

Phylogenetic and functional diversity of termites

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Abstract

This document describes in detail all the analyses performed for the phylogenetic and functional diversity of termites in response to ant predation, density of trees, P, and N content. It provides an R script following the analyses step by step, from downloading the data from public and permanent repositories to creating graphs and statistical tables. These are some of the ecological questions we tried to answer in this study:

- Termites have a strong turnover along P content, but their densities are strongly associated with the density of predatory ants.
- Why are termite species replacing each other along the environmental gradients?
- Does the phylogenetic community structure indicates environmental filtering or competition to sort the species?
- How ant density affects the co-occurrence of termite species? Are some termites more vulnerable to ant predation?

Contents

| | | |
|----|--|----|
| 1 | Load required packages | 3 |
| 2 | Import data | 3 |
| 3 | Extract data from tables | 3 |
| 4 | Calculate pairwise trait distance between species | 4 |
| 5 | Calculate phylogenetic distance and rearrange columns to match species names in the data | 5 |
| 6 | Contingency table of traits | 5 |
| 7 | Calculates Moran's <i>I</i> and mantel correlograms | 5 |
| 8 | Plot trait distances against phylogenetic distance | 8 |
| 9 | Plot mantel correlograms | 9 |
| 10 | Create response variables | 10 |
| 11 | Summarize composition and phylocomposition in PCoA axes | 12 |

| | |
|---|-----------|
| 12 Regression analyses by response variable | 13 |
| 12.1 Overall PD | 13 |
| 12.2 Overall MPD | 14 |
| 12.3 Overall MNTD | 14 |
| 12.4 Overall Sorensen | 15 |
| 12.5 Overall PhyloSorensen | 16 |
| 12.6 Overall Unifrac | 17 |
| 12.7 Wood feeders PD | 18 |
| 12.8 Wood feeders MPD | 18 |
| 12.9 Wood feeders MNTD | 19 |
| 12.10Wood feeders Sorensen | 20 |
| 12.11Wood feeders PhyloSorensen | 21 |
| 12.12Wood feeders Unifrac | 22 |
| 12.13Soil feeders PD | 22 |
| 12.14Soil feeders MPD | 23 |
| 12.15Soil feeders MNTD | 24 |
| 12.16Soil feeders Sorensen | 25 |
| 12.17Soil feeders PhyloSorensen | 26 |
| 12.18Soil feeders Unifrac | 26 |
| 13 Plot phylogenetic diversity against <i>P</i> | 28 |
| 14 Diagrams: spp. presence by phylo and predictor variable | 29 |
| 15 Summary of results in Table 1. | 31 |

1 Load required packages

Some of the analyses run in our study were coded along the text, some analyses were in pre built packages, and some were transformed in functions, which are publicly available on-line.

The following lines load the required libraries, and download and source the necessary functions

```
library(ape)
library(picante)
library(tree)
library(vegan)
library(FD)
source("http://files.figshare.com/1672057/poncho.R") # poncho function for figures
```

2 Import data

Similarly to the functions, we made our datasets publicly available on-line. They are downloaded using the next chunk of code. If you have problems running these lines, you might have an internet connection problem. Try to download the files to your directory using the provided links, and then read the files directly from your folder.

```
# To be changed - All files will download from the internet in the final version

iso.RFAD<-read.csv("http://files.figshare.com/1922298/Dambros2009_Isoptera.RFAD.csv",row.names=1)#termi
traits<-read.csv("http://files.figshare.com/1922300/Dambros2014_IsopteraTraits.RFAD.csv",row.names=1)#t
env.RFAD<-read.csv("http://files.figshare.com/1922301/PPBio2014_Environment.RFAD.csv",row.names=1)#env.
termite.phylo<-read.nexus("http://files.figshare.com/1922299/Dambros2014_IsopteraPhylo.RFAD.nex")#termi

#standardize variables
env.RFAD.std<-data.frame(env.RFAD[,1:5],deconstand(env.RFAD[,-c(1:5)],"standardize"))
```

To facilitate handling objects and to reduce the number of objects in the workspace, we incorporated the trait information by species into the long format table with the termite record by colony

```
iso.RFAD$FG2<-traits$FG1[match(iso.RFAD$Taxon,rownames(traits))]
iso.RFAD$DEF<-traits$Maj[match(iso.RFAD$Taxon,rownames(traits))]
```

To avoid counting the same termite colony twice, rows with exactly the same information were deleted. Therefore, colonies of the same species found in the same 5x2 plot were counted just once.

```
iso.RFAD<-iso.RFAD[!duplicated(iso.RFAD[,c("Taxon","Location","Grid","Trail","Plot",
      "Distance_beginning","Side"))],]
iso.RFAD<-iso.RFAD[iso.RFAD$Grid=="RFAD",]# Select only the samples from Ducke Reserve
```

3 Extract data from tables

The termie data were stored in the long format. This means that each colony found is represented by a row in the spreadsheet. The species the colonies belong to are attribute of the colonies, so there is a column designating this attribute. All the analyses used in our study require a short table format, where species are

in columns and the location they were found are rows. The following lines extract the information from the long format table, and rearrange this information in the proper format for analyses. Finally, vectors with the species traits are created. These vectors are in the same order as the species in the new table.

```
attach(iso.RFAD)

#Create factor with complete location
loc<-factor(paste(Location,Grid,Trail,Plot),
           levels=paste(env.RFAD.std$Location,env.RFAD.std$Grid,env.RFAD.std$Trail,env.RFAD.std$Plot))

#Just record the levels in the split format
loc.split<-unique(data.frame(env.RFAD.std$Location,
                             env.RFAD.std$Grid,env.RFAD.std$Trail,env.RFAD.std$Plot))

#sum(loc!=paste(Location,Grid,Trail,Plot)) #Must be zero

termite.plot<-tapply(Frequency,list(loc,Taxon),sum)# Create table with species frequency by location
termite.plot[is.na(termite.plot)]<-0 # Species non detected in a given location are real zeros
termite.plot<-termite.plot[,colSums(termite.plot)>0] # Trim species with zero occurrences

#check if the environmental and termite tables are in the same order
#cbind(rownames(termite.plot),env[,2:5])

termite.plot.PA<-(termite.plot>0)+0 # Abund to PA: Easier and faster than ifelse(termite.plot>0,1,0)

# Extract species feeding and defense group as vectors
TG.RFAD<-FG2[match(colnames(termite.plot),Taxon)]
DEF.RFAD<-DEF[match(colnames(termite.plot),Taxon)]

detach(iso.RFAD)
```

4 Calculate pairwise trait distance between species

We created a pairwise similarity matrix between all pairs of species. The matrix was filled with 1s and 0s, representing species pairs sharing or not a particular trait. This was done independently for feeding and defense strategy. See footnote¹ for explanation on the calculation.

```
TGn<-as.integer(TG.RFAD)# Transform the names of feeding groups in numbers
names(TGn)<-colnames(termite.plot.PA)# Assign the names of species to the vector of feeding groups

TG.dist<-as.dist((((TGn)%*%t(TGn))-(TGn)^2)!=0)#See footnote

DEFn<-as.integer(DEF.RFAD)# Transform the names of feeding groups in numbers
names(DEFn)<-colnames(termite.plot.PA)# Assign the names of species to the vector of feeding groups

DEF.dist<-as.dist((((DEFn)%*%t(DEFn))-(DEFn)^2)!=0)#See footnote
```

¹Multiply the vector by itself creating a pairwise matrix with one species multiplied by the other. Then subtract from the new pairwise matrix, the values of the species multiplied by itself. If the species trait value multiplied by its own value (square) equals the species value multiplied by the value of its pair, the pair has the same trait. Pair has the same trait, 1, otherwise 0

