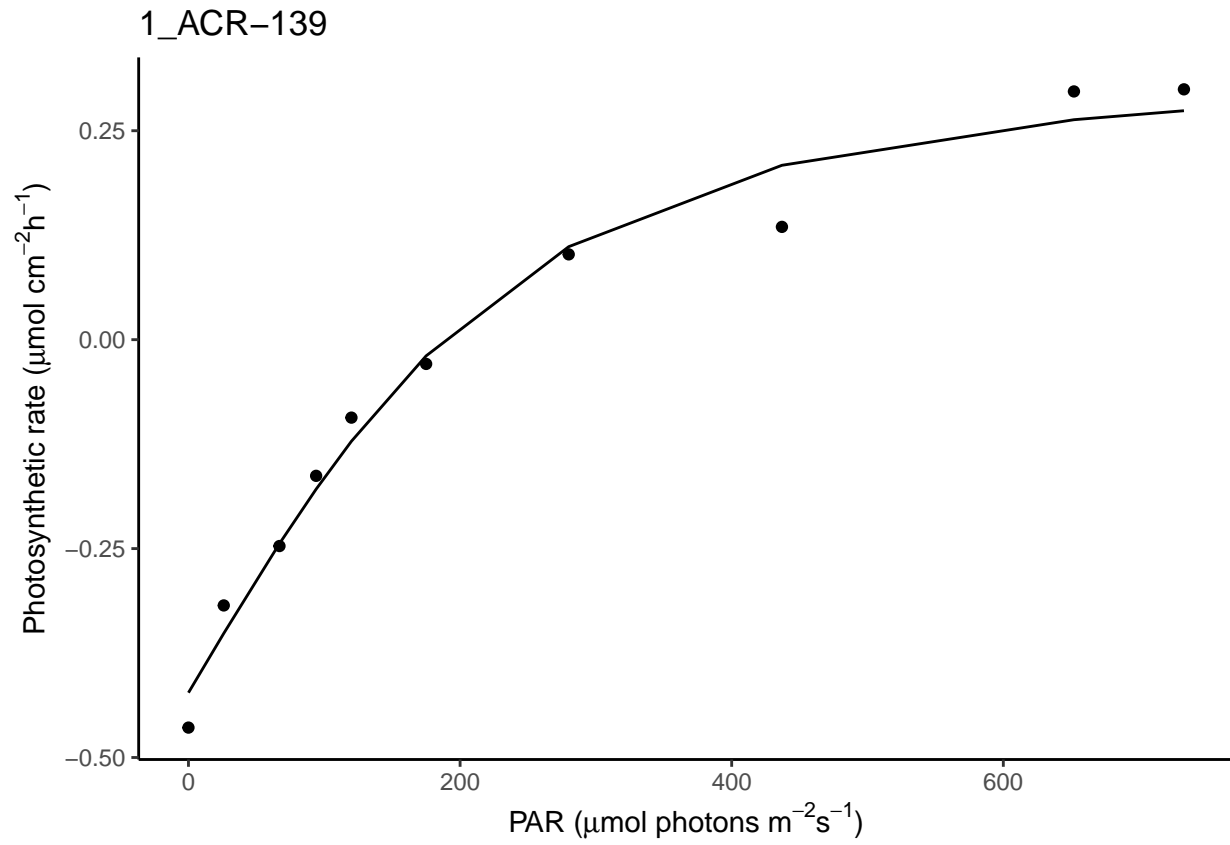
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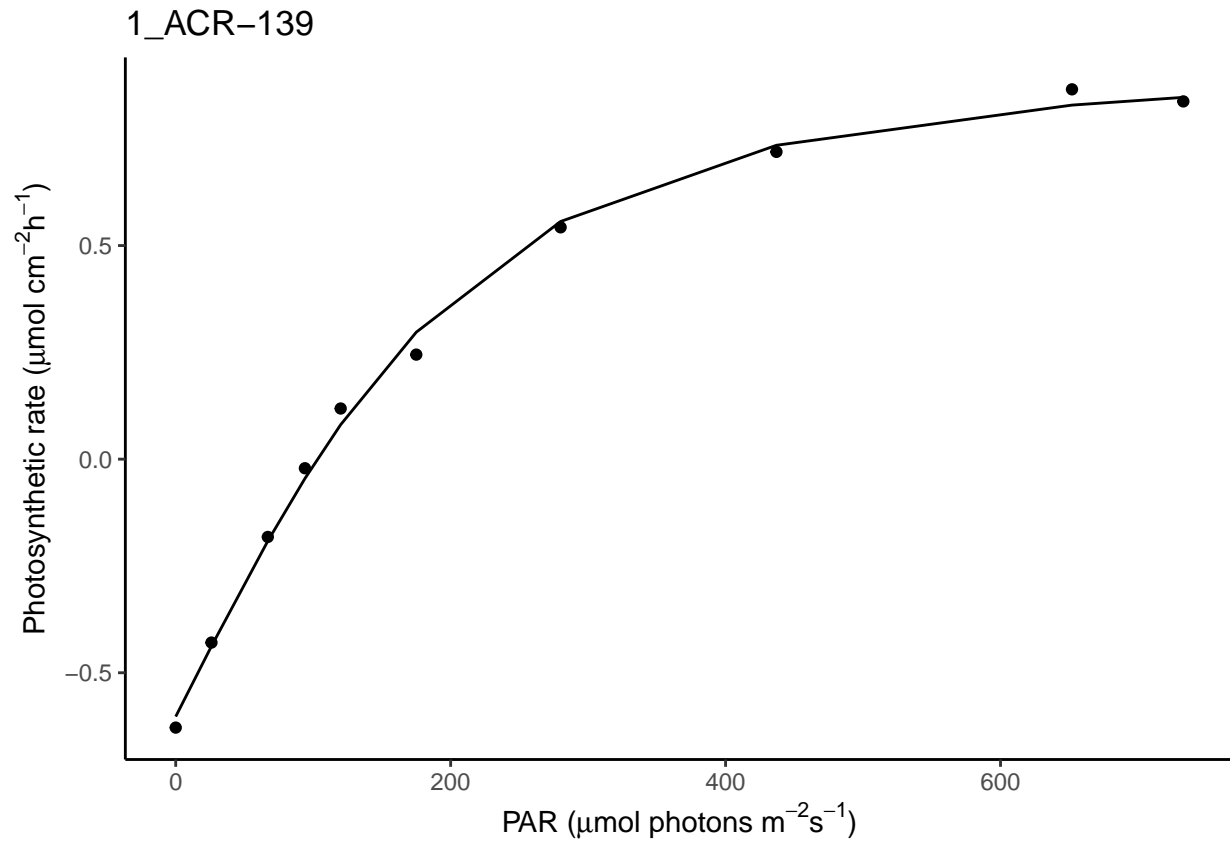
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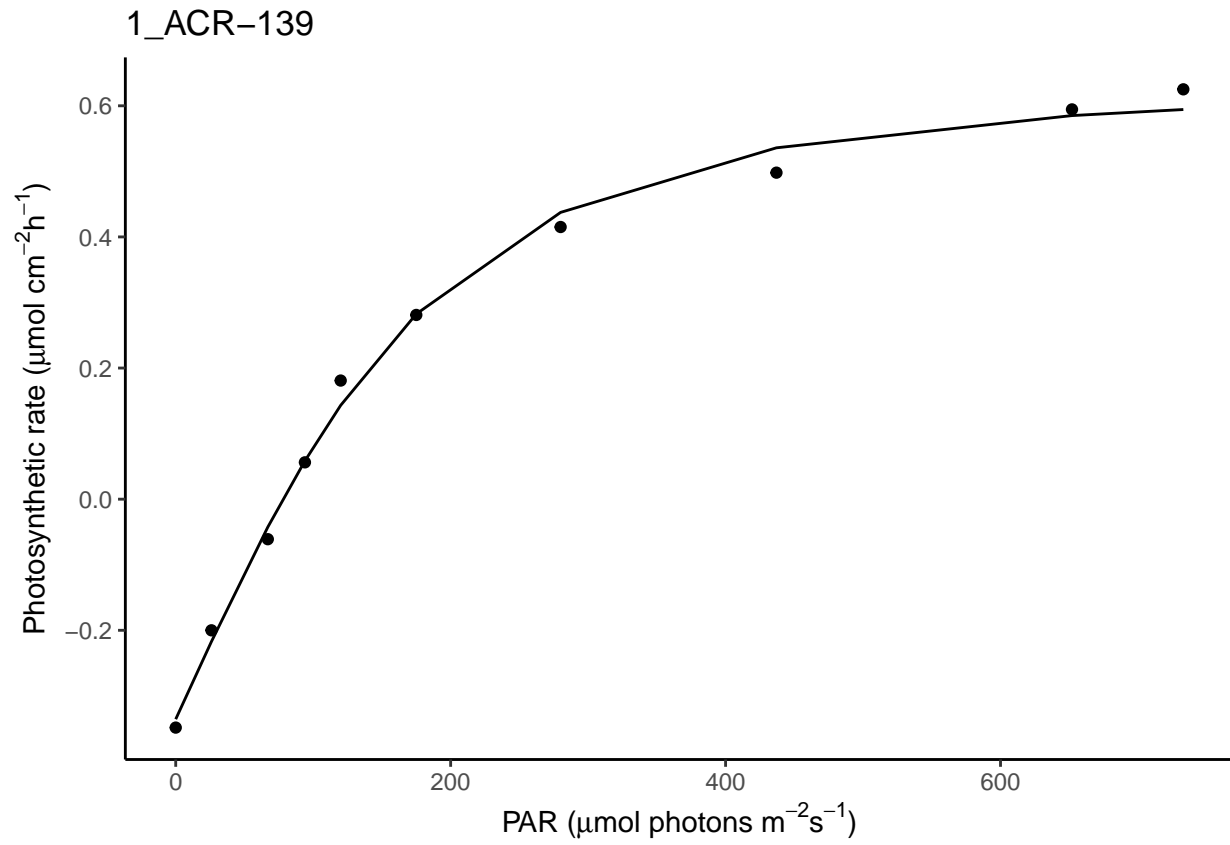
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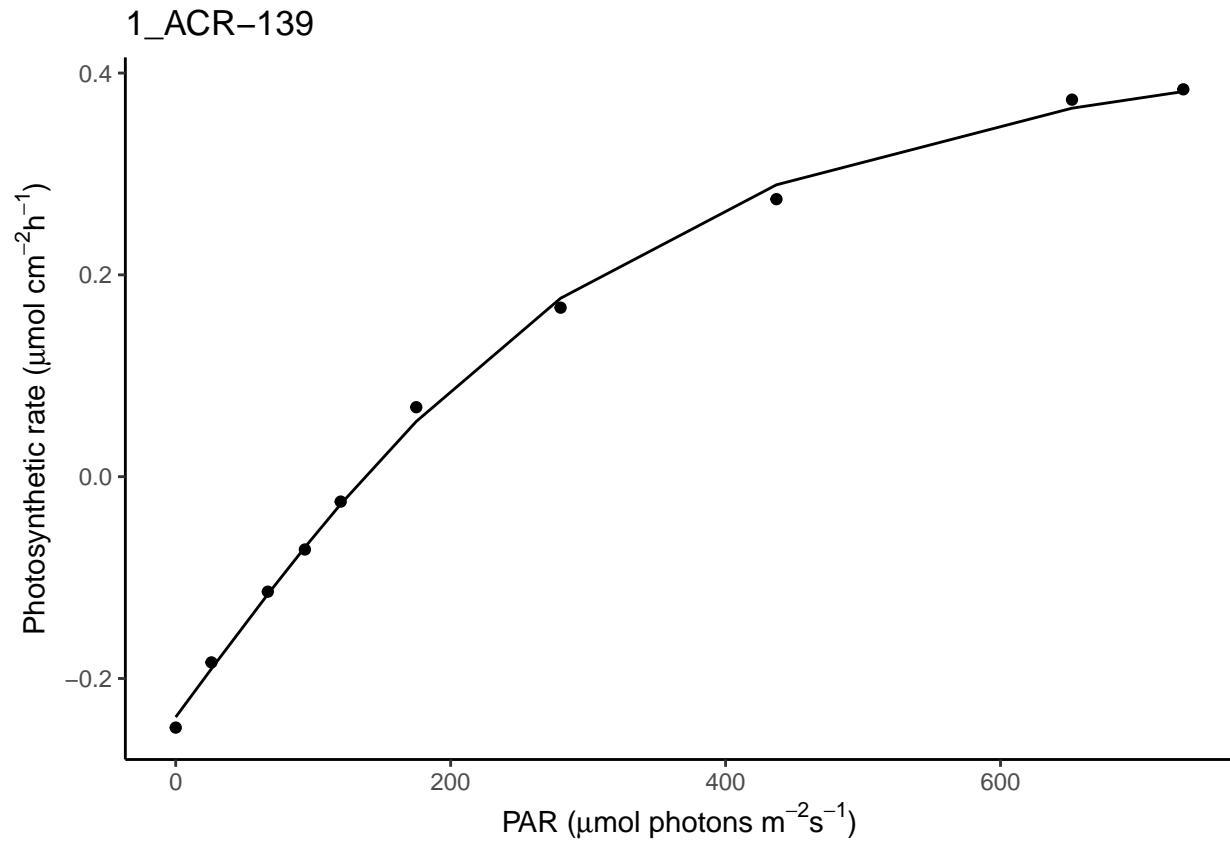
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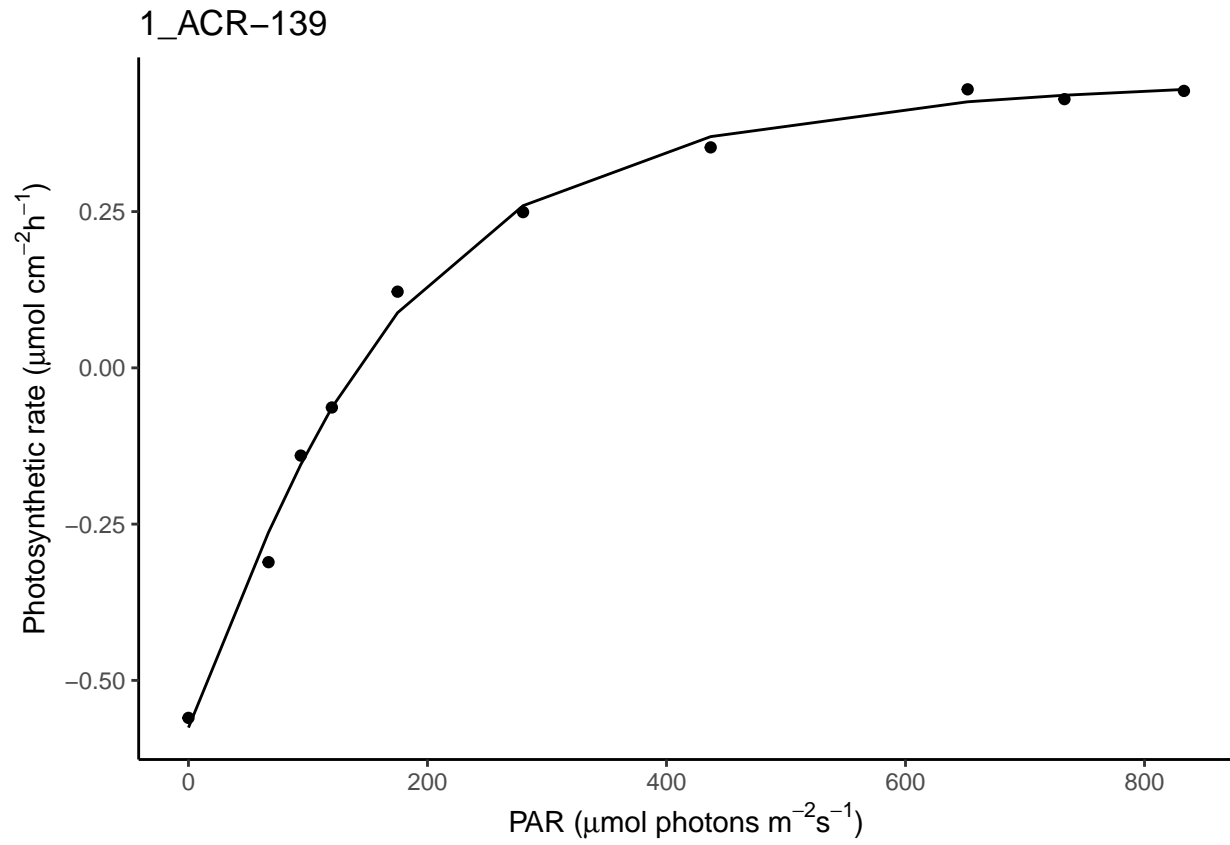
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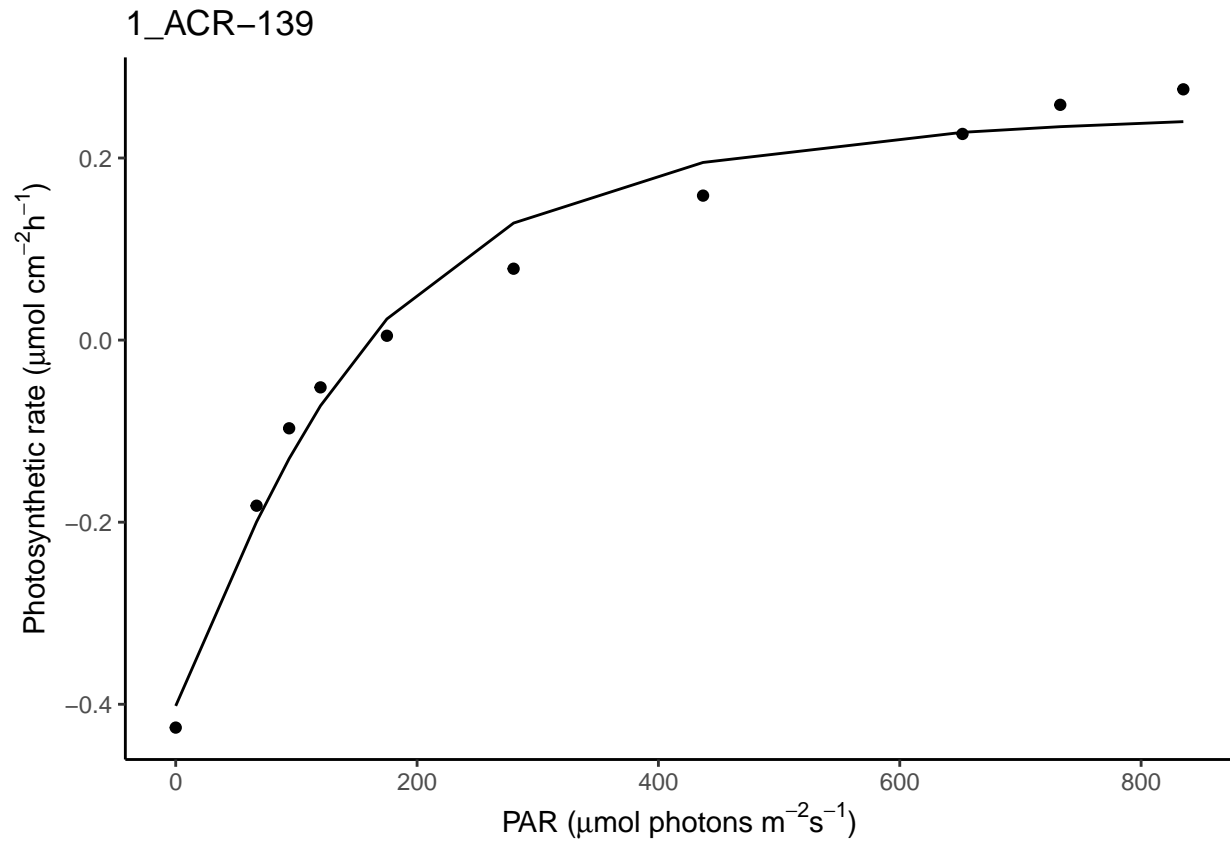
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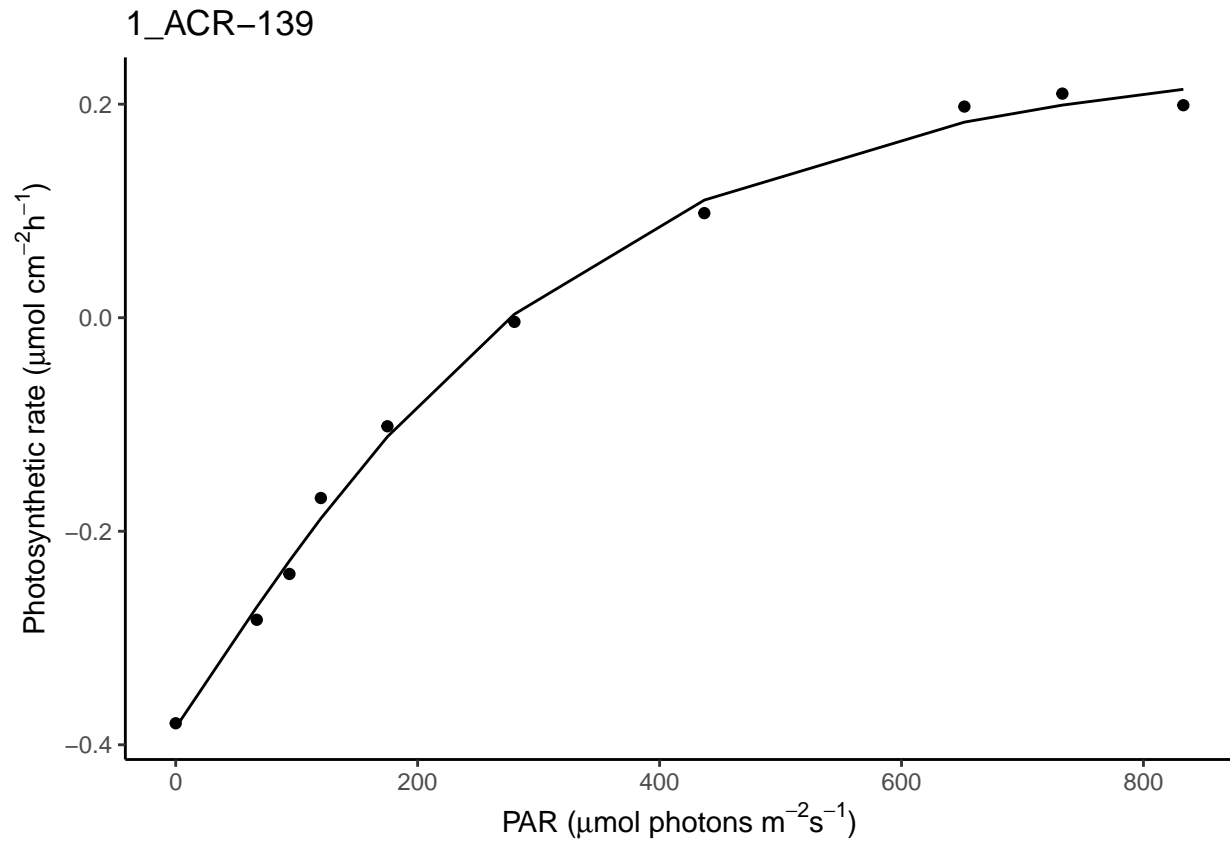
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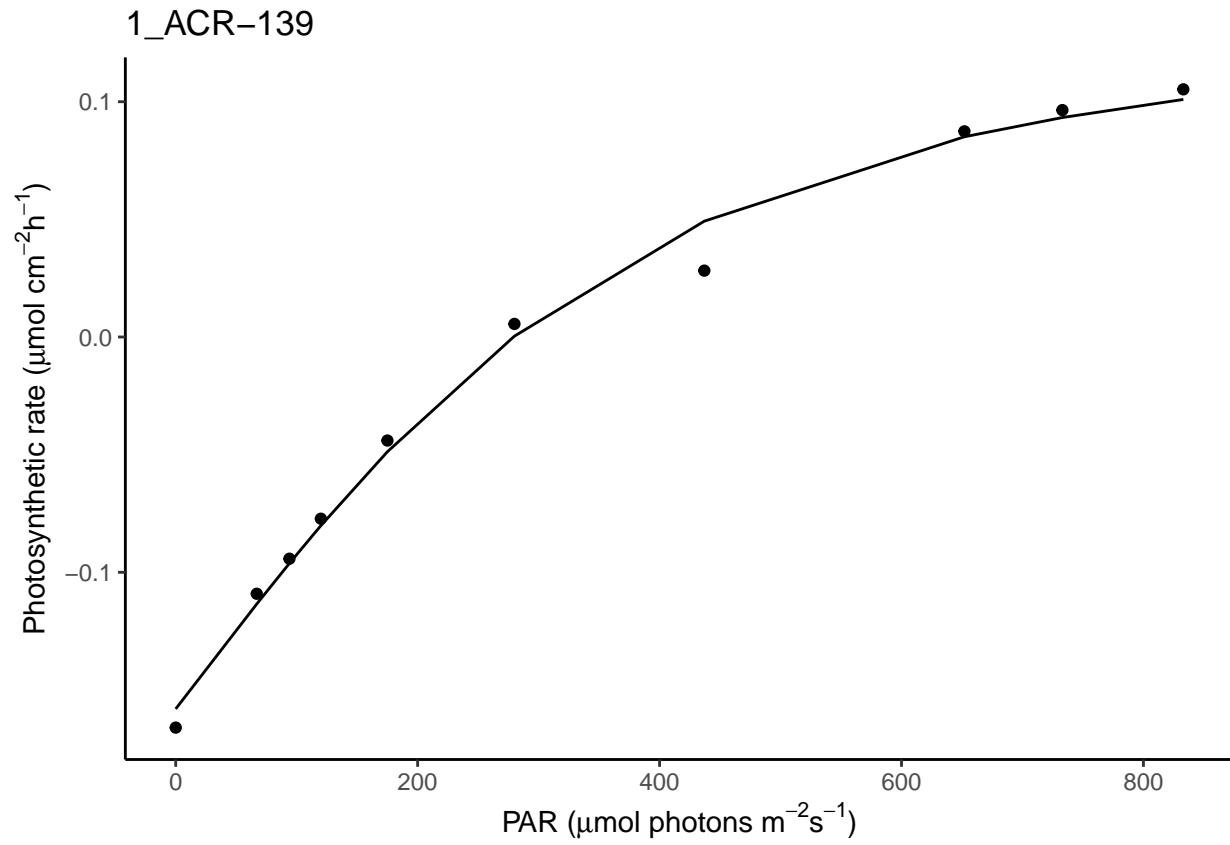
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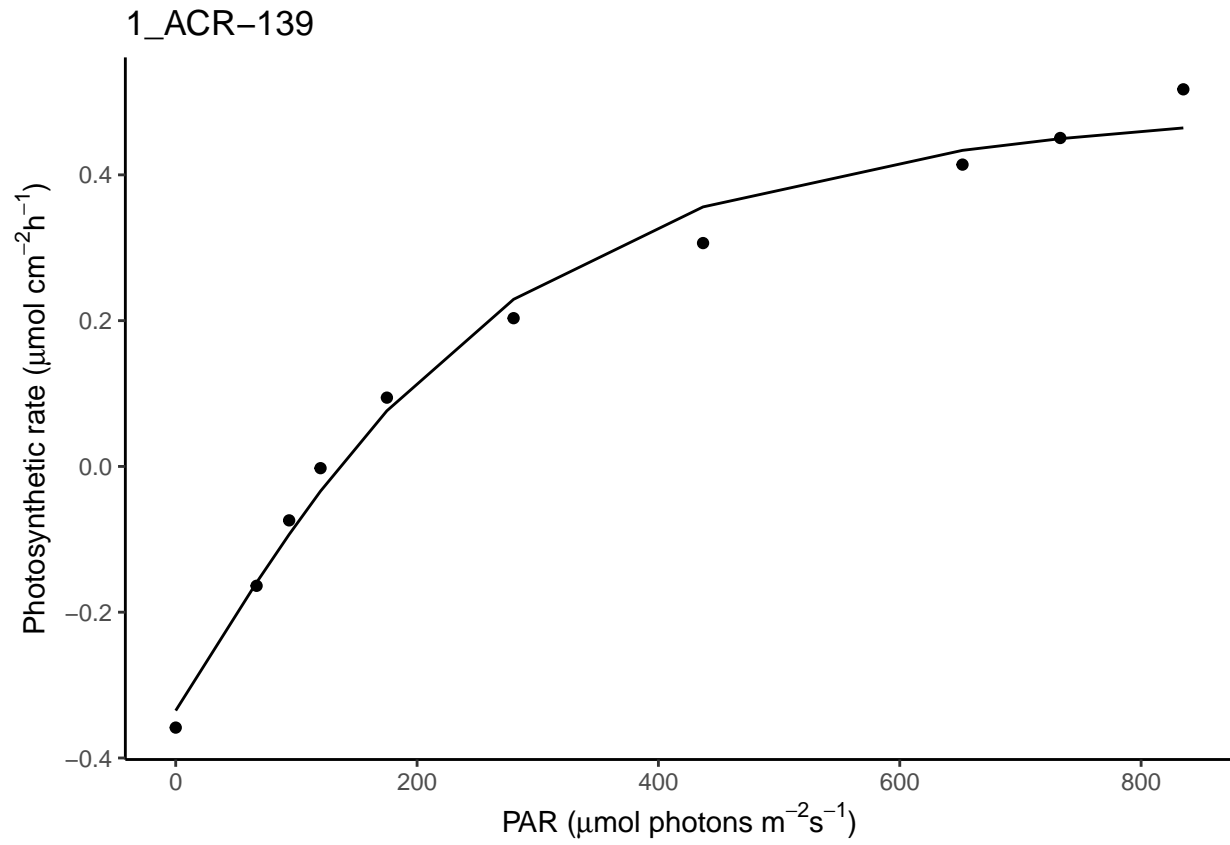
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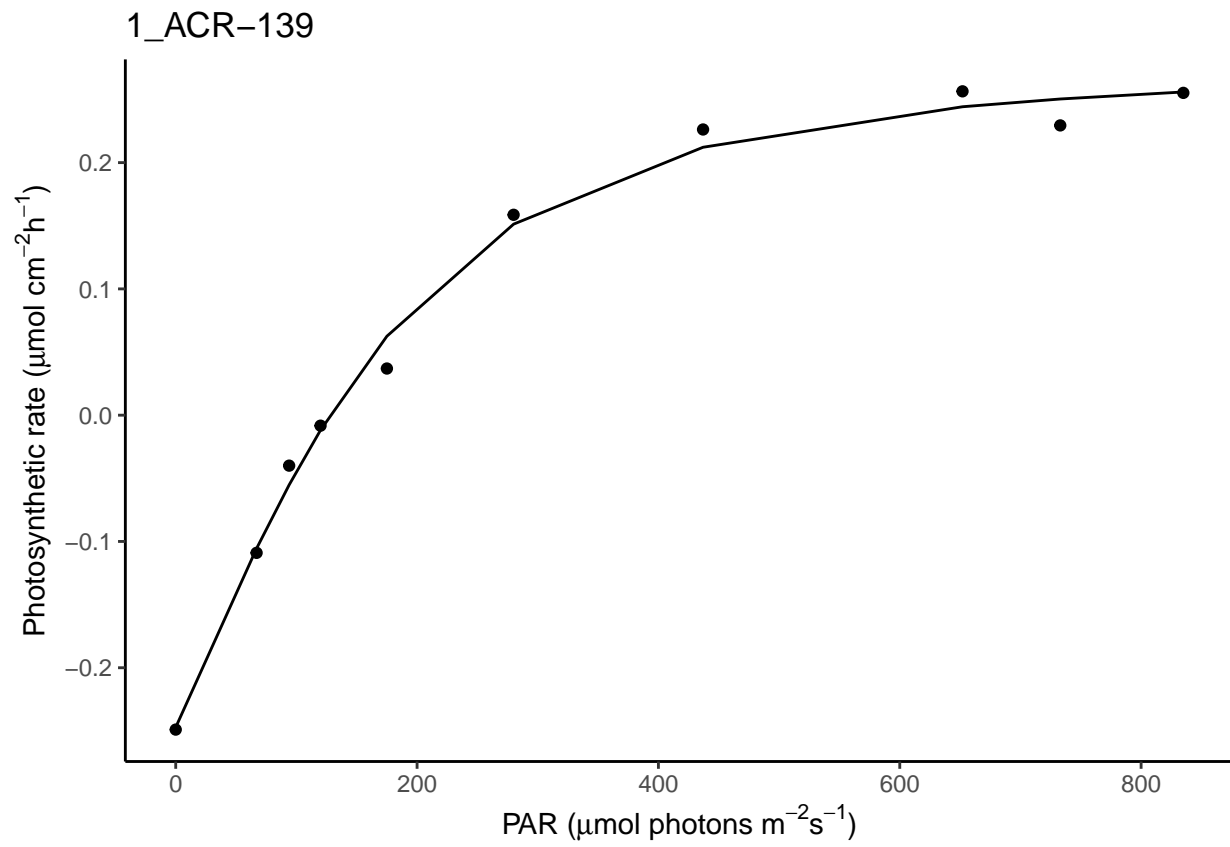
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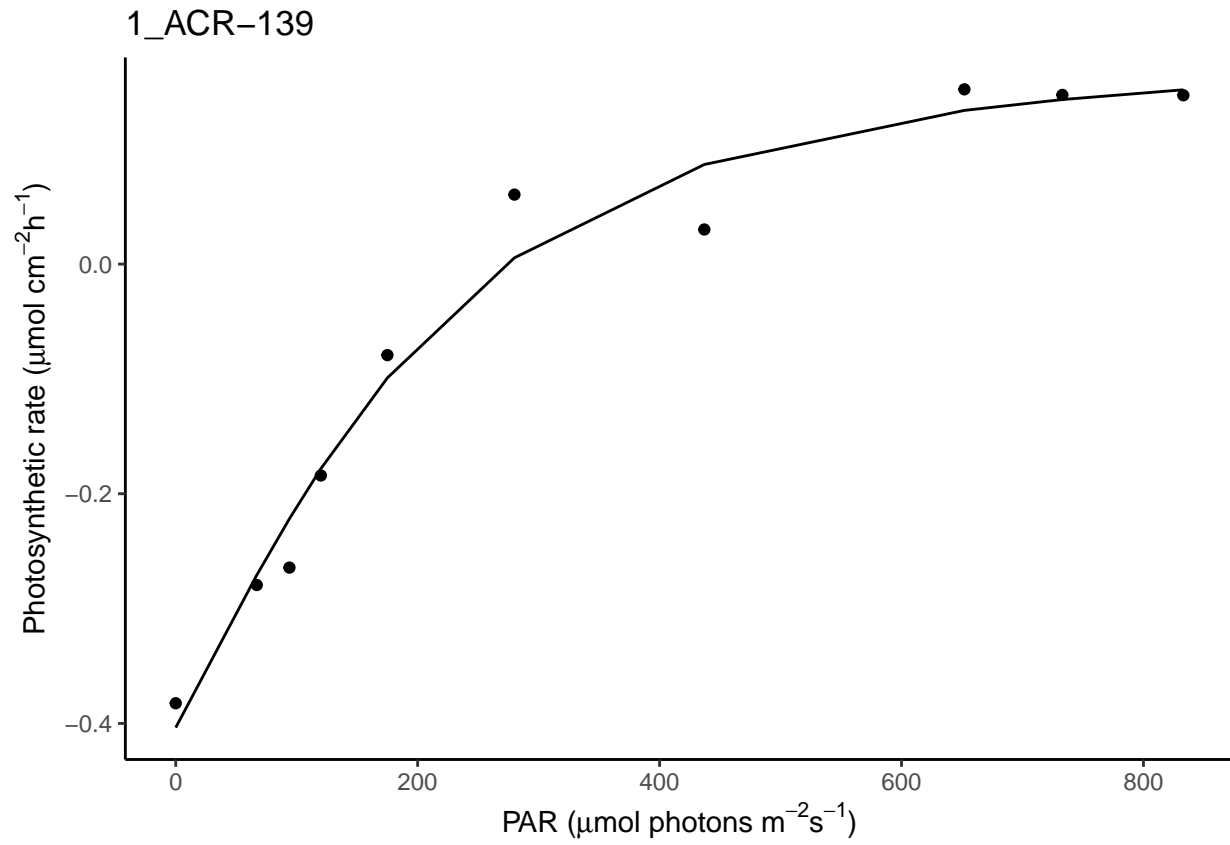
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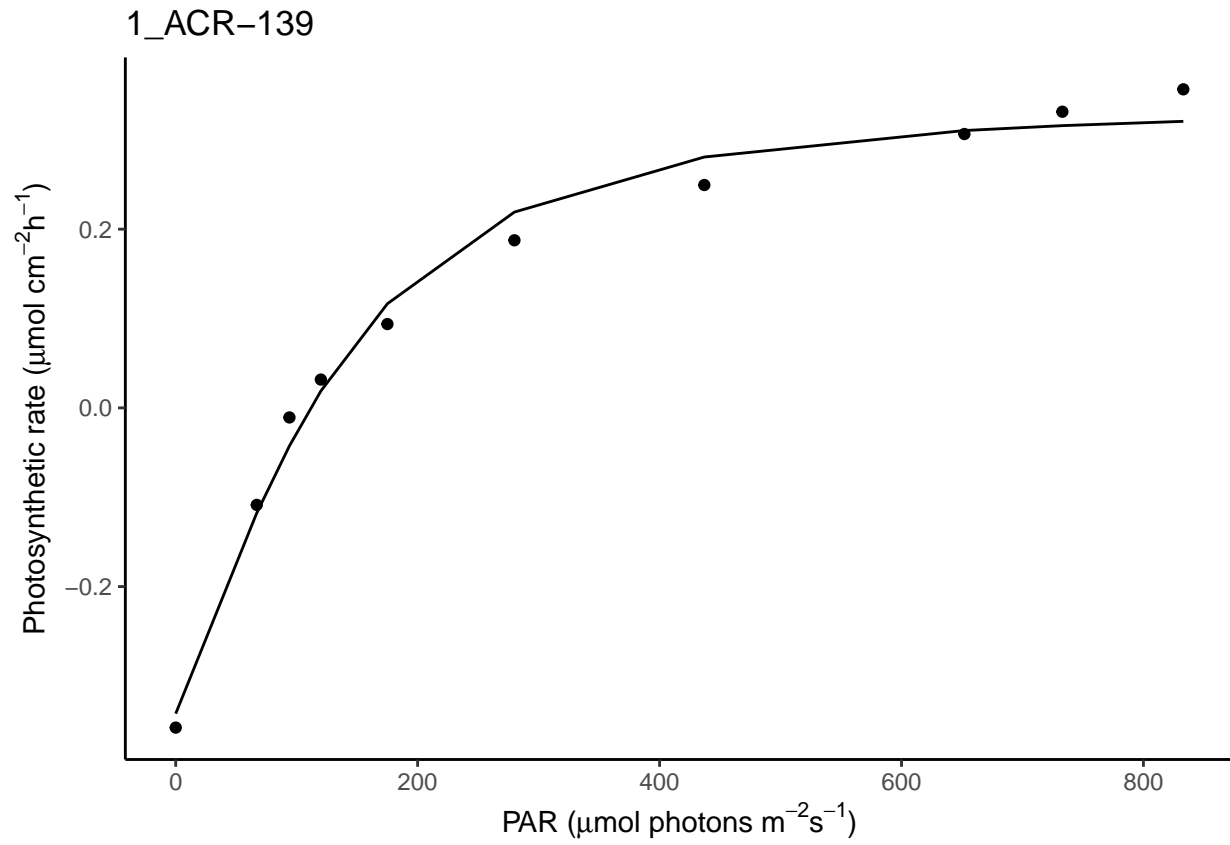
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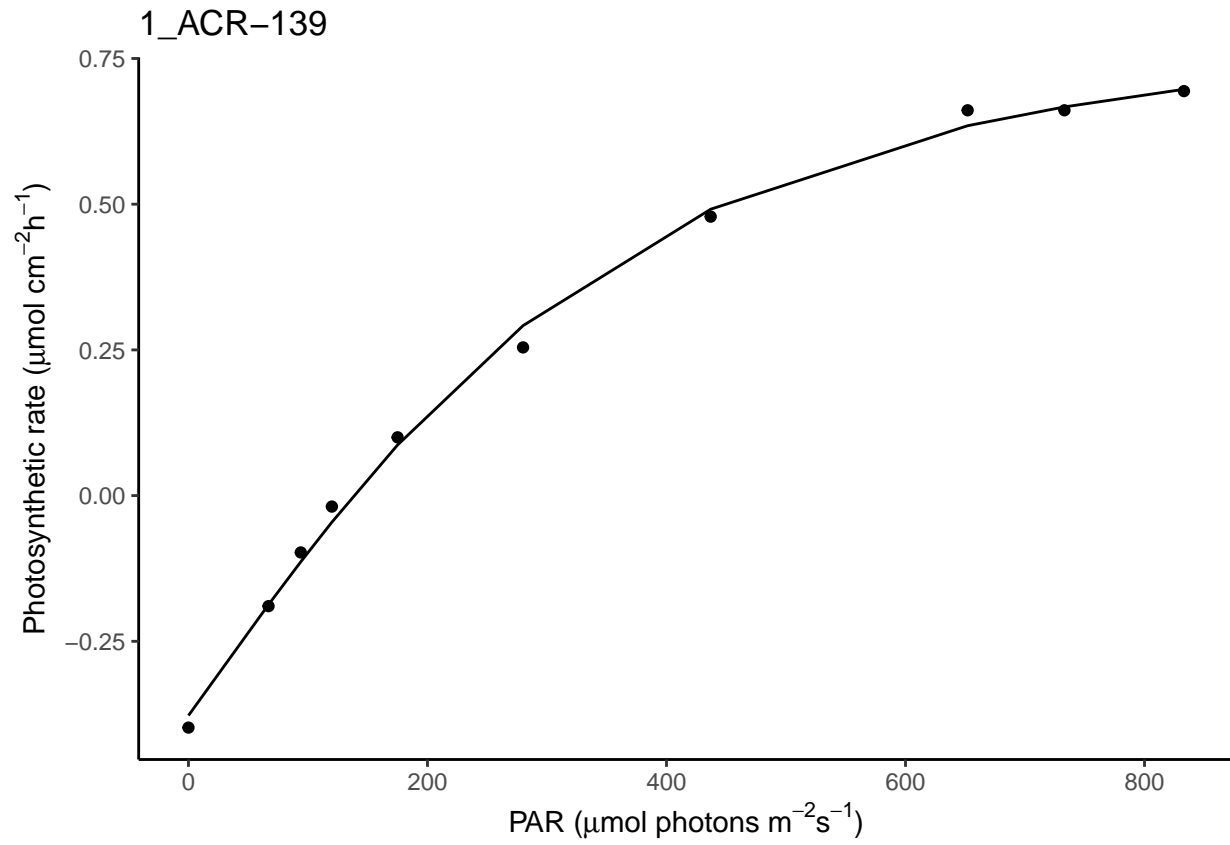
augmented\$colony_id: POC-372



