

```

library("lme4")
library("lmerTest")
library("nlme")
library("contrast")
library("ggplot2")
library("lsmeans")
library("car")
library("glmmADMB")
library("phia")

# Multiple plot function
# From: http://www.cookbook-
# r.com/Graphs/Multiple\_graphs\_on\_one\_page\_\(ggplot2\)/
# ggplot objects can be passed in ..., or to plotlist (as a list of
# ggplot objects)
# - cols: Number of columns in layout
# - layout: A matrix specifying the layout. If present, 'cols' is
# ignored.
#
# If the layout is something like matrix(c(1,2,3,3), nrow=2, byrow=TRUE),
# then plot 1 will go in the upper left, 2 will go in the upper right,
# and
# 3 will go all the way across the bottom.
#
multiplot <- function(..., plotlist=NULL, file, cols=1, layout=NULL) {
  library(grid)
  # Make a list from the ... arguments and plotlist
  plots <- c(list(...), plotlist)
  numPlots = length(plots)
  # If layout is NULL, then use 'cols' to determine layout
  if (is.null(layout)) {
    # Make the panel
    # ncol: Number of columns of plots
    # nrow: Number of rows needed, calculated from # of cols
    layout <- matrix(seq(1, cols * ceiling(numPlots/cols)),
                      ncol = cols, nrow = ceiling(numPlots/cols))
  }
  if (numPlots==1) {
    print(plots[[1]])
  } else {
    # Set up the page
    grid.newpage()
    pushViewport(viewport(layout = grid.layout(nrow(layout),
ncol(layout))))
    # Make each plot, in the correct location
    for (i in 1:numPlots) {
      # Get the i,j matrix positions of the regions that contain this
      subplot
      matchidx <- as.data.frame(which(layout == i, arr.ind = TRUE))
      print(plots[[i]], vp = viewport(layout.pos.row = matchidx$row,
                                      layout.pos.col = matchidx$col))
    }
  }
}

# To normalize variable when required

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```

normalize <- function(v) (v-mean(v))/sd(v)

# PATH to change
setwd("/Users/sylvain/Documents/Boulot/Recherche/Thematiques/Capsella/Competition/Xuyue/Article/V3/")

##### #
# Loading and filtering datasets #####
##### #

data_all <- read.table("CompetitionCapsella_dataset.csv", header = T, sep = ";") # raw data
# To ensure proper format for variables
data_all$block <- as.factor(data_all$block)
data_all$accession <- as.factor(data_all$accession)
# To write competition index as in the article
data_all$IcDiam1 <- 1 - data_all$alphadiameter1
data_all$IcDiam2 <- 1 - data_all$alphadiameter2
data_all$IcGrowth <- 1 - data_all$alphagrowthrate
data_all$IcGrowth <-
ifelse(data_all$alphagrowthrate>=0,data_all$alphagrowthrate,NA)
data_all$IcFlower <- 1 - data_all$alphaflowernumber
# Re-ordering for plotting
data_all$species <- relevel(data_all$species,"Cg")
levels(data_all$species) <- c("C. grandiflora","C. bursa-pastoris","C. orientalis","C. rubella")
data_all$area <- relevel(data_all$area,"Europe")
data_all$area <- relevel(data_all$area,"Middle_east")
levels(data_all$area) <- c("Middle East","Europe","Central Asia","China","Greece","Out of")
# Data set without non-flowering plants
data_all_flower <- subset(x = data_all, data_all$flowernumber>0)
# Only competition treatment for all populations
data_all_comp <- subset(x = data_all, (data_all$treatment=="competitor"))
# Dataset with only Cbp
data_cbp <-subset(x=data_all, (data_all$species == "C. bursa-pastoris"))
#cbp alone and competition treatment
data_cbp_flower <- subset(x = data_cbp, data_cbp$flowernumber>0) #only competition treatment for all populations
data_cbp_comp <- subset(x=data_all, (data_all$species == "C. bursa-pastoris" & data_all$treatment=="competitor" )) #only cbp competition treatment
# Mean per accession over block for data presentation
meanblock <-
aggregate(data_all,by=list("treatment"=data_all$treatment,"species"=data_all$species,"population"=data_all$allpopulation,"area"=data_all$area,"accession"=data_all$accession),FUN = function(x) mean(x,na.rm=T))
alone <- meanblock[meanblock$treatment=="alone",][,-c(6:13)]
comp <- meanblock[meanblock$treatment=="competitor",][,-c(6:13)]
data_meanblock <-
merge(alone,comp,by=c("species","population","area","accession"))
rm(meanblock,alone,comp)

