Supplementary Material

Table S1. Species of lichenicolous fungi , their lichen hosts, and numbers identifying plots and subplots in which the samples were collected. The table is taken from Fleischhaker et al. (2015) [24].

Lichenicolous fungal species	Host lichen species	Plot IDs (subplot IDs)
Arthonia protoparmeliae*	*Protoparmelia badia*	6(.1)
Arthonia varians	*Lecanora bicincta, Lecanora rupicola*	2(.3), 5(.1.2.3), 6(.2.3), 7(.3), 8(.1.3), 9(.1)
Arthonia sp. 1*	*Lecanora polytropa*	3(.1), 5(.2)
Arthonia sp. 2*	*Lecanora polytropa*	2(.2)
Carbonea aggregantula - Cv*	*Candelariella vitellina*	5(.3), 7(.3)
Carbonea assimilis*	*Tephromela atra*	7(.2), 8(.3)
Carbonea intrudens	*Rhizocarpon geographicum*	1(.1), 4(.3), 5(.1)
Carbonea supersparsa	*Lecanora polytropa*	2(.1), 4(.2), 7(.3), 9(.1), 9(.3)
Carbonea vitellinaria	*Candelariella vitellina*	5(.3), 6(.2)
Cecidonia umbonella	*Lecidea lapicida* var. *pantherina*	6(.2), 7(.1.3), 8(.1.3), 9(.2)
Cercidospora epipolytropa	*Lecanora polytropa*	1(.1.2), 3(.3), 4(.1.2.3), 5(.2), 6(.1.2.3), 7(.1.3), 8(.1.2.3), 9(.2.3), 10(.2)
Cercidospora solearispora*	*Aspicilia simoensis*	5(.2)
Deuteromyces sp.*	*Rhizocarpon geographicum*	1(.2)
Endococcus macrosporus	*Rhizocarpon geographicum*	4(.1.3), 5(.1.3), 6(.1.2.3), 7(.1.2.3), 8(.1.2.3), 9(.2.3), 10(.1.2.3)
Endococcus perpusillus*	*Schaereria fuscocinerea*	2(.1.3), 9(.2)
Endococcus propinquus - Ac	*Aspicilia caesiocinerea*	2(.3), 3(.1), 4(.2), 5(.1)
Endococcus propinquus - Rg	*Rhizocarpon geographicum*	4(.2)
Endococcus verrucosus	*Aspicilia simoensis*	2(.1), 5(.1.2.3), 6(.1.3), 9(.1.3)
Gyrophthorus sp.*	*Umbilicaria cylindrica*	2(.2), 8(.3)
Lichenoconium lecanorae	*Lecanora polytropa*	2(.2), 3(.3), 4(.2.3), 5(.2), 6(.2), 7(.2.3), 8(.1.2.3), 9(.2.3)
Lichenodiplis lecanorae*	*Tephromela atra*	10(.2)

Muellerella atricola*	*Tephromela atra*	5(.3), 6(.1), 7(.3), 10(.1.2)
Muellerella pygmaea - Ca	*Calvitimela armeniaca*	9(.1)
Muellerella pygmaea - Ia	*Immersaria arthroocarpa*	3(.3)
Muellerella pygmaea - Li	*Lecanora intricata*	1(.1.3), 2(1.2.), 5(.1.2.3), 6(.1), 10(.3)
Muellerella pygmaea - Lp	*Lecanora polytropa*	1(.1), 2(.1.3), 3(.1.2.3), 4(.1.2), 5(.1.2.3), 6(.1.2.3), 7(.1.2.3), 8(.1.2.3), 9(.1.2.3), 10(.1.2.3)
Muellerella pygmaea - Pb	*Protoparmelia badia*	8(.2)
Muellerella pygmaea - Rg	*Rhizocarpon geographicum*	2(.1.2.3), 3(.1.2.3), 4(.2.3), 5(.1.2.3), 6(.1.3), 7(.1.2.3), 8(.1.3), 9(.1.2.3), 10(.2.3)
Muellerella pygmaea - Sf	*Schaereria fuscocinerea*	8(.1), 9(.1)
Muellerella pygmaea s. str.	*Lecidea lapicida* var. *lapicida*, *Lecidea lapicida* var. *pantherina*	1(.1.2.3), 2(.2.3), 3(.1.2.3), 4(.1.2.3), 5(.1.2.3), 6(.1.2.3), 7(.1.2.3), 8(.1.3), 9(.1.2.3), 10(.1.2)
Opegrapha geographicola*	*Rhizocarpon geographicum*	8(.1)
Phacographa protoparmeliae*	*Protoparmelia badia*	3(.2), 7(.1), 8(.3)
Phoma sp.*	*Protoparmelia badia*	6(.3), 9(.1), 10(.1)
Polycoccum microsticticum	*Acarospora fuscata*	2(.2), 5(.2)
Polycoccum sporastatiae	*Sporastatia polyspora*	9(.2.3)
Rosellinula haplospora*	*Aspicilia simoensis*	10(.3)
Sagediopsis fissurisedens	*Aspilidea myrinii*	4(.1.3), 6(.3), 7(.2), 8(.2.3), 9(.1.2.3), 10(.3)
Sclerococcum sphaerale	*Pertusaria corallina*	1(.3), 4(.3), 6(.2)