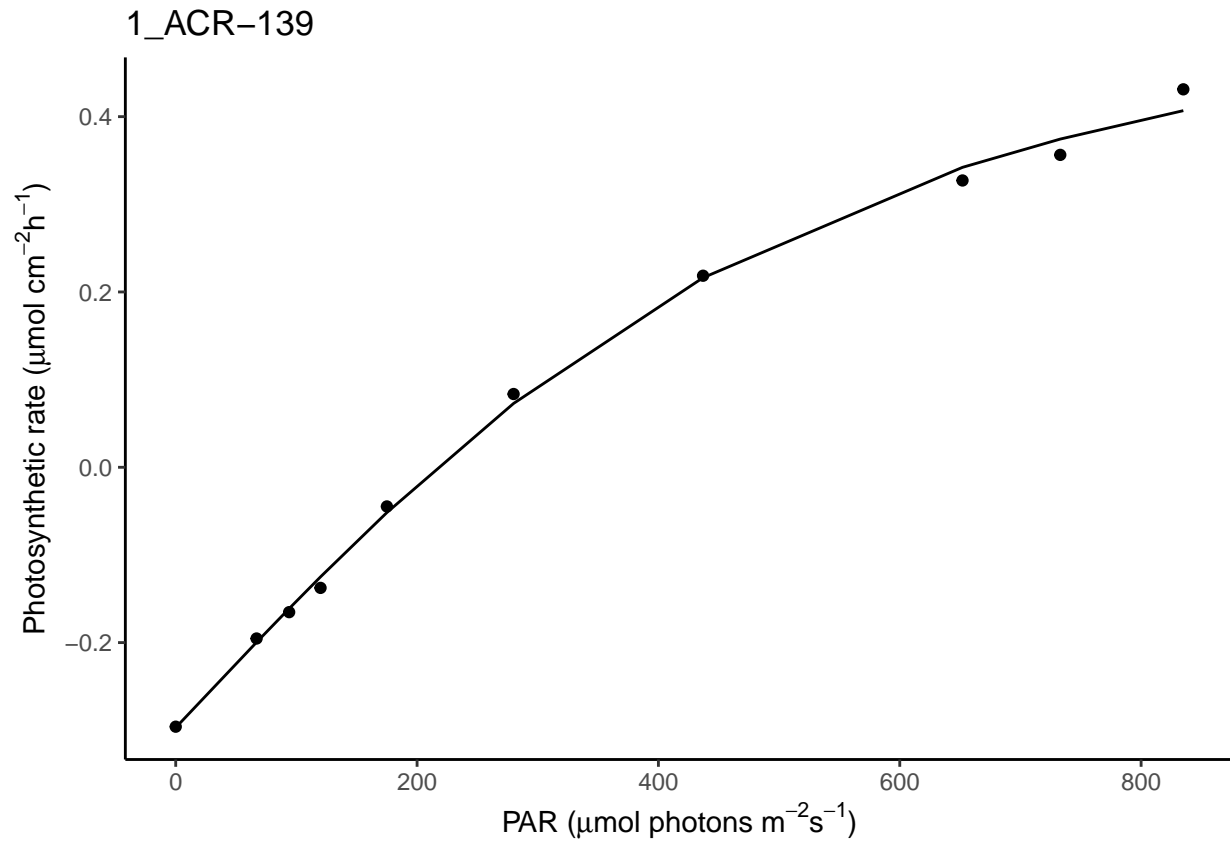
augmented\$colony_id: P0C-373



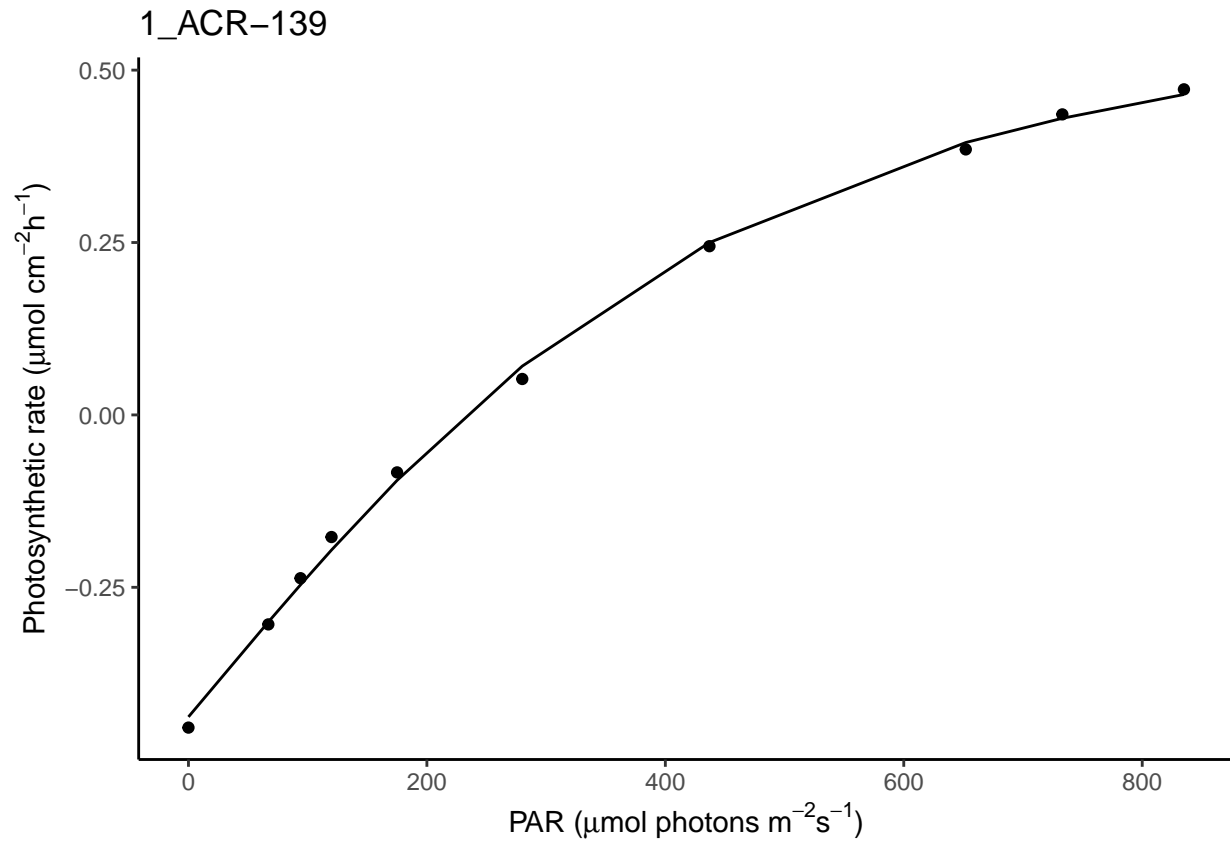
augmented\$colony_id: POC-375



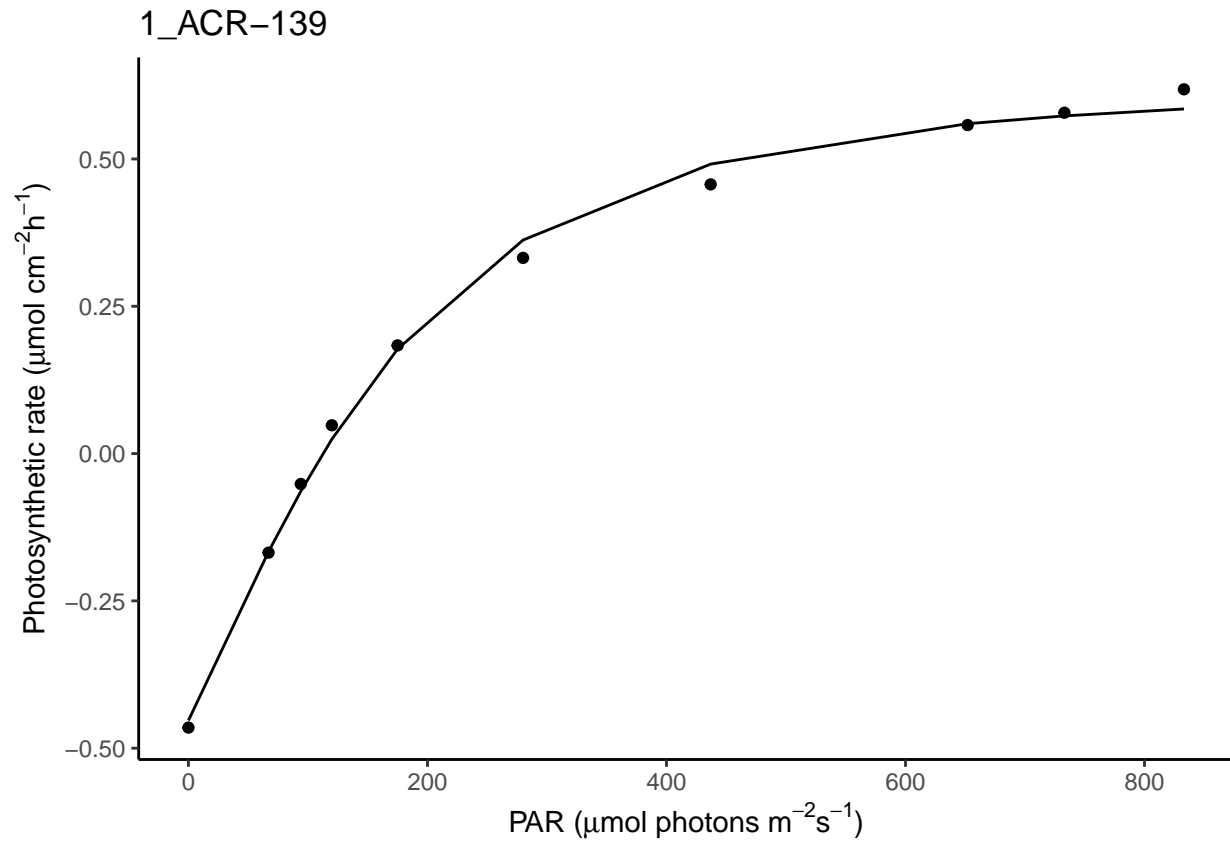
augmented\$colony_id: POC-377



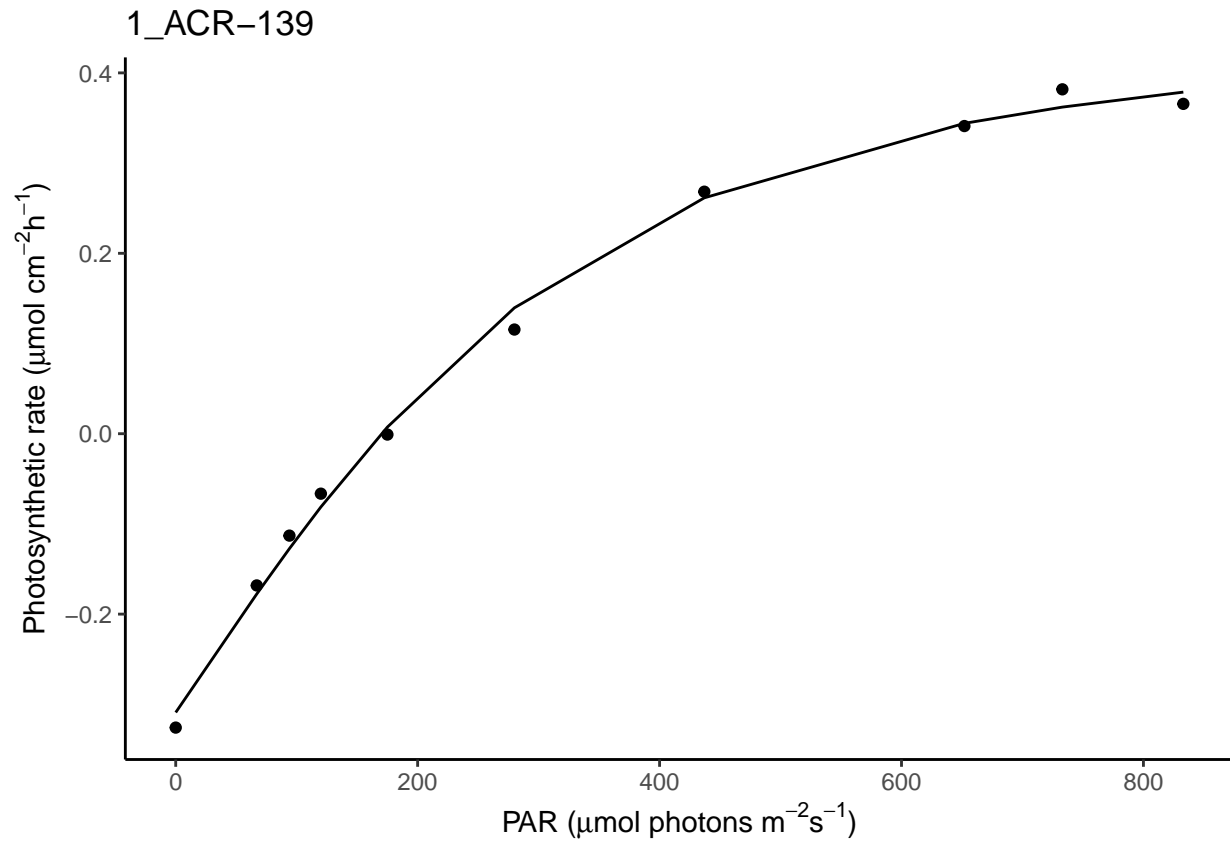
augmented\$colony_id: POC-378



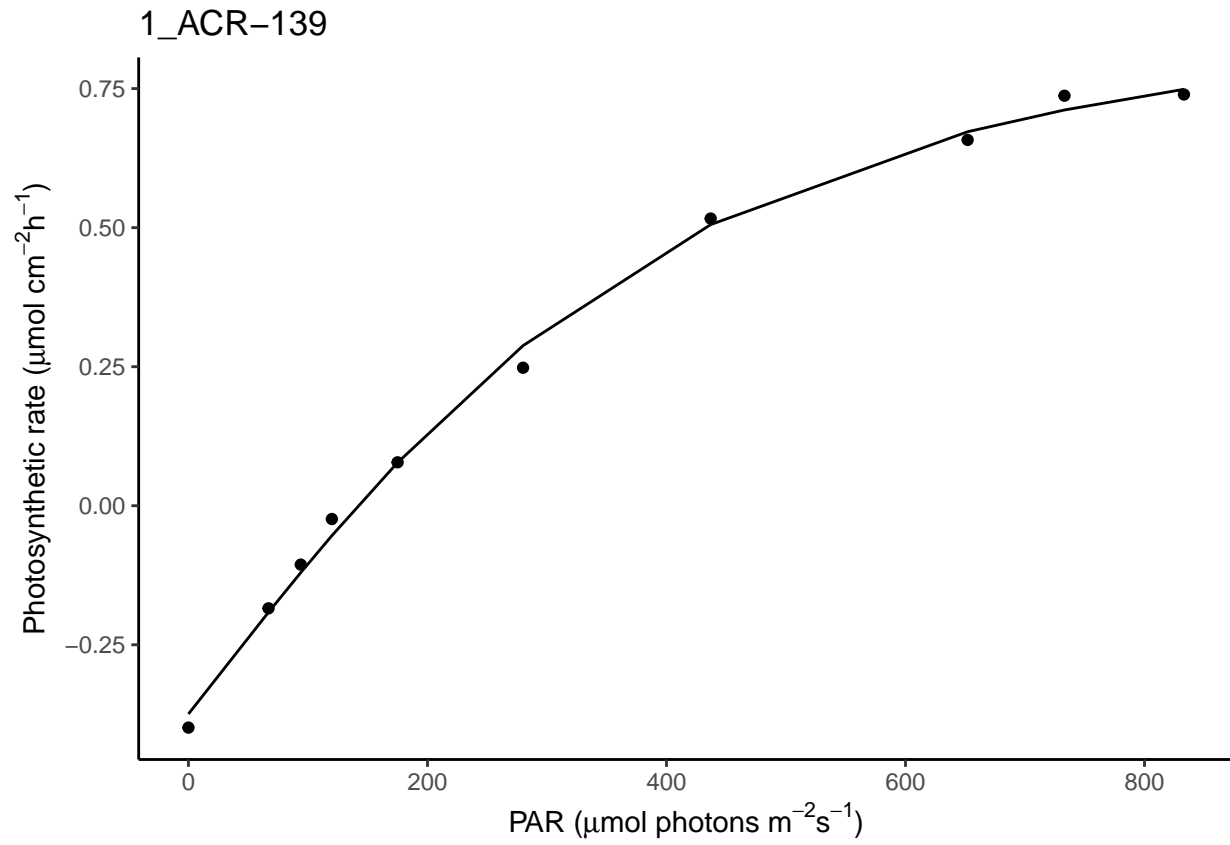
augmented\$colony_id: POC-386



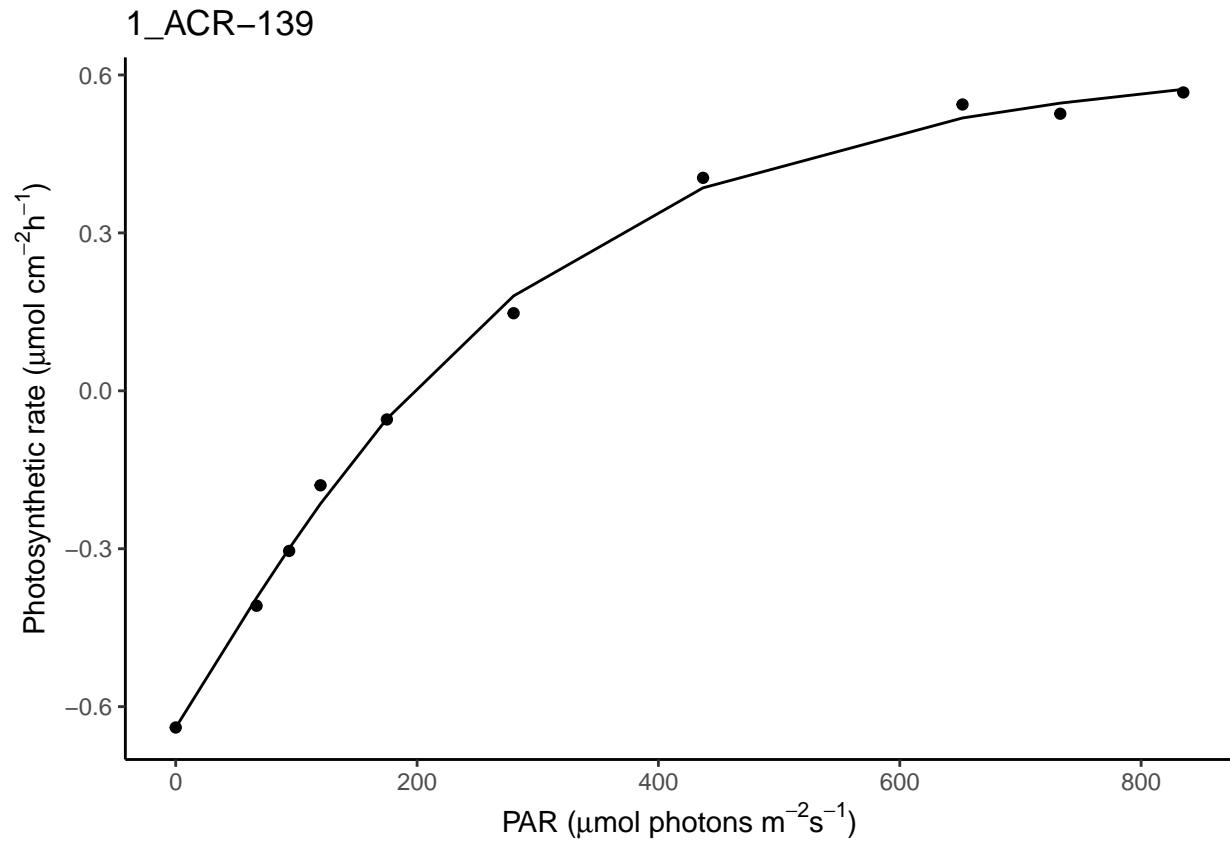
augmented\$colony_id: POC-391



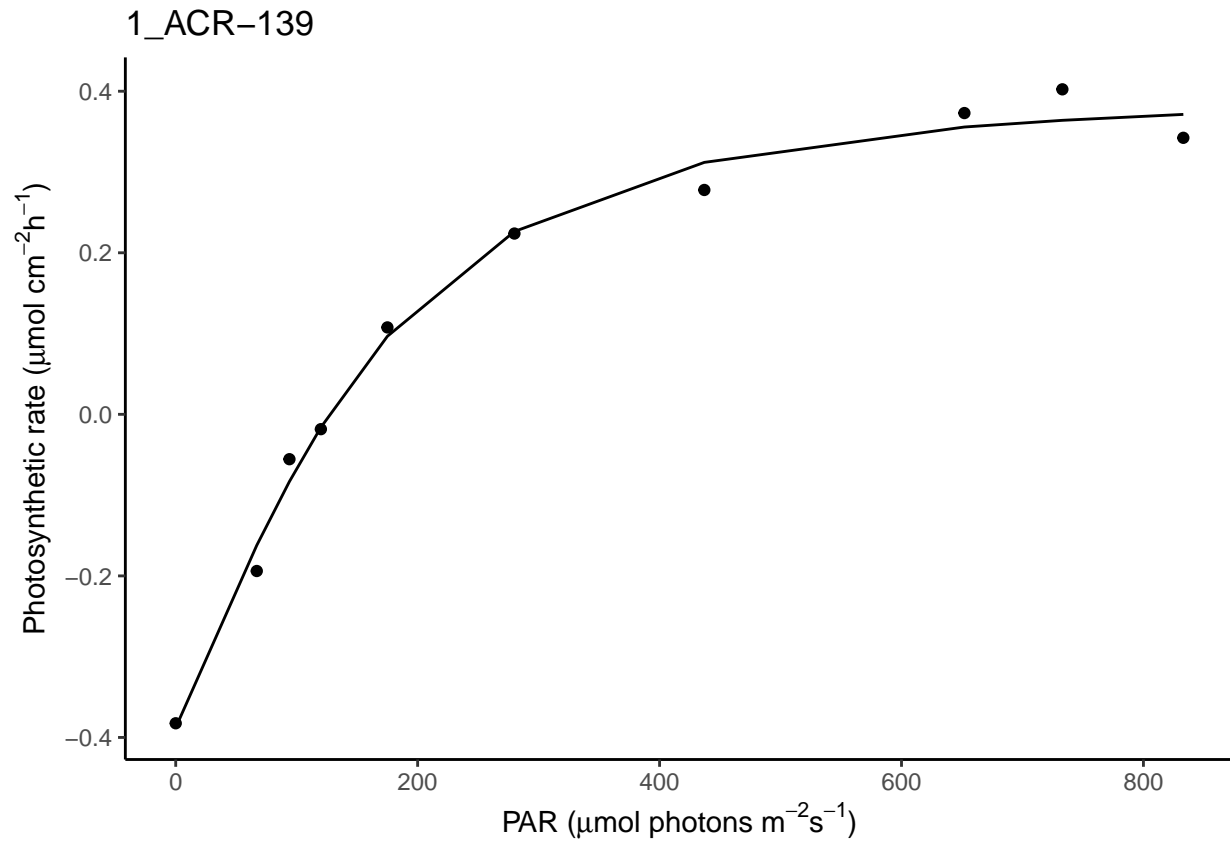
augmented\$colony_id: POC-394



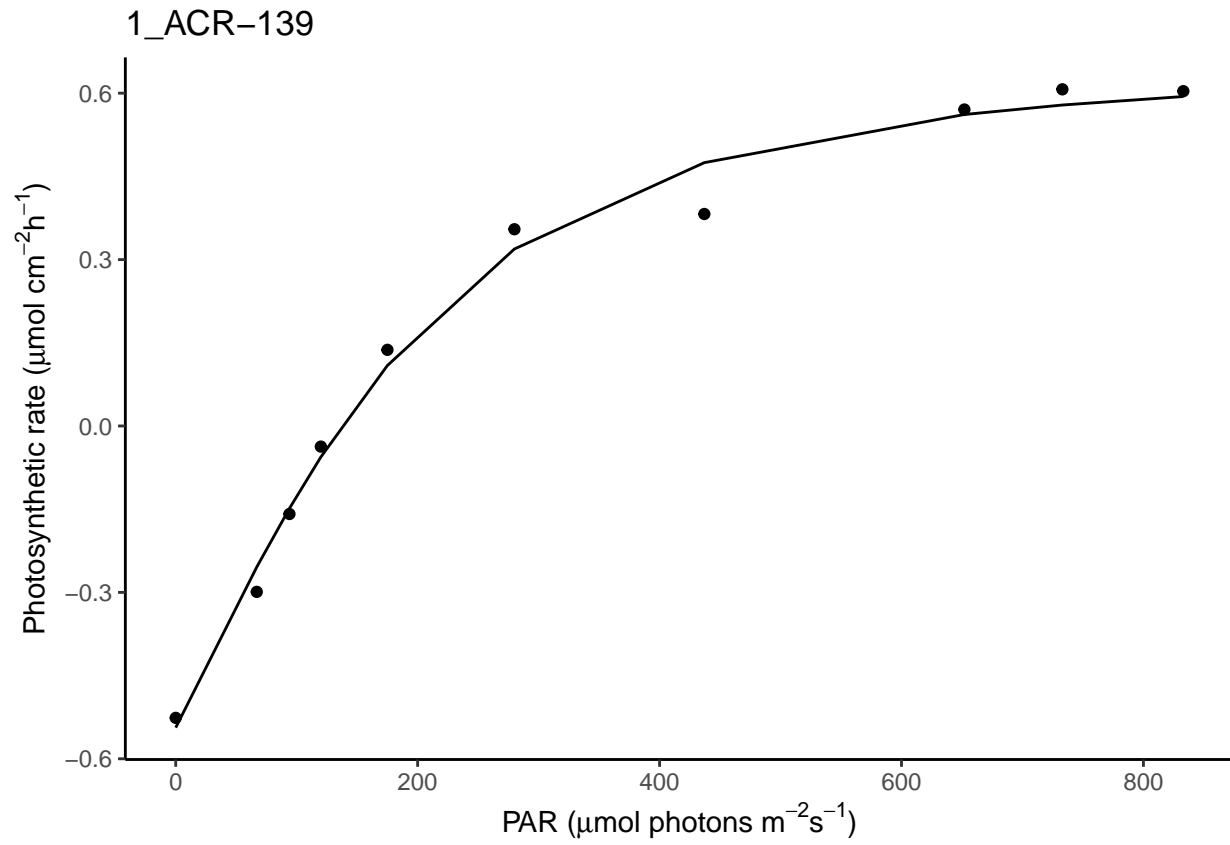
augmented\$colony_id: P0C-395



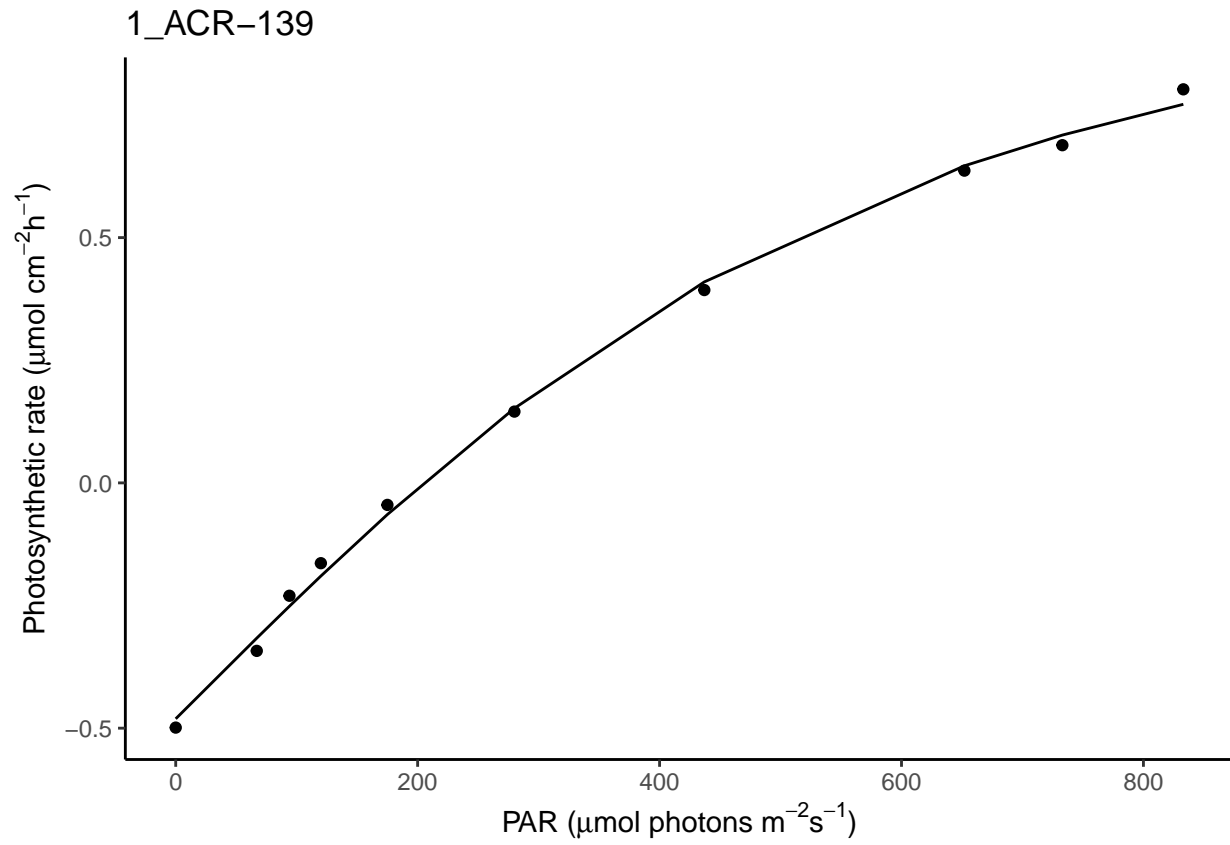