5 Calculate phylogenetic distance and rearrange columns to match species names in the data

Use the `cophenetic` function from the `ape` package to calculate pairwise phylogenetic distances between species. Then match the species in this matrix with those present in the species `x` matrix. Finally, transform the pairwise matrix in a `dist` object (triangular matrix).

```
phylo.dist<-cophenetic(termite.phylo)
phylo.dist<-as.dist(phylo.dist[match(colnames(termite.plot.PA),colnames(phylo.dist)),
  match(colnames(termite.plot.PA),colnames(phylo.dist))])
```

6 Contingency table of traits

```
fisher.test(TG.RFAD,DEF.RFAD,workspace = 500000,simulate.p.value = T)
```

```
##
## Fisher's Exact Test for Count Data with simulated p-value (based
## on 2000 replicates)
##
## data:  TG.RFAD and DEF.RFAD
## p-value = 0.0004998
## alternative hypothesis: two.sided
```

7 Calculates Moran's I and mantel correlograms

```
Moran.I(TGn,as.matrix(phylo.dist))
```

```
## $observed
## [1] -0.06302
##
## $expected
## [1] -0.01266
##
## $sd
## [1] 0.005232
##
## $p.value
## [1] 6.236e-22
```

```
Moran.I(DEFn,as.matrix(phylo.dist))
```

```
## $observed
## [1] -0.04564
##
## $expected
## [1] -0.01266
```

```
##
## $sd
## [1] 0.005238
##
## $p.value
## [1] 3.026e-10
```

```
TG.mantel<-mantel.correlog(TG.dist,phylo.dist)
DEF.mantel<-mantel.correlog(DEF.dist,phylo.dist)
```

```
TG.mantel
```

```
##
## Mantel Correlogram Analysis
##
## Call:
##
## mantel.correlog(D.eco = TG.dist, D.geo = phylo.dist)
##
##      class.index    n.dist Mantel.cor Pr(Mantel) Pr(corrected)
## D.c1.1      2.8462  286.0000    0.2178     0.00     0.001 ***
## D.c1.2      4.5385  128.0000    0.0450     0.02     0.016 *
## D.c1.3      6.2308  180.0000    0.1181     0.00     0.003 **
## D.c1.4      7.9231  348.0000   -0.1802     0.00     0.004 **
## D.c1.5      9.6154  130.0000   -0.0423     0.08     0.078 .
## D.c1.6     11.3077  374.0000   -0.0361     0.12     0.156
## D.c1.7     13.0000    0.0000         NA         NA         NA
## D.c1.8     14.6923  198.0000         NA         NA         NA
## D.c1.9     16.3846  672.0000         NA         NA         NA
## D.c1.10    18.0769 2160.0000         NA         NA         NA
## D.c1.11    19.7692  938.0000         NA         NA         NA
## D.c1.12    21.4615  444.0000         NA         NA         NA
## D.c1.13    23.1538  462.0000   -0.1056     0.04         NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
DEF.mantel
```

```
##
## Mantel Correlogram Analysis
##
## Call:
##
## mantel.correlog(D.eco = DEF.dist, D.geo = phylo.dist)
##
##      class.index    n.dist Mantel.cor Pr(Mantel) Pr(corrected)
## D.c1.1      2.8462  286.0000    0.4295     0.00     0.001 ***
## D.c1.2      4.5385  128.0000    0.2380     0.00     0.002 **
## D.c1.3      6.2308  180.0000    0.2389     0.00     0.003 **
## D.c1.4      7.9231  348.0000    0.4187     0.00     0.004 **
## D.c1.5      9.6154  130.0000    0.1737     0.00     0.005 **
## D.c1.6     11.3077  374.0000    0.0297     0.16     0.159
## D.c1.7     13.0000    0.0000         NA         NA         NA
```

```
## D.cl.8      14.6923  198.0000      NA      NA      NA
## D.cl.9      16.3846  672.0000      NA      NA      NA
## D.cl.10     18.0769 2160.0000      NA      NA      NA
## D.cl.11     19.7692  938.0000      NA      NA      NA
## D.cl.12     21.4615  444.0000      NA      NA      NA
## D.cl.13     23.1538  462.0000    -0.1399    0.00      NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

8 Plot trait distances against phylogenetic distance

```

par(mfrow=c(1,2),mar=c(5,2,4,2)+.1,oma=c(0,3,0,0),xpd=NA) #set graphical parameter space

plot(1-tapply(as.vector(TG.dist),as.vector(phylo.dist),mean)~sort(unique(phylo.dist)),
ylab="Probability of shared trait",xlab="Phylogenetic distance",cex.lab=1.5,pch=21,bg=1)

c1<-coef(glm(y~x,family=binomial(link="log"),data=data.frame(y=1-tapply(as.vector(TG.dist),
as.vector(phylo.dist),mean),x=sort(unique(phylo.dist)))))#line fit using glm

points(exp(cbind(1,seq(2,24,.1))%*%c1)~x,data=data.frame(x=seq(2,24,.1)),type="l")#plot line

title("A"),adj=0,cex.main=1.5)

plot(1-tapply(as.vector(DEF.dist),as.vector(phylo.dist),mean)~sort(unique(phylo.dist)),
ylab="",xlab="Phylogenetic distance",cex.lab=1.5,pch=21,bg=1)

c1<-coef(glm(y~x,family=binomial(link="log"),start = c(a=0,b=-.5),data=data.frame(y=1-tapply(
as.vector(DEF.dist),as.vector(phylo.dist),mean),x=sort(unique(phylo.dist)))))#line fit using glm

points(exp(cbind(1,seq(2,24,.1))%*%c1)~x,data=data.frame(x=seq(2,24,.1)),type="l")#plot line

title("B"),adj=0,cex.main=1.5)

```

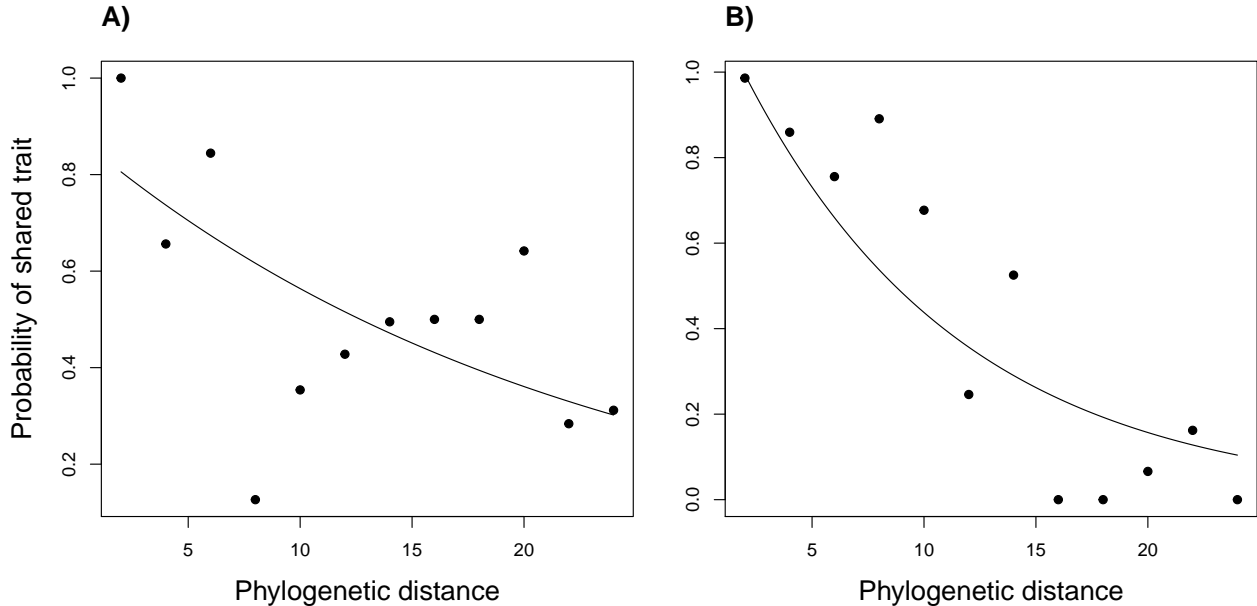


Figure 1: Mean pairwise trait similarity in feeding (A) and defense (B) strategy against mean pairwise phylogenetic distance

9 Plot mantel correlograms

