

Rock Lichen data from Sunset Crater

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Analysis Summary

- Dead trees and non-lichen species were removed from lichen community analyses.
- Lichen communities were adequately sampled, based on species accumulation curves, with moth resistant trees accumulating slightly more lichen species.
- Lichen communities (abundance, richness, diversity, composition) were significantly, generally negatively, affected by moth susceptibility.
- Several tree variables, including light availability, leaf litter abundance and rock abundance, were impacted by moth susceptibility.
- Analysis of causal pathways supported an indirect link between moth susceptibility and impacts on lichen communities via decreasing rock (i.e. habitat) availability through increased leaf abscission and accumulation on rocks under trees.
- These results support a genetically based link between intraspecific variation in susceptibility to an insect herbivore and community dynamics in an arid ecosystem.
- Given the possible impacts of climate change on this system, this study supports the conclusion that community and ecosystem impacts need to be considered in an evolutionary context.

```
# 0. Supporting functions and libraries
## Support functions

dif <- function(x){
  out=x[1]
  for (i in 2:length(x)){
    out=out-x[i]
  }
  return(out)
}

## Libraries
my.libs <- c("vegan", "ecodist", "xtable")
if (any(!(my.libs %in% installed.packages()[, 1]))){
  sapply(my.libs[!(my.libs %in% installed.packages()[, 1])],
    install.packages)
}else{}
sapply(my.libs, require, character.only = TRUE)
```

Load Data

The following are variable descriptions (Variable, Type, Range, Definition):

- Moth,categorical,0 or 1,Was the tree susceptible (0) or resistant (1) to moth attack?
- Live/Dead,categorical,0 or 1,Was the tree dead (0) or alive (1)?

- Litter %,continuous,0 to 100,Percent cover inside quadrat
- Rocks > 3cm? %,continuous,0 to 100,Percent cover of rocks > 3cm? inside quadrat
- Rocks < 3cm? %,continuous,0 to 100,Percent cover of rocks < 3cm? inside quadrat
- Shrubs %,continuous,0 to 100,Percent cover of shrubs inside quadrat
- Grass %,continuous,0 to 100,Percent cover of grass inside quadrat
- Branches %,continuous,0 to 100,Percent cover of branches on ground inside quadrat
- Distance,continuous,0 to 100,“Distance from main trunk, converted to percent of crown radius at that azimuth”
- Azimuth,continuous,0 to 360,Compass direction from main trunk
- Slope,continuous,0 to 90,Topographical steepness
- Aspect,continuous,0 to 360,Compass direction of slope
- Light,continuous,,Amount of light available to epiliths

```
## Data are in ../data/scrl
l.dat <- read.csv("../data/scrl/spp_env_combined.csv")

## Summary of data
summary(l.dat)

## remove dead trees
l.dat <- l.dat[l.dat[, "Live.Dead"] != 0, ]

## Lichen species list
spp.l <- c("Acacon", "Acasup", "Acaobp", "Sterile.sp", "Brown.cr",
"Lobalp", "Canros", "Calare", "Phydub", "Rhichr", "Xanlin", "Xanpli",
"Xanele", "GrBr.cr", "Gray.cr")
spp.moss <- c("Synrur", "Cerpur.Bryarg")

## Create a community matrix
com <- l.dat[, colnames(l.dat) %in% spp.l]
com.moss <- l.dat[, colnames(l.dat) %in% spp.moss]

## Add the tree labels to the rownames
rownames(com) <- paste(l.dat[, "Moth"], l.dat[, "Tree.pairs"], sep = "_")
rownames(com.moss) <- paste(l.dat[, "Moth"], l.dat[, "Tree.pairs"], sep = "_")
rownames(l.dat) <- paste(l.dat[, "Moth"], l.dat[, "Tree.pairs"], sep = "_")
```