augmented\$colony_id: POC-40



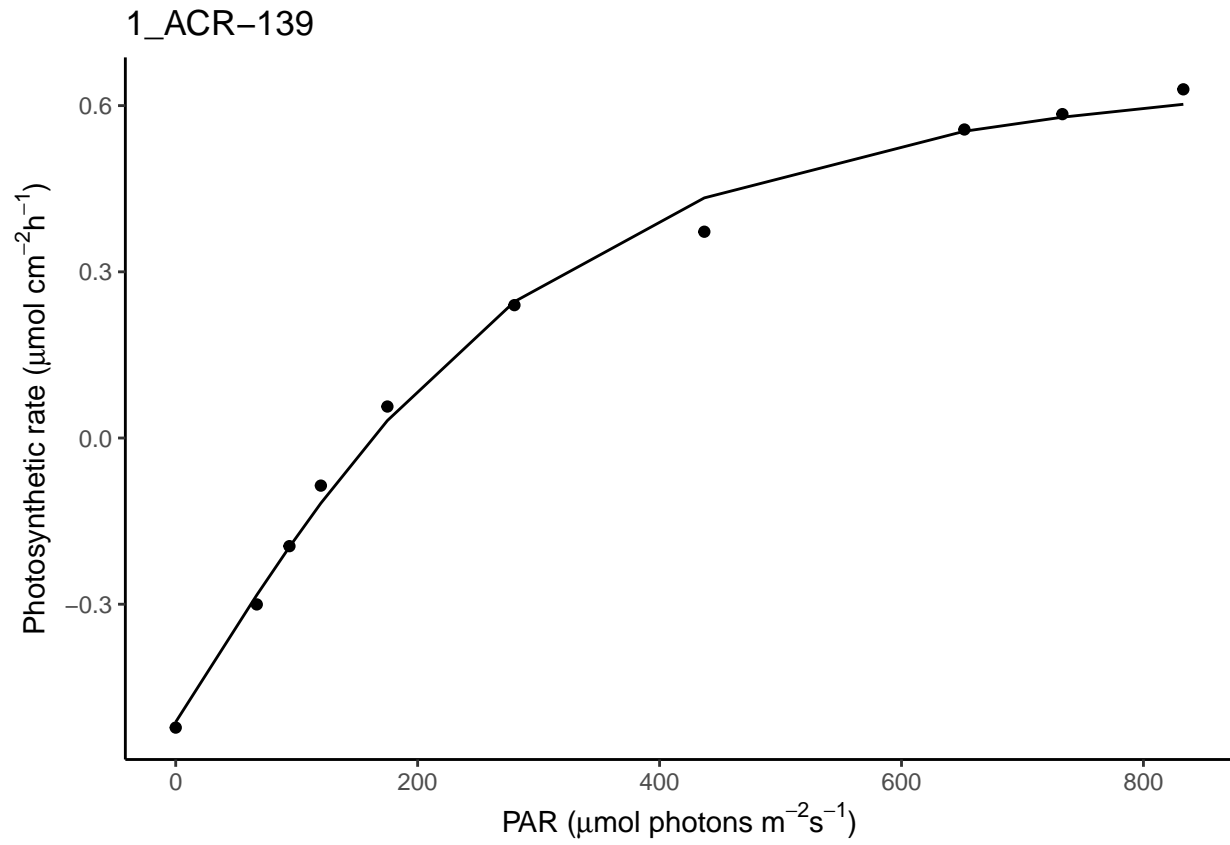
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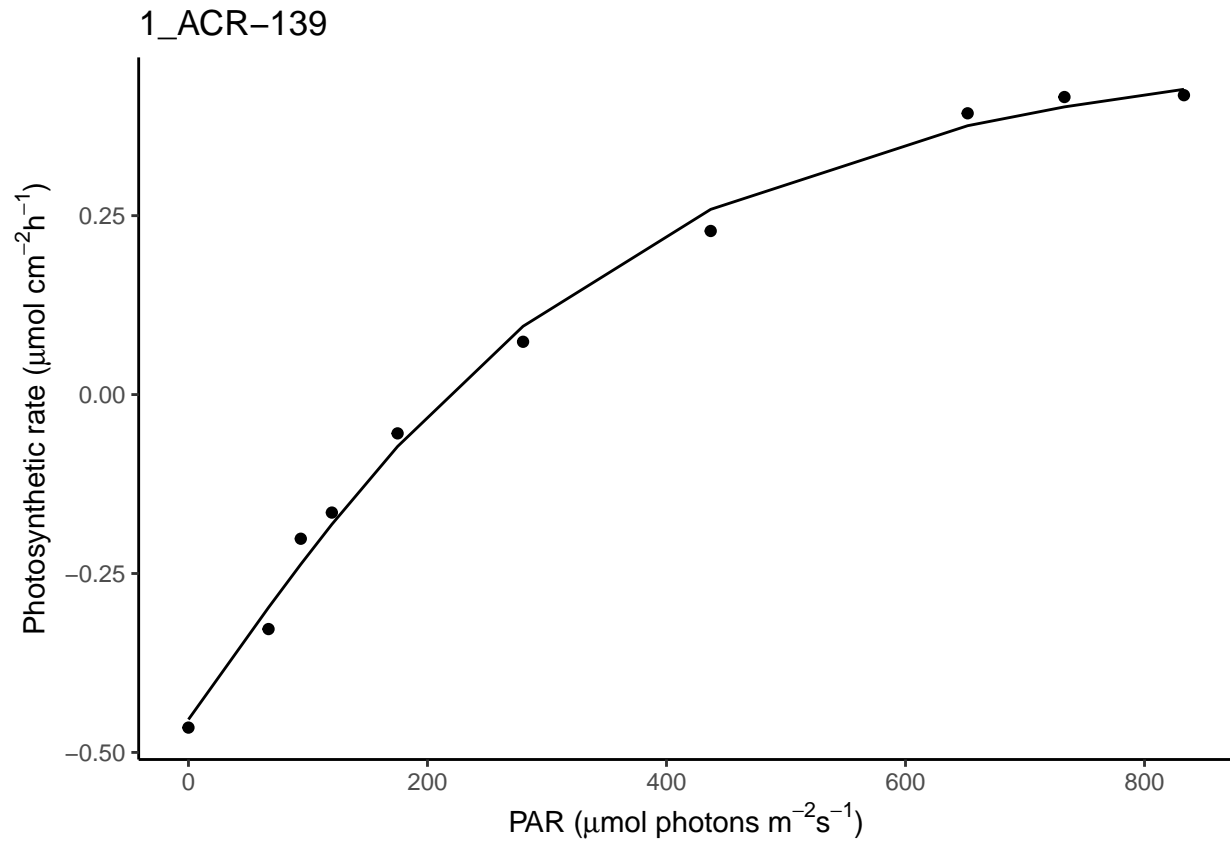
augmented\$colony_id: POC-42



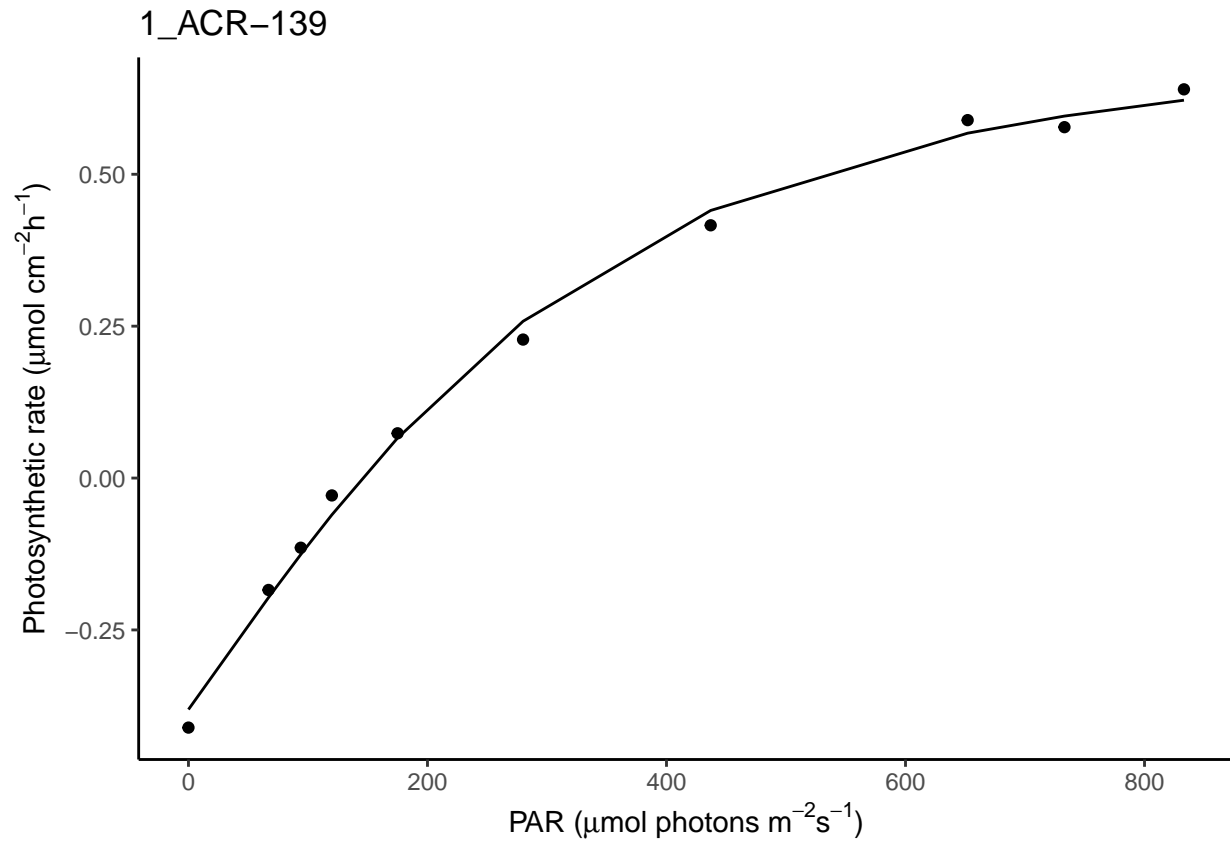
augmented\$colony_id: POC-43



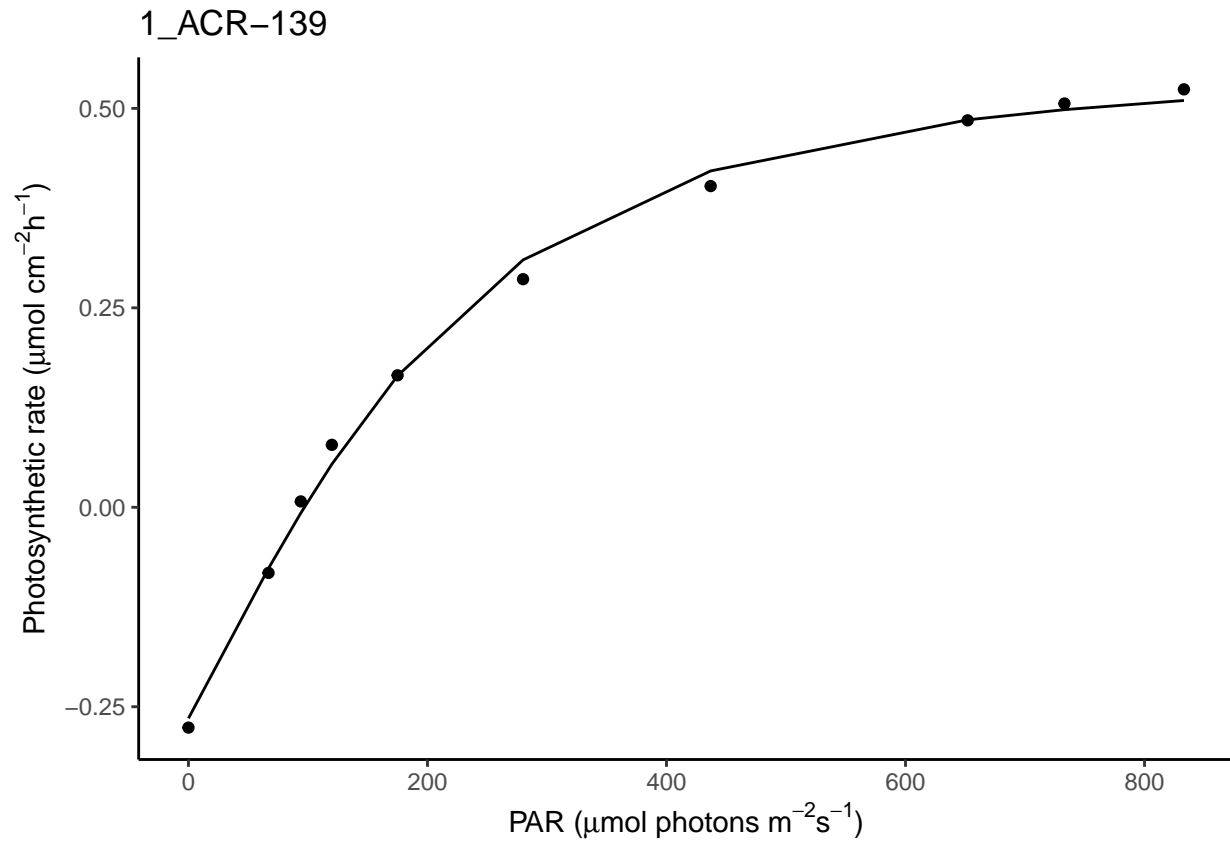
augmented\$colony_id: POC-44



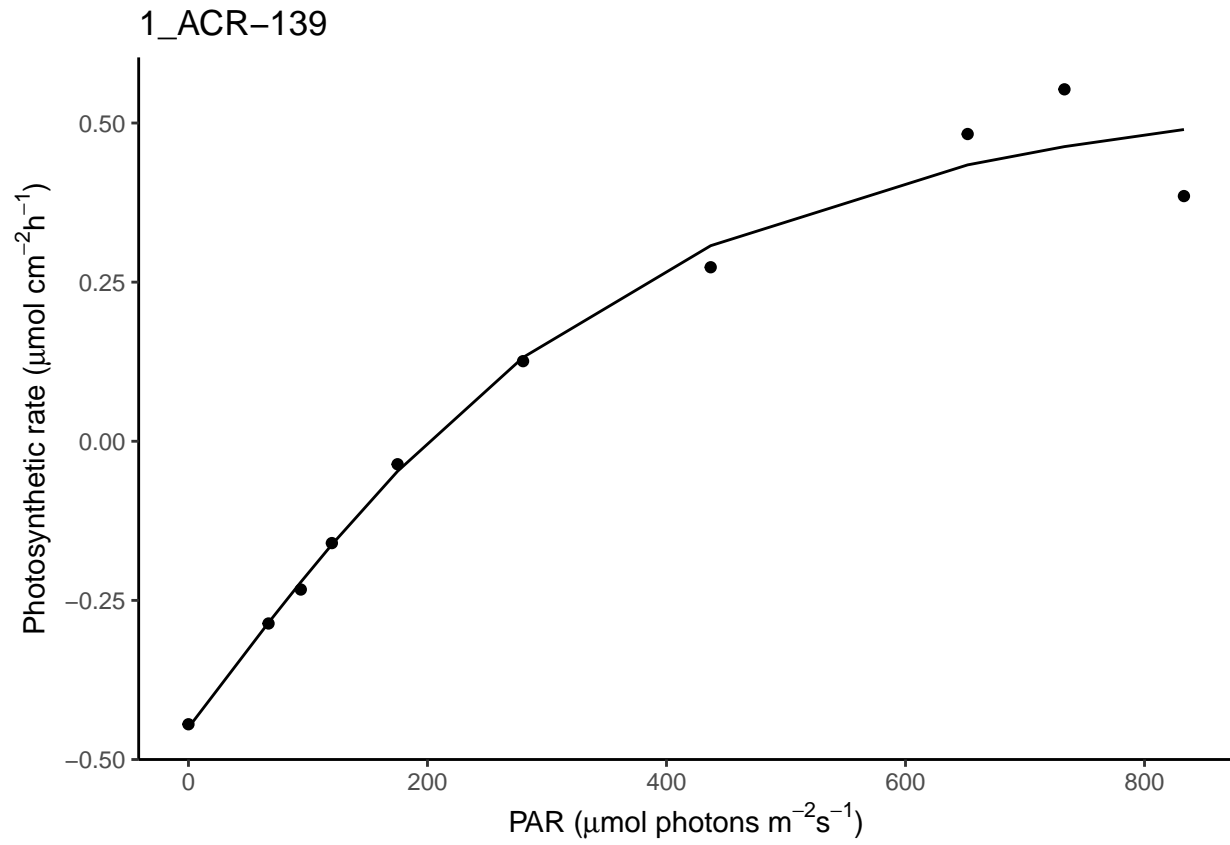
augmented\$colony_id: POC-45



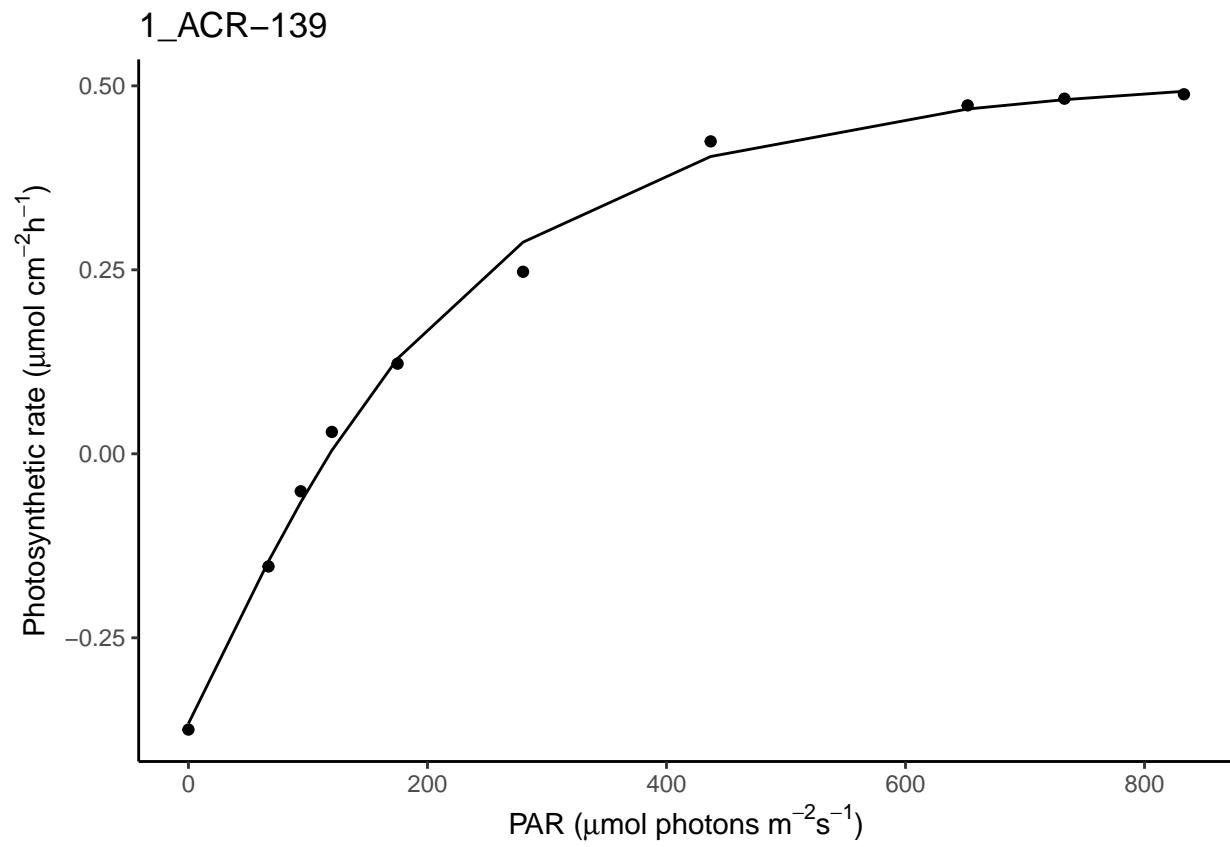
augmented\$colony_id: POC-47



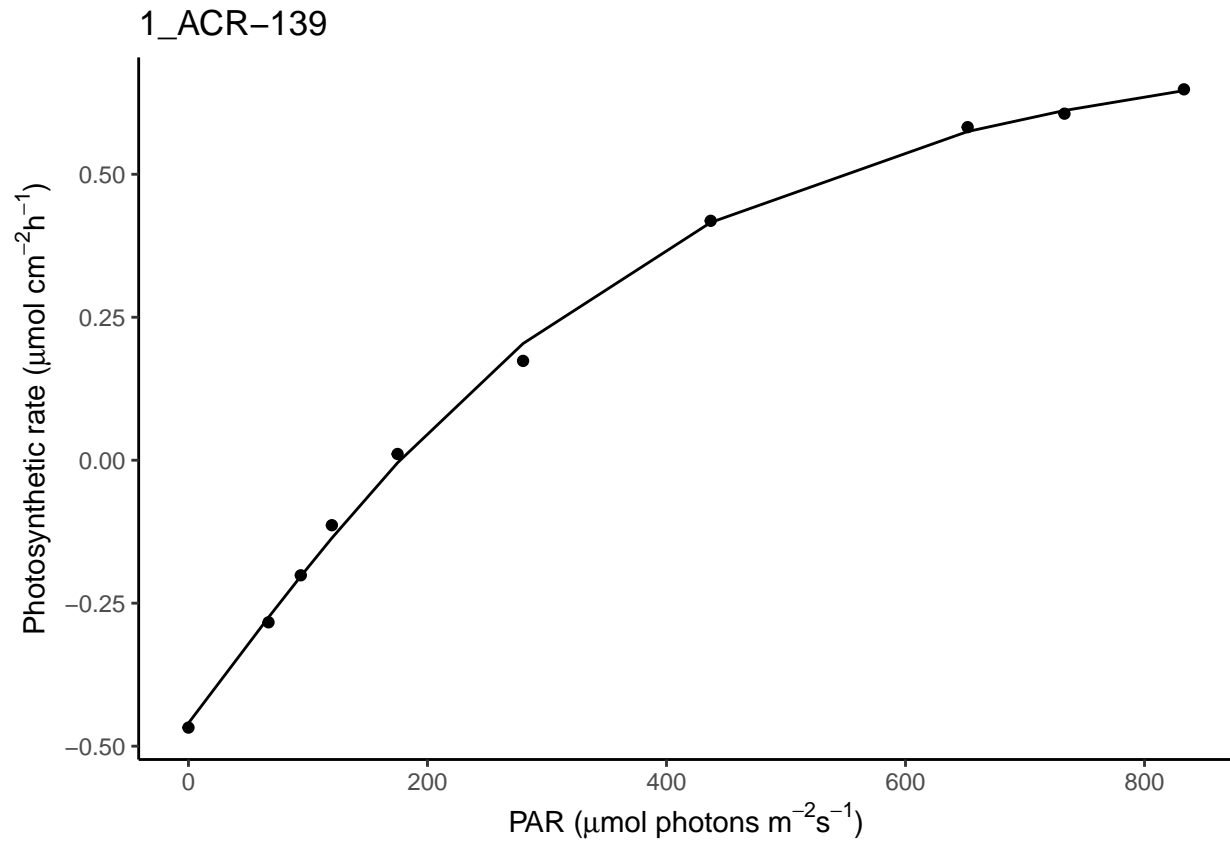
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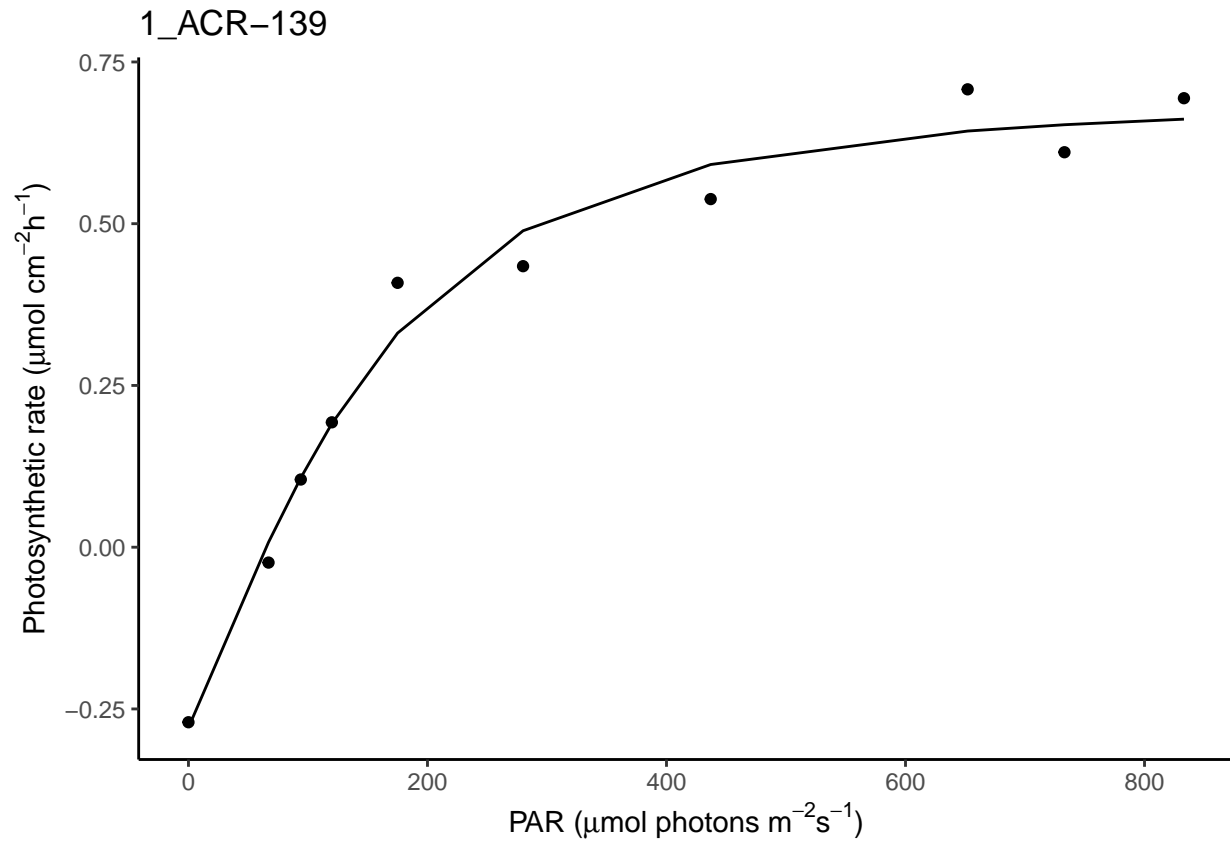
augmented\$colony_id: POC-50



