

Body size and symbiotic status influence gonad development in *Aiptasia pallida* anemones

Symbiosis

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Relevant R code:

#MALE SIZE

```
males<-read.csv("boxplot males.csv")
by(males$MeanSize, males$Group, shapiro.test)
bartlett.test(MeanSize~Group, data=males)
wilcox.test(MeanSize~Group, data=males)
par(mai=c(1.2,1.5,0.5,4))
stripchart(males$Follicles~males$Group, vertical=TRUE, method="jitter", pch=1, cex=2, xlab="",
           ylab="", las=1, cex.lab=1.6, cex.axis=1.5)
points(c(1,2), tapply(males$Follicles, males$Group, median), pch="___", cex=4)
mtext("Number of Sperm Follicles",side=2,line=3.5, cex=2, at=30)
mtext("Group", side=1, line=3, cex = 2)
par(mai=c(1.4,1.6,0.5,0.5))
plot(FolliclesSym~MeanSize, data=males, pch=1, cex=2, xlab="", ylab="", cex.axis=2.5, mgp=c(3,1.5,0),
     ylim=c(0,70), xlim=c(1,4.5))
lines(FolliclesApo~MeanSize, data=males, type="p",pch=2, cex=2, xlab="", ylab="", cex.axis=2.5,
     mgp=c(3,1.5,0), ylim=c(0,70), xlim=c(1,4.5))
leg.txt<-c("Sym", "Apo")
legend(1, 70, leg.txt,pch=c(1,2), pt.cex=2, cex=1.5)
mtext("Number of Sperm Follicles",side=2,line=3.9, cex=3, at=35)
mtext("Body Column Diameter (mm)", side=1, line=4, cex = 3, at=2.75)
cor.test(males$FolliclesSym, males$MeanSize, method="spearman")
```

#FEMALE SIZE

```
females<-read.csv("boxplot females.csv")
by(females$MeanSize, females$Group, shapiro.test)
bartlett.test(MeanSize~Group, data=females)
wilcox.test(MeanSize~Group, data=females)
par(mai=c(1.2,1.5,0.5,4))
stripchart(females$Oocytes~females$Group, vertical=TRUE, method="jitter", pch=1, cex=2, xlab="",
           ylab="", las=1, cex.lab=1.6, cex.axis=1.5)
points(c(1,2), tapply(females$Oocytes, females$Group, median), pch="___", cex=4)
mtext("Number of Oocytes",side=2,line=3.5, cex=2, at=195)
mtext("Group", side=1, line=3, cex = 2)
par(mai=c(1.4,1.6,0.5,0.5))
plot(OocytesSym~MeanSize, data=females, pch=1, cex=2, xlab="", ylab="", cex.axis=2.5,
     mgp=c(3,1.5,0), ylim=c(0,400), xlim=c(1,4.5))
lines(OocytesApo~MeanSize, data=females, type="p", pch=2, cex=2, xlab="", ylab="", cex.axis=2.5,
     mgp=c(3,1.5,0), ylim=c(0,400), xlim=c(1,4.5))
leg.txt<-c("Sym", "Apo")
legend(1, 400, leg.txt,pch=c(1,2), pt.cex=2, cex=1.5)
mtext("Number of Oocytes",side=2,line=3.9, cex=3, at=200)
mtext("Body Column Diameter (mm)", side=1, line=4, cex = 3, at=2.75)
cor.test(females$OocytesSym, females$MeanSize, method="spearman")#
```

STRIP CHART WITH SEPARATE PLOTS

```
alldata<-read.csv("anemone data one column.csv")
par(mai=c(1.2,1.2,0.5,0.5))
stripchart(alldata$MeanSize~alldata$Group, vertical=TRUE, method="jitter",
           pch=" ", xlab="Group", ylab="Body Column Diameter (mm)", las=1, cex.lab=1.6, cex.axis=1.5)
points(c(1,2,3,4), tapply(alldata$MeanSize, alldata$Group, median), pch="___", cex=4)
stripchart(alldata$MeanSize[alldata$YesNo=="no"] ~ alldata$Group[alldata$YesNo=="no"],
           method="jitter", vertical=TRUE, pch=1, col="black", cex=2, las=1, add=TRUE)
stripchart(alldata$MeanSize[alldata$YesNo=="yes"] ~ alldata$Group[alldata$YesNo=="yes"],
           method="jitter", vertical=TRUE, pch=8, col="black", cex=2, las=1, add=TRUE)
leg.txt<-c("No Gonads", "Gonads")
legend(0.72, 4.5, leg.txt, pch=c(1,8), pt.cex=2, cex=1.5)
```

GENERALIZED LINEAR MODELS

```
# install package ("MuMIn")
library(MuMIn)
```

FEMALES

```
females<-read.csv("boxplot females.csv")
gmffemale1<-glm(Oocytes~MeanSize+Group, females, family="poisson")
gmffemale2<-glm(Oocytes~MeanSize, females, family="poisson")
gmffemale3<-glm(Oocytes~Group, females, family="poisson")
gmffemale4<-glm(Oocytes~1, females, family="poisson")
AIC(gmffemale1,gmffemale2,gmffemale3,gmffemale4)
summary(gmffemale1)
gmpffemale1<-glm(OocytesBinomial~MeanSize+Group, females, family="binomial")
gmpffemale2<-glm(OocytesBinomial~MeanSize, females, family="binomial")
gmpffemale3<-glm(OocytesBinomial~Group, females, family="binomial")
gmpffemale4<-glm(OocytesBinomial~1, females, family="binomial")
AIC(gmpffemale1,gmpffemale2,gmpffemale3,gmpffemale4)
averagegmpffemale<-model.avg(gmpffemale2,gmpffemale1,revised.var=TRUE)
summary(averagegmpffemale)
```

MALES

```
males<-read.csv("boxplot males.csv")
gmmale1<-glm(Follicles~MeanSize+Group, males, family="poisson")
gmmale2<-glm(Follicles~MeanSize, males, family="poisson")
gmmale3<-glm(Follicles~Group, males, family="poisson")
gmmale4<-glm(Follicles~1, males, family="poisson")
AIC(gmmale1,gmmale2,gmmale3,gmmale4)
summary(gmmale1)
gmpmale1<-glm(FolliclesBinomial~MeanSize+Group, males, family="binomial")
gmpmale2<-glm(FolliclesBinomial~MeanSize, males, family="binomial")
gmpmale3<-glm(FolliclesBinomial~Group, males, family="binomial")
gmpmale4<-glm(FolliclesBinomial~1, males, family="binomial")
AIC(gmpmale1,gmpmale2,gmpmale3,gmpmale4)
averagegmpmale<-model.avg(gmpmale2,gmpmale1,revised.var=TRUE)
summary(averagegmpmale)
```