```

```
##### #  
# ANALYSES ####  
##### #
```

```
# Among species comparison ####
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# Vegetative traits ####
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```
# Diameter t1  
model_d1 <- lmer(squarediameter1 ~ (block+species+treatment)^2  
+(1|accession) ,data=data_all,na.action = "na.omit",REML=F)  
anova(model_d1)  
ranova(model_d1)  
# Test of main effects by keeping only significant interaction  
model_d1sign <- lmer(squarediameter1 ~ block+block:species  
+(species+treatment) +(1|accession) ,data=data_all,na.action =  
"na.omit",REML=F)  
anova(model_d1sign)
```

```
# Diameter t2  
model_d2 <- lmer(squarediameter2 ~ (block+species+treatment)^2  
+(1|accession) ,data=data_all,na.action = "na.omit",REML=F)  
anova(model_d2)  
ranova(model_d2)  
# Test of main effects by keeping only significant interaction  
model_d2sign <- lmer(squarediameter2 ~ (block+species+treatment)  
+(1|accession) ,data=data_all,na.action = "na.omit",REML=F)  
anova(model_d2sign)
```

```
# Growth rate  
model_growth <- lmer(squaregrowthrate ~ (block+species+treatment)^2  
+(1|accession) ,data=data_all,na.action = "na.omit",REML=F)  
anova(model_growth)  
ranova(model_growth)  
# Test of main effects by keeping only significant interaction  
model_growthsign <- lmer(squaregrowthrate ~  
block*species+block*treatment +(1|accession) ,data=data_all,na.action =  
"na.omit",REML=F)  
anova(model_growthsign)
```

```
# Reproductive traits ####
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```
#Flowering rate #  
model_flowering <- glmer(flowering ~  
(block+squarediameter2+species+treatment)^2 +  
(1|accession),family=binomial(link=logit),data=data_all,  
glmerControl(optimizer = c("bobyqa",  
"Nelder_Mead"), restart_edge = FALSE, boundary.tol = 1e-5, calc.derivs=F,  
use.last.params=FALSE, sparseX = FALSE, tolPwrss=1e-6, compDev=TRUE,  
nAGQ0initStep=TRUE)
```

```

)
model_flowering_fix <- glm(flowering ~
(block+squarediameter2+species+treatment)^2
,family=binomial(link=logit),data=data_all)
Anova(model_flowering,type=3)
anova(model_flowering,model_flowering_fix)

# Test of main effects by keeping only significant interactions
model_floweringsign <- glmer(flowering ~
(block+squarediameter2+species+treatment) +
(1|accession),family=binomial(link=logit),data=data_all,
glmerControl(optimizer = c("bobyqa",
"Nelder_Mead"), restart_edge = FALSE, boundary.tol = 1e-5, calc.derivs=F,
use.last.params=FALSE, sparseX = FALSE, tolPwrss=1e-6, compDev=TRUE,
nAGQ0initStep=TRUE)
)
Anova(model_floweringsign,type=3)

# Number of flowers #
model_nbFlowerDiam <- glmer.nb(flowernumber ~ (block + species +
squarediameter2+treatment)^2 + (1|accession),data=data_all_flower,
glmerControl(optimizer = c("bobyqa",
"Nelder_Mead"), restart_edge = FALSE, boundary.tol = 1e-5, calc.derivs=F,
use.last.params=FALSE, sparseX = FALSE, tolPwrss=1e-6, compDev=TRUE,
nAGQ0initStep=TRUE))
model_nbFlowerDiam_fix <- glm.nb(flowernumber ~
(block+squarediameter2+species + treatment)^2,
data=data_all_flower,na.action = "na.omit")
Anova(model_nbFlowerDiam,type=3)
anova(model_nbFlowerDiam,model_nbFlowerDiam_fix)

# Test of main effects by keeping only significant interactions
model_nbFlowerDiamsign <- glmer.nb(flowernumber ~ block +
(species+treatment)^2 +(squarediameter2+treatment)^2 +
(1|accession),data=data_all_flower,
glmerControl(optimizer = c("bobyqa",
"Nelder_Mead"), restart_edge = FALSE, boundary.tol = 1e-5, calc.derivs=F,
use.last.params=FALSE, sparseX = FALSE, tolPwrss=1e-6, compDev=TRUE,
nAGQ0initStep=TRUE))
Anova(model_nbFlowerDiamsign,type=3)
testInteractions(model_nbFlowerDiamsign,pairwise="species",
across="treatment",adjustment = "fdr")

summary(model_nbFlowerDiamsign)

# Figure 1

m1 <- as.data.frame(summary(lsmmeans(model_d2,c("species","treatment"))))
Mean1 <- merge(m1[c(1:4),],m1[c(5:8),],by="species")
Mean1$species <- relevel(Mean1$species,"C. grandiflora")
Mean1 <- Mean1[order(Mean1$species),]
Mean1$CI <- round(Mean1$lsmmean.y /Mean1$lsmmean.x,2)
Mean1$species <- relevel(Mean1$species,"C. grandiflora")
Mean1$label <- paste("Ic = ",Mean1$CI)