Skyttea tephromelarum	*Tephromela atra*	1(.2), 5(.2), 8(.1)
Sphaerellothecium atryneae	*Lecanora bicincta*, *Lecanora swartzii*	3(.1), 6(.1), 8(.1), 10(.1.2.3)
Sphaerellothecium contextum	*Protoparmelia badia*	7(.3), 9(.3)
Sphinctrina sp.*	*Lecidea lapicida* var. *pantherina*, *Rhizocarpon geographicum*	6(.2), 7(.3)
Stigmidium eucline	*Varicellaria lactea*	1(.2), 3(.2), 8(.1), 9(.2)

Stigmidium gyrophorarum	*Umbilicaria cylindrica*	2(.2), 7(.3), 10(.1.2.3)
Taeniolella atricerebrina	*Tephromela atra*	1(.1.2.3), 2(.2.3), 3(.1.2.3), 4(.1.3), 6(.1.2.3), 8(.2), 9(.2.3), 10(.1.2.3)
Taeniolella sp.*	*Lecanora bicincta*	1(.2), 9(.3), 10(.1)

Supplementary Material R scritp

###SCRIPT De Carolis et al. 2023 "Lichen and lichenicolous fungal communities tested as suitable systems for the application of cross-taxon analysis"

```
library(vegan)
library(ggplot2)
library(cowplot)
library(multcompView)
library(viridis)
library(tidyverse)
library(hrbrthemes)
library(multcompView)
library(ggplot2)
library(latticeExtra)
library(Rarefy)
require(ade4)
require(adiv)
require(ape)
require(phyloregion)
require(raster)
library(entropart)
library(corrplot)
library(car)


####Variable Description
### 1) "lich" is the composition matrix of lichens. It include the first column with the PLOT ID and the second one with the SUBPLOT ID; 2) "lifu" is the composition matrix of fungi. It include the first column with the PLOT ID and the second one with the SUBPLOT ID
subplot<-as.factor(lich[,2])###transform the subplot ID in a factor
plot<-as.factor(lich[,1])####transform the plot ID in a factor
sp_lich<-lich[,4:ncol(lich)]#save as a new dataframe the "lich" matrix excluding the ID columns
sp_lifu<-lifu[,4:ncol(lifu)]#save as a new dataframe the "lifu" matrix excluding the ID columns

###estimation of species richness, shannon's index, eveness (Pielou index)
lich_rich<- specnumber(sp_lich)#n° of species in each sampling unit
lich_shan<- diversity(sp_lich)#shannon index for each sampling unit
lich_evene<- lich_shan/log(sp_lich)#Pielou index for each sampling unit
lifu_rich<- specnumber(sp_lifu)#n° of species in each sampling unit
lifu_shan<- diversity(sp_lifu)#shannon index for each sampling unit
lifu_evene<- lifu_shan/log(sp_lifu)#Pielou index for each sampling unit


lich_rich_data <- as.data.frame(lich_rich)
lifu_rich_data <- as.data.frame(lifu_rich)
lich_shan_data <- as.data.frame(lich_shan)
```

```r
lifu_shan_data <- as.data.frame(lifu_shan)
lich_evene_data <- as.data.frame(lich_evene)
lifu_evene_data <- as.data.frame(lifu_evene)

###Analyses Of Variance of diversity indexes
# Analyses Of Variance lichens
analis_varia_rich<- aov(lich_rich_data$lich_rich~as.factor(lich$Plot.1))
analis_varia_shann<- aov(lich_shan_data$lich_shan~as.factor(lich$Plot.1))
analis_varia_even <- aov(lich_evene_data$lich_evene~as.factor(lich$Plot.1))
# Analyses Of Variance lichenicolous fungi
analis_varia_rich_lifu <- aov(lifu_rich_data$lifu_rich~as.factor(lifu$Plot.1))
analis_varia_shann_lifu <- aov(lifu_shan_data$lifu_shan~as.factor(lifu$Plot.1))
analis_varia_even_lifu <- aov(lifu_evene_data$lifu_evene~as.factor(lifu$Plot.1))

###boxplot graph rich