```
par(mfrow=c(1,2),oma=c(0,1,0,0))#set graphical parameter space

plot(TG.mantel$mantel.res[,3]~TG.mantel$mantel.res[,1],pch=21,bg=TG.mantel$mantel.res[,5]<0.05,
xlim=c(2,12),type="o",ylab="Mantel correlation",xlab="Phylogenetic distance",cex.lab=1.5)
abline(h=0,lty=2,col=2)

title("A"),adj=0,cex.main=2)

plot(DEF.mantel$mantel.res[,3]~DEF.mantel$mantel.res[,1],pch=21,bg=DEF.mantel$mantel.res[,5]<0.05,
xlim=c(2,12),type="o",ylab="Mantel correlation",xlab="Phylogenetic distance",cex.lab=1.5)
abline(h=0,lty=2,col=2)

title("B"),adj=0,cex.main=2)
```

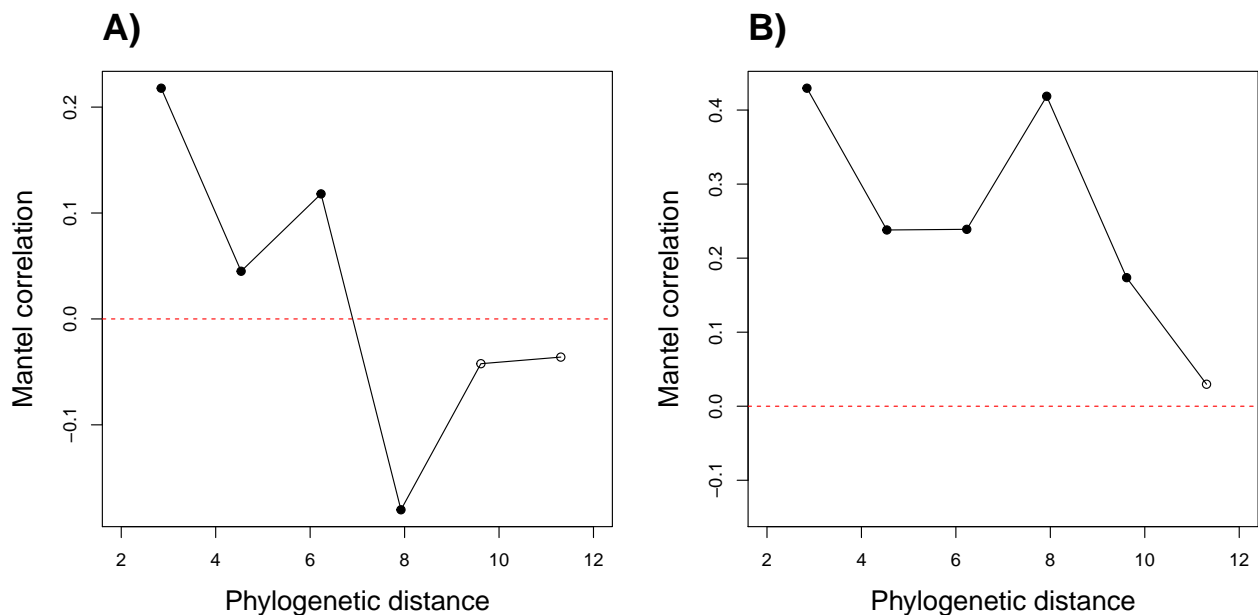


Figure 2: Correlgram plot showing the correlation between trait and phylogenetic distance by distance classes. A: Feeding stragy; B: Defense strategy. Solid dots represent significant correlations at 0.05 level.

10 Create response variables

In the following lines, there are the code to create all the response variables used in our study. In the following sections, individual regressions of these variables against the predictor variables present in the environmental dataset are performed.

```
# Overall diversity

termite.N<-rowSums(termite.plot)
termite.S<-rowSums(termite.plot>0)

termite.N.w<-rowSums(termite.plot[,TG.RFAD=="W"])
termite.S.w<-rowSums(termite.plot[,TG.RFAD=="W"]>0)

termite.N.s<-rowSums(termite.plot[,TG.RFAD=="S"])
termite.S.s<-rowSums(termite.plot[,TG.RFAD=="S"]>0)

# Sorensen simiarity matrices (triangular matrices)

sor.dist<-vegdist(termite.plot,"bray",binary = T)
sor.dist.w<-vegdist(termite.plot[,TG.RFAD=="W"],"bray",binary = T)
sor.dist.s<-vegdist(termite.plot[,TG.RFAD=="S"],"bray",binary = T)

# Total phylodiversity (PD, MPD, and MNTD)

ses.pd<-ses.pd(termite.plot[,],termite.phylo,null.model = "taxa.labels")
ses.mpd<-ses.mpd(termite.plot[,],cophenetic(termite.phylo),null.model = "taxa.labels",
abundance.weighted=TRUE)
ses.mntd<-ses.mntd(termite.plot[,],cophenetic(termite.phylo),null.model = "taxa.labels",
abundance.weighted=TRUE)

# Wood feeders phylodiversity (PD, MPD, and MNTD)

ses.pd.w<-ses.pd(termite.plot[,TG.RFAD=="W"],termite.phylo,null.model = "taxa.labels")
ses.mpd.w<-ses.mpd(termite.plot[,TG.RFAD=="W"],cophenetic(termite.phylo),null.model = "taxa.labels",
abundance.weighted=TRUE)
ses.mntd.w<-ses.mntd(termite.plot[,TG.RFAD=="W"],cophenetic(termite.phylo),null.model = "taxa.labels",
abundance.weighted=TRUE)

# Soil feeders phylodiversity (PD, MPD, and MNTD)

ses.pd.s<-ses.pd(termite.plot[,TG.RFAD=="S"],termite.phylo,null.model = "taxa.labels")
ses.mpd.s<-ses.mpd(termite.plot[,TG.RFAD=="S"],cophenetic(termite.phylo),null.model = "taxa.labels",
abundance.weighted=TRUE)
ses.mntd.s<-ses.mntd(termite.plot[,TG.RFAD=="S"],cophenetic(termite.phylo),null.model = "taxa.labels",
abundance.weighted=TRUE)

# Total phylocompositon (Unifrac,PhyloSorensen, and betaMNTD [not used])

ufrac.dist<-unifrac(termite.plot,termite.phylo)
psor.dist<-phylosor(termite.plot,termite.phylo)
betaMNTD.dist<-comdistnt(termite.plot,cophenetic(termite.phylo))

# Wood-feeders phylocompositon (Unifrac,PhyloSorensen, and betaMNTD [not used])
```

```

ufrac.dist.w<-unifrac(termite.plot[,TG.RFAD=="W"],termite.phylo)
psor.dist.w<-phylosor(termite.plot[,TG.RFAD=="W"],termite.phylo)
betaMNTD.dist.w<-comdistnt(termite.plot[,TG.RFAD=="W"],cophenetic(termite.phylo))

# Soil-feeders phylocomposition (Unifrac,PhyloSorensen, and betaMNTD [not used])

ufrac.dist.s<-unifrac(termite.plot[,TG.RFAD=="S"],termite.phylo)
psor.dist.s<-phylosor(termite.plot[,TG.RFAD=="S"],termite.phylo)
betaMNTD.dist.s<-comdistnt(termite.plot[,TG.RFAD=="S"],cophenetic(termite.phylo))

# Functional diversity

names(TG.RFAD)<-colnames(termite.plot)
names(DEF.RFAD)<-colnames(termite.plot)

TG.fdis<-fdisp(TG.dist,termite.plot)$FDis
DEF.fdis<-fdisp(DEF.dist,termite.plot)$FDis