```

```

G1 <- ggplot() + geom_segment(aes(x = 0, y = squarediameter2.x, xend = 1,
yend = squarediameter2.y), data=data_meanblock, col="grey")
G1 <- G1 + scale_y_log10(limits = c(10, 22), breaks = c(10, 15, 20)) +
xlim(-0.01, 1.01)
G1 <- G1 +
geom_segment(aes(x=0, y=lsmean.x, xend=1, yend=lsmean.y), data=Mean1, col="black", size=1.5)
G1 <- G1 + geom_errorbar(aes(x=0, ymin=lower.CL.x, ymax=upper.CL.x),
width=1, data=Mean1, col="black", size=1.5)
G1 <- G1 + geom_errorbar(aes(x=1, ymin=lower.CL.y, ymax=upper.CL.y),
width=1, data=Mean1, col="black", size=1.5)
G1 <- G1 + facet_grid(.~species)
G1 <- G1 + geom_text(aes(x, y, label=lab), data=data.frame(x=0, y=10,
lab="Alone"), hjust=0.1, size=5)
G1 <- G1 + geom_text(aes(x, y, label=lab), data=data.frame(x=1, y=10,
lab="Competitor"), hjust=0.9, size=5)
G1 <- G1 + geom_text(aes(x, y, label=lab), data=data.frame(x=0.5, y=22,
lab=Mean1$label, species=levels(data_meanblock$species)), size=5)
G1 <- G1 + theme_bw() + theme(legend.title = element_blank(), legend.text
= element_text(size=14, face = "italic"),
axis.text.x=element_blank(),
axis.ticks.x=element_blank(), axis.title.x=element_blank(), axis.title.y =
element_text(size = 16),
strip.text.x = element_text(size = 14, face =
"italic"), axis.text.y=element_text(size=14))
G1 <- G1 + theme(panel.grid.major = element_blank(),
legend.position="none", panel.grid.minor = element_blank())
G1 <- G1 + ylab("Rosette surface (in cm2)")
G1