# create data
names <- c( rep(1:10, each = 3))
value_rich_lich <- lich_rich_data$lich_rich
value_rich_lifu <- lifu_rich_data$lifu_rich
value_shan_lich <- lich_shan_data$lich_shan
value_shan_lifu <- lifu_shan_data$lifu_shan
value_even_lich <- lich_evene_data$lich_evene
value_even_lifu <- lifu_evene_data$lifu_evene

# boxplot richness
ggplot(lich_rich_data, aes(x=as.factor(names), y=value_rich_lich))+
  geom_boxplot(fill="slateblue", alpha=0.2) +
  xlab("plot")#plot lich_rich
ggplot(lifu_rich_data, aes(x=as.factor(names), y=value_rich_lifu)) +
  geom_boxplot(fill="red", alpha=0.2) +
  xlab("plot")#plot lifu_rich

#boxplot shannon_lich
ggplot(lich_shan_data, aes(x=as.factor(names), y=value_shan_lich)) +
  geom_boxplot(fill= "slateblue", alpha = 0.2)+
  xlab("plot")
#plot shannon_lifu
ggplot(lifu_shan_data, aes(x=as.factor(names), y=value_shan_lifu)) +
  geom_boxplot(fill= "red", alpha = 0.2)+
  xlab("plot")

#boxplot eveness
ggplot(lich_evene_data, aes(x=as.factor(names_even), y=value_even_lich)) +
  geom_boxplot(fill= "slateblue", alpha = 0.2)+
  xlab("plot")
ggplot(lifu_evene_data, aes(x=as.factor(names_even), y=value_even_lifu)) +
  geom_boxplot(fill= "red", alpha = 0.2)+
  xlab("plot")


###accumulation curves
lich_accurves<- specaccum(lich_acc[,-1], method = "exact",  w = NULL)
plot(lich_accurves)
lifu_accurves<- specaccum(Lifu_acc[,-1], method = "exact",  w = NULL)
plot(lich_accurves)
lines(lifu_accurve, col="red")
str(lich_accurve)
x <- c(1:30)
```

```
plot(x, lich_accurve$richness/lifu_accurve$richness )
plot(x, lifu_accurve$richness/lich_accurve$richness )


###spatial Rarefacion curves
Lichens <- as.data.frame(lich)
Coord <- as.data.frame(coordinate_sampling)

#LICHENS
dist_sp <- dist(Coord, method = "euclidean")
Lich_rarefaction <- directionalSAC(lich[,4:50],dist_sp)
plot(1:30,Lich_rarefaction$N_Exact, xlab ="plot", ylab="species",pch=1)
points(1:30,Lich_rarefaction$N_SCR, pch=2)

#LIfu
dist_sp <- dist(Coord, method = "euclidean")
Lifu_rarefaction <- directionalSAC(lifu[,4:44],dist_sp)
plot(1:30,Lifu_rarefaction$N_Exact,  xlab ="plot", ylab="species",pch=1)
points(1:30,Lifu_rarefaction$N_SCR,pch=2)


###Diversity Partitioning Analysis
#lifu
indici_spaziale<-data.frame(seq(1:30),rep(1:10, each=3),rep(1,30))
lifu_part<-adipart(t(Lifu_DIVPART),indici_spaziale, index="richness", nsimul=9999)
plot(lifu_part)
#lich
indici_spaziale<-data.frame(seq(1:30),rep(1:10, each=3),rep(1,30))
lich_part<-adipart(t(Lich_DIVPART),indici_spaziale, index="richness", nsimul=9999)
plot(lich_part)


##########Correlation between indeces
indexdiversit <- data.frame(lich_rich, lich_shan, lich_evene, lifu_rich, lifu_shan, lifu_evene)
matrixcorr <- cor(indexdiversit)
test <- cor.mtest(indexdiversit)
corrplot(matrixcorr, p.mat = test$p, method = "color", diag = FALSE, type = "upper",
      sig.level = c(.001, .01, .05), pch.cex = .9,
      insig = "label_sig", pch.col = "white")
##########################################################
##########################################################

#MANTEL TEST correspondence in species richness

vettore_richness_lich <- lich_rich_data$lich_rich
vettore_richness_lifu <- lifu_rich_data$lifu_rich
