library (stringr); library (vegan); library(reshape2); library (ggplot2); library(ggpubr)

myBotu <- read.table("otu\_rarefy\_16s.DDS.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

myBtaxa<- read.table("tax\_rarefy\_16s.DDS.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

dim(myBotu); dim(myBtaxa)

design <- read.table("design\_rarefy\_16s.DDS.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

otu\_its\_RA <- t(t(myBotu)/colSums(myBotu))\*100

PHYLAnames\_its <- names(sort(table(myBtaxa[,"Genus"]), decr=T))

length(PHYLAnames\_its)

y <- NULL

otunames <- rownames(otu\_its\_RA)

for (i in PHYLAnames\_its){

x <- array(colSums(otu\_its\_RA [rownames(myBtaxa)[which(myBtaxa$Genus == paste(i))],,drop=FALSE]))

y <- rbind(y,x) }

rownames(y) <- paste(PHYLAnames\_its)

colnames(y) <- paste(colnames(otu\_its\_RA))

CLASS\_mat\_its <- y

head(CLASS\_mat\_its) #查看

colSums(CLASS\_mat\_its)

dim(CLASS\_mat\_its)

**write.table**(CLASS\_mat\_its, file="Genus.abd.DDS.txt", sep="\t",quote=F)

S.Genus<- as.data.frame( t(CLASS\_mat\_its [ c("Pseudomonas", "Bacillus", "Lysobacter", "Arthrobacter", "Sphingobium"), ]) )

S.Genus$Trt <- design $ Trt

p.Pse <- **ggplot**(S.Genus, aes(x=Trt, y= Pseudomonas, fill=Trt)) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, size=0, geom="bar")+

**stat\_summary**(fun.data=mean\_se, geom="errorbar", position=position\_dodge(0.70),

width=0.40, linewidth=0.75, colour="black") +

scale\_fill\_manual(values = c("dodgerblue", "darkorange")) +

scale\_y\_continuous (limits=c(0, 1.0), expand=c(0, 0.0001)) +

labs(x=NULL, y="Pseudomonas sp. (RA %)") +

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), axis.title=element\_text(size=12) )

p.Pse

data = S.Genus

(sum(data[rownames(data)[data$Trt=="DDS"],]$Pseudomonas)-sum(data[rownames(data)[data$Trt=="Control"], ]$Pseudomonas))/sum(data[rownames(data)[data$Trt=="VOC"], ]$Pseudomonas)\*100

**stats::t.test**(data $ Pseudomonas ~ data $Trt, p.adj="BH", var.equal=F) #Welch’s T test

###############################################################

p.Bac <- **ggplot**(S.Genus, aes(x=Trt, y= Bacillus, fill=Trt)) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, size=0, geom="bar")+

**stat\_summary**(fun.data=mean\_se, geom="errorbar", position=position\_dodge(0.70),

width=0.40, linewidth=0.75, colour="black") +

scale\_fill\_manual(values = c("dodgerblue", "darkorange")) +

scale\_y\_continuous (limits=c(0, 1.05), expand=c(0, 0.0001)) +

labs(x=NULL, y="Bacillus sp. (RA %)") +

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), axis.title=element\_text(size=12) )

p.Bac

data = S.Genus

(sum(data[rownames(data)[data$Trt=="DDS"],]$Bacillus)-sum(data[rownames(data)[data$Trt=="Control"], ]$ Bacillus))/sum(data[rownames(data)[data$Trt=="Control"], ]$ Bacillus)\*100

**stats::t.test**(data $ Bacillus ~ data $Trt, p.adj="BH", var.equal=F) #Welch’s T test

**ggarrange**(p.Pse, p.Bac, ncol=4, nrow=1, align="hv", legend="none" )