```

```

m2 <-
as.data.frame(summary(lsmmeans(model_nbFlowerDiamsign, c("species", "treatment"))))
Mean2 <- merge(m2[c(1:4), ], m2[c(5:8), ], by="species")
Mean2$species <- relevel(Mean2$species, "C. grandiflora")
Mean2 <- Mean2[order(Mean2$species), ]
Mean2$lsmean.x <- exp(Mean2$lsmean.x)
Mean2$lsmean.y <- exp(Mean2$lsmean.y)
Mean2$asympt.LCL.x <- exp(Mean2$asympt.LCL.x)
Mean2$asympt.LCL.y <- exp(Mean2$asympt.LCL.y)
Mean2$asympt.UCL.x <- exp(Mean2$asympt.UCL.x)
Mean2$asympt.UCL.y <- exp(Mean2$asympt.UCL.y)
Mean2$CI <- round(Mean2$lsmean.y/Mean2$lsmean.x, 2)
Mean2$label <- paste("Ic = ", Mean2$CI)

```

```

G2 <- ggplot() + geom_segment(aes(x = 0, y = flowernumber.x, xend = 1,
yend = flowernumber.y), data=data_meanblock, col="grey")
G2 <- G2 +
scale_y_log10(breaks=c(250, 500, 1000, 2000, 3000), limits=c(200, 4000)) +
xlim(-0.01, 1.01)
G2 <- G2 +
geom_segment(aes(x=0, y=lsmean.x, xend=1, yend=lsmean.y), data=Mean2, col="black", size=1.5)

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G2 <- G2 + geom_errorbar(aes(x=0,ymin=asyp.LCL.x, ymax=asyp.UCL.x),
width=1,data=Mean2,col="black",size=1.5)
G2 <- G2 + geom_errorbar(aes(x=1,ymin=asyp.LCL.y, ymax=asyp.UCL.y),
width=1,data=Mean2,col="black",size=1.5)
G2 <- G2 + facet_grid(.~species)
G2 <- G2 + geom_text(aes(x, y, label=lab), data=data.frame(x=0, y=200,
lab="Alone"),hjust=0.1,size=5)
G2 <- G2 + geom_text(aes(x, y, label=lab), data=data.frame(x=1, y=200,
lab="Competitor"),hjust=0.9,size=5)
G2 <- G2 + geom_text(aes(x, y, label=lab), data=data.frame(x=0.5, y=3500,
lab=Mean2$label,species=levels(data_meanblock$species)),size=5)
G2 <- G2 + geom_text(aes(x, y, label=lab), data=data.frame(x=0.7, y=3800,
lab=c("a","b","c","c"),species=levels(data_meanblock$species)),size=5,fontface = "bold")
G2 <- G2 + theme_bw() + theme(legend.title = element_blank(),legend.text =
element_text(size=14,face = "italic"),
axis.text.x=element_blank(),
axis.ticks.x=element_blank(),axis.title.x=element_blank(),axis.title.y =
element_text(size = 16),
strip.text.x = element_text(size = 14,face =
"italic"),axis.text.y=element_text(size=14))
G2 <- G2 + theme(panel.grid.major = element_blank(),
legend.position="none",panel.grid.minor = element_blank())
G2 <- G2 + ylab("Flowers number")
G2

```

```

pdf(file = "Figure1.pdf",width = 12 ,height = 10)
multiplot(G1,G2)
dev.off()

```

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# Within Cbp comparison ####

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# Vegetative traits ####

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```

# Diameter t1
model_d1cbp <- lmer(squarediameter1 ~ (block+area+treatment)^2
+(1|accession) ,data=data_cbp,na.action = "na.omit",REML=F)
anova(model_d1cbp)
ranova(model_d1cbp)
# Test of main effects by keeping only significant interactions
model_d1cbpsign <- lmer(squarediameter1 ~ (block+area+treatment)
+(1|accession) ,data=data_cbp,na.action = "na.omit",REML=F)
anova(model_d1cbpsign)