vettore_richness_lich_pa <- lich_rich_data$lich_rich
vettore_richness_lifu_pa <- lifu_rich_data$lifu_rich

distance_richness_lich <- vegdist(vettore_richness_lich, method = "euclidean")
distance_richness_lifu <- vegdist(vettore_richness_lifu, method = "euclidean")
distance_richness_lich_pa <- vegdist(vettore_richness_lich_pa, method = "euclidean")
distance_richness_lifu_pa <- vegdist(vettore_richness_lifu_pa, method = "euclidean")

mtest <- mantel(distance_richness_lich, distance_richness_lifu, method = "pearson", 9999)
mtest_pa <- mantel(distance_richness_lich_pa, distance_richness_lifu_pa, method = "pearson", 9999)

#######MANTEL TEST IN COMPOSITON####
```

```
matr_composition_lich <- lich_shan_data
matr_composition_lifu <- lifu_shan_data
matr_composition_lich_PA <- lich_PA_compos[,2:50]
matr_composition_lifu_PA <- lifu_PA_composition[,2:41]

distance_compo_lich <- vegdist(matr_composition_lich, method = "bray")
distance_compo_lifu <- vegdist(matr_composition_lifu, method = "bray")
distance_compo_lich_pa <- vegdist(matr_composition_lich_PA, method = "jaccard")
distance_compo_lifu_pa <- vegdist(matr_composition_lifu_PA, method = "jaccard")

mtestcompositionPA <- mantel(distance_compo_lich,distance_compo_lifu, method = "pearson", 9999)

#####CO-correspondence analyses
subplot<-as.factor(lich[,2])
plot<-as.factor(lich[,1])
sp_lich<-lich[,4:ncol(lich)]
sp_lifu<-lifu[,4:ncol(lifu)]

diss_lich<-vegdist(sqrt(lich[,4:ncol(lich)]), method="bray")
diss_lifu<-vegdist(sqrt(lifu[,4:ncol(lifu)]), method="bray")
plot(diss_lich,diss_lifu)

#Dissimilarity matrices
pers_manteljac<-mantel(diss_lich, diss_lifu, method="pearson", permutations=4999)
sper_manteljac<-mantel(diss_lich, diss_lifu, method="spearman", permutations=4999)
scatterplot(1-diss_lifu~1-diss_lich, reg.line=lm, smooth=FALSE, spread=FALSE, id.method='mahal', id.n = 2,
boxplots=FALSE, span=0.5, xlab="Lichens Similarity", ylab="Lifu Similarity")

# to normalize the data we use the square root method
sqrtlich<-sqrt(sp_lich)
sqrtlifu<-sqrt(sp_lifu)

###co-correspondence, all the below analyses are used to co-correspondence analyses with presence/absence
data

library(cocorresp)
coca_bis<-coca(sp_lifu~.,data=sp_lich)
coca_pa<-coca(sqrtlifu~.,data=sqrtlich)

summary(coca_pa)
summary(coca_bis)

plot(coca_pa)
plot(coca_pa, which = "response", main = "Lifu")
plot(coca_pa, which = "predictor", main = "Lichens")

summary(coca_bis)
plot(coca_bis)
plot(coca_bis, which = "response", main = "Lifu")
plot(coca_bis, which = "predictor", main = "Lichens")

### Cross validation analyses of axes
x_pa<-crossval(sqrtlifu,sqrtlich, n.axes=4)
permtest_pa<-permutest(coca_pa,permutations = 4999)
summary(permtest_pa)


x_bis<-crossval(sp_lifu,sp_lich, n.axes=4)
```

```
permtest_bis<-permutest(coca_bis,permutations = 4999)
summary(permtest_bis)

##############PLOT SQRT#########
scorespecieslich<-data.frame(coca_pa$scores$species$X)
scorespecieslifu<-data.frame(coca_pa$scores$species$Y)
scoresitelich<-data.frame(coca_pa$scores$site$X)

par(mfrow=c(1,2))
plot(scorespecieslich$Comp.1,scorespecieslich$Comp.2,xlim=c(-10,+10),ylim=c(-15,+15),cex.axis=1,cex.lab=1,
xlab="Axis 1",ylab="Axis 2",main="Lichens",cex.main=1, pch=".")