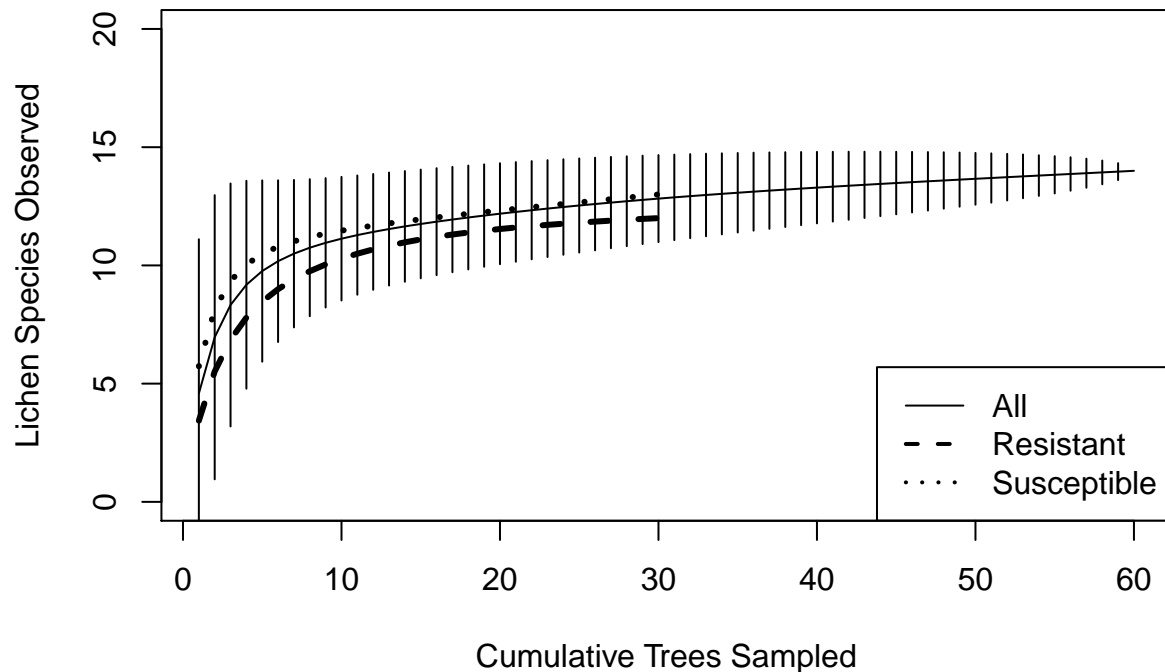
Species accumulation

Are the communities on each tree type adequately sampled?

```
spa.all <- specaccum(com)
spa.res <- specaccum(com[l.dat[, "Moth"] == 0, ])
spa.sus <- specaccum(com[l.dat[, "Moth"] == 1, ])

plot(spa.all,
     ylim = c(0, 20),
     xlab = "Cumulative Trees Sampled",
     ylab = "Lichen Species Observed")
lines(spa.res$sites, spa.res$richness,
      ylim = c(0, 20), lty = 2, lwd = 3)
lines(spa.sus$sites, spa.sus$richness,
      ylim = c(0, 20), lty = 3, lwd = 3)
```

```
legend("bottomright",
      legend = c("All", "Resistant", "Susceptible"),
      lty = c(1, 2, 3), lwd = c(1, 2, 2))
```



Moth trees have different microenvironments

- paired t-tests

Moth trees have different lichen communities (FIGURE ch.plot A, R, H)

less abundant and diverse (paired t-tests, in text)

```
abun <- apply(com, 1, sum)
rich <- apply(com, 1, function(x) sum(sign(x)))
shan <- apply(com, 1, diversity, index = "shannon")
tt.a <- t.test(tapply(abun, l.dat[, "Tree.pairs"], diff))
tt.r <- t.test(tapply(rich, l.dat[, "Tree.pairs"], diff))
tt.h <- t.test(tapply(shan, l.dat[, "Tree.pairs"], diff))
tt.arh <- do.call(rbind,
                  list(a = unlist(tt.a), r = unlist(tt.r), h = unlist(tt.h)))
data.frame(tt.arh)
```

##	statistic.t	parameter.df	p.value	conf.int1
## a	-2.35680534636893	29	0.0253991007560338	-2.89259563276878
## r	-2.83579994251995	29	0.00824742800912123	-3.95880113980294
## h	-2.43278934693583	29	0.0213834528180339	-0.783514237345595
##	conf.int2	estimate.mean.of.x	null.value.mean	stderr
## a	-0.204737700564558	-1.54866666666667	0	0.657104189386137

```
## r -0.641198860197056 -2.3 0 0.811058624239964
## h -0.0678109108683953 -0.425662574106995 0 0.174968940341312
## alternative method data.name
## a two.sided One Sample t-test tapply(abun, l.dat[, "Tree.pairs"], diff)
## r two.sided One Sample t-test tapply(rich, l.dat[, "Tree.pairs"], diff)
## h two.sided One Sample t-test tapply(shan, l.dat[, "Tree.pairs"], diff)
```