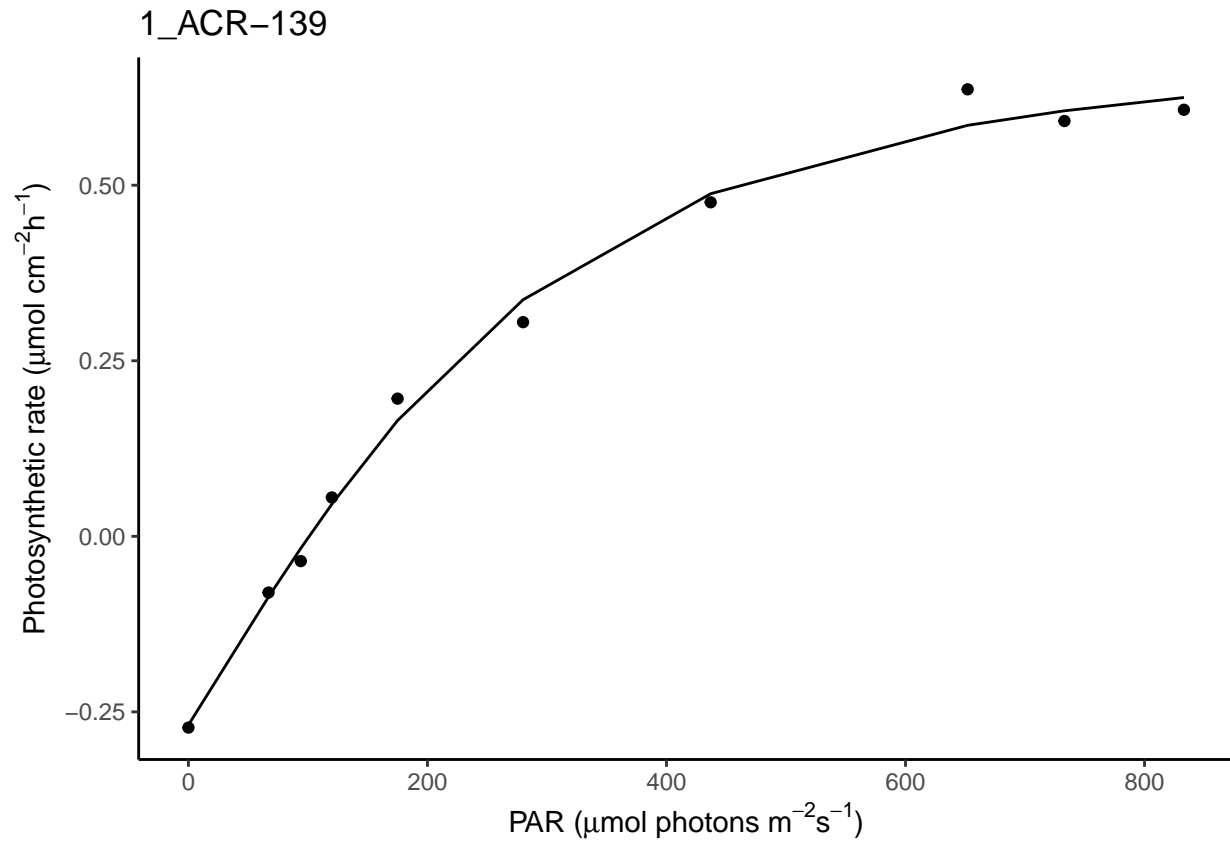
augmented\$colony_id: POC-52



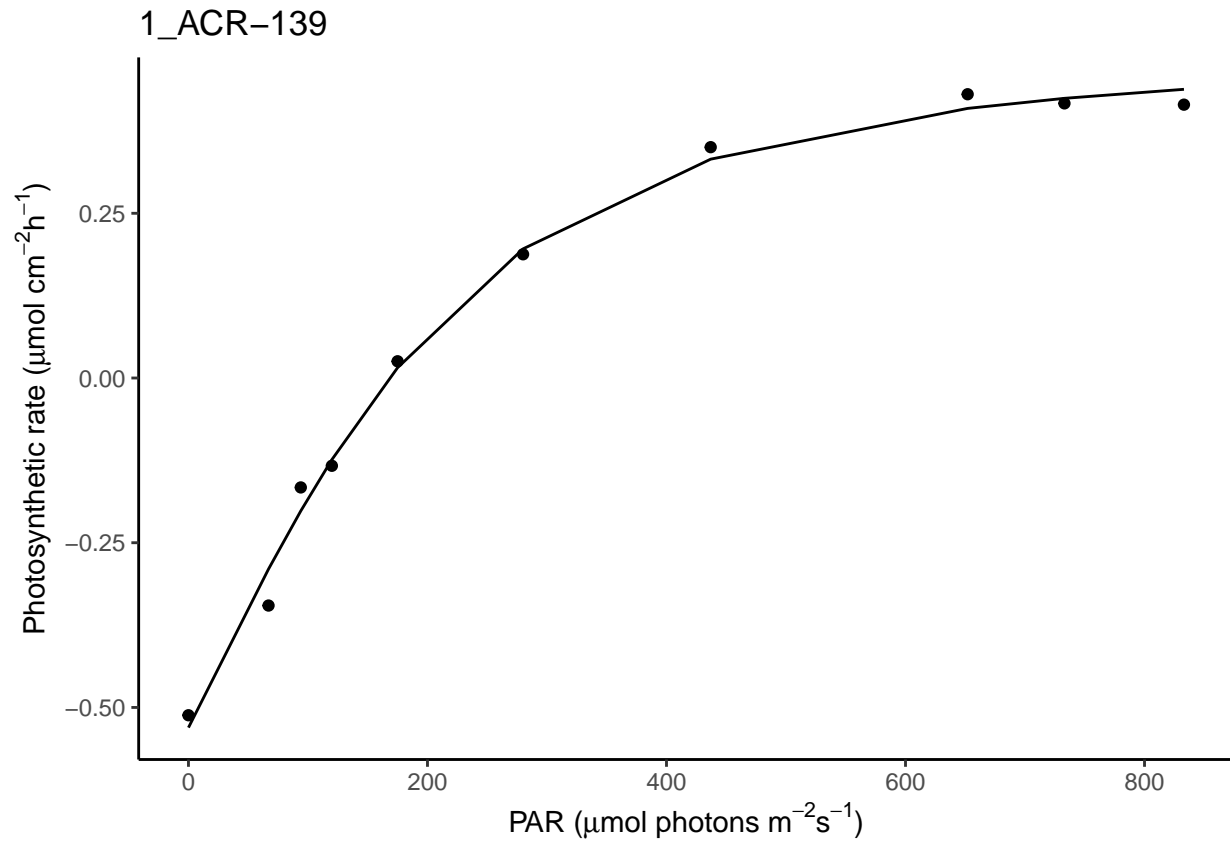
augmented\$colony_id: POC-53



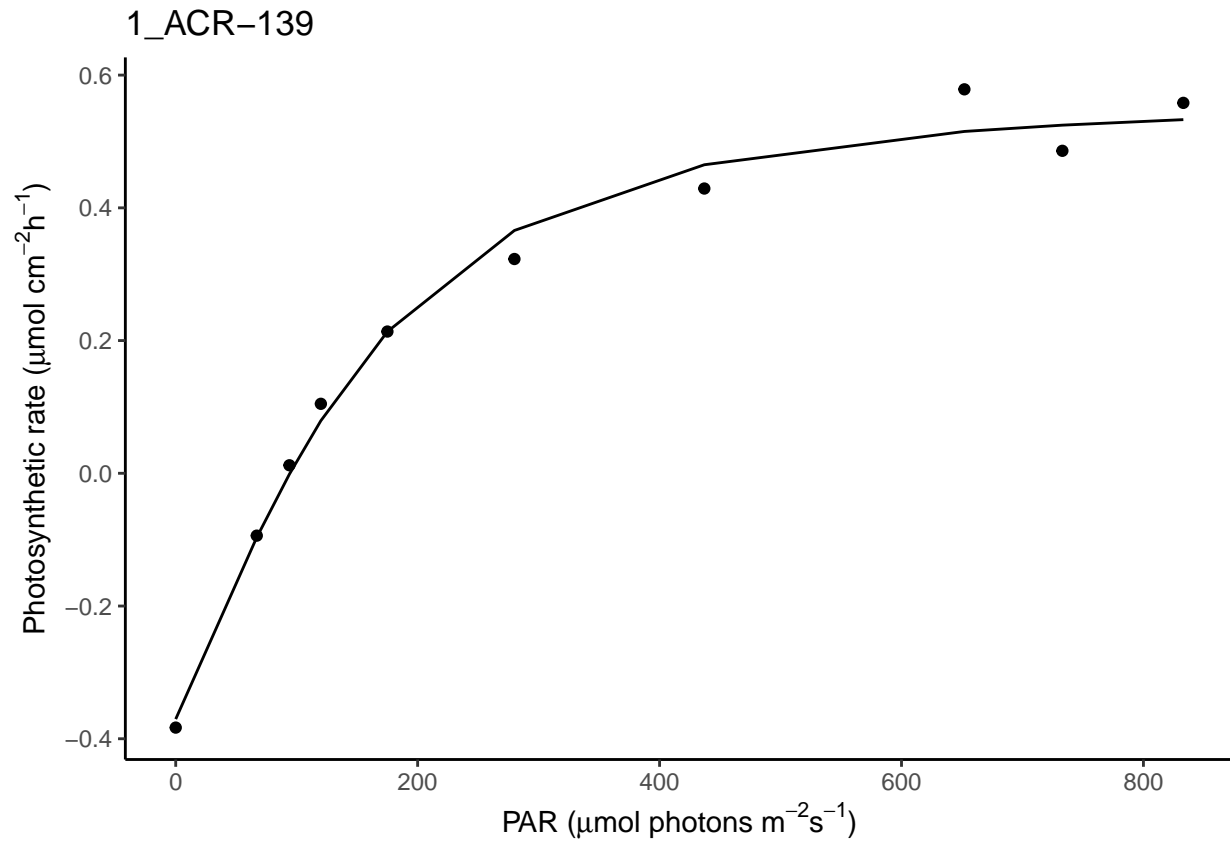
augmented\$colony_id: POC-55



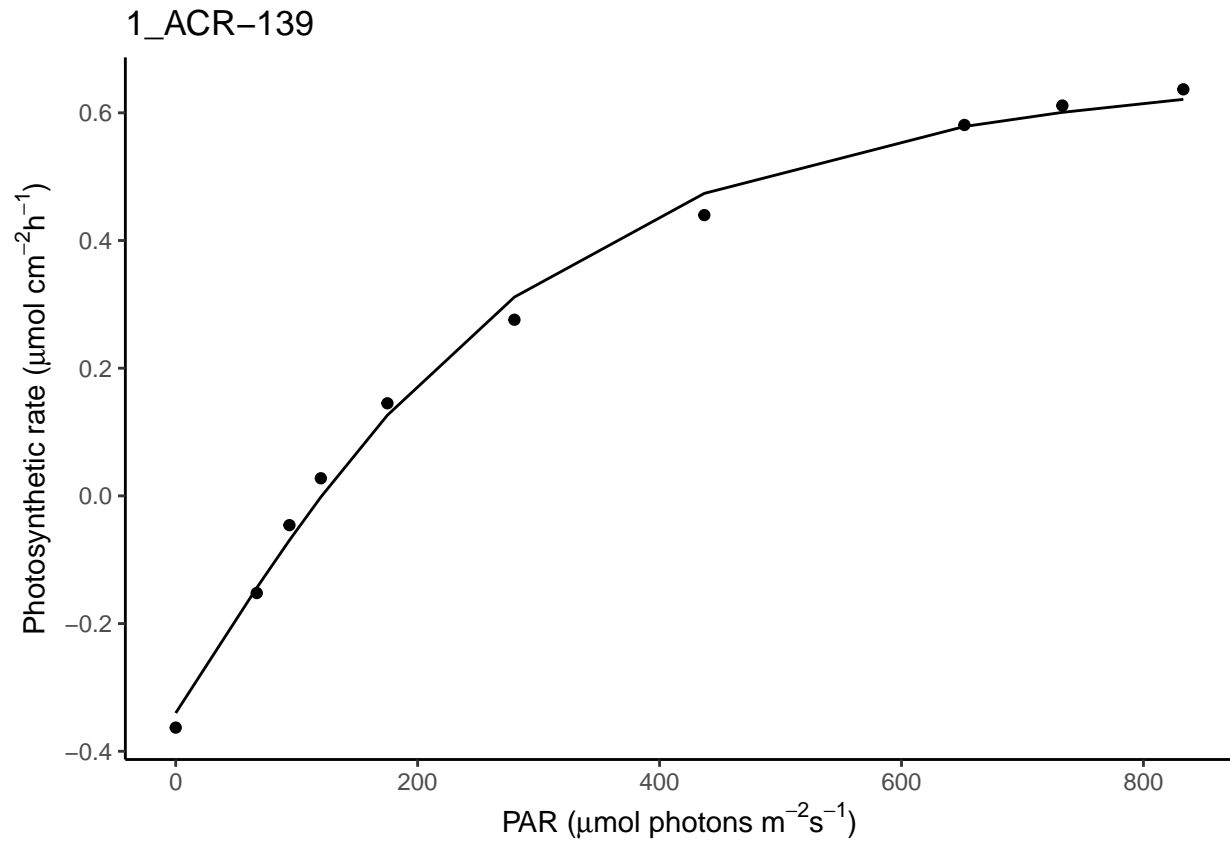
augmented\$colony_id: POC-56



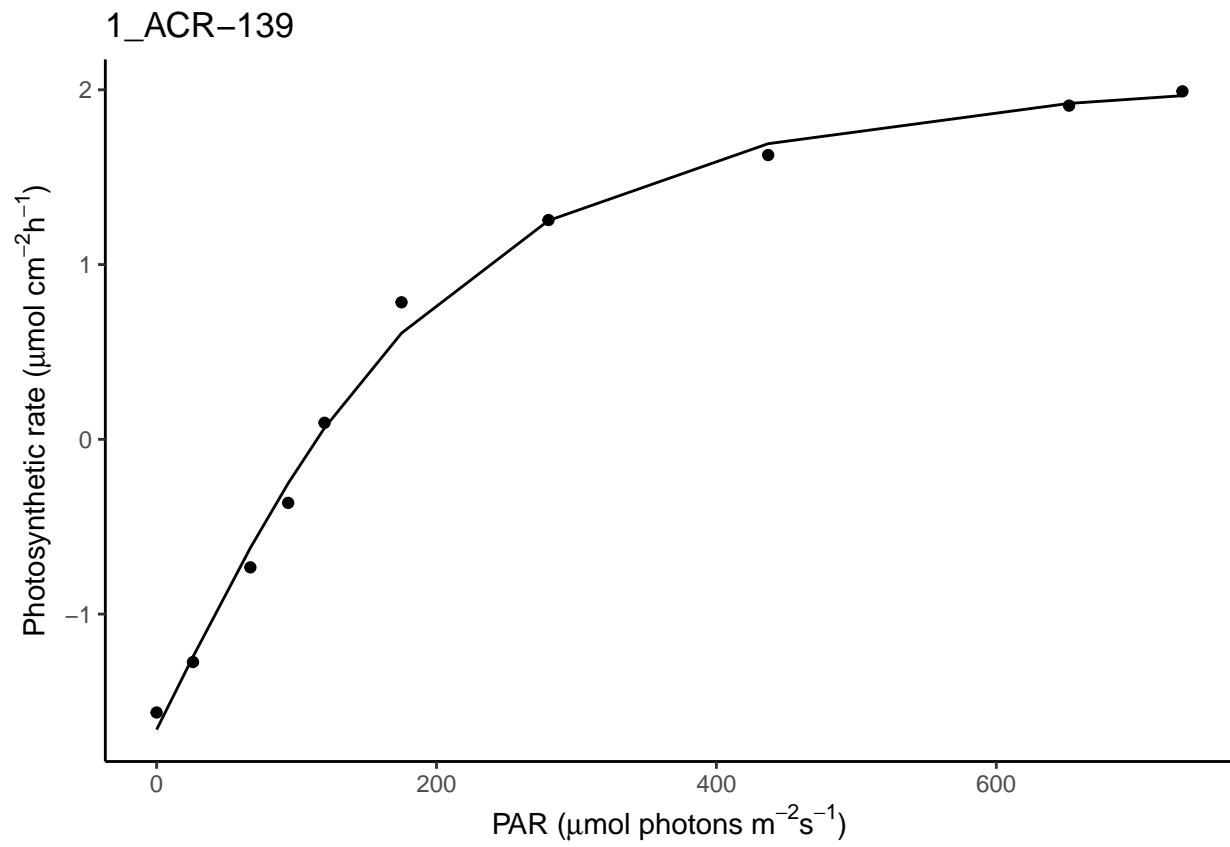
augmented\$colony_id: POC-57



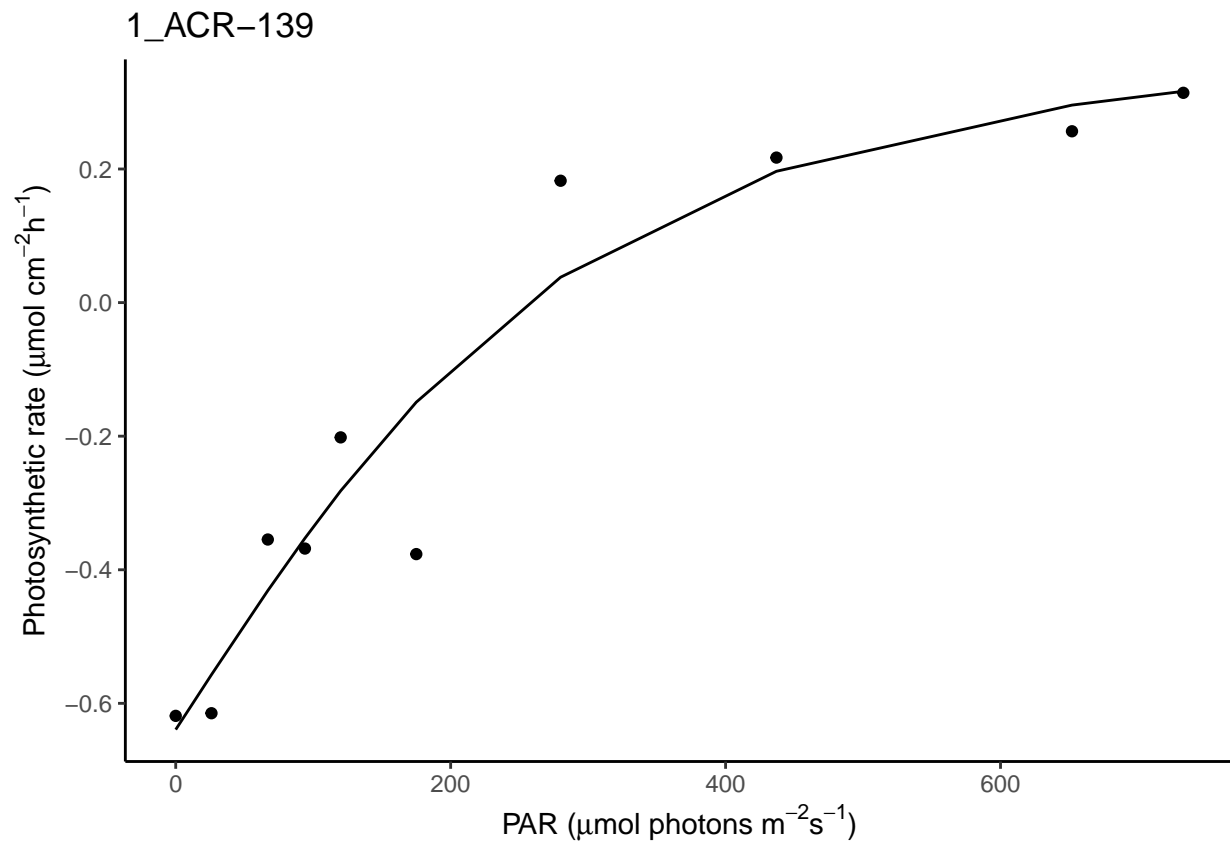
augmented\$colony_id: POC-68



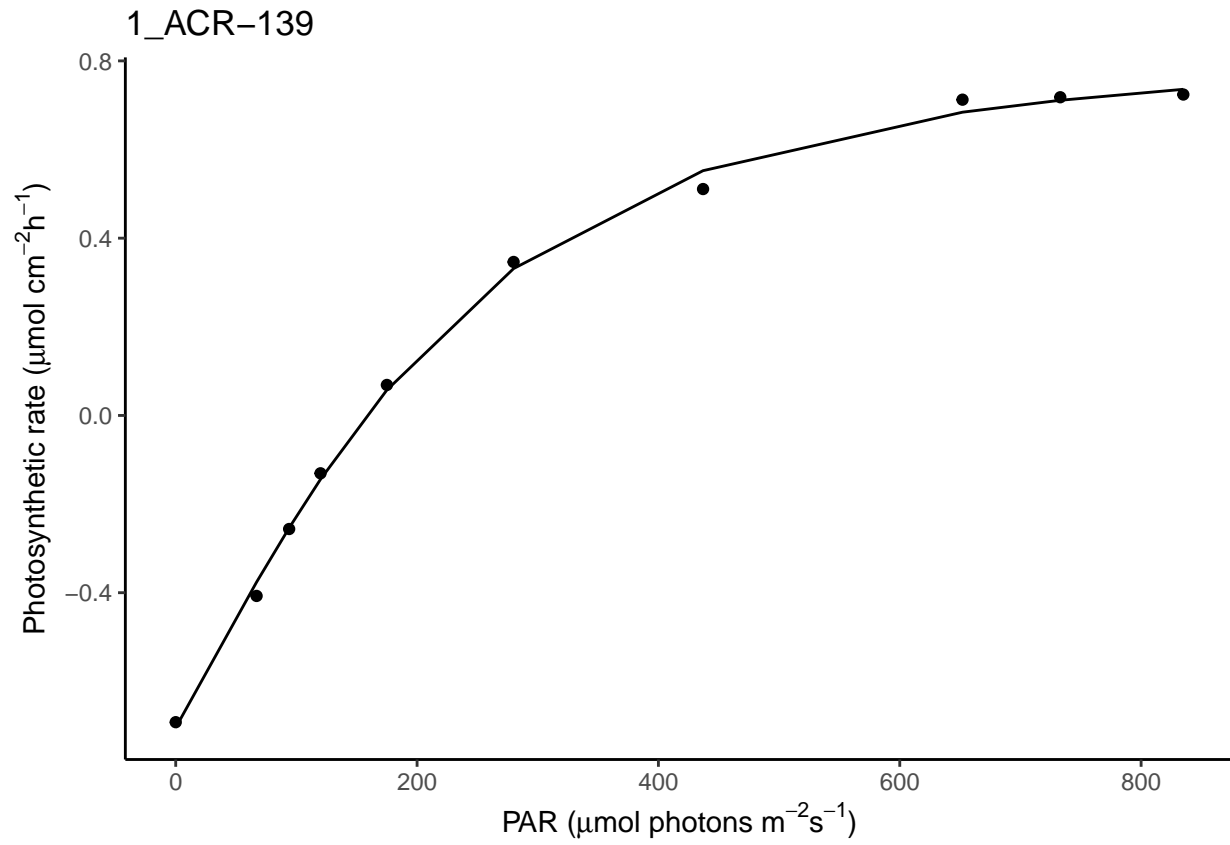
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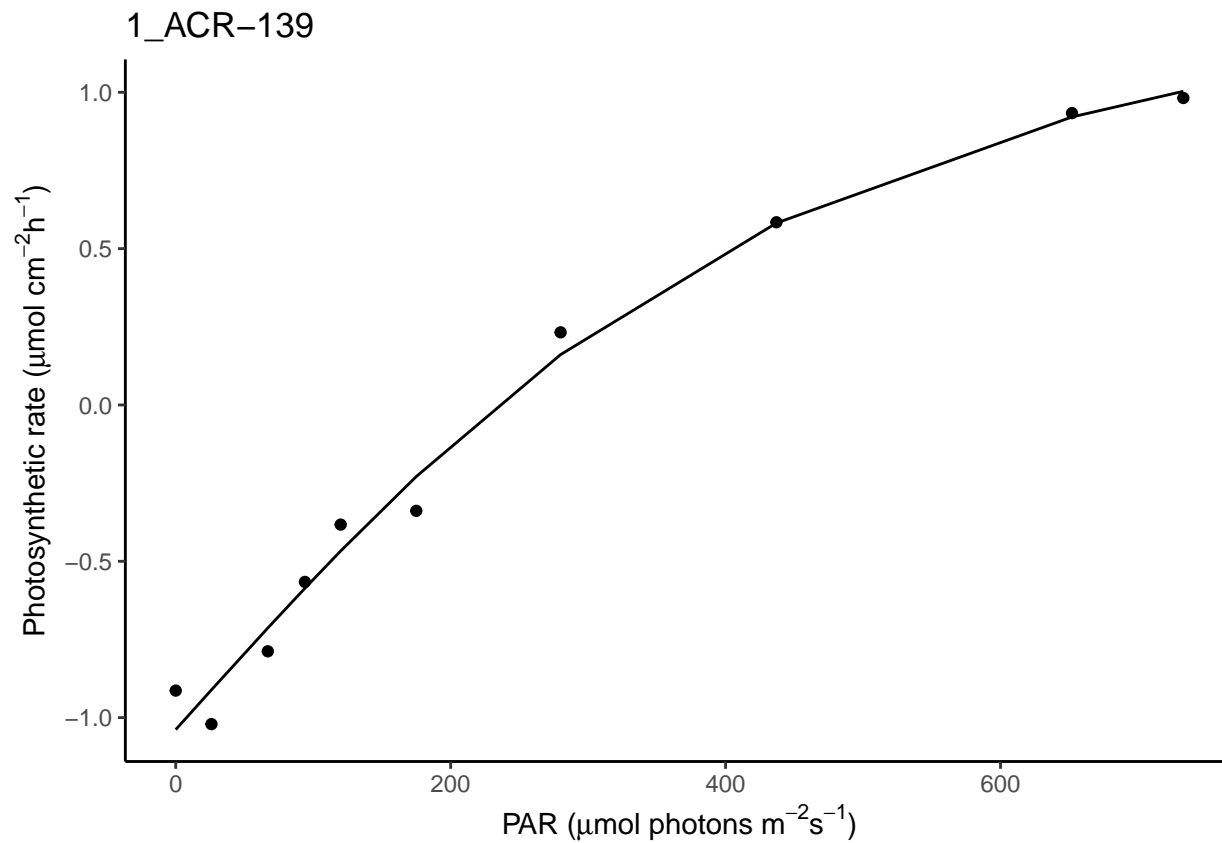
augmented\$colony_id: POR-214