text(scorespecieslich$Comp.1,scorespecieslich$Comp.2,labels=row.names(scorespecieslich),cex=0.6,col="black")
points(scoresitelich$Comp.1,scoresitelich$Comp.2,cex=0.5,col="blue")
text(scoresitelich$Comp.1,scoresitelich$Comp.2, labels=row.names(scoresitelich),cex=0.6,col="blue")
plot(scorespecieslifu$Comp.1,scorespecieslifu$Comp.2,xlim=c(-1.5,+1.5),ylim=c(-1.5,+2),cex.axis=1,cex.lab=1,
xlab="Axis 1",ylab="Axis 2",main="Lifu",cex.main=1, pch=".")
text(scorespecieslifu$Comp.1,scorespecieslifu$Comp.2,labels=row.names(scorespecieslifu),cex=0.6,col="black")
points(scoresitelich$Comp.1,scoresitelich$Comp.2,cex=0.5,col="blue")
text(scoresitelich$Comp.1,scoresitelich$Comp.2, labels=row.names(scoresitelich),cex=0.6,col="blue")

###TEST BETA DISPERSION
fattore<-as.numeric(fattore)
fattore1<-factor(rep(c(1,2),c(63,41)))
summary(fattore1)
dist_speci<-vegdist(t(tutte_specie), method = "bray")

beta_habitat<-betadispersion2(dist_speci, fattore1, 999)
dim(matrix(dist_speci))

###Differences in beta diversity tested using the betadispersion2 function, also available in Bacaro et al. 2012,
2013

betadispersion2<-function(data, factor, permutation)
{
  require(vegan)
  x<-as.dist(data)
  x.estend <- as.vector(x)
  if (missing(permutation) )
    permutation<- 9999
  N <- attributes(x)$Size
  grouping <- as.factor(factor)
  matched <- function(irow, icol, grouping) {
    grouping[irow] == grouping[icol]
  }
  irow <- as.vector(as.dist(row(matrix(nrow = N, ncol = N))))
  icol <- as.vector(as.dist(col(matrix(nrow = N, ncol = N))))
  within <- matched(irow, icol, grouping)
  cl.vec <- rep("Between", length(x))
  take <- as.numeric(irow[within])
  cl.vec[within] <- levels(grouping)[grouping[take]]
  cl.vec <- factor(cl.vec, levels = c("Between", levels(grouping)))
  frame<-data.frame(x.estend, cl.vec)
  reduced<-frame[!cl.vec=="Between",]
  oneway <- lm(x.estend ~ cl.vec, data=reduced)
  promo<-anova(oneway,test="F")
  F.mod<-promo[1,4]
  Average_Beta_Within<-tapply(reduced$x.estend, list(cl.vec=reduced$cl.vec), mean, na.rm=TRUE)
  permF <-array(dim=c(permutation,1))
```

```
for (i in 1:permutation)
{
  permutated<-sample(reduced$x.estend)
  model<- lm(permutated ~ reduced$cl.vec)
  vin<-anova(model,test="F")
  permF[i,1]<-vin[1,4]
}
tab <- data.frame(Df = promo[,1], SumsOfSqs = promo[,2],
          MeanSqs = promo[,3], F.Model = promo[,4],
          P = c((rowSums(t(permF) >= F.mod) + 1)/(permutation + 1), NA))
rownames(tab) <- c("Factor","Residuals")
colnames(tab)[ncol(tab)] <- "Pr(>F)"
class(tab) <- c("anova", class(tab))
Average_Beta_Within<-data.frame(Average_Beta_Within)
col1<-row.names(Average_Beta_Within)
col2<-Average_Beta_Within[,1]
Summary_beta<-data.frame(col1,col2)
Summary<-data.frame(Summary_beta[2:nrow(Summary_beta),])
colnames(Summary)<-c("Group", "Average Beta")
output<-list(tab,Summary)
output

}
```