# Diameter t2
model_d2cbp <- lmer(squarediameter2 ~ (block +area+treatment)^2
+(1|accession) ,data=data_cbp,na.action = "na.omit",REML=F)
anova(model_d2cbp)
ranova(model_d2cbp)
# Test of main effects by keeping only significant interactions
model_d2cbpsign <- lmer(squarediameter2 ~ block + (area+treatment)^2
+(1|accession) ,data=data_cbp,na.action = "na.omit",REML=F)
testInteractions(model_d2cbpsign,pairwise="area",
across="treatment",adjustment = "fdr")
anova(model_d2cbpsign)

```

```

# Growth rate
model_growthcbp <- lmer(squaregrowthrate ~ (block+area+treatment)^2
+(1|accession) ,data=data_cbp,na.action = "na.omit",REML=F)
anova(model_growthcbp)
ranova(model_growthcbp)
# Test of main effects by keeping only significant interactions
model_growthcbpsign <- lmer(squaregrowthrate ~ area+(block+treatment)^2
+(1|accession) ,data=data_cbp,na.action = "na.omit",REML=F)
anova(model_growthcbpsign)

# Reproductive traits ####

#Flowering rate #
model_floweringcbp <- glmer(flowering ~ (block +
scale(squarediameter2)+ area+treatment)^2 +
(1|accession),family=binomial(link=logit),data=data_cbp,
glmerControl(optimizer = c("bobyqa",
"Nelder_Mead"), optCtrl = list(maxfun=50000),restart_edge = FALSE,
boundary.tol = 1e-5, calc.derivs=F, use.last.params=FALSE, sparseX =
FALSE, tolPwrss=1e-6, compDev=TRUE, nAGQ0initStep=TRUE)
)
model_flowering_fixcbp <- glm(flowering ~ (block +
scale(squarediameter2)+ area+treatment)^2
,family=binomial(link=logit),data=data_cbp)
Anova(model_floweringcbp,type=3)
anova(model_floweringcbp,model_flowering_fixcbp)
# Test of main effects by keeping only significant interaction
model_floweringcbpsign <- glmer(flowering ~ (block +
scale(squarediameter2)+ area+treatment) +
(1|accession),family=binomial(link=logit),data=data_cbp,
glmerControl(optimizer = c("bobyqa",
"Nelder_Mead"), optCtrl = list(maxfun=50000),restart_edge = FALSE,
boundary.tol = 1e-5, calc.derivs=F, use.last.params=FALSE, sparseX =
FALSE, tolPwrss=1e-6, compDev=TRUE, nAGQ0initStep=TRUE)
)
Anova(model_floweringcbpsign,type=3)

# Number of flowers #
model_nbFlowerDiamcbp <- glmer.nb(flowernumber ~ (block +
scale(squarediameter2) + area + treatment)^2 +
(1|accession),data=data_cbp_flower,
glmerControl(optimizer = c("bobyqa",
"Nelder_Mead"), optCtrl = list(maxfun=50000),restart_edge = FALSE,
boundary.tol = 1e-5, calc.derivs=F, use.last.params=FALSE, sparseX =
FALSE, tolPwrss=1e-6, compDev=TRUE, nAGQ0initStep=TRUE))
model_nbFlowerDiam_fixcbp <- glm.nb(flowernumber ~ (block +
squarediameter2 + area + treatment)^2, data=data_cbp_flower,na.action =
"na.omit")
Anova(model_nbFlowerDiamcbp,type=3)
anova(model_nbFlowerDiamcbp,model_nbFlowerDiam_fixcbp)