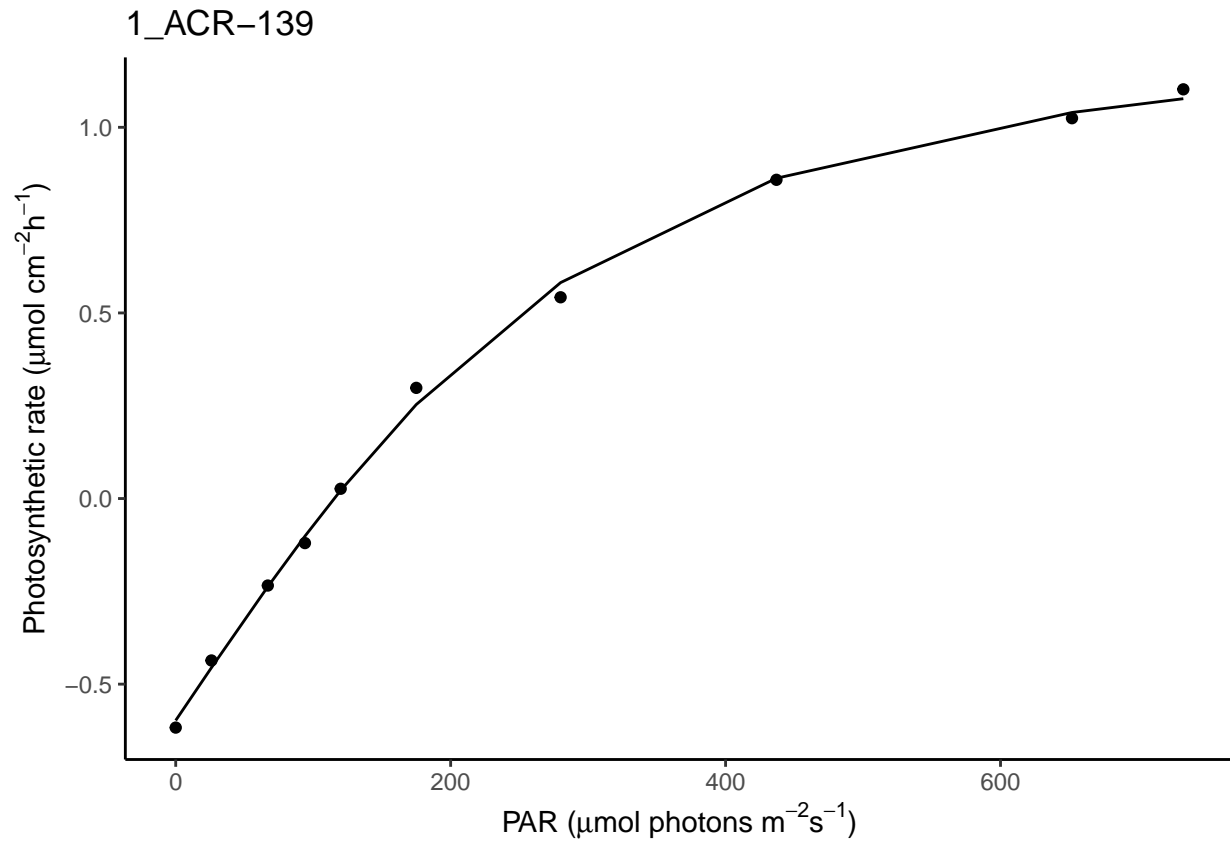
augmented\$colony_id: POR-216



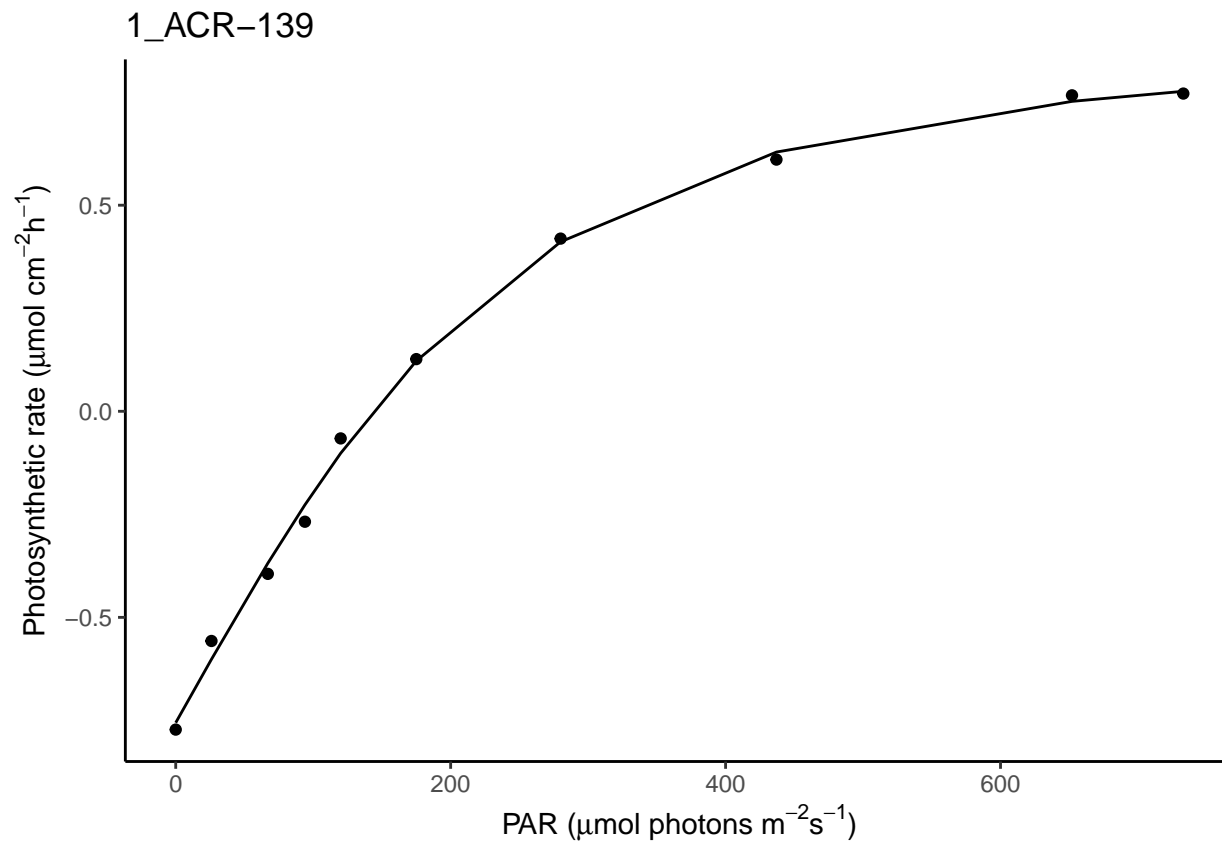
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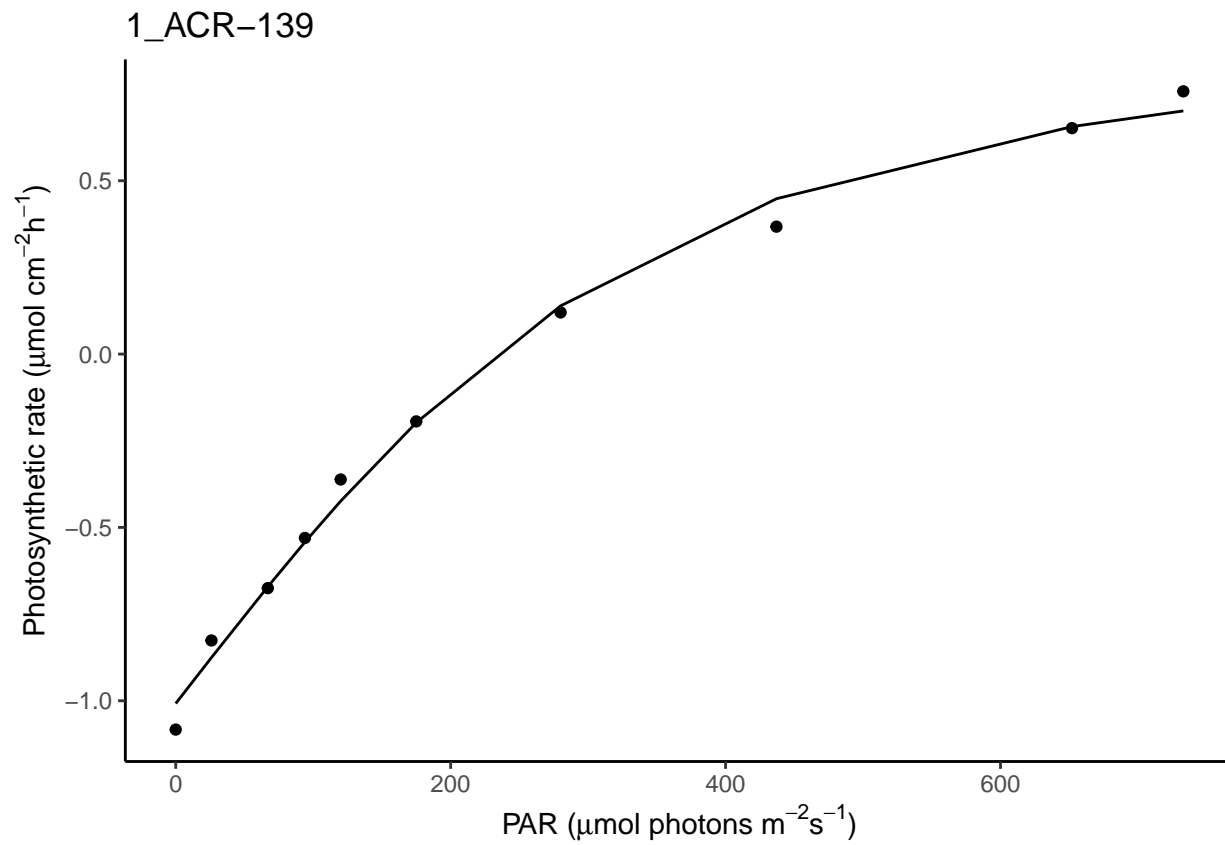
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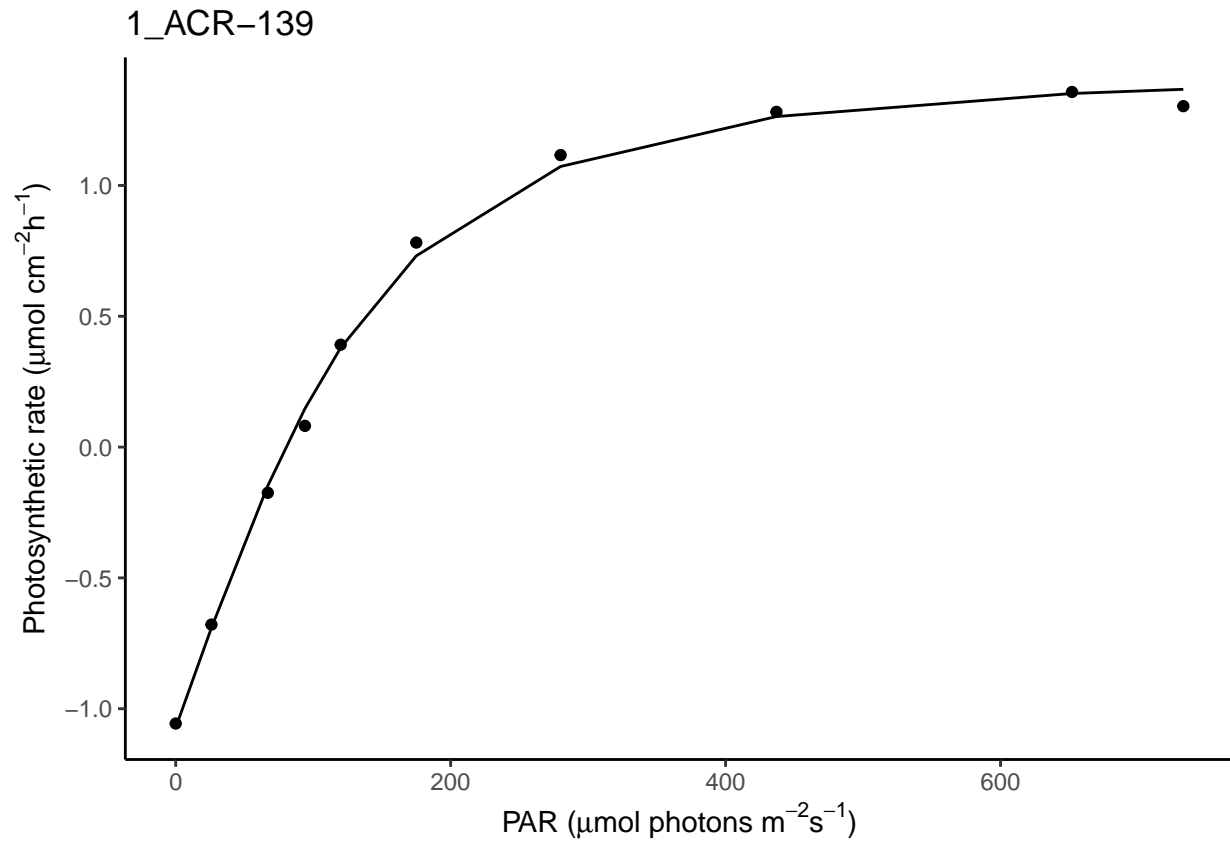
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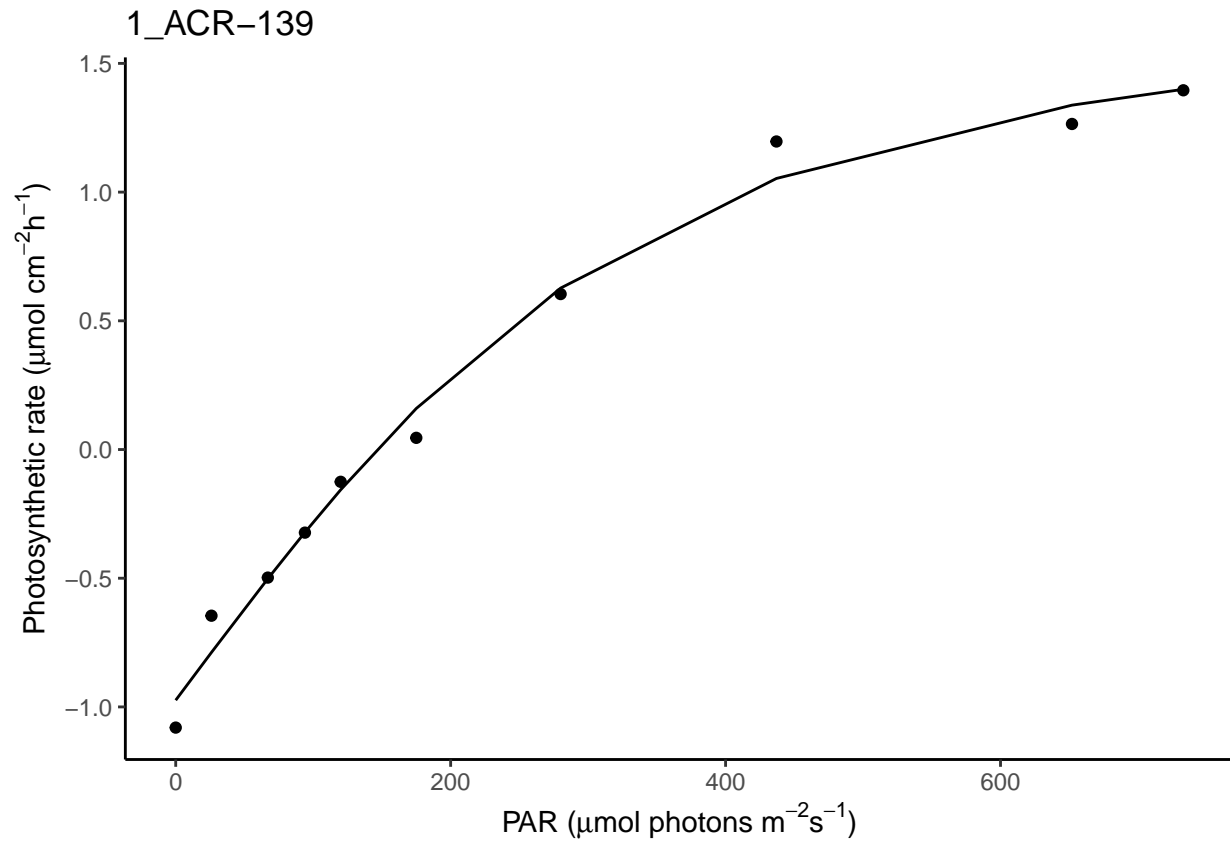
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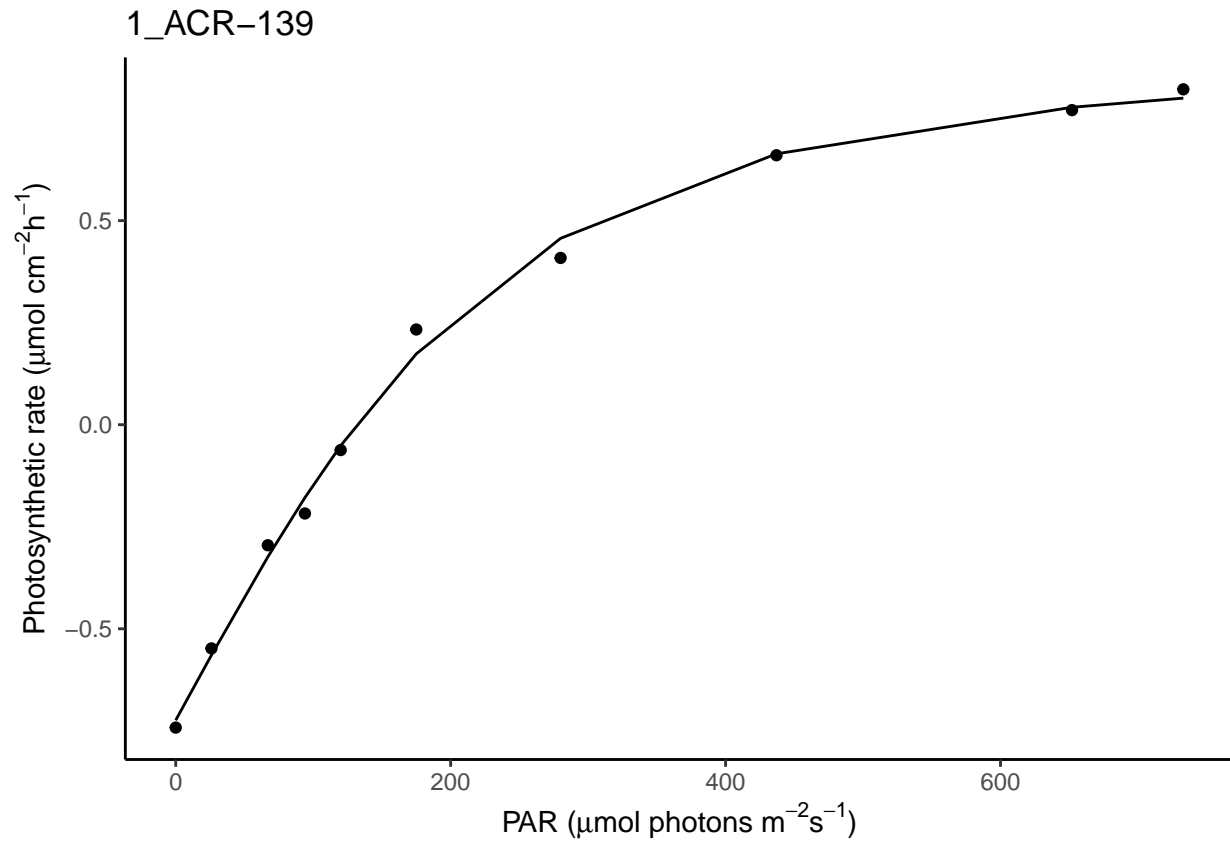
augmented\$colony_id: POR-240



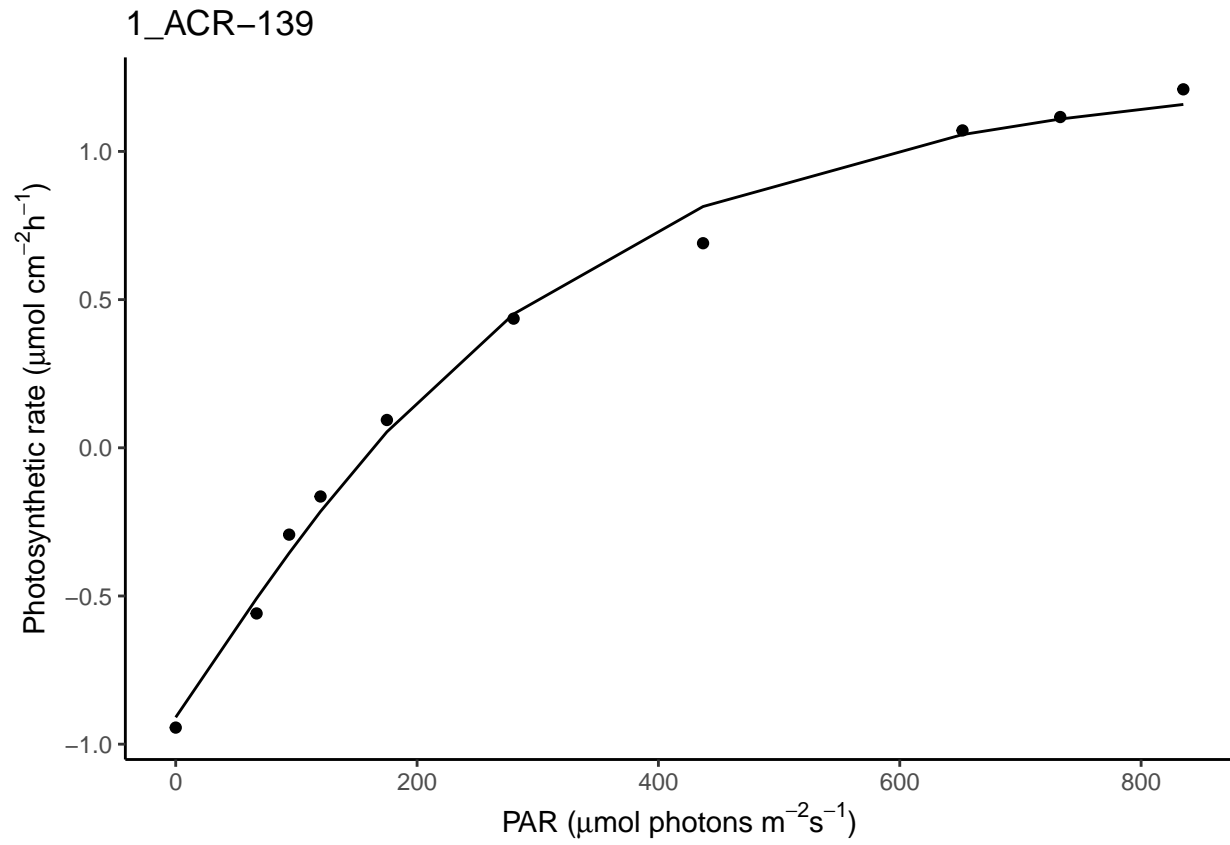
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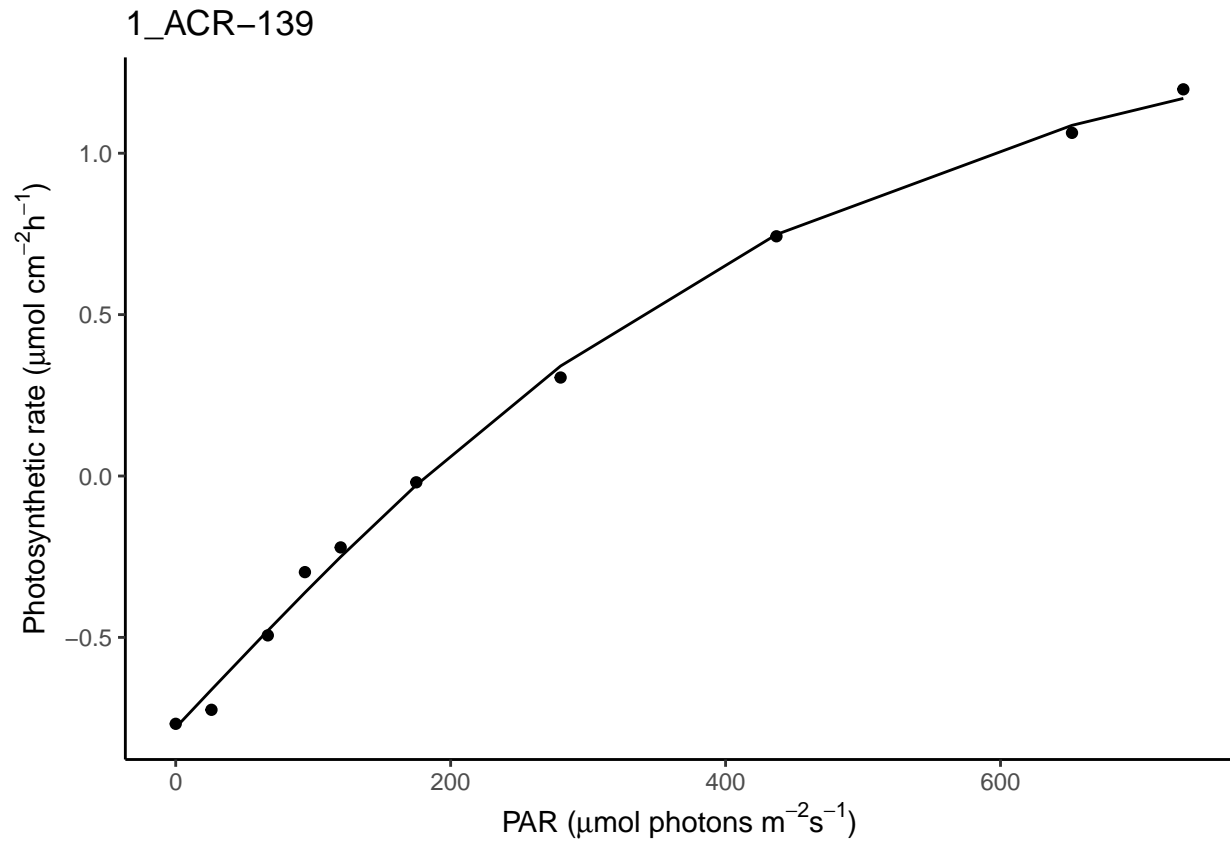
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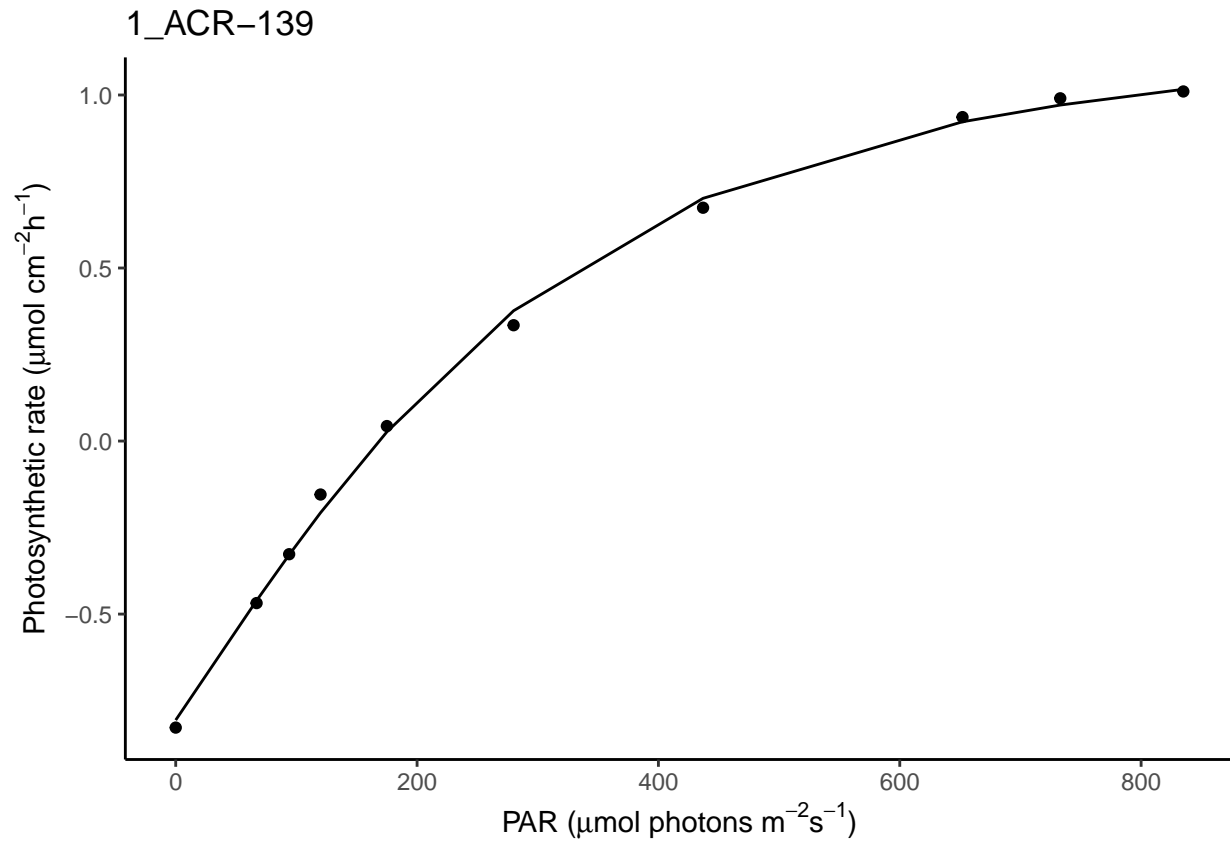
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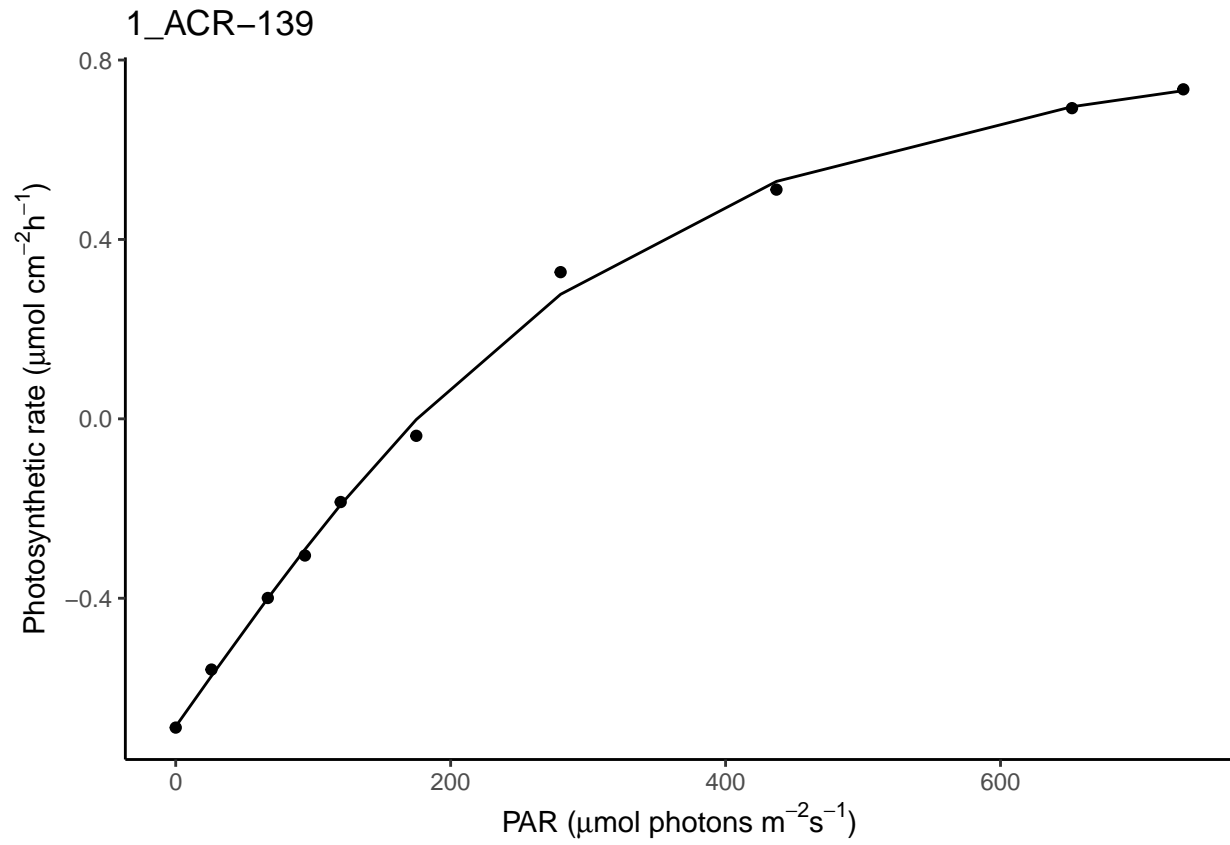
augmented\$colony_id: POR-253