#standardied effect size for trait diversity

nrep=999

TG.fdis.sim<-matrix(nrow=nrow(termite.plot),ncol=nrep)
TG.dist.null<-TG.dist

DEF.fdis.sim<-matrix(nrow=nrow(termite.plot),ncol=nrep)
DEF.dist.null<-DEF.dist

for(i in 1:nrep){

TG.dist.null[i]<-sample(TG.dist)
DEF.dist.null[i]<-sample(DEF.dist)

TG.fdis.sim[,i]<-fdisp(TG.dist.null,termite.plot)$FDis
DEF.fdis.sim[,i]<-fdisp(DEF.dist.null,termite.plot)$FDis

}

TG.fdis.ses<-(TG.fdis-rowMeans(TG.fdis.sim))/apply(TG.fdis.sim,1,sd)
DEF.fdis.ses<-(DEF.fdis-rowMeans(DEF.fdis.sim))/apply(DEF.fdis.sim,1,sd)

# Functional composition

TG.pcoa<-prcomp(t(aggregate(t(termite.plot),by = list(TG.RFAD),sum)[-1]))$x[,1]
DEF.pcoa<-prcomp(t(aggregate(t(termite.plot),by = list(DEF.RFAD),sum)[-1]))$x[,1]

TG.nmnds<-scores(metaMDS(t(aggregate(t(termite.plot),by = list(TG.RFAD),sum)[-1])))[,1]
DEF.nmnds<-scores(metaMDS(t(aggregate(t(termite.plot),by = list(DEF.RFAD),sum)[-1])))[,1]

```

```

# Separate nestedness and turnover on functional composition (Baselga 2010)
# Not performed because all groups are represented in all sites (dissimilarity using sor = 0)

#TG.sim.dist<-beta.sim(t(aggregate(t(termite.plot),by = list(TG.RFAD),sum)[-1]))
#TG.nes.dist<-beta.nes(t(aggregate(t(termite.plot),by = list(TG.RFAD),sum)[-1]))

#nes.dist.w<-beta.nes(termite.plot[,TG.RFAD=="W"])
#nes.dist.s<-beta.nes(termite.plot[,TG.RFAD=="S"])

```

11 Summarize composition and phylocomposition in PCoA axes

Similar to Duarte et al. (2011), we summarized the phylogenetic dissimilarity matrices in PCoA axes, representing phylogenetic composition. This was performed to all indexes used in our study (Sorensen, PhyloSor, and UniFrac).

```

pcoa.sor<-scores(cmdscale(sor.dist))

pcoa.psor<-scores(cmdscale(psor.dist))
pcoa.ufrac<-scores(cmdscale(ufrac.dist))

pcoa.sor.w<-scores(cmdscale(sor.dist.w))

pcoa.psor.w<-scores(cmdscale(psor.dist.w))
pcoa.ufrac.w<-scores(cmdscale(ufrac.dist.w))

pcoa.sor.s<-scores(cmdscale(sor.dist.s))
pcoa.psor.s<-scores(cmdscale(psor.dist.s))
pcoa.ufrac.s<-scores(cmdscale(ufrac.dist.s))

```

12 Regression analyses by response variable

For each response variable, we run a multiple regression against the predictor variables. P-values using t and F statistics were similar, but we based our results on the F-statistics results. This answer the question: *Does the inclusion of a given variable significantly increases the explanatory power of the model?* You can see a summary of these results as a table in the end of the document

12.1 Overall PD

```
summary(M1<-lm(ses.pd$pd.obs.z~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = ses.pd$pd.obs.z ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5329 -0.2666  0.0075  0.5862  1.0744
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.28184    0.13694     2.06  0.0501 .
## ant.pred.N        0.08698    0.15369     0.57  0.5765
## P                -0.48340    0.15577    -3.10  0.0047 **
## N.percentage      0.21316    0.15883     1.34  0.1916
## Vegetation.structure -0.00679    0.15542    -0.04  0.9655
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.75 on 25 degrees of freedom
## Multiple R-squared:  0.393, Adjusted R-squared:  0.296
## F-statistic: 4.05 on 4 and 25 DF, p-value: 0.0115
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: ses.pd$pd.obs.z
##              Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N    1  0.06   0.06   0.10 0.75467
## P             1  7.97   7.97  14.17 0.00091 ***
## N.percentage  1  1.08   1.08   1.92 0.17842
## Vegetation.structure 1  0.00   0.00   0.00 0.96551
## Residuals    25 14.06   0.56
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.2 Overall MPD

```
summary(M1<-lm(ses.mpd$mpd.obs.z~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = ses.mpd$mpd.obs.z ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##   Min     1Q  Median     3Q    Max
## -1.131 -0.462  0.104  0.414  0.853
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.6059     0.1096   5.53 9.6e-06 ***
## ant.pred.N       -0.0276     0.1230  -0.22  0.82
## P                -0.1643     0.1247  -1.32  0.20
## N.percentage     -0.0670     0.1271  -0.53  0.60
## Vegetation.structure -0.0450     0.1244  -0.36  0.72
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6 on 25 degrees of freedom
## Multiple R-squared:  0.067, Adjusted R-squared:  -0.0823
## F-statistic: 0.449 on 4 and 25 DF,  p-value: 0.772
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: ses.mpd$mpd.obs.z
##              Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N    1  0.00   0.000    0.00  0.98
## P             1  0.52   0.523    1.45  0.24
## N.percentage  1  0.08   0.076    0.21  0.65
## Vegetation.structure 1  0.05   0.047    0.13  0.72
## Residuals    25  9.01   0.360
```

12.3 Overall MNTD

```
summary(M1<-lm(ses.mntd$mntd.obs.z~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = ses.mntd$mntd.obs.z ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
```

```
##      Min      1Q  Median      3Q      Max
## -1.3123 -0.5632 -0.0558  0.4676  1.6240
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.2084   0.1473    1.41  0.16953
## ant.pred.N       -0.0103   0.1653   -0.06  0.95080
## P                -0.7183   0.1675   -4.29  0.00024 ***
## N.percentage      0.2073   0.1708    1.21  0.23619
## Vegetation.structure -0.0161   0.1672   -0.10  0.92414
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.807 on 25 degrees of freedom
## Multiple R-squared:  0.519, Adjusted R-squared:  0.442
## F-statistic: 6.75 on 4 and 25 DF, p-value: 0.000794
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: ses.mntd$mntd.obs.z
##              Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N    1  0.03   0.03   0.05   0.83
## P             1 16.49  16.49  25.33 3.4e-05 ***
## N.percentage  1  1.04   1.04   1.60   0.22
## Vegetation.structure 1  0.01   0.01   0.01   0.92
## Residuals    25 16.27   0.65
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.4 Overall Sorensen

```
summary(M1<-lm(pcoa.sor[,1]~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = pcoa.sor[, 1] ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min      1Q  Median      3Q      Max
## -0.2016 -0.0807 -0.0144  0.1102  0.1702
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.40e-17  2.19e-02   0.00   1.00
## ant.pred.N   2.57e-02  2.45e-02   1.05   0.30
## P            1.33e-01  2.49e-02   5.36  1.5e-05 ***
## N.percentage -3.93e-02  2.53e-02  -1.55   0.13
## Vegetation.structure -3.57e-02  2.48e-02  -1.44   0.16
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.12 on 25 degrees of freedom
## Multiple R-squared:  0.676, Adjusted R-squared:  0.625
## F-statistic: 13.1 on 4 and 25 DF,  p-value: 7.11e-06
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: pcoa.sor[, 1]
##
##      Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N      1  0.015   0.015    1.02   0.32
## P                1  0.681   0.681   47.53 3.2e-07 ***
## N.percentage    1  0.023   0.023    1.61   0.22
## Vegetation.structure 1  0.030   0.030    2.07   0.16
## Residuals      25  0.358   0.014
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.5 Overall PhyloSorensen

```
summary(M1<-lm(pcoa.psor[,1]~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = pcoa.psor[, 1] ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.2505 -0.0502 -0.0037  0.0423  0.4365
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  5.98e-17  2.29e-02   0.00   1.00
## ant.pred.N   -3.88e-02  2.57e-02  -1.51   0.14
## P            1.59e-02  2.60e-02   0.61   0.55
## N.percentage  3.79e-03  2.65e-02   0.14   0.89
## Vegetation.structure 3.24e-02  2.59e-02   1.25   0.22
##
## Residual standard error: 0.125 on 25 degrees of freedom
## Multiple R-squared:  0.134, Adjusted R-squared:  -0.00431
## F-statistic: 0.969 on 4 and 25 DF,  p-value: 0.442
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
```



```
## Response: pcoa.psor[, 1]
##           Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N      1  0.036  0.0357   2.27  0.14
## P                1  0.000  0.0005   0.03  0.87
## N.percentage    1  0.000  0.0003   0.02  0.90
## Vegetation.structure 1  0.024  0.0244   1.56  0.22
## Residuals      25  0.392  0.0157
```

