### in vitro

library(ggplot2); library(ggpubr); library (readr); library (dplyr); library(car)

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

IAA.plot <- **ggplot**(IAA.data, aes(x= **factor**(Strain, levels=c('Pse', 'Bac')), y= IAA , fill= Strain) ) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=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("cyan3", "cyan1")) +

scale\_y\_continuous (limits=c(0, 21), expand=c(0, 0.0001))+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), legend.position="none", axis.title=element\_text(size=12) )

IAA.plot

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

ACC.plot <- **ggplot**(IAA.data, aes(x= **factor**(Strain, levels=c('Pse', 'Bac')), y= ACC , fill= Strain) ) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=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("cyan3", "cyan1")) +

scale\_y\_continuous (limits=c(0, 65), expand=c(0, 0.0001))+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), legend.position="none", axis.title=element\_text(size=12) )

ACC.plot

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

**ggarrange**(IAA.plot, ACC.plot, ncol=2, nrow=1, align="hv", legend="none" )

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

Pcontent.NBRIP <- **ggplot**(mydata, aes(x= **factor**(Strain, levels=c('Pse', 'Bac')), y= InoP.NBRIP , fill= Strain) ) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=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("cyan3", "cyan1")) +

scale\_y\_continuous (limits=c(0, 150), expand=c(0, 0.0001))+

labs(x=NULL, y="Soluble P concentration (ug/ml)")+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), legend.position="none", axis.title=element\_text(size=12) )

Pcontent.NBRIP

**stats::t.test**(mydata $ InoP.NBRIP ~ mydata $ Strain, p.adj="BH", var.equal=F) #Welch’s T test

Pcontent.PS <- **ggplot**(mydata, aes(x= **factor**(Strain, levels=c('Pse', 'Bac')), y= InoP.PS , fill= Strain) ) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=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("cyan3", "cyan1")) +

scale\_y\_continuous (limits=c(0, 80), expand=c(0, 0.0001))+

labs(x=NULL, y="Soluble P concentration (ug/ml)")+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), legend.position="none", axis.title=element\_text(size=12) )

Pcontent.PS

**stats::t.test**(mydata $ InoP.PS ~ mydata $ Strain, p.adj="BH", var.equal=F) #Welch’s T test

pHdrop <- **ggplot**(mydata, aes(x= **factor**(Strain, levels=c('Pse', 'Bac')), y= pHdrop , fill= Strain) ) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=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("cyan3", "cyan1")) +

scale\_y\_continuous (limits=c(0, 1.25), expand=c(0, 0.0001))+

labs(x=NULL, y="pH drop (Unit)")+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), legend.position="none", axis.title=element\_text(size=12) )

pHdrop

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

Phytase <- **ggplot**(mydata, aes(x= **factor**(Strain, levels=c('Pse', 'Bac')), y= Phytase , fill= Strain) ) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=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("cyan3", "cyan1")) +

scale\_y\_continuous (limits=c(0, 30), expand=c(0, 0.0001))+

labs(x=NULL, y="Phytase activity (U/ml)")+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), legend.position="none", axis.title=element\_text(size=12) )

Phytase

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

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

OrganicAcid <- **ggplot**(OrganicAcid.data, aes(x= Acid, y= Content, fill = Isolate )) + #

geom\_bar(fun = mean, position=position\_dodge(), stat="summary", width=0.7, colour = "transparent") +

stat\_summary(fun.data = 'mean\_se', geom = "errorbar", colour = "black",

width=0.40, linewidth =0.75, position=position\_dodge(0.7)) +

scale\_fill\_manual(values = c("cyan3", "cyan1")) +

scale\_y\_continuous (limits=c(0, 170), expand=c(0, 0.0001))+

labs(x=NULL, y="Content (ug/ml)")+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), legend.position="none", axis.title=element\_text(size=12) )

OrganicAcid

mydata <- **filter**(OrganicAcid.data, Acid =="Malonicacid") # "Gluconicacid" "OxalicAcid" "Isobutyricacid" "Aceticacid" "Quinicacid" "Malonicacid"

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

**ggarrange**(Pcontent.NBRIP, pHdrop, Pcontent.PS, Phytase, ncol=4, nrow=1, align="hv", legend="none" )

### pot experiment###

library(ggplot2); library(ggpubr); library (readr); library (dplyr); library(car)

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

Biomass.bar <- **ggplot**(mydata, aes(x= **factor**(Trt, levels=c('CK', 'Pse', 'Bac', 'Two')), y=Biomass, fill=Trt) ) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=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("cyan3", "grey60", "cyan1", "cyan4")) +

scale\_y\_continuous (limits=c(0, 5.5), expand=c(0, 0.0001))+

labs(x=NULL, y="Plant dry biomass (g/plant)")+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), legend.position="none", axis.title=element\_text(size=12) )

Biomass.bar

library(car); library(multcompView); library(lsmeans); library(multcomp); library (dplyr)

model<-lm(Biomass~Trt, data= mydata); #summary(model); #Anova(model, type="II")

marginal=lsmeans(model, ~Trt); #pairs(marginal, adjust="fdr")

cld(marginal, alpha=0.05, Letters=letters, adjust="fdr", reversed=T)

Puptake.bar <- **ggplot**(mydata, aes(x= **factor**(Trt, levels=c('CK', 'Pse', 'Bac', 'Two')), y= Puptake, fill=Trt) ) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=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("cyan3", "grey60", "cyan1", "cyan4")) +

scale\_y\_continuous (limits=c(0, 30), expand=c(0, 0.0001))+

labs(x=NULL, y="P uptake (mg/plant)")+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), legend.position="none", axis.title=element\_text(size=12) )

Puptake.bar

model<-lm(Puptake~Trt, data= mydata); #summary(model); #Anova(model, type="II")

marginal=lsmeans(model, ~Trt); #pairs(marginal, adjust="fdr")

cld(marginal, alpha=0.05, Letters=letters, adjust="fdr", reversed=T)

RhizoP.bar <- **ggplot**(mydata, aes(x= **factor**(Trt, levels=c('CK', 'Pse', 'Bac', 'Two')), y= OlsenP, fill=Trt) ) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=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("cyan3", "grey60", "cyan1", "cyan4")) +

scale\_y\_continuous (limits=c(0, 100), expand=c(0, 0.0001))+

labs(x=NULL, y="Rhizosphere soil Olsen P content (mg/kg)")+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), legend.position="none", axis.title=element\_text(size=12) )

RhizoP.bar

model<-lm(OlsenP~Trt, data= mydata); #summary(model); #Anova(model, type="II")

marginal=lsmeans(model, ~Trt); #pairs(marginal, adjust="fdr")

cld(marginal, alpha=0.05, Letters=letters, adjust="fdr", reversed=T)

**ggarrange**(Biomass.bar, Puptake.bar, RhizoP.bar, ncol=3, nrow=1, align="hv", legend="none" )