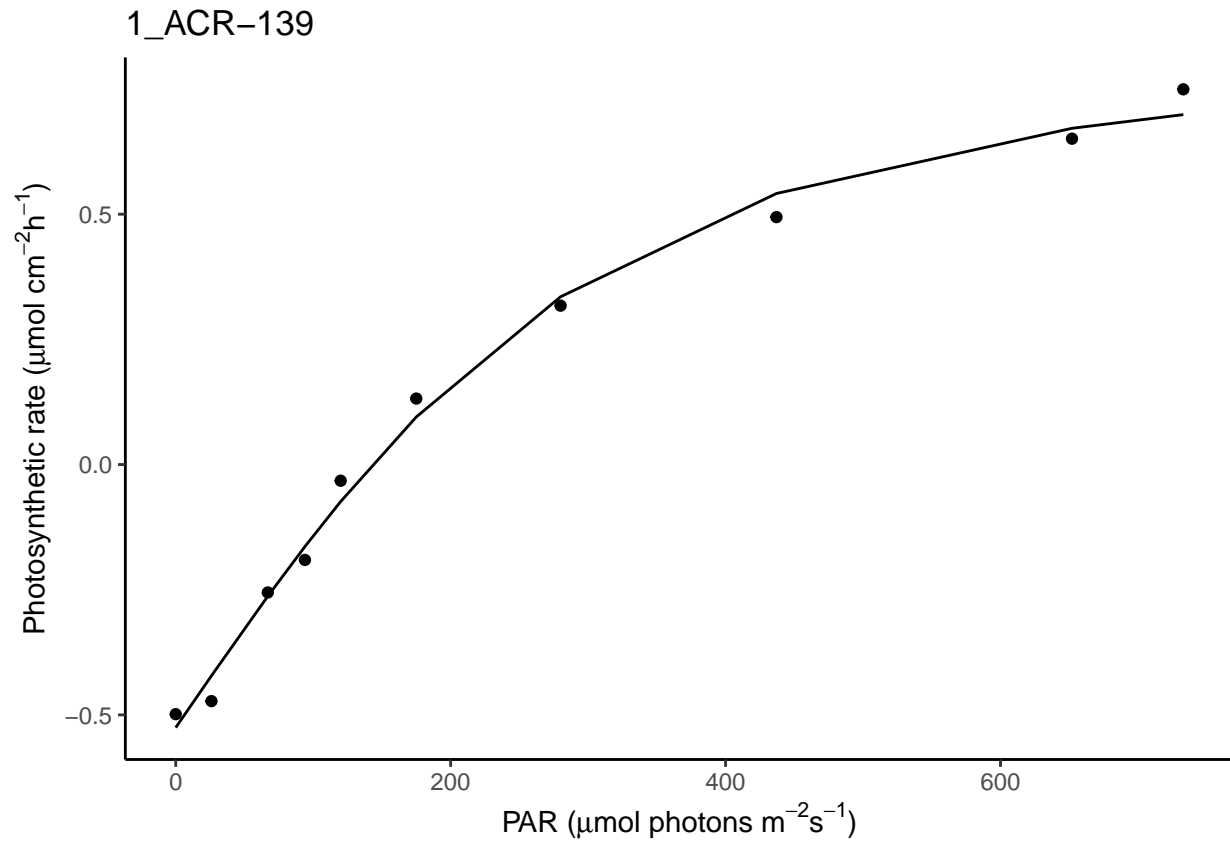
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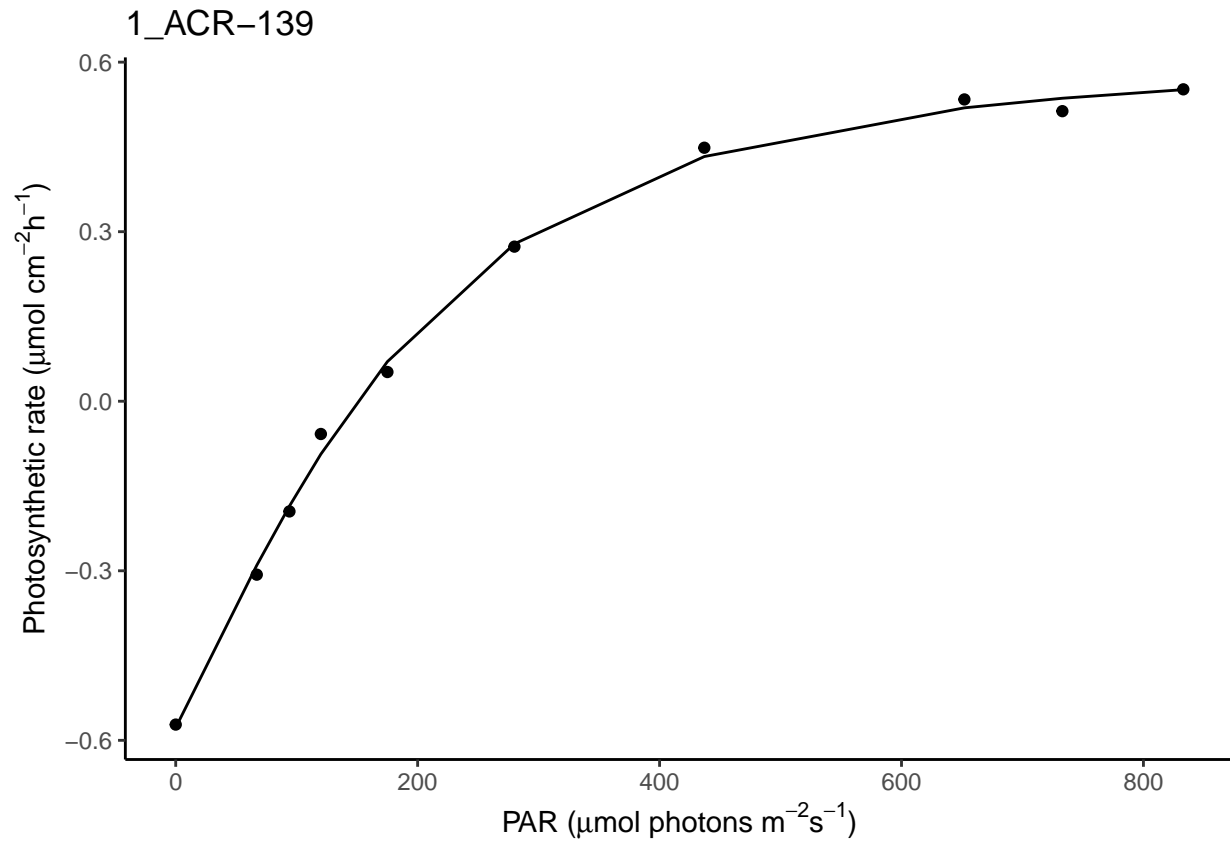
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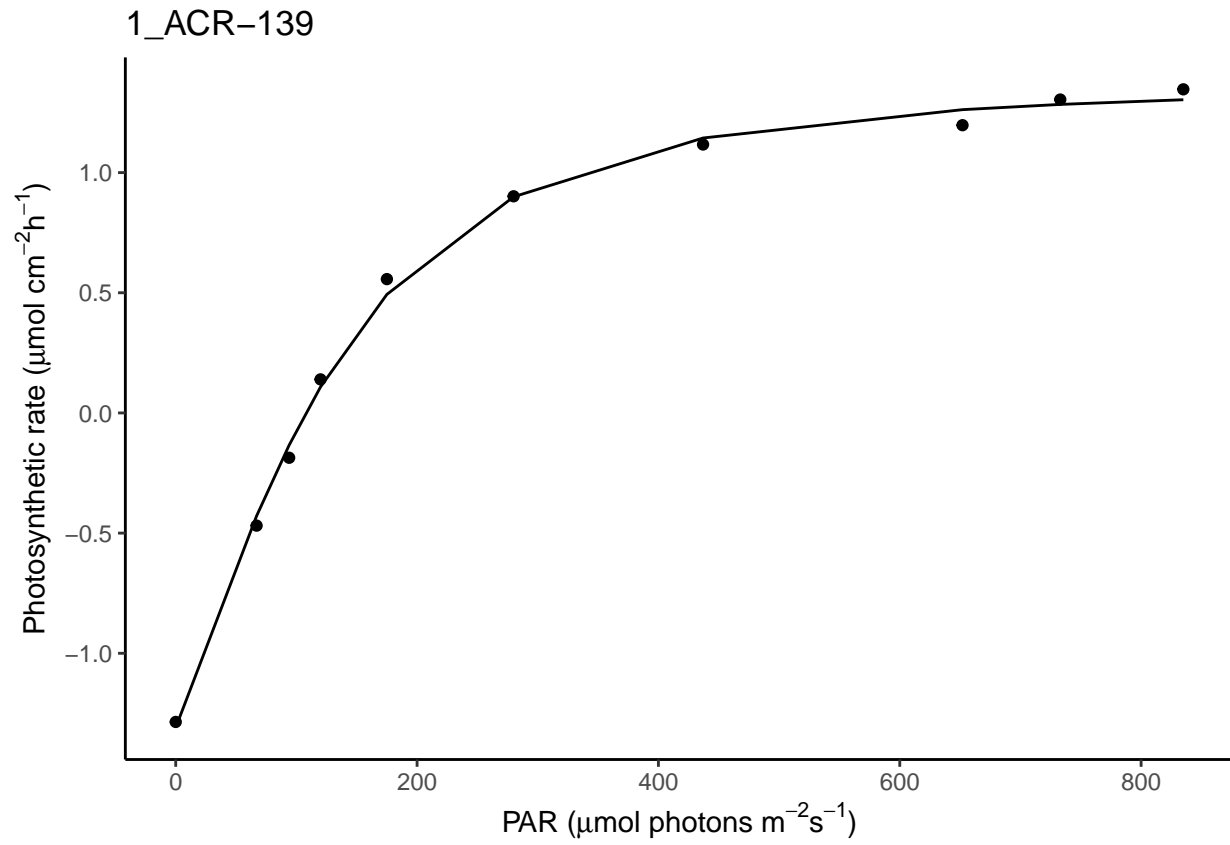
augmented\$colony_id: POR-266



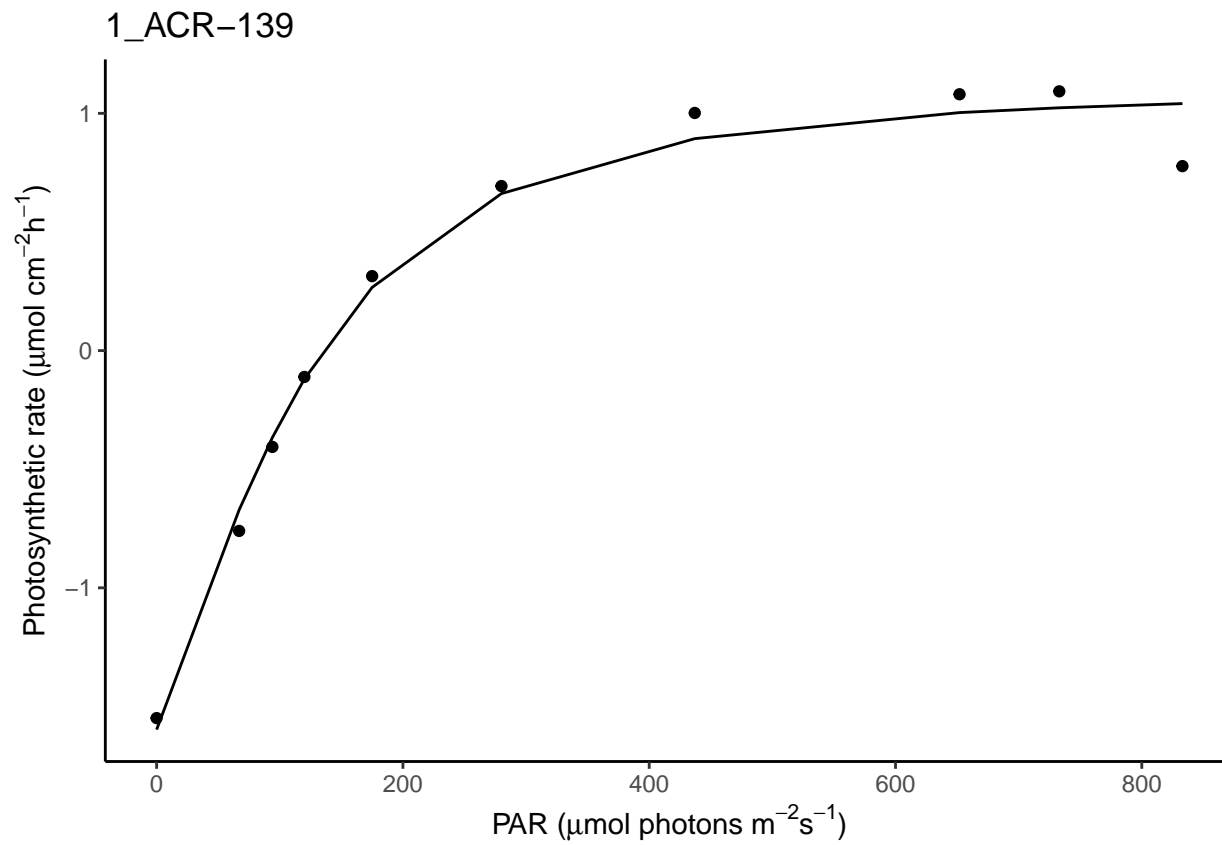
augmented\$colony_id: POR-338



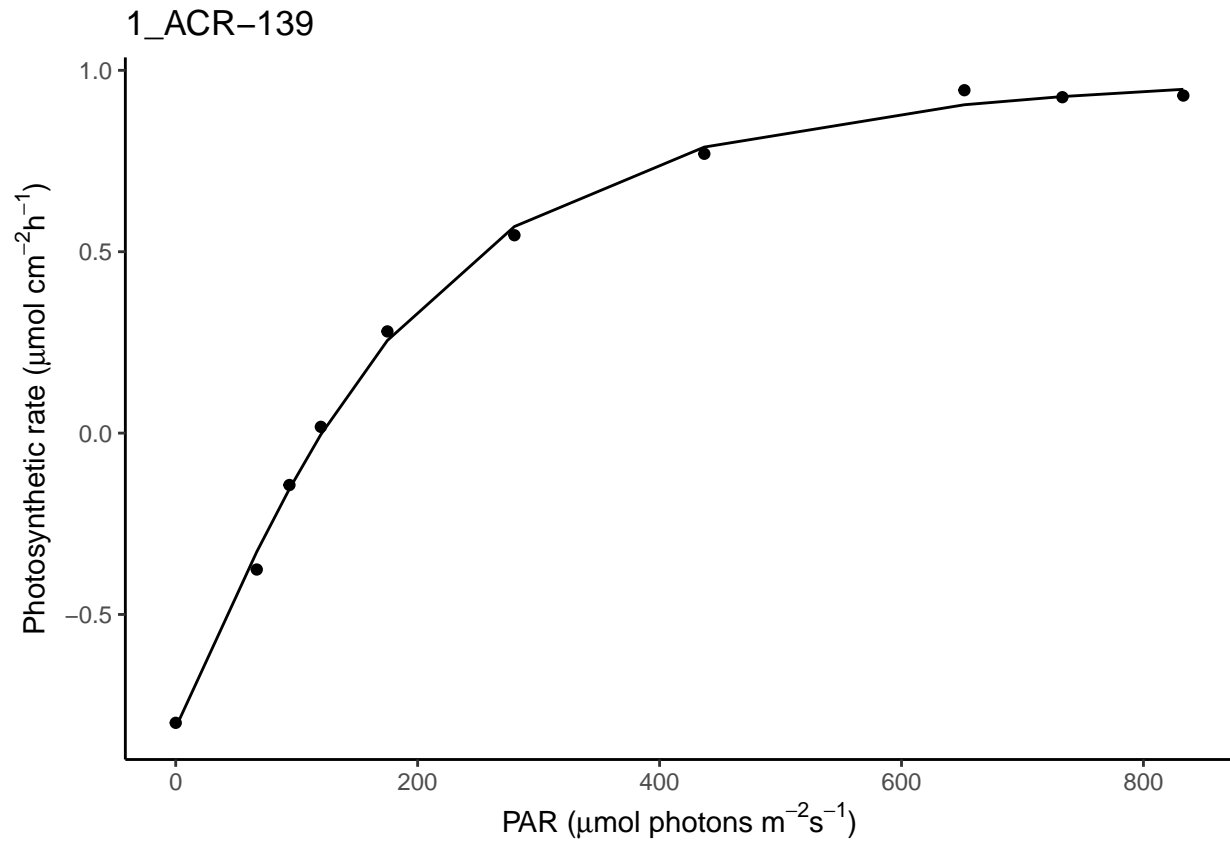
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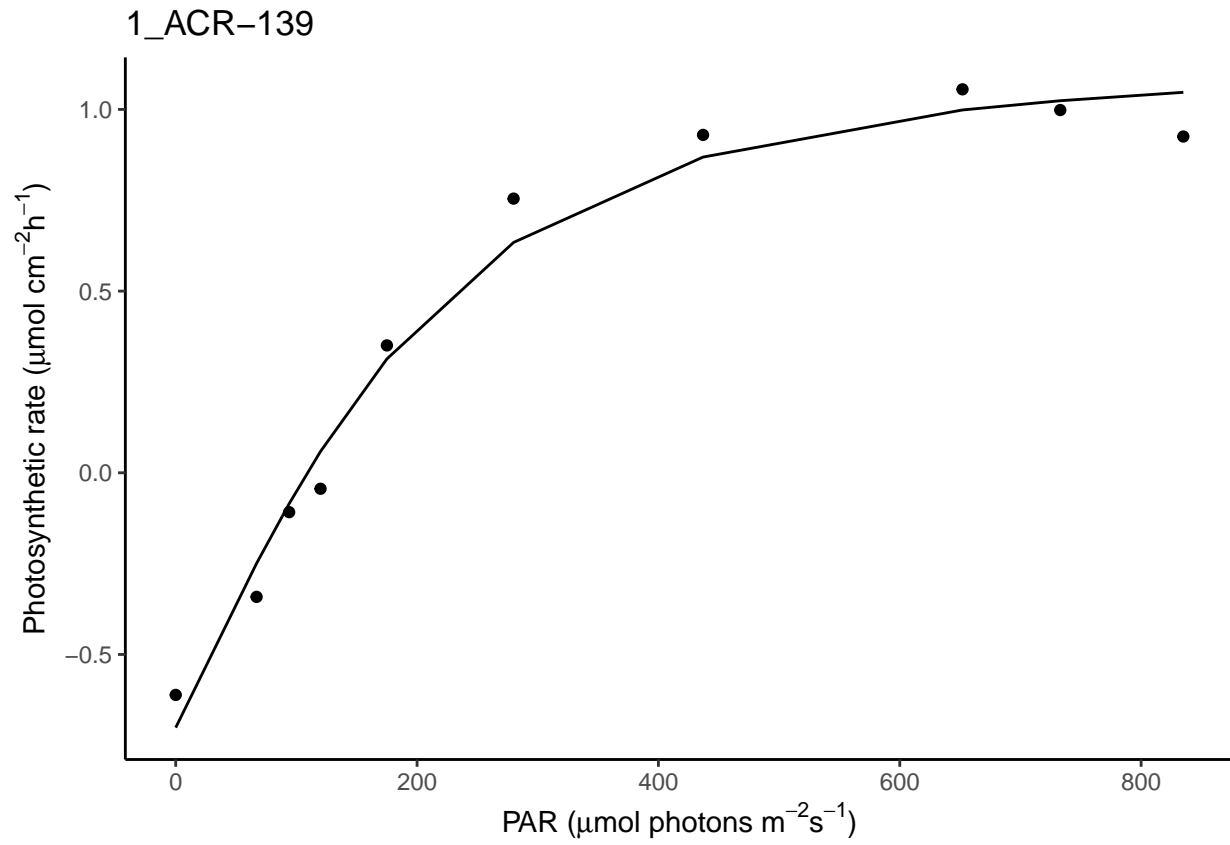
augmented\$colony_id: POR-341



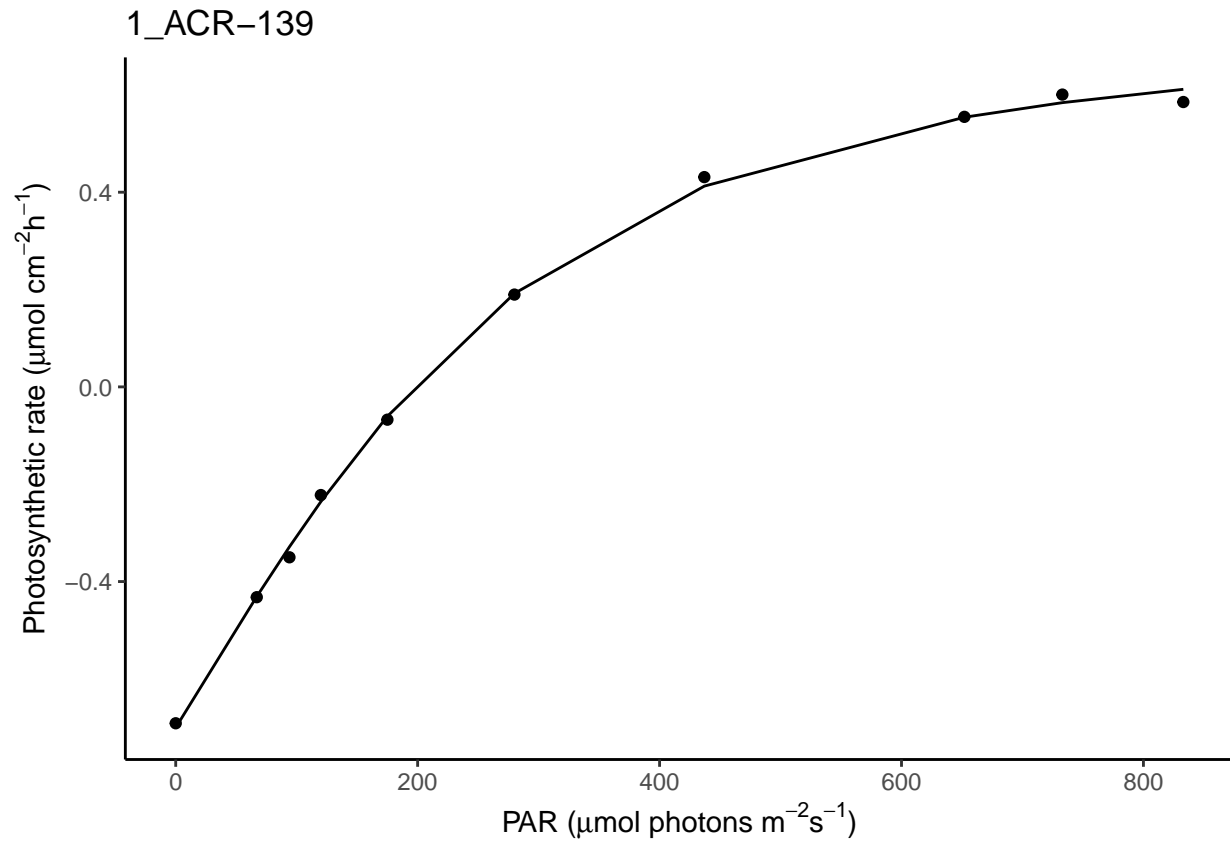
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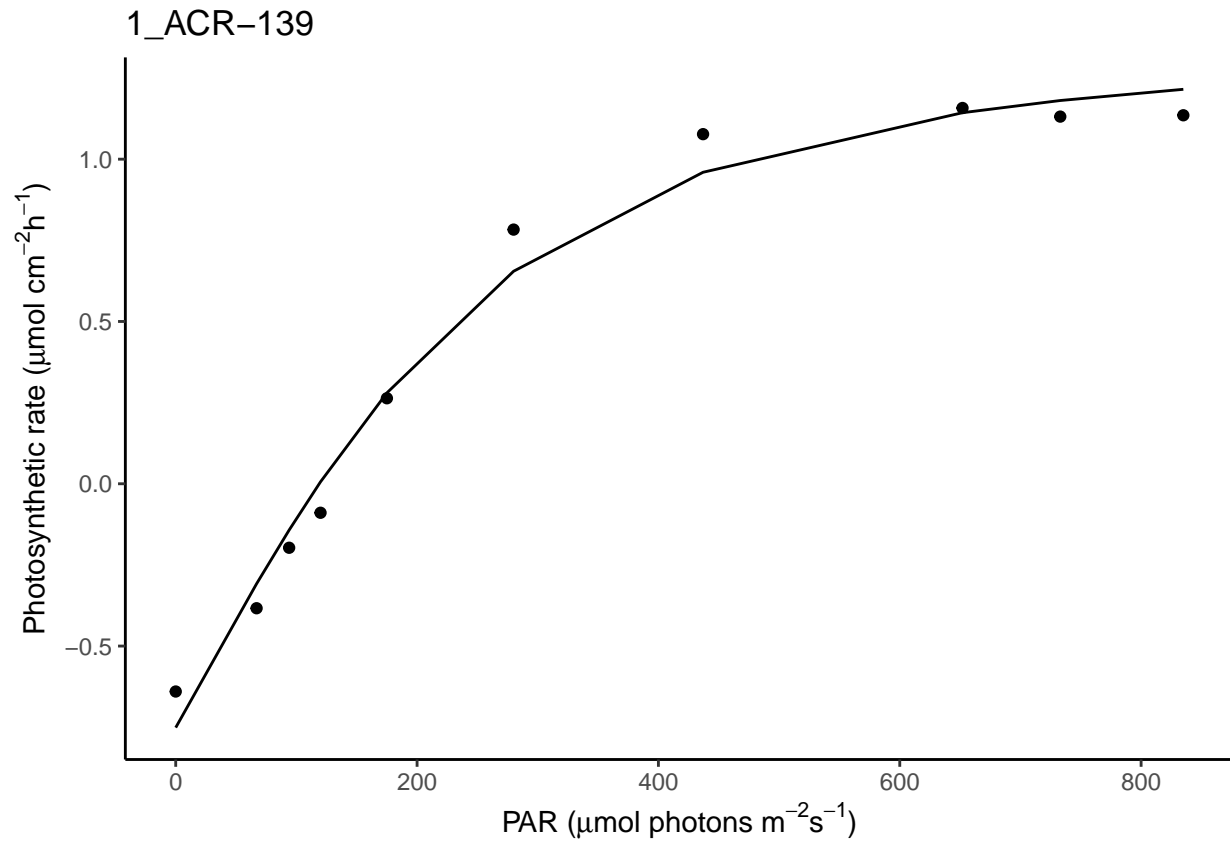
augmented\$colony_id: POR-353



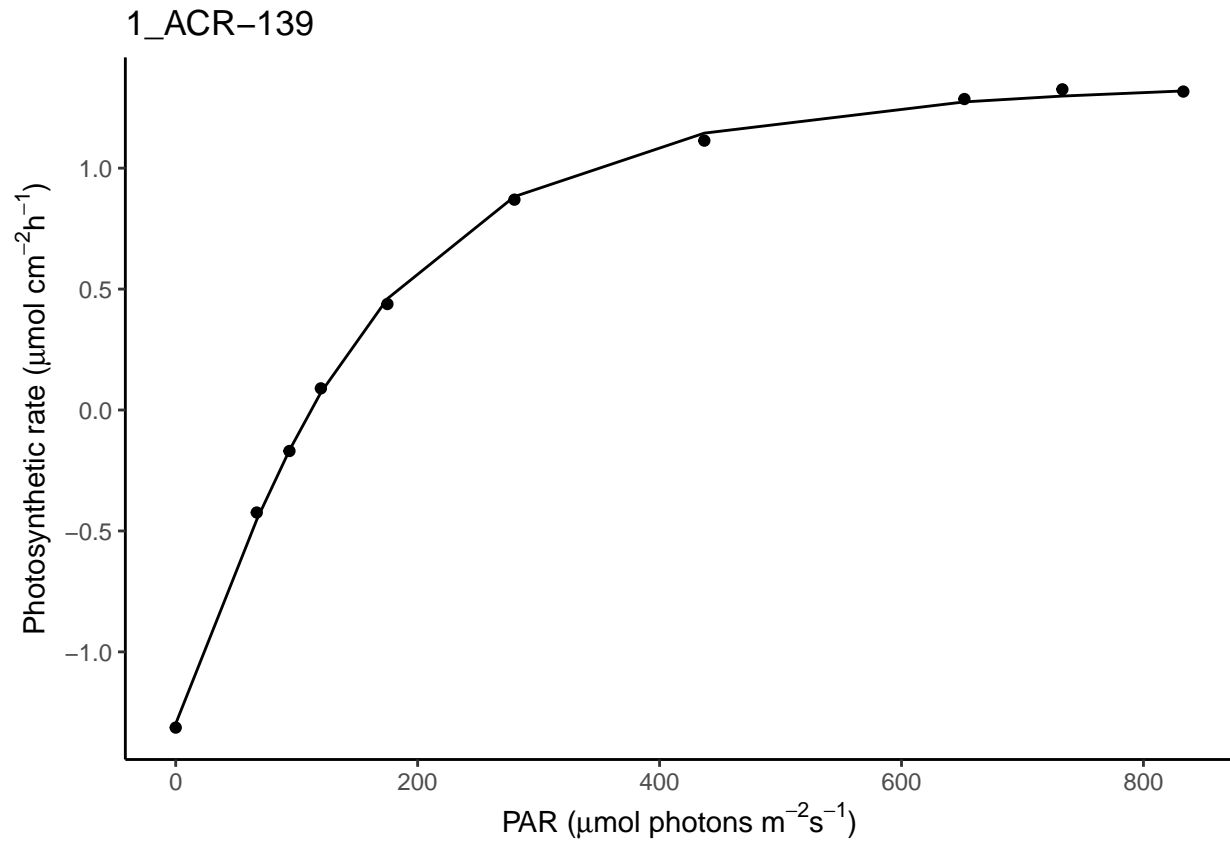
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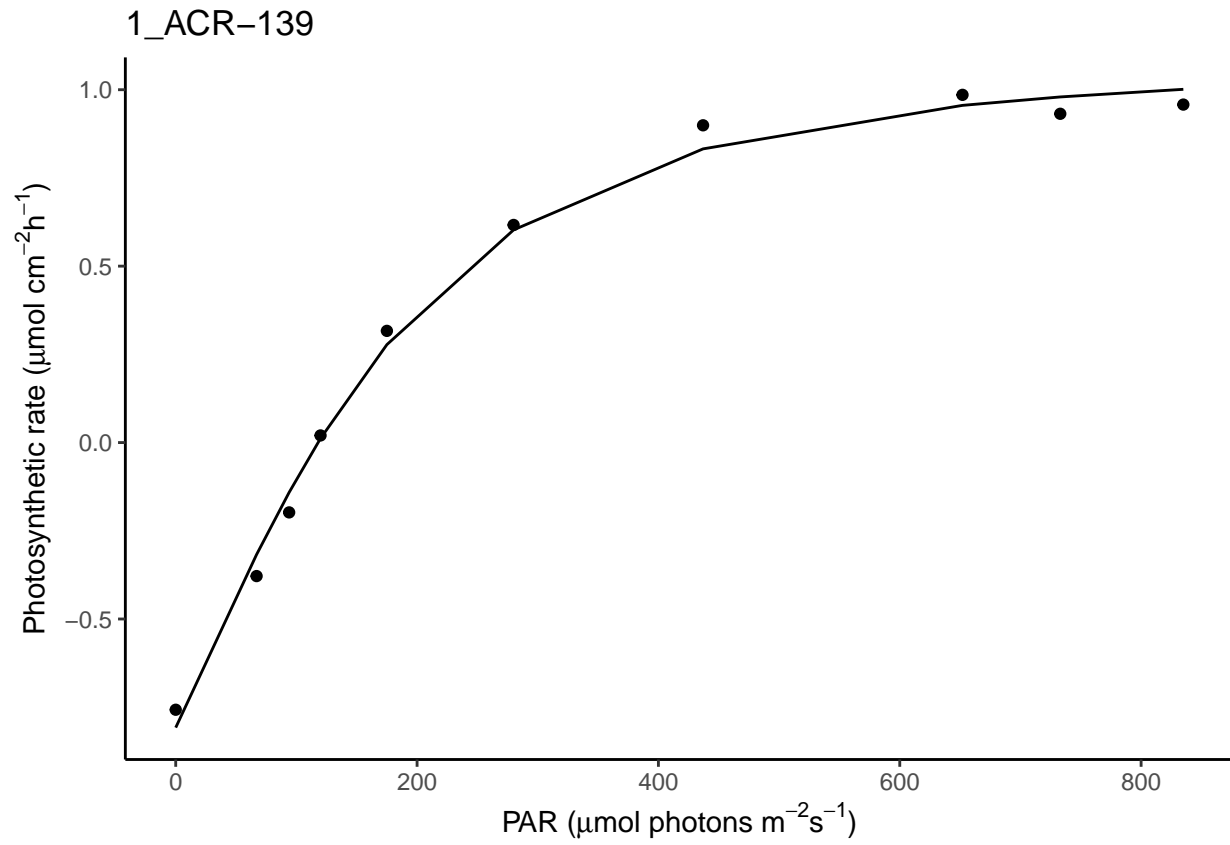
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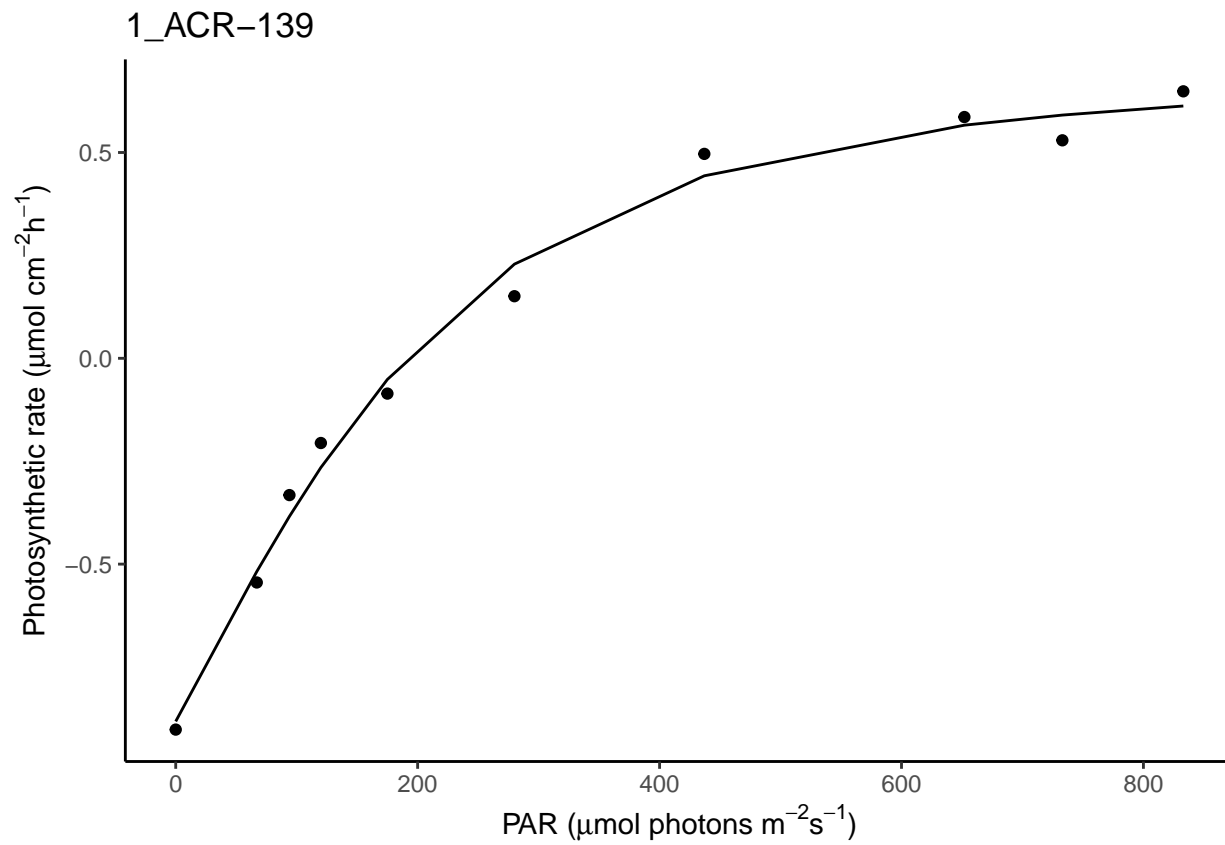
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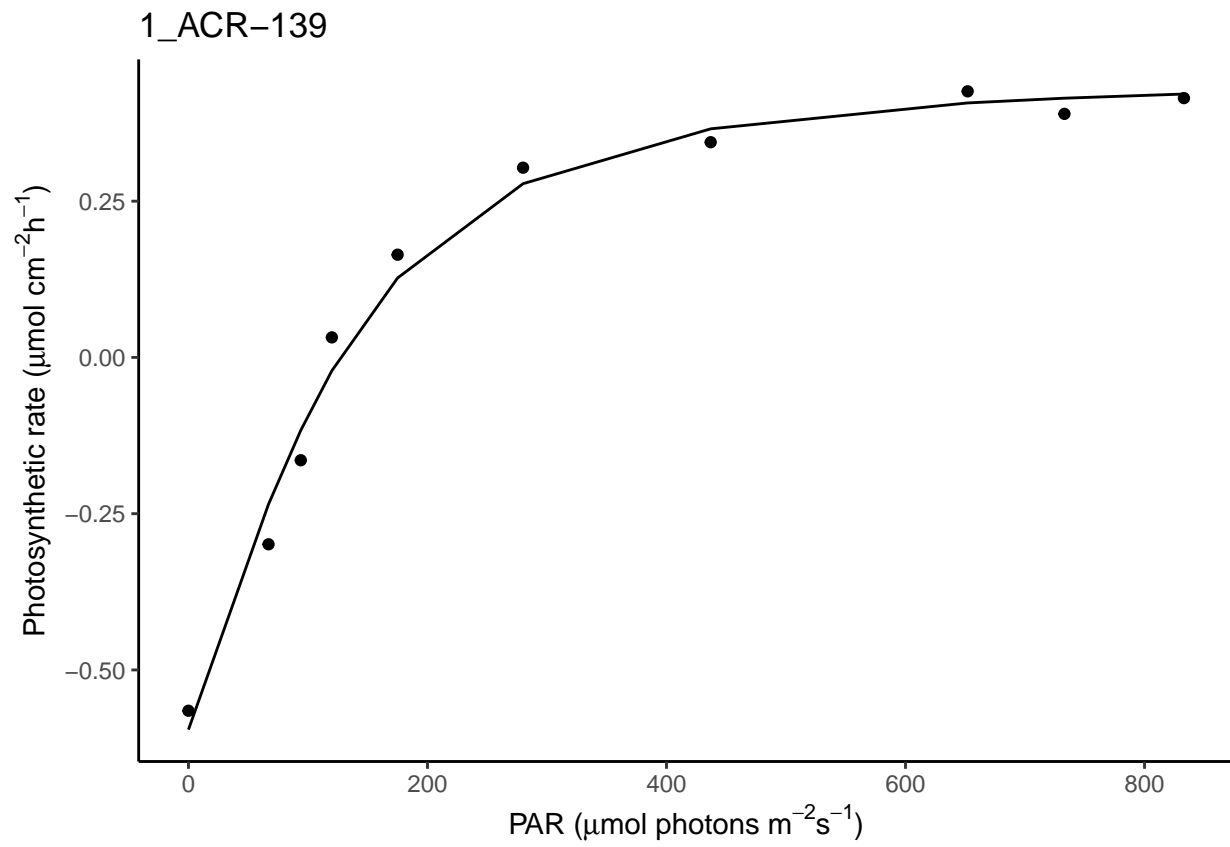
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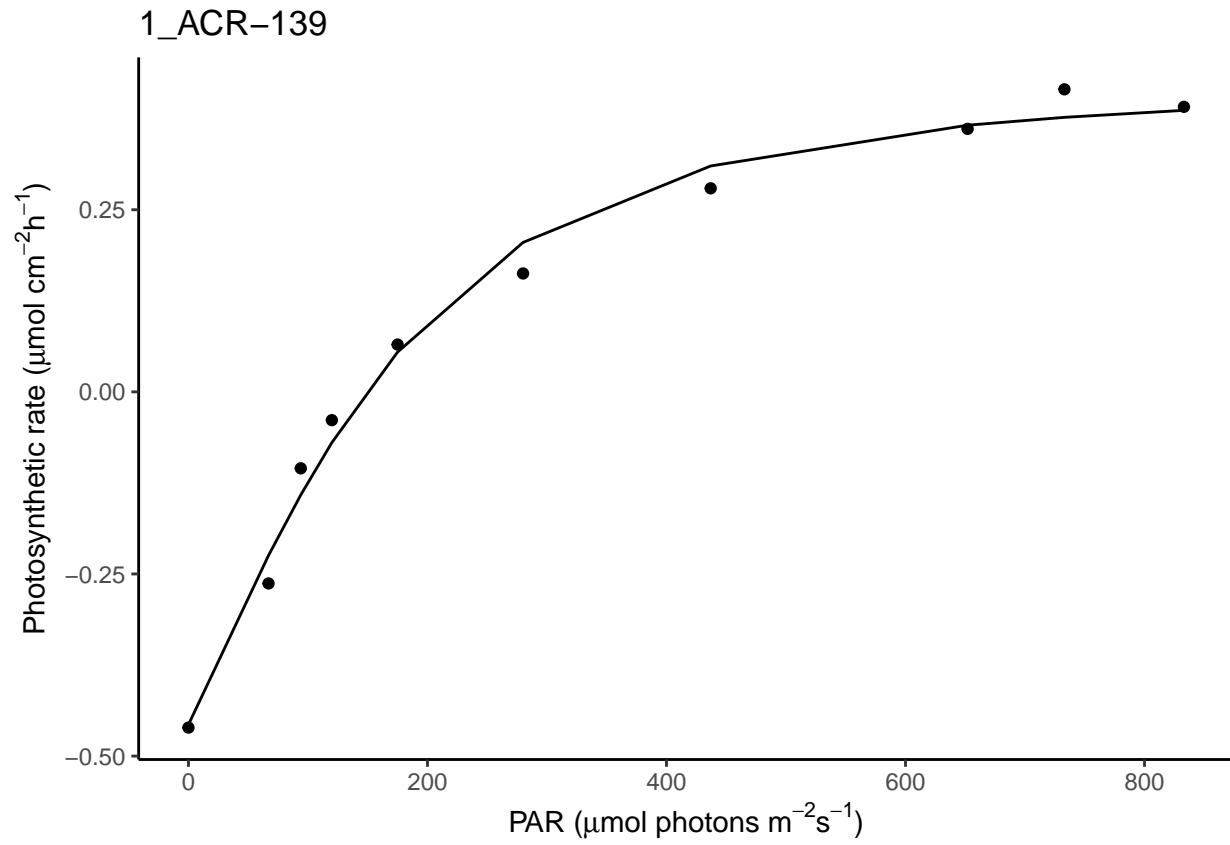
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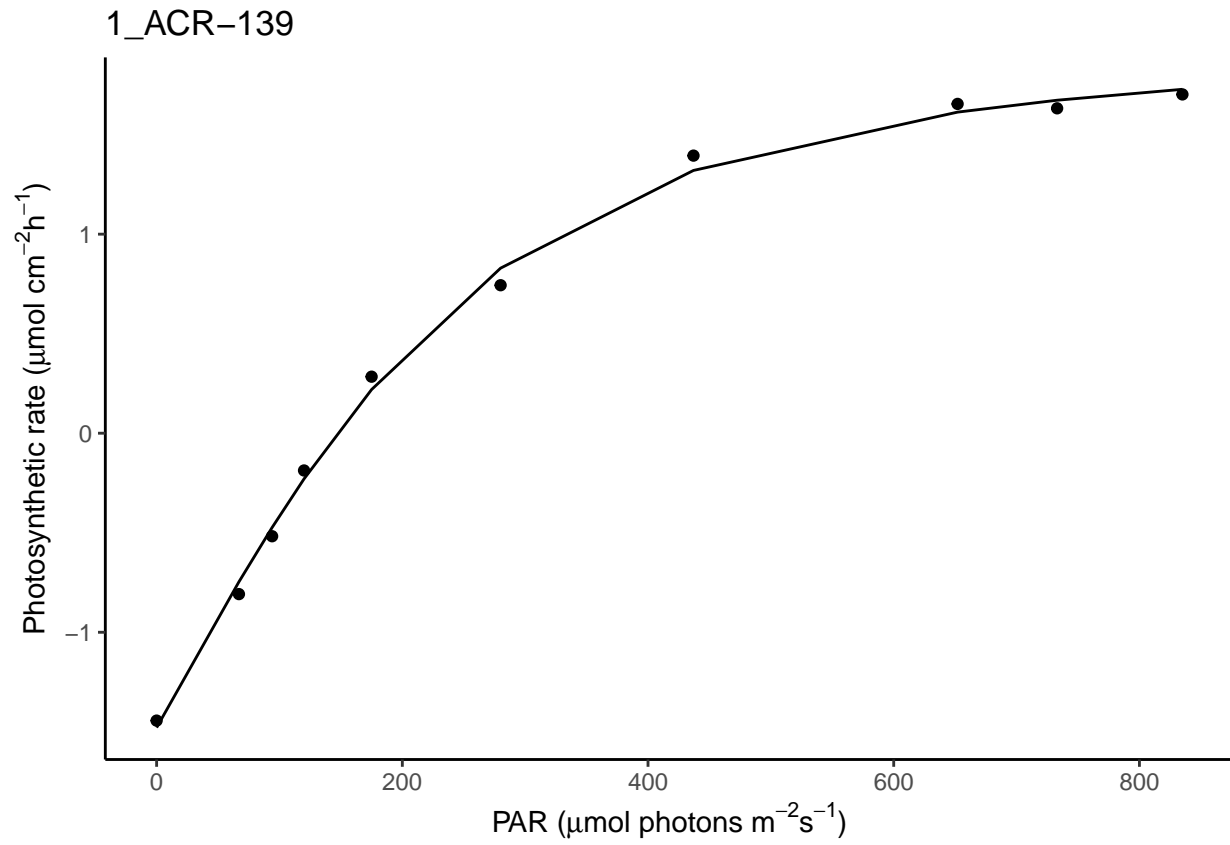
augmented\$colony_id: POR-367