12.6 Overall Unifrac

```
summary(M1<-lm(pcoa.ufrac[,1]~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = pcoa.ufrac[, 1] ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.3921 -0.0463  0.0242  0.0975  0.2435
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.63e-18   2.77e-02   0.00    1.00
## ant.pred.N     -2.95e-02   3.11e-02  -0.95    0.35
## P              -8.77e-02   3.15e-02  -2.78    0.01 *
## N.percentage  -2.53e-02   3.21e-02  -0.79    0.44
## Vegetation.structure -3.34e-02  3.14e-02  -1.06    0.30
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.152 on 25 degrees of freedom
## Multiple R-squared:  0.247, Adjusted R-squared:  0.127
## F-statistic: 2.05 on 4 and 25 DF, p-value: 0.117
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: pcoa.ufrac[, 1]
##           Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N      1  0.011  0.0106   0.46  0.503
## P                1  0.145  0.1451   6.30  0.019 *
## N.percentage    1  0.008  0.0075   0.33  0.572
## Vegetation.structure 1  0.026  0.0259   1.13  0.299
## Residuals      25  0.575  0.0230
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.7 Wood feeders PD

```
summary(M1<-lm(ses.pd.w$pd.obs.z~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = ses.pd.w$pd.obs.z ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.2507 -0.6317  0.0578  0.6999  1.0524
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.1297     0.1437   -0.90  0.3753 .
## ant.pred.N       0.2889     0.1613    1.79  0.0853 .
## P              -0.5816     0.1634   -3.56  0.0015 **
## N.percentage     0.2505     0.1666    1.50  0.1453
## Vegetation.structure 0.0774     0.1631    0.47  0.6393
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.787 on 25 degrees of freedom
## Multiple R-squared:  0.507, Adjusted R-squared:  0.428
## F-statistic: 6.42 on 4 and 25 DF, p-value: 0.00107
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: ses.pd.w$pd.obs.z
##              Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N    1   1.91    1.91    3.09 0.09107 .
## P             1  12.58   12.58   20.31 0.00013 ***
## N.percentage  1   1.27    1.27    2.06 0.16383
## Vegetation.structure 1   0.14    0.14    0.23 0.63931
## Residuals    25  15.48    0.62
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.8 Wood feeders MPD

```
summary(M1<-lm(ses.mpd.w$mpd.obs.z~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = ses.mpd.w$mpd.obs.z ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
```

```
##
## Residuals:
##   Min     1Q   Median     3Q      Max
## -1.410 -0.488  0.110  0.308  1.014
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.6266    0.1104    5.68 6.6e-06 ***
## ant.pred.N     0.0383    0.1239    0.31  0.760
## P             -0.2926    0.1256   -2.33  0.028 *
## N.percentage   0.0119    0.1280    0.09  0.927
## Vegetation.structure -0.0582    0.1253   -0.46  0.646
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.605 on 25 degrees of freedom
## Multiple R-squared:  0.204, Adjusted R-squared:  0.0763
## F-statistic:  1.6 on 4 and 25 DF,  p-value: 0.206
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: ses.mpd.w$mpd.obs.z
##              Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N    1  0.06  0.063    0.17  0.682
## P             1  2.18  2.182    5.97  0.022 *
## N.percentage  1  0.01  0.014    0.04  0.844
## Vegetation.structure 1  0.08  0.079    0.22  0.646
## Residuals    25  9.14  0.366
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.9 Wood feeders MNTD

```
summary(M1<-lm(ses.mntd.w$mntd.obs.z~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = ses.mntd.w$mntd.obs.z ~ ant.pred.N + P + N.percentage +
##   Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##   Min     1Q   Median     3Q      Max
## -1.4896 -0.6311 -0.0748  0.5829  1.5447
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.37609    0.15671   -2.40  0.024 *
## ant.pred.N     0.06962    0.17588    0.40  0.696
## P             -0.83211    0.17826   -4.67  8.8e-05 ***
```

```
## N.percentage      0.30560    0.18176    1.68    0.105
## Vegetation.structure 0.00521    0.17786    0.03    0.977
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.858 on 25 degrees of freedom
## Multiple R-squared:  0.58, Adjusted R-squared:  0.513
## F-statistic: 8.63 on 4 and 25 DF, p-value: 0.000161
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: ses.mntd.w$mntd.obs.z
##          Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N      1  0.01   0.01   0.02  0.888
## P                1 23.25  23.25  31.55 7.6e-06 ***
## N.percentage    1  2.17   2.17   2.94  0.099 .
## Vegetation.structure 1  0.00   0.00   0.00  0.977
## Residuals      25 18.42   0.74
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.10 Wood feeders Sorensen

```
summary(M1<-lm(pcoa.sor.w[,1]~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = pcoa.sor.w[, 1] ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.2304 -0.0899  0.0408  0.1003  0.2523
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  5.31e-18  2.49e-02   0.00    1.00
## ant.pred.N   -2.20e-02  2.80e-02  -0.79    0.44
## P            -1.32e-01  2.84e-02  -4.66  8.9e-05 ***
## N.percentage  3.42e-02  2.89e-02   1.18    0.25
## Vegetation.structure 5.17e-02  2.83e-02   1.83    0.08 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.137 on 25 degrees of freedom
## Multiple R-squared:  0.629, Adjusted R-squared:  0.57
## F-statistic: 10.6 on 4 and 25 DF, p-value: 3.63e-05
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: pcoa.sor.w[, 1]
##           Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N      1  0.005   0.005    0.29   0.59
## P                1  0.711   0.711   38.16 1.8e-06 ***
## N.percentage    1  0.012   0.012    0.65   0.43
## Vegetation.structure 1  0.062   0.062    3.34   0.08 .
## Residuals      25  0.466   0.019
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.11 Wood feeders PhyloSorensen

```
summary(M1<-lm(pcoa.psor.w[,1]~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = pcoa.psor.w[, 1] ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.3748 -0.0566  0.0009  0.0644  0.2322
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.77e-18  2.49e-02   0.00   1.00
## ant.pred.N    6.34e-03  2.80e-02   0.23   0.82
## P            -1.63e-02  2.84e-02  -0.57   0.57
## N.percentage -2.35e-02  2.89e-02  -0.81   0.42
## Vegetation.structure -2.90e-02  2.83e-02  -1.02   0.32
##
## Residual standard error: 0.137 on 25 degrees of freedom
## Multiple R-squared:  0.0602, Adjusted R-squared:  -0.0901
## F-statistic: 0.401 on 4 and 25 DF,  p-value: 0.806
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: pcoa.psor.w[, 1]
##           Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N      1  0.003  0.00345    0.18   0.67
## P                1  0.000  0.00006    0.00   0.96
## N.percentage    1  0.007  0.00684    0.37   0.55
## Vegetation.structure 1  0.020  0.01955    1.05   0.32
## Residuals      25  0.466  0.01866
```

12.12 Wood feeders Unifrac