# Test of main effects by keeping only significant interactions

model_nbFlowerDiamcbpsign <- glmer.nb(flowernumber ~ block +
scale(squarediameter2) + (area + treatment)^2 +
(1|accession),data=data_cbp_flower,

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                                glmerControl(optimizer = c("bobyqa",
"Nelder_Mead"), optCtrl = list(maxfun=50000),restart_edge = FALSE,
boundary.tol = 1e-5, calc.derivs=F, use.last.params=FALSE, sparseX =
FALSE, tolPwrss=1e-6, compDev=TRUE, nAGQ0initStep=TRUE))
Anova(model_nbFlowerDiamcbpsign,type=3)
testInteractions(model_nbFlowerDiamcbpsign,pairwise="area",
across="treatment",adjustment = "fdr")
summary(model_nbFlowerDiamcbpsign)

# Figure 2

m1cbp <-
as.data.frame(summary(lsmmeans(model_d2cbpsign,c("area","treatment"))))
Mean1cbp <- merge(m1cbp[c(1:4),],m1cbp[c(5:8),],by="area")
Mean1cbp$area <- relevel(Mean1cbp$area ,"Europe")
Mean1cbp$area <- relevel(Mean1cbp$area ,"Middle East")
Mean1cbp <- Mean1cbp[order(Mean1cbp$area),]
Mean1cbp$CI <- round(Mean1cbp$lsmmean.y /Mean1cbp$lsmmean.x,2)
Mean1cbp$label <- paste("Ic = ",Mean1cbp$CI)

G1cbp <- ggplot() + geom_segment(aes(x = 0, y = squarediameter2.x, xend =
1, yend =
squarediameter2.y),data=data_meanblock[data_meanblock$species=="C. bursa-
pastoris",],col="grey")
G1cbp <- G1cbp + scale_y_log10(limits = c(10, 24),breaks = c(10,15,20)) +
xlim(-0.01,1.01)
G1cbp <- G1cbp +
geom_segment(aes(x=0,y=lsmmean.x,xend=1,yend=lsmmean.y),data=Mean1cbp,col="
black",size=1.5)
G1cbp <- G1cbp + geom_errorbar(aes(x=0,ymin=lower.CL.x, ymax=upper.CL.x),
width=1,data=Mean1cbp,col="black",size=1.5)
G1cbp <- G1cbp + geom_errorbar(aes(x=1,ymin=lower.CL.y, ymax=upper.CL.y),
width=1,data=Mean1cbp,col="black",size=1.5)
G1cbp <- G1cbp + facet_grid(.~area)
G1cbp <- G1cbp + geom_text(aes(x, y, label=lab), data=data.frame(x=0,
y=10, lab="Alone"),hjust=0.1,size=5)
G1cbp <- G1cbp + geom_text(aes(x, y, label=lab), data=data.frame(x=1,
y=10, lab="Competitor"),hjust=0.9,size=5)
G1cbp <- G1cbp + geom_text(aes(x, y, label=lab), data=data.frame(x=0.5,
y=23, lab=Mean1cbp$label,area=levels(Mean1cbp$area)),size=5)
G1cbp <- G1cbp + geom_text(aes(x, y, label=lab), data=data.frame(x=0.7,
y=23.5, lab=c("a","b","
a,b","b"),area=levels(Mean1cbp$area)),size=5,fontface = "bold")
G1cbp <- G1cbp + theme_bw() + theme(legend.title =
element_blank(),legend.text = element_text(size=14,face = "italic"),
axis.text.x=element_blank(),
axis.title.x=element_blank(),axis.title.y =
element_text(size = 16),
strip.text.x = element_text(size = 14,face
= "italic"),axis.text.y=element_text(size=14))
G1cbp <- G1cbp + theme(panel.grid.major = element_blank(),
legend.position="none",panel.grid.minor = element_blank())
G1cbp <- G1cbp + ylab("Rosette surface (in cm2)")
G1cbp

```