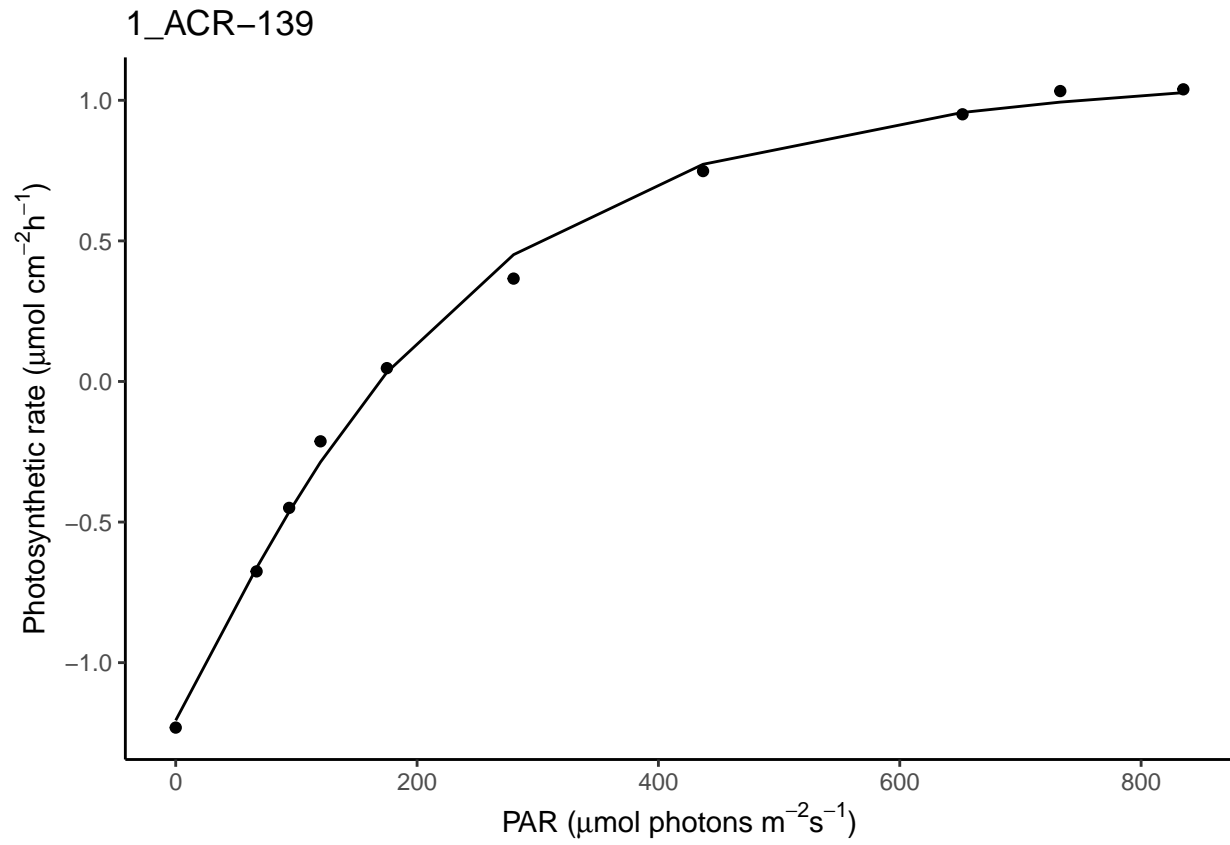
augmented\$colony_id: POR-381



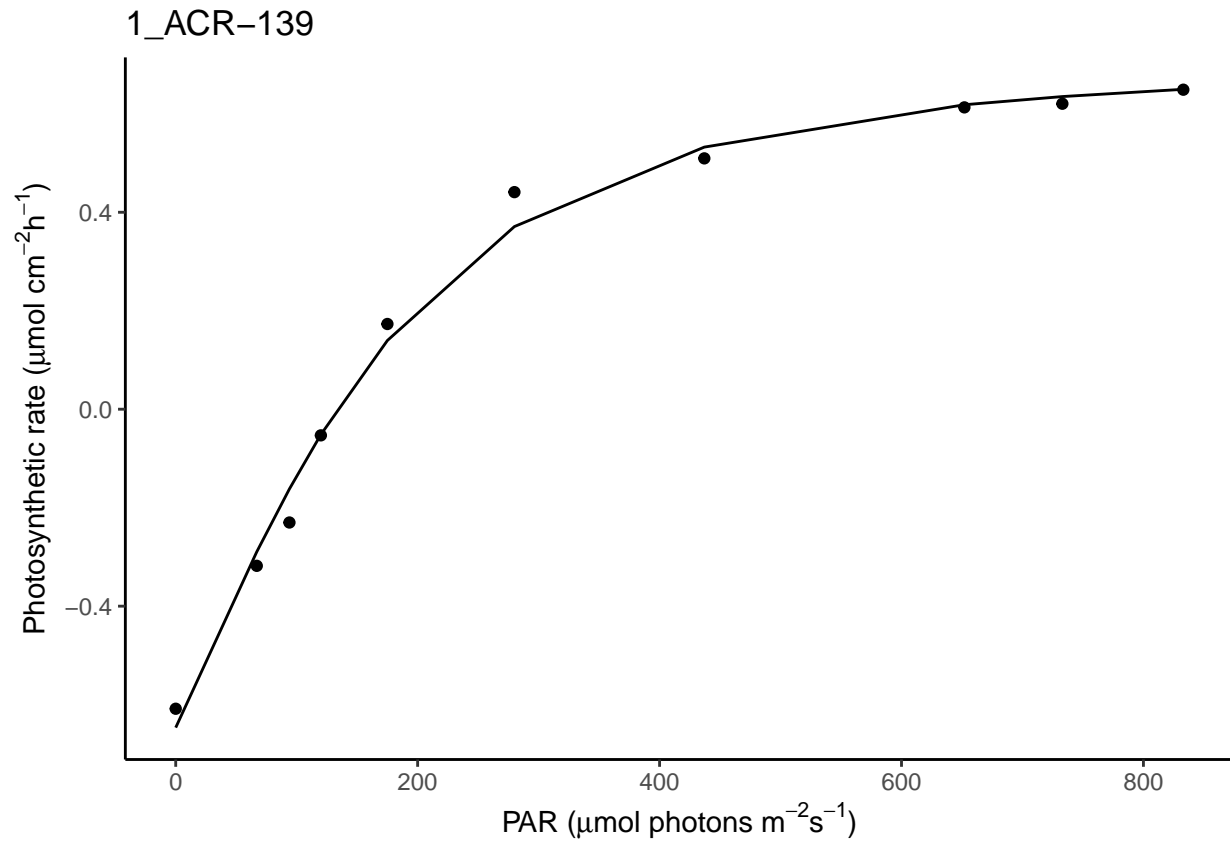
augmented\$colony_id: POR-383



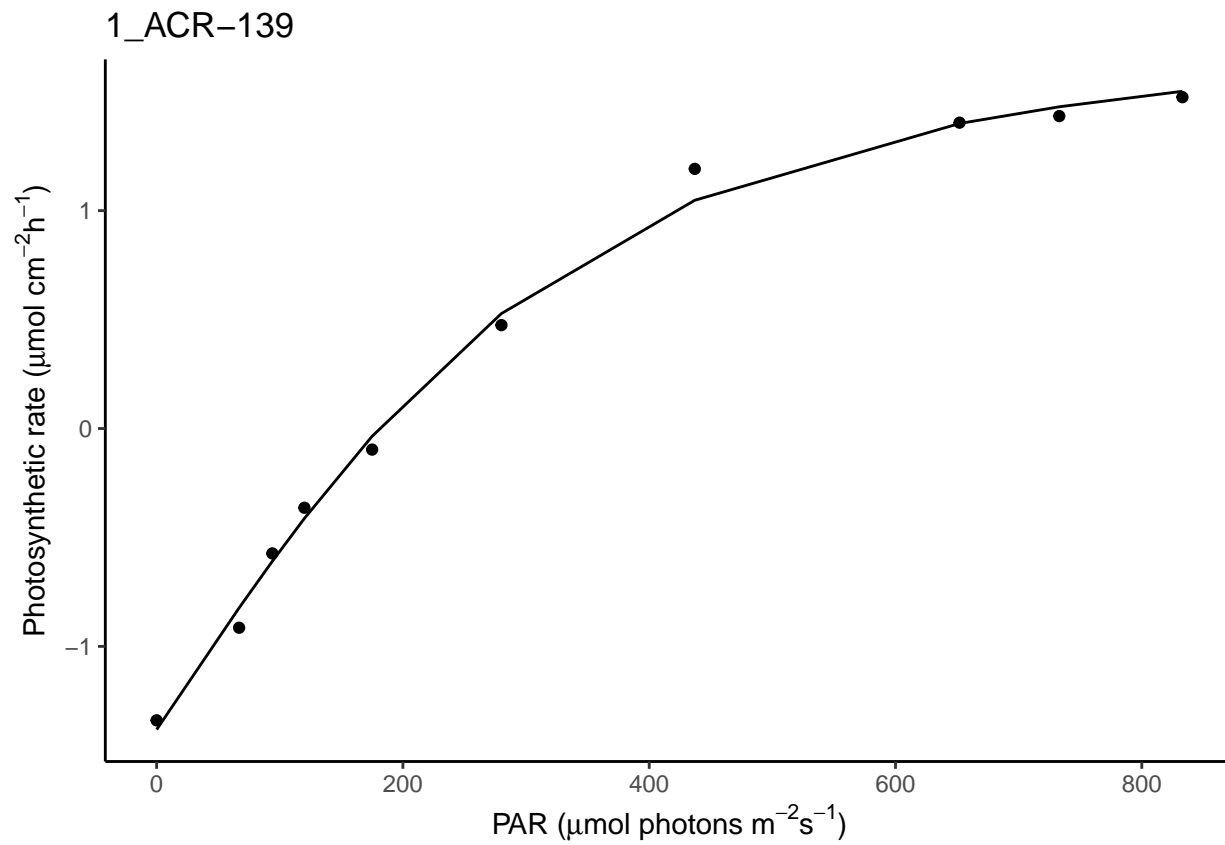
augmented\$colony_id: POR-384



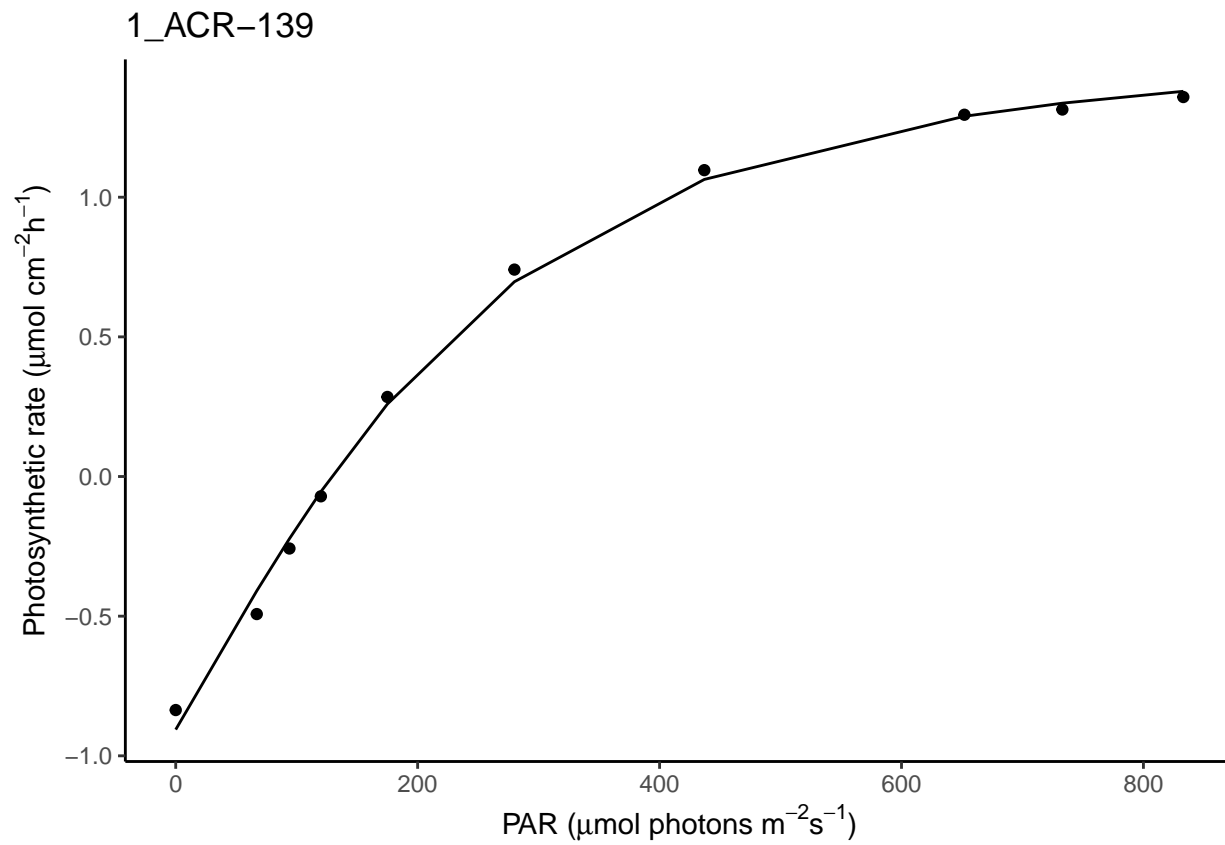
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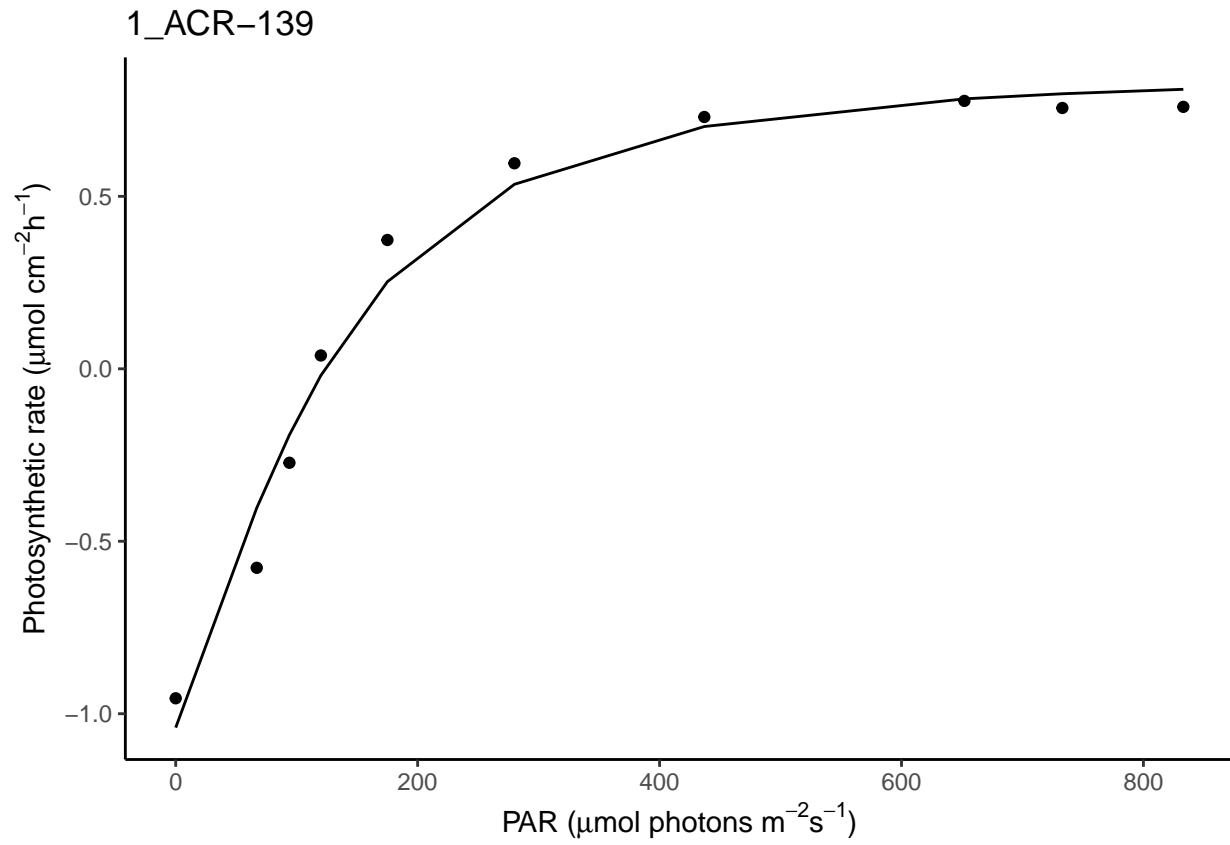
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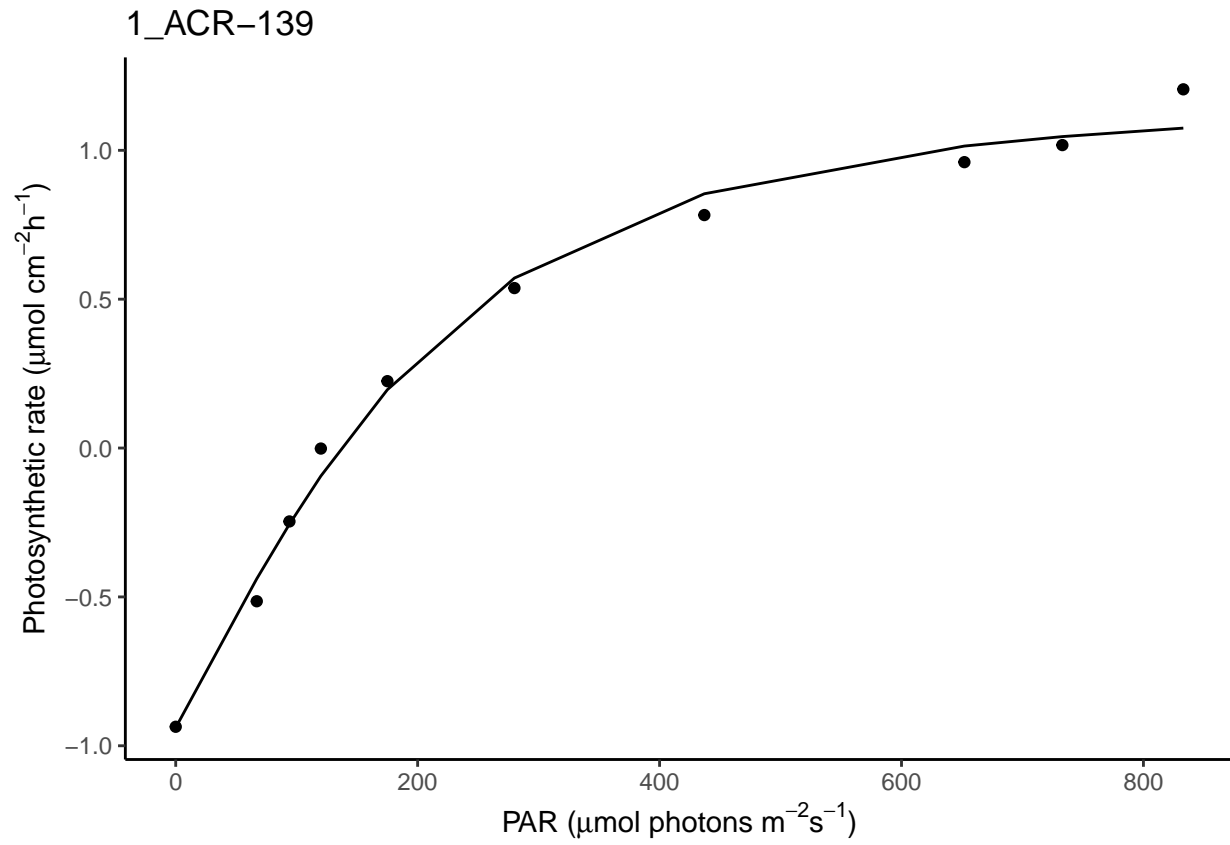
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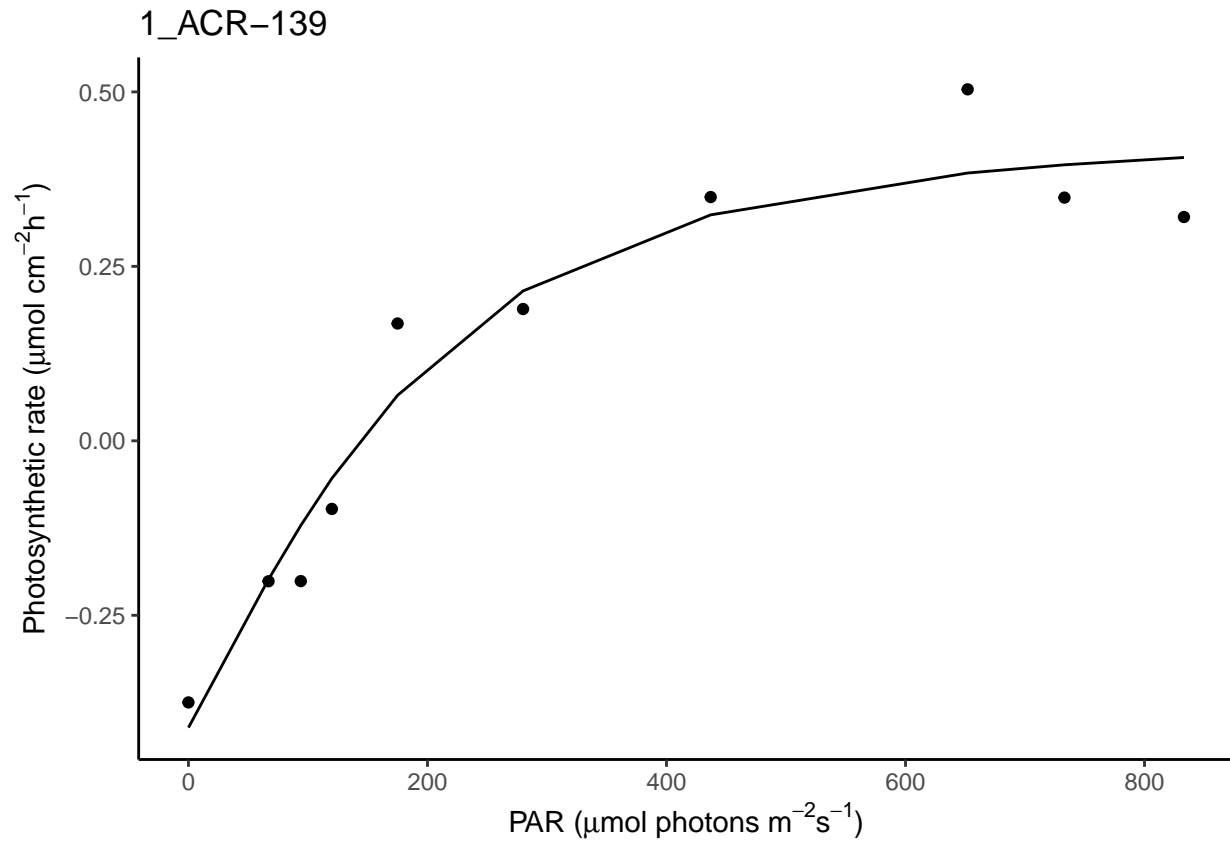
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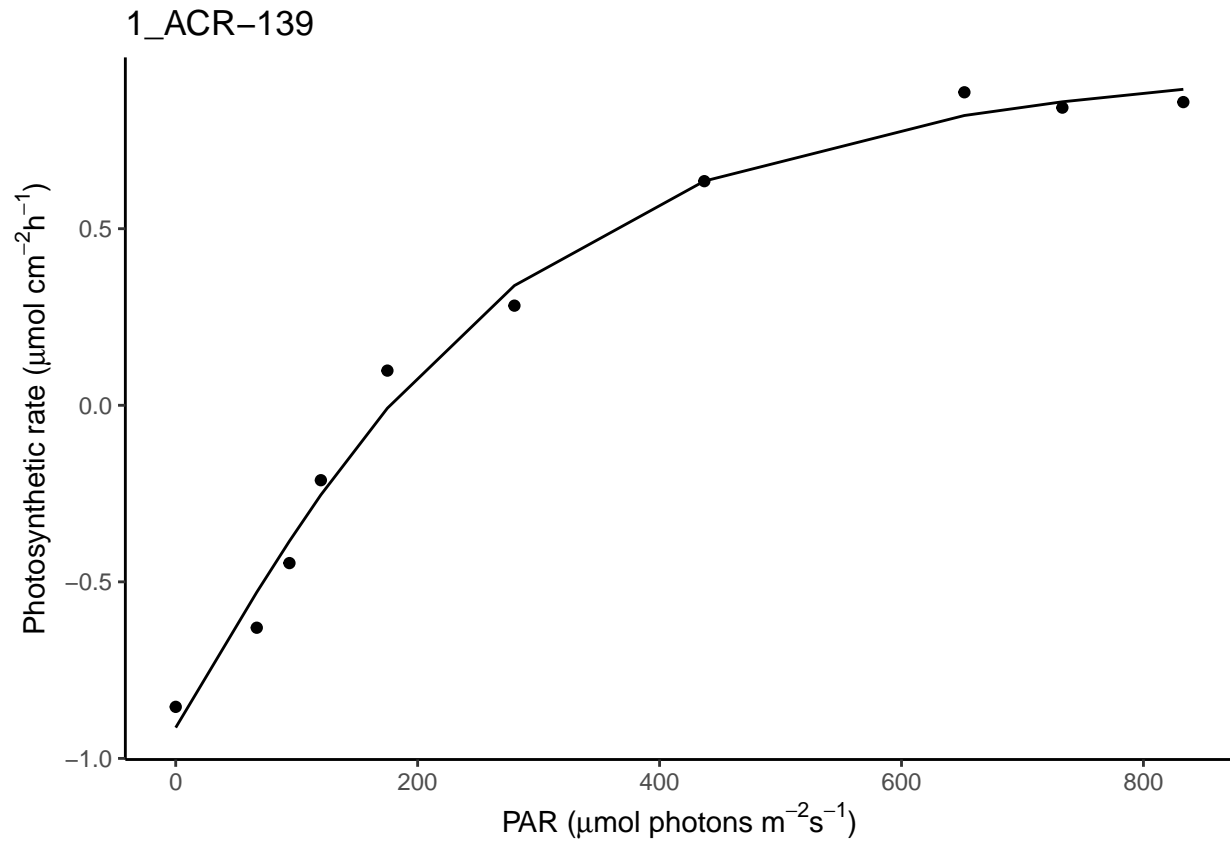
augmented\$colony_id: POR-72