```
summary(M1<-lm(pcoa.ufrac.w[,1]~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = pcoa.ufrac.w[, 1] ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.2525 -0.1542  0.0613  0.1167  0.2806
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.23e-17   3.10e-02   0.00    1.00
## ant.pred.N     1.73e-03   3.48e-02   0.05    0.96
## P              3.65e-02   3.53e-02   1.03    0.31
## N.percentage  2.94e-02   3.60e-02   0.82    0.42
## Vegetation.structure 5.19e-02   3.52e-02   1.47    0.15
##
## Residual standard error: 0.17 on 25 degrees of freedom
## Multiple R-squared:  0.0939, Adjusted R-squared:  -0.0511
## F-statistic: 0.647 on 4 and 25 DF,  p-value: 0.634
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: pcoa.ufrac.w[, 1]
##              Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N    1  0.000  0.0001    0.00  0.95
## P             1  0.005  0.0045    0.16  0.70
## N.percentage  1  0.007  0.0075    0.26  0.61
## Vegetation.structure 1  0.063  0.0627    2.17  0.15
## Residuals    25  0.722  0.0289
```

12.13 Soil feeders PD

```
summary(M1<-lm(ses.pd.s$pd.obs.z~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = ses.pd.s$pd.obs.z ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.2088 -0.2252 -0.0204  0.3551  0.9883
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.1464    0.1155   -1.27   0.217
## ant.pred.N      0.0872    0.1335    0.65   0.520
## P               0.3332    0.1293    2.58   0.017 *
## N.percentage    0.2271    0.1317    1.72   0.098 .
## Vegetation.structure 0.0148    0.1336    0.11   0.913
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.619 on 24 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  0.272, Adjusted R-squared:  0.151
## F-statistic: 2.24 on 4 and 24 DF, p-value: 0.0944
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: ses.pd.s$pd.obs.z
##           Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N      1  0.01  0.007   0.02  0.893
## P               1  2.27  2.275   5.94  0.023 *
## N.percentage    1  1.15  1.148   3.00  0.096 .
## Vegetation.structure 1  0.00  0.005   0.01  0.913
## Residuals      24  9.19  0.383
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.14 Soil feeders MPD

```
summary(M1<-lm(ses.mpd.s$mpd.obs.z~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = ses.mpd.s$mpd.obs.z ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7133 -0.4416  0.0285  0.6331  1.0150
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.45859    0.14096   -3.25  0.0034 **
## ant.pred.N      -0.00416    0.16292   -0.03  0.9798
## P               0.40406    0.15778    2.56  0.0171 *
## N.percentage    0.19888    0.16073    1.24  0.2279
## Vegetation.structure 0.18715    0.16305    1.15  0.2624
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.755 on 24 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  0.232, Adjusted R-squared:  0.104
## F-statistic: 1.81 on 4 and 24 DF,  p-value: 0.16
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: ses.mpd.s$mpd.obs.z
##
##      Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N      1  0.21   0.206   0.36 0.553
## P                1  2.54   2.539   4.45 0.045 *
## N.percentage    1  0.63   0.629   1.10 0.304
## Vegetation.structure 1  0.75   0.751   1.32 0.262
## Residuals      24 13.68   0.570
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.15 Soil feeders MNTD

```
summary(M1<-lm(ses.mntd.s$mntd.obs.z~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = ses.mntd.s$mntd.obs.z ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8130 -0.5484  0.0906  0.4659  1.4809
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.5895    0.1694  -3.48  0.0019 **
## ant.pred.N      0.0446    0.1957   0.23  0.8218
## P              0.5542    0.1896   2.92  0.0074 **
## N.percentage   0.1998    0.1931   1.03  0.3112
## Vegetation.structure 0.1697    0.1959   0.87  0.3950
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.907 on 24 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  0.269, Adjusted R-squared:  0.147
## F-statistic: 2.21 on 4 and 24 DF,  p-value: 0.0982
```



```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: ses.mntd.s$mntd.obs.z
##           Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N      1   0.09   0.09   0.11  0.747
## P                1   5.91   5.91   7.18  0.013 *
## N.percentage    1   0.66   0.66   0.80  0.380
## Vegetation.structure 1   0.62   0.62   0.75  0.395
## Residuals      24  19.74   0.82
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.16 Soil feeders Sorensen

```
summary(M1<-lm(pcoa.sor.s[,1]~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = pcoa.sor.s[, 1] ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.4195 -0.1378  0.0315  0.1662  0.2835
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  8.85e-18  3.98e-02   0.00   1.00
## ant.pred.N    6.10e-02  4.47e-02   1.36   0.18
## P            -5.88e-02  4.53e-02  -1.30   0.21
## N.percentage  3.83e-02  4.62e-02   0.83   0.41
## Vegetation.structure 3.79e-02  4.52e-02   0.84   0.41
##
## Residual standard error: 0.218 on 25 degrees of freedom
## Multiple R-squared:  0.221, Adjusted R-squared:  0.0968
## F-statistic: 1.78 on 4 and 25 DF,  p-value: 0.165
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: pcoa.sor.s[, 1]
##           Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N      1  0.100  0.1002   2.11  0.159
## P                1  0.183  0.1835   3.86  0.061 .
## N.percentage    1  0.021  0.0210   0.44  0.513
## Vegetation.structure 1  0.033  0.0334   0.70  0.410
## Residuals      25  1.189  0.0476
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

12.17 Soil feeders PhyloSorensen

```
summary(M1<-lm(pcoa.psor.s[,1]~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = pcoa.psor.s[, 1] ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.3304 -0.0401  0.0051  0.0455  0.3333
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.11e-17   2.34e-02   0.00    1.00
## ant.pred.N     -2.17e-03   2.63e-02  -0.08    0.94
## P              -3.20e-02   2.66e-02  -1.20    0.24
## N.percentage  -2.88e-03   2.72e-02  -0.11    0.92
## Vegetation.structure -2.18e-02   2.66e-02  -0.82    0.42
##
## Residual standard error: 0.128 on 25 degrees of freedom
## Multiple R-squared:  0.0634, Adjusted R-squared:  -0.0864
## F-statistic: 0.423 on 4 and 25 DF,  p-value: 0.79
```

```
anova(M1)
```

```
## Analysis of Variance Table
##
## Response: pcoa.psor.s[, 1]
##           Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N    1  0.000  0.00023    0.01  0.91
## P             1  0.016  0.01647    1.00  0.33
## N.percentage  1  0.000  0.00009    0.01  0.94
## Vegetation.structure 1  0.011  0.01109    0.67  0.42
## Residuals    25  0.412  0.01646
```

12.18 Soil feeders Unifrac

```
summary(M1<-lm(pcoa.ufrac.s[,1]~ant.pred.N+P+N.percentage+Vegetation.structure,data=env.RFAD.std))
```

```
##
## Call:
## lm(formula = pcoa.ufrac.s[, 1] ~ ant.pred.N + P + N.percentage +
##     Vegetation.structure, data = env.RFAD.std)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.3008 -0.1299 -0.0108  0.1283  0.4231
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept) -3.94e-17  3.90e-02   0.00   1.00
## ant.pred.N  -5.38e-02  4.38e-02  -1.23   0.23
## P           -1.44e-04  4.44e-02   0.00   1.00
## N.percentage  1.44e-02  4.53e-02   0.32   0.75
## Vegetation.structure 2.97e-02  4.43e-02   0.67   0.51
##
## Residual standard error: 0.214 on 25 degrees of freedom
## Multiple R-squared:  0.0873, Adjusted R-squared:  -0.0587
## F-statistic: 0.598 on 4 and 25 DF,  p-value: 0.667
```

anova(M1)

```
## Analysis of Variance Table
##
## Response: pcoa.ufrac.s[, 1]
##           Df Sum Sq Mean Sq F value Pr(>F)
## ant.pred.N      1  0.082  0.0823   1.80  0.19
## P                1  0.005  0.0051   0.11  0.74
## N.percentage     1  0.001  0.0014   0.03  0.86
## Vegetation.structure 1  0.021  0.0205   0.45  0.51
## Residuals       25  1.144  0.0457
```

13 Plot phylogenetic diversity against P

One of the strongest findings in this study was the strong relation of phylogenetic diversity metrics with P content.