```

m2cbp <-
as.data.frame(summary(lsmmeans(model_nbFlowerDiamcbpsign,c("area","treatme
nt"))))
Mean2cbp <- merge(m2cbp[c(1:4),],m2cbp[c(5:8),],by="area")
Mean2cbp$area <- relevel(Mean2cbp$area,"Europe")
Mean2cbp$area <- relevel(Mean2cbp$area,"Middle East")
Mean2cbp <- Mean2cbp[order(Mean2cbp$area),]
Mean2cbp$lsmmean.x <- exp(Mean2cbp$lsmmean.x)
Mean2cbp$lsmmean.y <- exp(Mean2cbp$lsmmean.y)
Mean2cbp$asympt.LCL.x <- exp(Mean2cbp$asympt.LCL.x)
Mean2cbp$asympt.LCL.y <- exp(Mean2cbp$asympt.LCL.y)
Mean2cbp$asympt.UCL.x <- exp(Mean2cbp$asympt.UCL.x)
Mean2cbp$asympt.UCL.y <- exp(Mean2cbp$asympt.UCL.y)
Mean2cbp$CI <- round(Mean2cbp$lsmmean.y/Mean2cbp$lsmmean.x,2)
Mean2cbp$label <- paste("Ic =",Mean2cbp$CI)

G2cbp <- ggplot() + geom_segment(aes(x = 0, y = flownumber.x, xend = 1,
yend = flownumber.y),data=data_meanblock[data_meanblock$species=="C.
bursa-pastoris",],col="grey")
G2cbp <- G2cbp +
scale_y_log10(breaks=c(250,500,1000,2000),limits=c(200,2000)) + xlim(-
0.01,1.01)
G2cbp <- G2cbp +
geom_segment(aes(x=0,y=lsmmean.x,xend=1,yend=lsmmean.y),data=Mean2cbp,col="
black",size=1.5)
G2cbp <- G2cbp + geom_errorbar(aes(x=0,ymin=asympt.LCL.x,
ymax=asympt.UCL.x), width=1,data=Mean2cbp,col="black",size=1.5)
G2cbp <- G2cbp + geom_errorbar(aes(x=1,ymin=asympt.LCL.y,
ymax=asympt.UCL.y), width=1,data=Mean2cbp,col="black",size=1.5)
G2cbp <- G2cbp + facet_grid(.~area)
G2cbp <- G2cbp + geom_text(aes(x, y, label=lab), data=data.frame(x=0,
y=200, lab="Alone"),hjust=0.1,size=5)
G2cbp <- G2cbp + geom_text(aes(x, y, label=lab), data=data.frame(x=1,
y=200, lab="Competitor"),hjust=0.9,size=5)
G2cbp <- G2cbp + geom_text(aes(x, y, label=lab), data=data.frame(x=0.5,
y=1800, lab=Mean2cbp$label,area=c("Middle East","Europe","Central
Asia","China")),size=5)
G2cbp <- G2cbp + geom_text(aes(x, y, label=lab), data=data.frame(x=0.7,
y=1900, lab=c("a","b","a,b","c"),area=c("Middle East","Europe","Central
Asia","China")),size=5,fontface = "bold")
G2cbp <- G2cbp + theme_bw() + theme(legend.title =
element_blank(),legend.text = element_text(size=14,face = "italic"),
axis.text.x=element_blank(),
axis.title.x=element_blank(),axis.title.y =
element_text(size = 16),
strip.text.x = element_text(size = 14,face
= "italic"),axis.text.y=element_text(size=14))
G2cbp <- G2cbp + theme(panel.grid.major = element_blank(),
legend.position="none",panel.grid.minor = element_blank())
G2cbp <- G2cbp + ylab("Flowers number")
G2cbp

pdf(file = "Figure2.pdf",width = 12 ,height = 10)
multiplot(G1cbp,G2cbp)
dev.off()

```