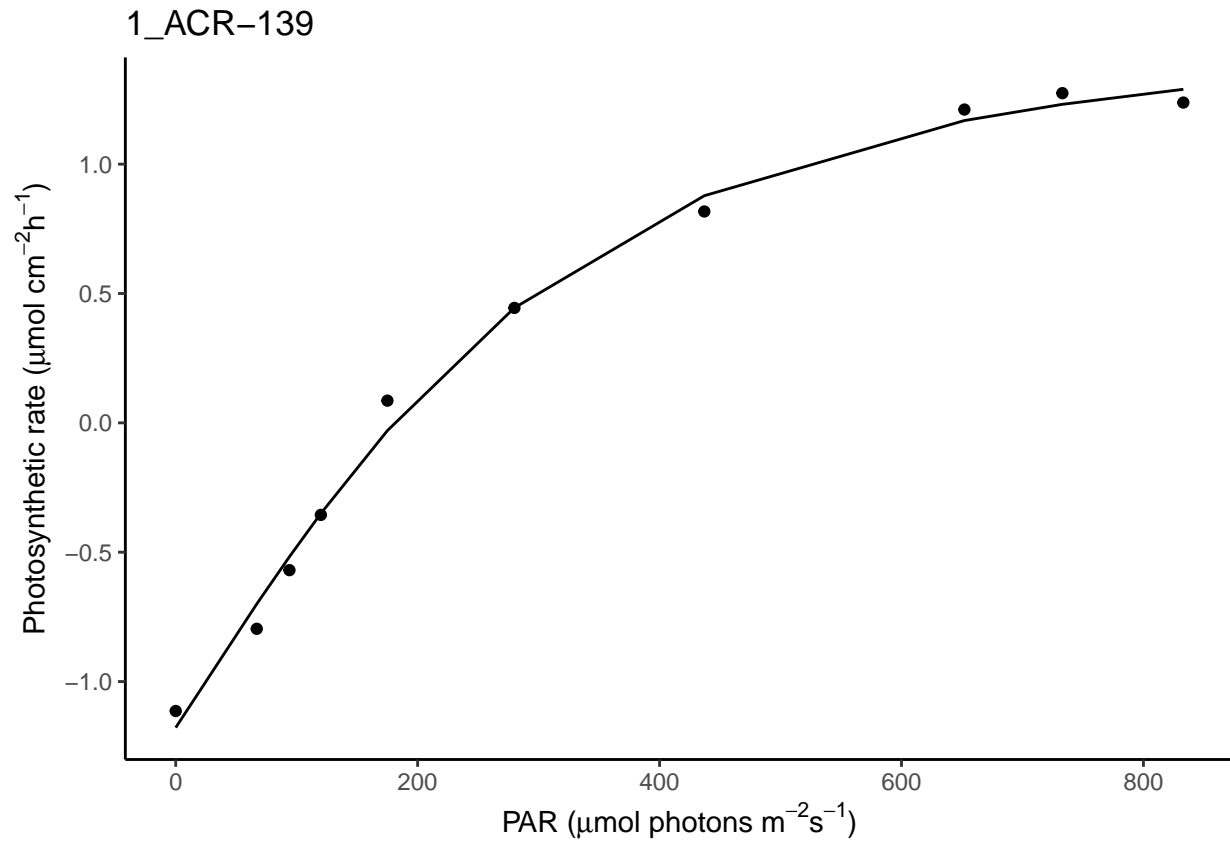
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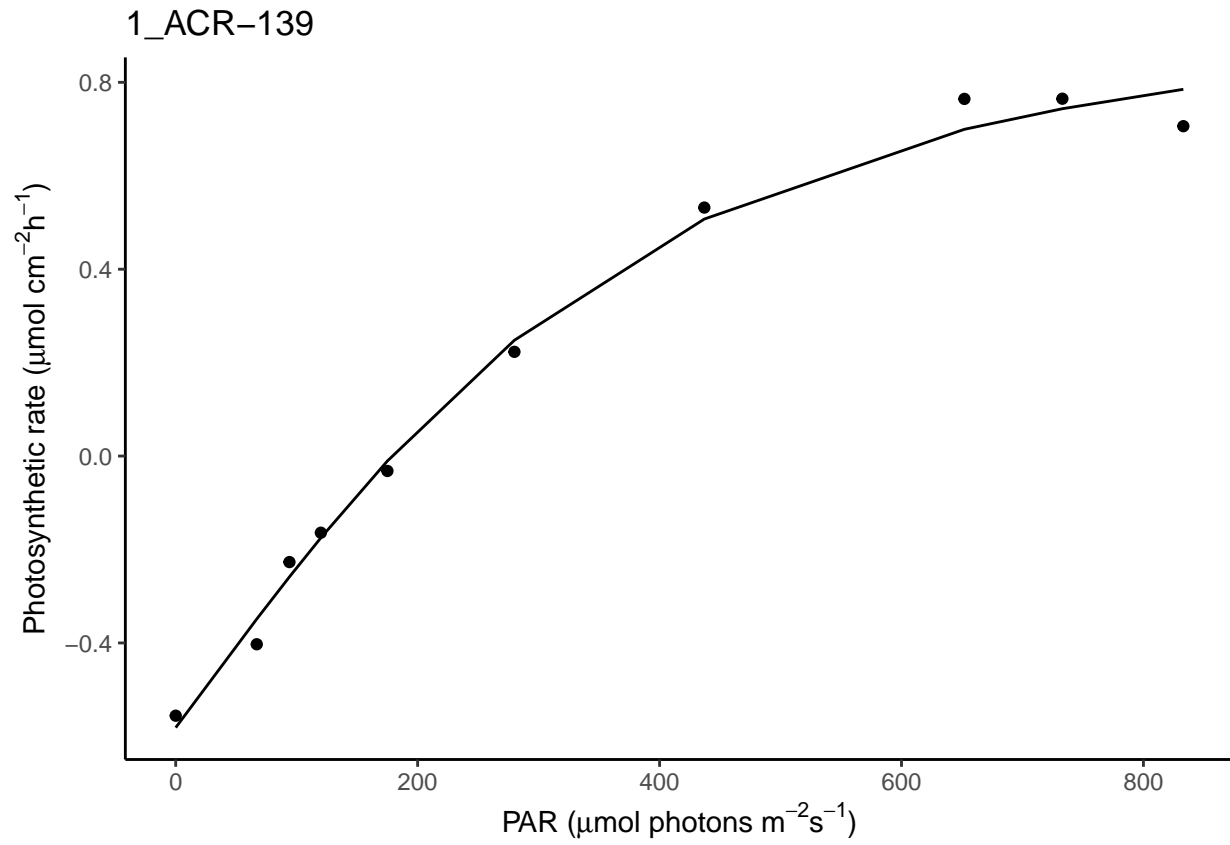
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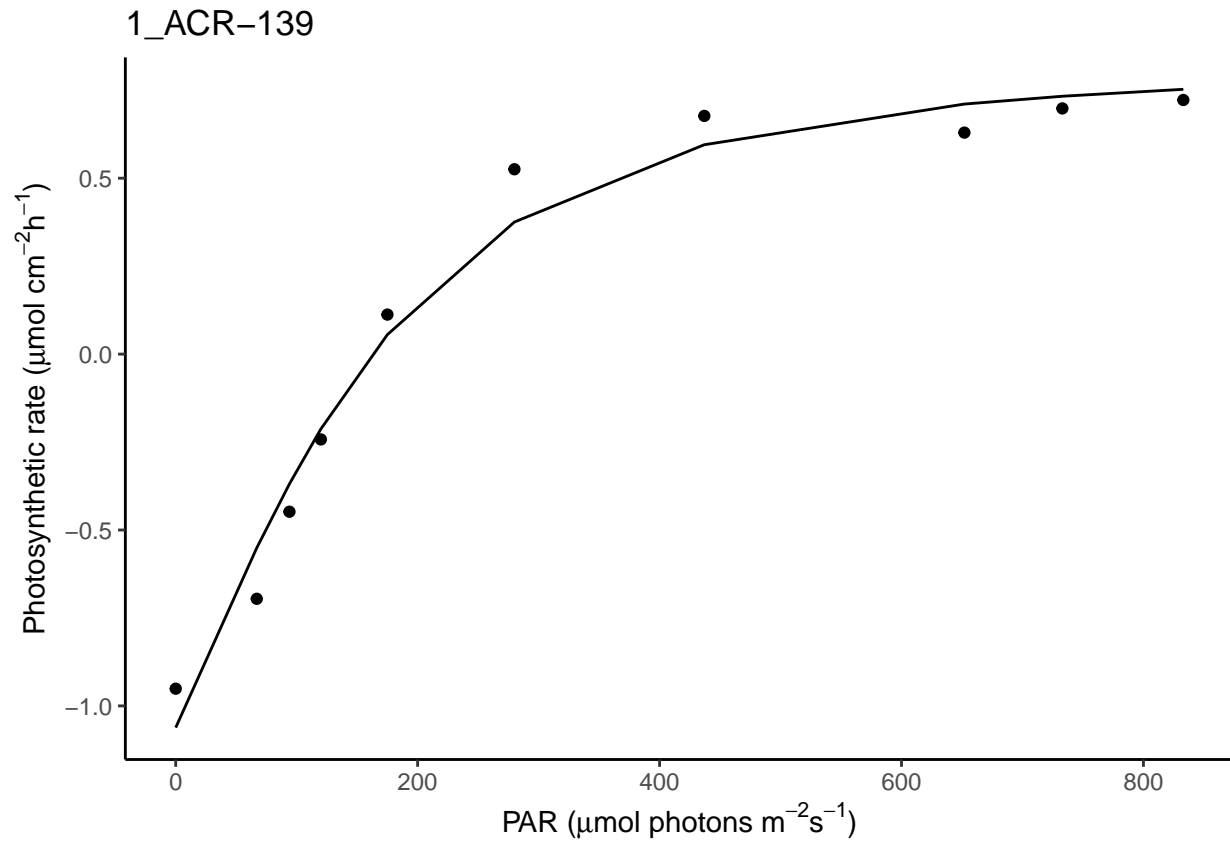
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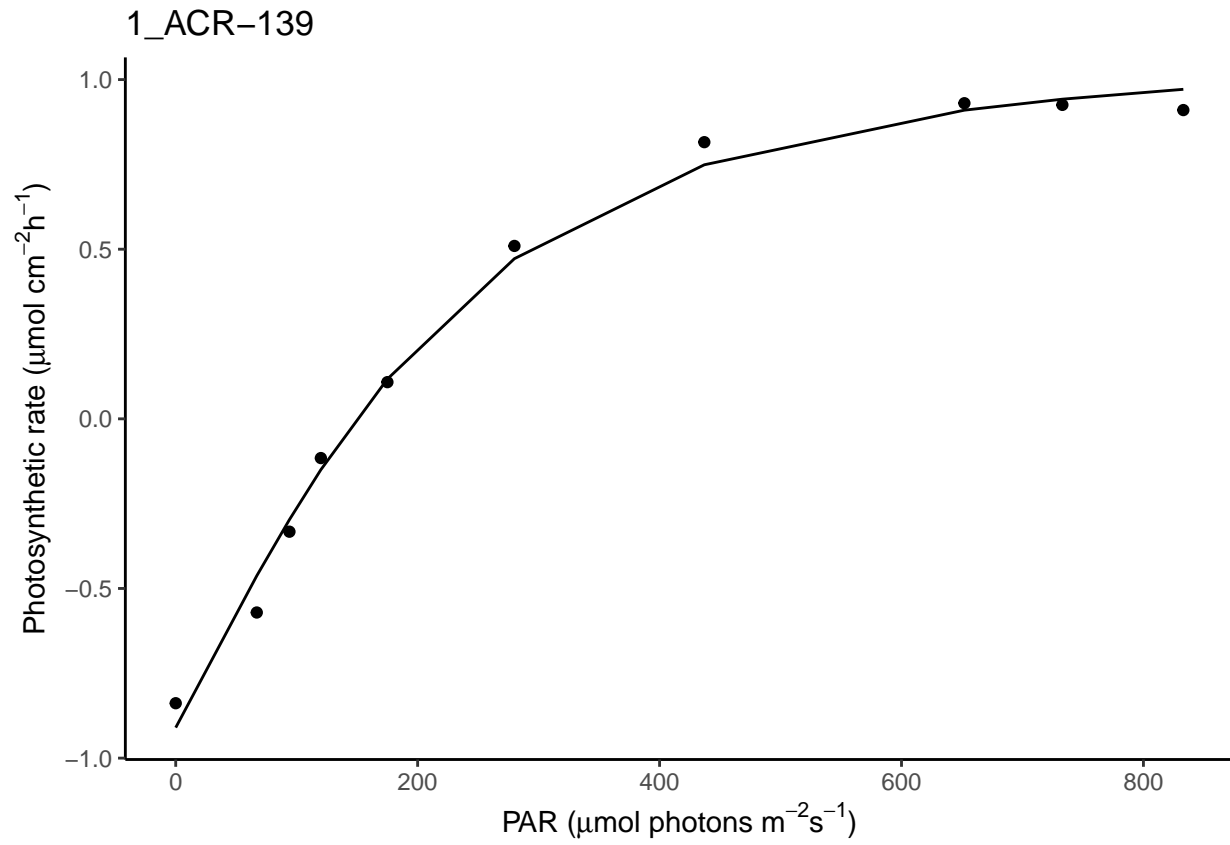
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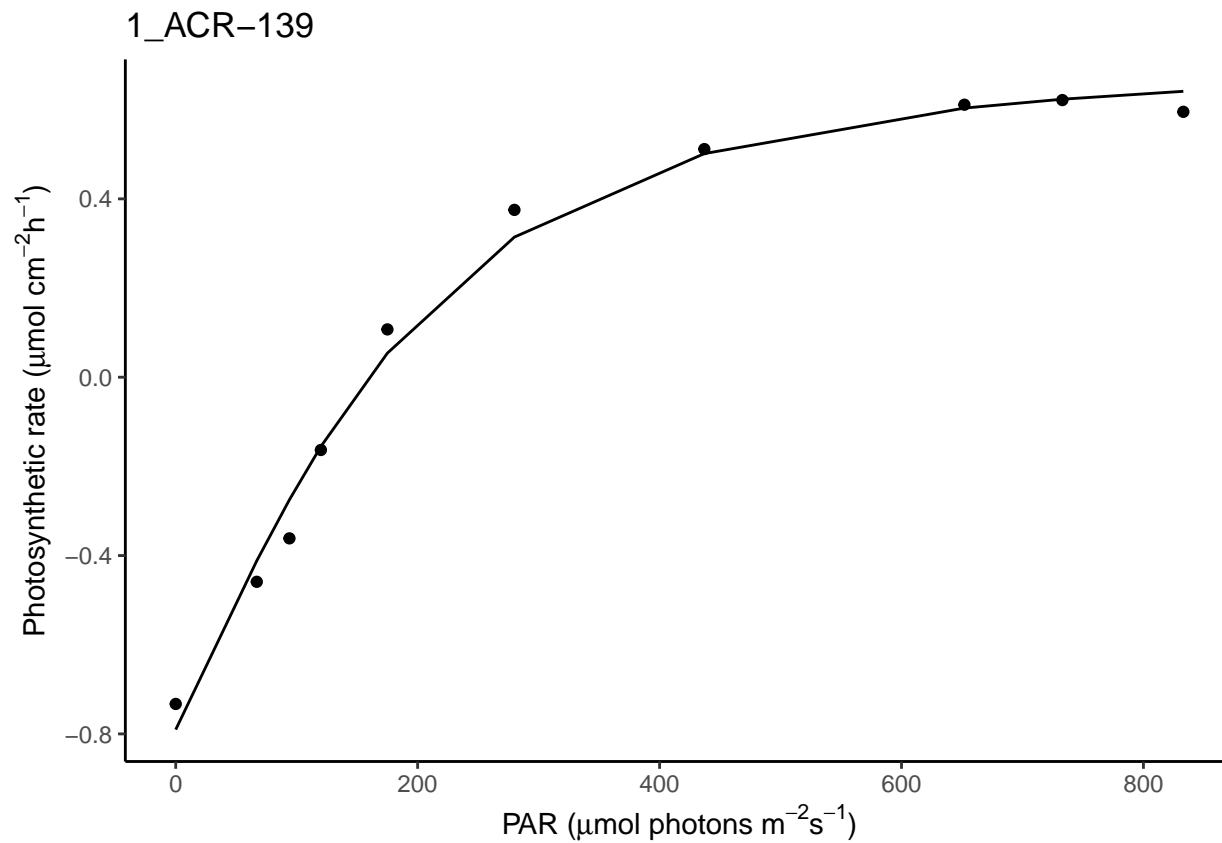
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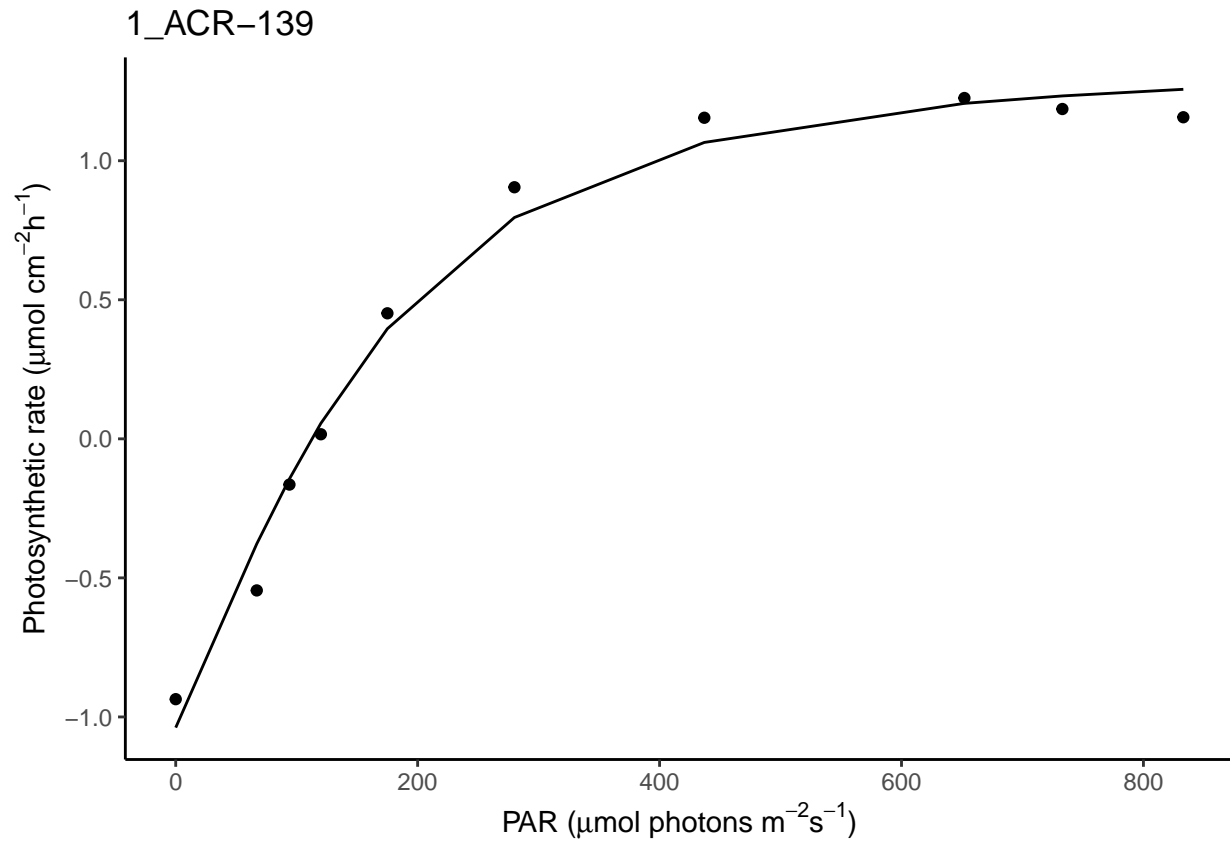
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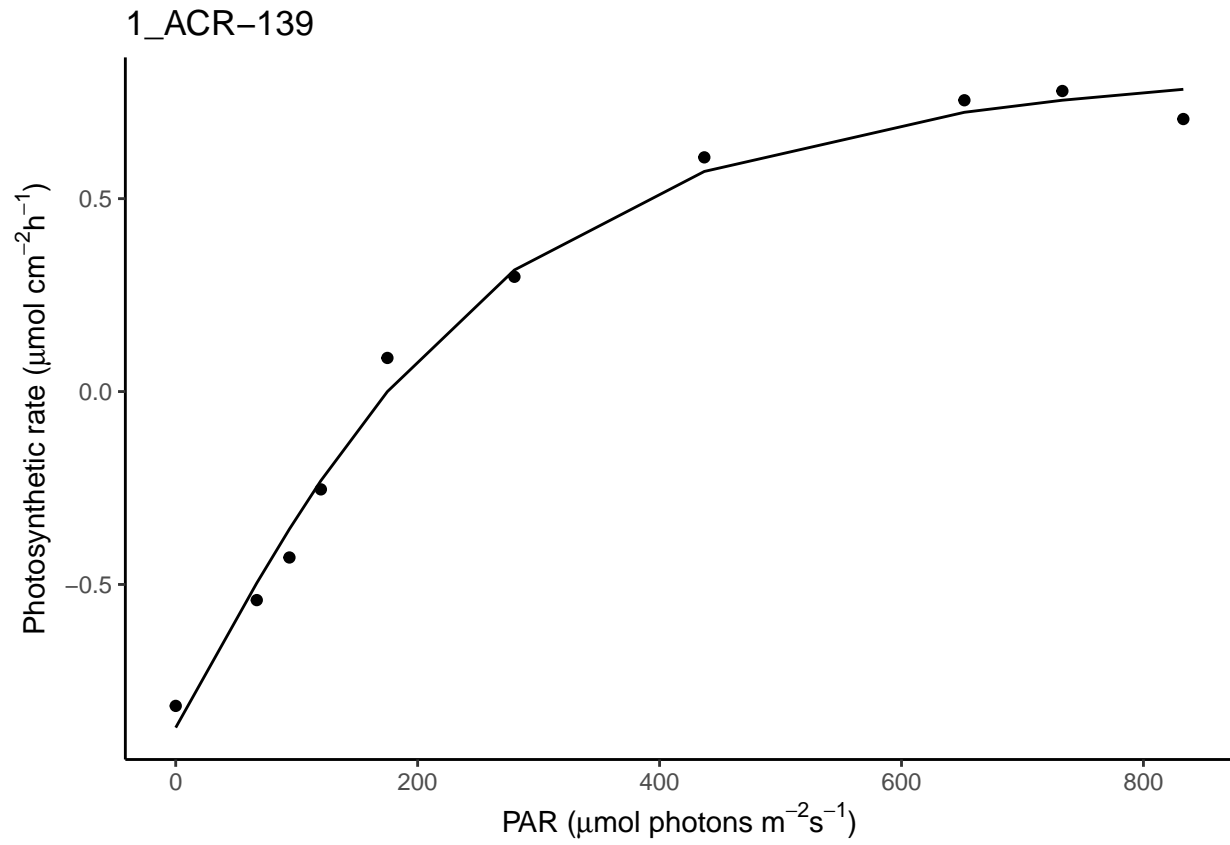
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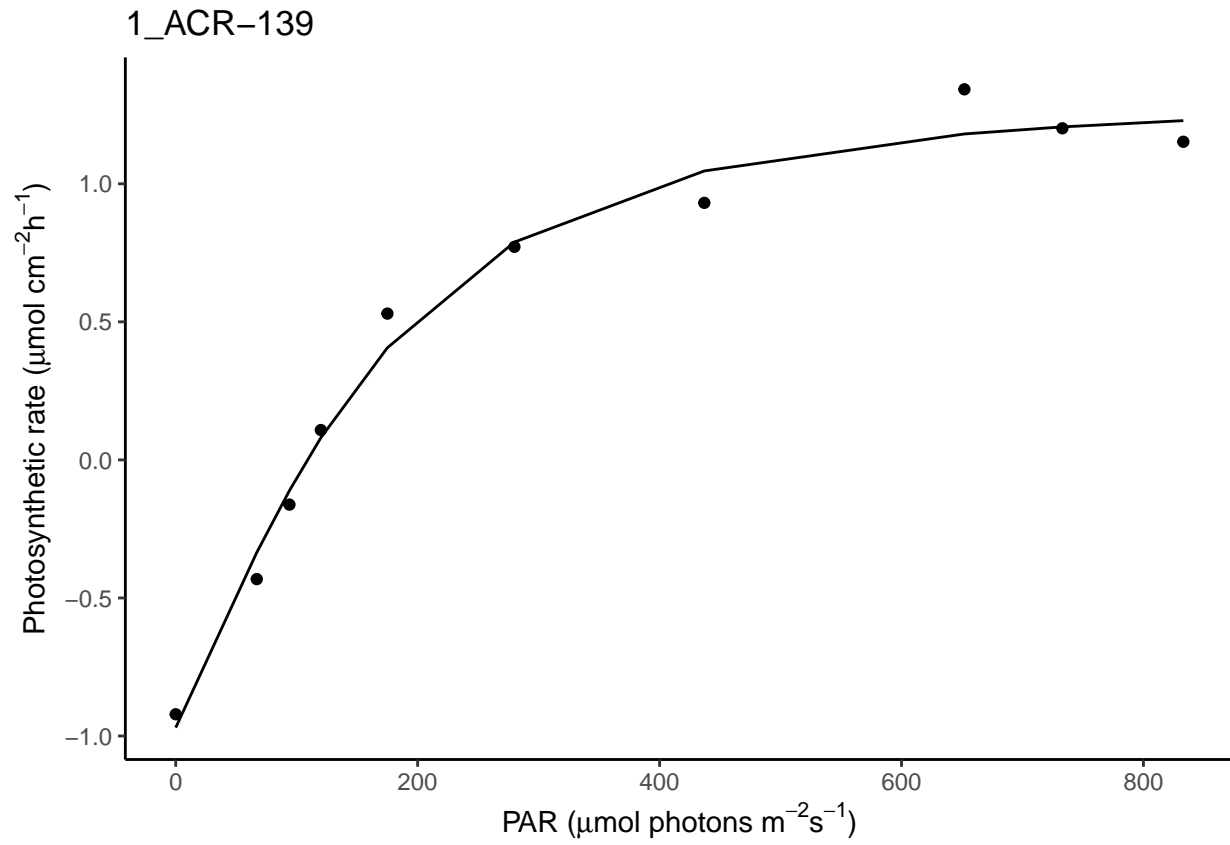
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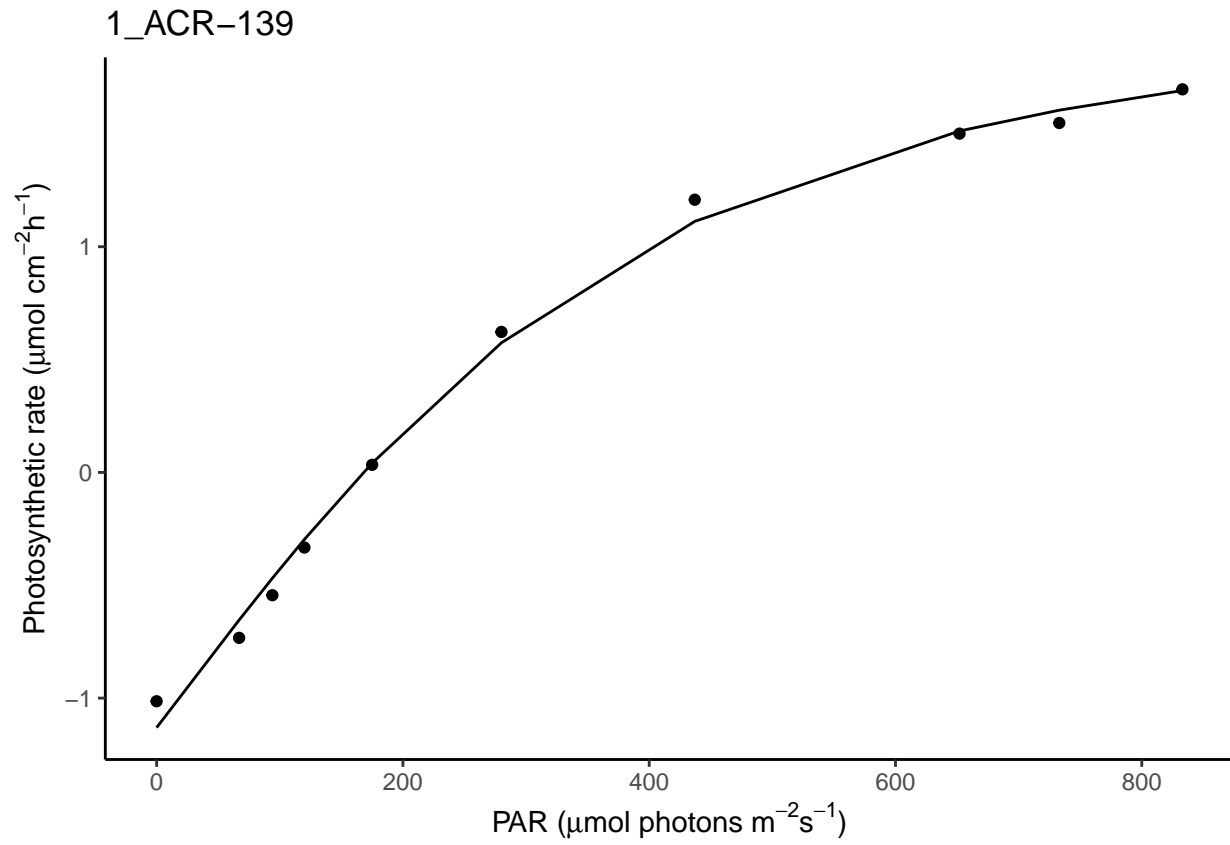
augmented\$colony_id: POR-81



augmented\$colony_id: POR-82



augmented\$colony_id: POR-83



#NEED TO FIND A WAY TO SAVE INDIVIDUALS