```
par(mfrow=c(1,3),mar=c(5,2,4,2)+.1,oma=c(0,3,0,0),xpd=NA)

plot(ses.mntd$mntd.obs.z~env.RFAD$P,cex.lab=1.5,xlab=expression("P "(mg/dm^3)), ylab= "Phylogenetic diversity",
     pch=21,col=0,bg=1,cex=1.2,ylim=c(-2.5,2.5))

c1<-coef(nls(y~a+b*exp(c*x),start=list(a=-3,b=5,c=-0.07),data=data.frame(y=ses.mntd$mntd.obs.z,
                               x=env.RFAD$P)))
points((c1[1]+c1[2]*exp(c1[3]*x))~x,data=data.frame(x=seq(1,12,.1)),type="l")

title("A)",adj=0,cex.main=1.5)

plot(ses.mntd.w$mntd.obs.z~env.RFAD$P,cex.lab=1.5,xlab=expression("P "(mg/dm^3)), ylab= "",pch=21,col=0,
     cex=1.2,ylim=c(-2.5,2.5))

c1<-coef(nls(y~a+b*exp(c*x),start=list(a=-3,b=5,c=-0.08),data=data.frame(y=ses.mntd.w$mntd.obs.z,
                               x=env.RFAD$P)))
points((c1[1]+c1[2]*exp(c1[3]*x))~x,data=data.frame(x=seq(1,12,.1)),type="l")

title("B)",adj=0,cex.main=1.5)

plot(ses.mntd.s$mntd.obs.z~env.RFAD$P,cex.lab=1.5,xlab=expression("P "(mg/dm^3)), ylab= "",pch=21,col=0,
     cex=1.2,ylim=c(-2.5,2.5))

c1<-coef(nls(y~a+b*exp(c*x),start=list(a=-2,b=-2,c=-0.07),data=data.frame(y=ses.mntd.s$mntd.obs.z,
                               x=env.RFAD$P)))
points((c1[1]+c1[2]*exp(c1[3]*x))~x,data=data.frame(x=seq(1,12,.1)),type="l")

title("C)",adj=0,cex.main=1.5)
```

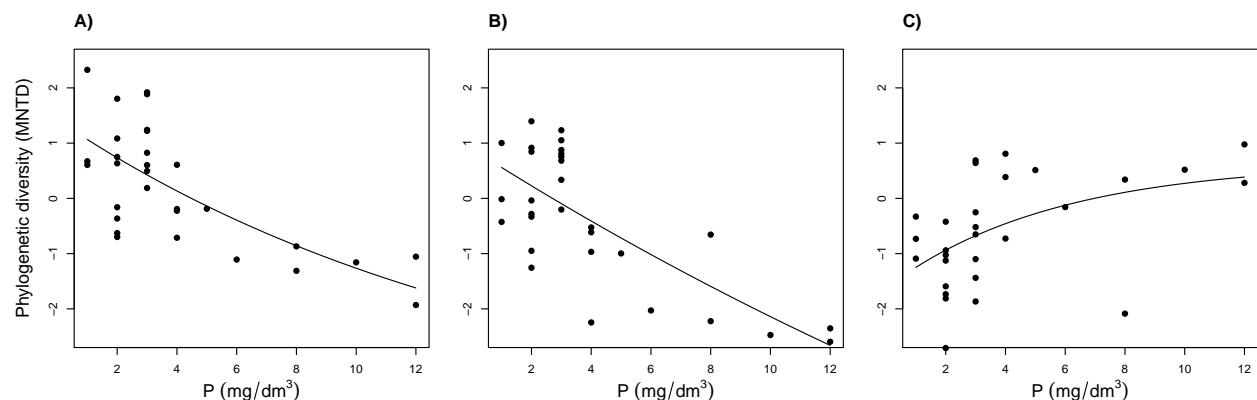


Figure 3: Phylogenetic diversity measured by MNTD against P . A: Overall phylogenetic diversity; B: Phylogenetic diversity for wood-feeding termites; C: Phylogenetic diversity for soil-feeding termites.

14 Diagrams: spp. presence by phylo and predictor variable

In these diagrams, species were color coded by their feeding and defense strategies. The species were ordered by their position in the phylogeny and the locations where they were found were ordered by P and ant predator density

```
palette(c("#004CFFFF", "black", "#00FF4DFF", "#00E5FFFF", "tomato", "yellow", "grey"))
```

```
poncho(termite.plot.PA, phy=termite.phylo, env=env.RFAD$P, col=as.integer(TG.RFAD)+1,
  file="phyloxPA", ylab.bottom = expression("P (mg/dm^3)"), xlab="Sampling units",
  col.gradient = "tomato", border="black")
```

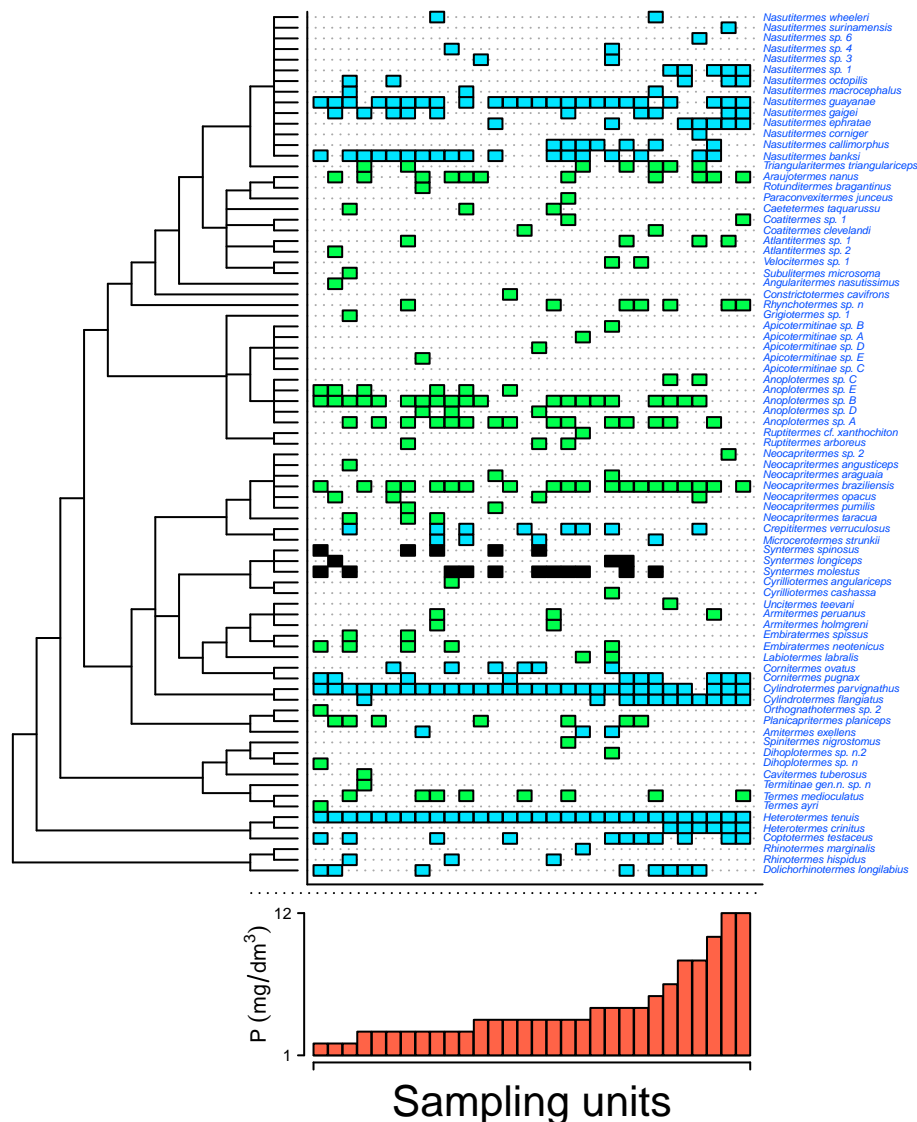


Figure 4: Diagram of species presence ordered by position in the termite phylogeny and P in the soil. Colors represent different feeding groups: Green: soil-feeding termites; Blue: wood-feeding termites; Black: leaf-litter-feeding termites.