```
# With PI as a covariable ####
```

```
model_d2Picbp <- lmer(squarediameter2 ~ scale(Pi) + (block +  
treatment)^2 + (1|accession) ,data=data_cbp,na.action = "na.omit",REML=F)  
anova(model_d2Picbp)  
summary(model_d2Picbp)  
model_d2Picbpsign <- lmer(squarediameter2 ~ block + scale(Pi)+treatment  
+ (1|accession) ,data=data_cbp,na.action = "na.omit",REML=F)  
anova(model_d2Picbpsign)
```

```
reg1 <-  
lm(squarediameter2~Pi,data=data_cbp[data_cbp$treatment=="alone",])  
reg2 <-  
lm(squarediameter2~Pi,data=data_cbp[data_cbp$treatment=="competitor",])  
Gpi1 <- ggplot() +  
geom_point(aes(x=Pi,y=squarediameter2,col=treatment),data=data_cbp)  
Gpi1 <- Gpi1 + scale_color_manual(values =  
c("black","grey"),breaks=data_cbp$treatment)  
Gpi1 <- Gpi1 +  
geom_abline(intercept=reg1$coefficients[1],slope=reg1$coefficients[2],col  
="black")  
Gpi1 <- Gpi1 +  
geom_abline(intercept=reg2$coefficients[1],slope=reg2$coefficients[2],col  
="grey")  
Gpi1 <- Gpi1 + theme_bw() + theme(axis.title.x = element_text(size =  
24),axis.title.y = element_text(size = 16),  
                                strip.text.x = element_text(size =  
14,face = "italic"),axis.text=element_text(size=10))  
Gpi1 <- Gpi1 + theme(panel.grid.major = element_blank(),  
legend.position="none",panel.grid.minor = element_blank()) +  
ylab("Rosette surface (in cm2)") +xlab(expression(pi))  
Gpi1
```

```
model_nbFlowerPicbp <- glm.nb(flowernumber ~ scale(Pi) + (block +  
treatment)^2 ,data=data_cbp_flower,na.action = "na.omit")  
summary(model_nbFlowerPicbp)  
Anova(model_nbFlowerPicbp,type=3)
```

```
model_nbFlowerPicbpsign <- glm.nb(flowernumber ~ block + scale(Pi) +  
treatment ,data=data_cbp_flower,na.action = "na.omit")  
Anova(model_nbFlowerPicbpsign,type=3)
```

```
reg1 <- lm(flowernumber~Pi,data=data_cbp[data_cbp$treatment=="alone",])  
reg2 <-  
lm(flowernumber~Pi,data=data_cbp[data_cbp$treatment=="competitor",])  
Gpi2 <- ggplot() +  
+geom_point(aes(x=Pi,y=flowernumber,col=treatment),data=data_cbp)  
Gpi2 <- Gpi2 + scale_color_manual(values =  
c("black","grey"),breaks=data_cbp$treatment)  
Gpi2 <- Gpi2 +  
geom_abline(intercept=reg1$coefficients[1],slope=reg1$coefficients[2],col  
="black")  
Gpi2 <- Gpi2 +  
geom_abline(intercept=reg2$coefficients[1],slope=reg2$coefficients[2],col  
="grey")
```

```
Gpi2 <- Gpi2 + theme_bw() + theme(legend.title =
element_blank(), legend.text = element_text(size=14, face = "italic"),
axis.title.x = element_text(size =
24), axis.title.y = element_text(size = 16),
strip.text.x = element_text(size =
14, face = "italic"), axis.text=element_text(size=10))
Gpi2 <- Gpi2 + theme(panel.grid.major = element_blank(),
legend.position="none", panel.grid.minor = element_blank()) +
ylab("Flowers number") + xlab(expression(pi))
Gpi2
```

```
pdf(file = "FigureSup.pdf", width = 8 , height = 4)
multiplot(Gpi1, Gpi2, cols=2)
dev.off()
```