```
poncho(termite.plot.PA,phy=termite.phylo,env=env.RFAD$ant.pred.N,col=as.integer(DEF.RFAD),
ylab.bottom = "Ant density",xlab="Sampling units",col.gradient = "tomato",border="black")
```

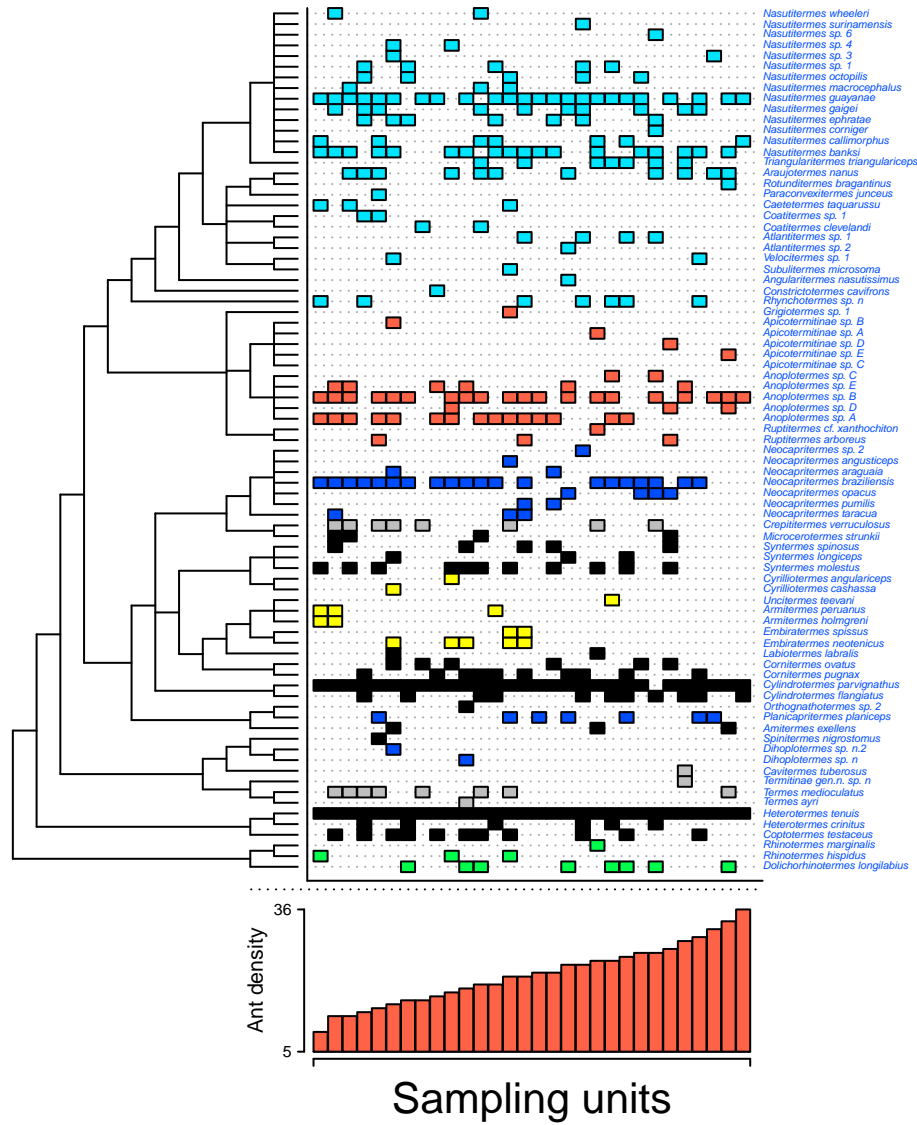


Figure 5: Diagram of species presence ordered by position in the termite phylogeny and ant predator density. Colors represent different defense strategy groups: Green: XXX; Blue: XXX; Black: XXX Red: No soldiers present - Other defeses; Dark blue: ; Grey: ; Yellow: .

```
## use file = "filename.pdf" to save as a pdf
```

```
palette("default")
```

15 Summary of results in Table 1.

- Code for generating table not shown. You can check the results in the Regressions section.²

| ## | response | N.ant.pred | P | N | N.trees | df | F | r2 |
|-------|------------|------------|-----------|---------|---------|----|--------|-----------|
| ## 1 | PD | 0.087 | -0.483*** | 0.213 | -0.007 | 25 | 4.047 | 29.589* |
| ## 2 | MPD | -0.028 | -0.164 | -0.067 | -0.045 | 25 | 0.449 | 0.000 |
| ## 3 | MNTD | -0.01 | -0.718*** | 0.207 | -0.016 | 25 | 6.747 | 44.217*** |
| ## 4 | PCoA.sor | 0.026 | 0.133*** | -0.039 | -0.036 | 25 | 13.059 | 62.453*** |
| ## 5 | PCoA.psor | -0.039 | 0.016 | 0.004 | 0.032 | 25 | 0.969 | 0.000 |
| ## 6 | PCoA.ufrac | -0.03 | -0.088* | -0.025 | -0.033 | 25 | 2.055 | 12.7 |
| ## 7 | PD | 0.289+ | -0.582*** | 0.251 | 0.077 | 25 | 6.422 | 42.785** |
| ## 8 | MPD | 0.038 | -0.293* | 0.012 | -0.058 | 25 | 1.599 | 7.627 |
| ## 9 | MNTD | 0.07 | -0.832*** | 0.306+ | 0.005 | 25 | 8.629 | 51.273*** |
| ## 10 | PCoA.sor | -0.022 | -0.132*** | 0.034 | 0.052+ | 25 | 10.611 | 57.001*** |
| ## 11 | PCoA.psor | 0.006 | -0.016 | -0.024 | -0.029 | 25 | 0.401 | 0.000 |
| ## 12 | PCoA.ufrac | 0.002 | 0.036 | 0.029 | 0.052 | 25 | 0.647 | 0.000 |
| ## 13 | PD | 0.087 | 0.333* | 0.227+ | 0.015 | 24 | 2.243 | 15.077+ |
| ## 14 | MPD | -0.004 | 0.404* | 0.199 | 0.187 | 24 | 1.809 | 10.362 |
| ## 15 | MNTD | 0.045 | 0.554* | 0.2 | 0.17 | 24 | 2.209 | 14.733+ |
| ## 16 | PCoA.sor | 0.061 | -0.059+ | 0.038 | 0.038 | 25 | 1.777 | 9.678 |
| ## 17 | PCoA.psor | -0.002 | -0.032 | -0.003 | -0.022 | 25 | 0.423 | 0.000 |
| ## 18 | PCoA.ufrac | -0.054 | 0.000 | 0.014 | 0.03 | 25 | 0.598 | 0.000 |
| ## 19 | TG.FD | -0.037 | -0.06** | -0.034 | -0.023 | 25 | 3.765 | 27.607* |
| ## 20 | DEF.FD | -0.03 | -0.015 | -0.031+ | -0.026+ | 25 | 2.371 | 15.906+ |
| ## 21 | PCoA.TG | 2.49*** | -1.368** | 0.933+ | 0.086 | 25 | 9.185 | 53.03*** |
| ## 22 | PCoA.DEF | 0.371 | 0.459 | -0.48 | -0.508 | 25 | 0.709 | 0.000 |

² r^2 is represented by zero when adjusted r^2 was less than zero