composition is different (PERMANOVA, in text and supplement)

```
com.ds <- cbind(com, ds = rep(0.0001, nrow(com)))
set.seed(123)
ptab.moth <- adonis2(com.ds~ Moth, data = l.dat,
                     strata = l.dat[, "Tree.pairs"],
                     by = "margin", nperm = 100000)
xtable(ptab.moth)
```

```
## % latex table generated in R 3.6.2 by xtable 1.8-4 package
## % Tue Apr 7 18:10:36 2020
## \begin{table}[ht]
## \centering
## \begin{tabular}{lrrrrr}
## \hline
## & Df & SumOfSqs & R2 & F & Pr(>$F) \\
## \hline
## Moth & 1 & 0.83 & 0.04 & 2.35 & 0.0230 \\
## Residual & 58 & 20.44 & 0.96 & & \\
## Total & 59 & 21.27 & 1.00 & & \\
## \hline
## \end{tabular}
## \end{table}
```

three main species were reduced by moths (FDR paired t-tests, in text + supplement)

```
ind.spp <- lapply(com, function(x, p) t.test(tapply(x, p, diff)), p = l.dat[, "Tree.pairs"])
isp <- apply(do.call(rbind, lapply(ind.spp, unlist)), 2, as.numeric)
```

```
## Warning in apply(do.call(rbind, lapply(ind.spp, unlist)), 2, as.numeric): NAs
## introduced by coercion
```

```
## Warning in apply(do.call(rbind, lapply(ind.spp, unlist)), 2, as.numeric): NAs
## introduced by coercion
```

```
## Warning in apply(do.call(rbind, lapply(ind.spp, unlist)), 2, as.numeric): NAs
## introduced by coercion
```

```
rownames(isp) <- names(ind.spp)
isp[, "p.value"] <- p.adjust(isp[, "p.value"], method = "fdr")
isp <- isp[order(isp[, "p.value"]), ]
head(isp[, 1:3])
```

```
##      statistic.t parameter.df    p.value
## Acacon    -3.377629         29 0.01390405
## Acasup    -3.242091         29 0.01390405
## Canros    -3.581884         29 0.01390405
## Lobalp    -2.041361         29 0.17642430
## Phydub    -1.922619         29 0.18031798
## Calare    -1.607607         29 0.22424946
```

Litter covering rocks was the main driver (FIGURE = ORDINATION)

light not litter predicted lichen composition (PERMANOVA, table 3, Ordination)

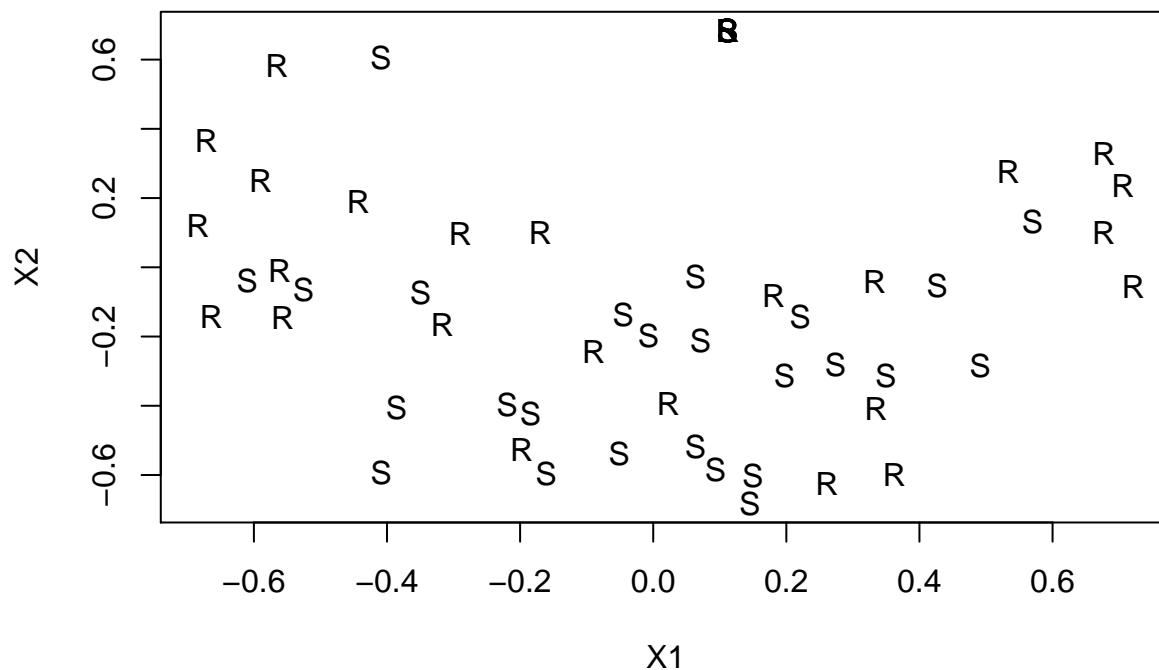
```
set.seed(123)
ptab.env <- adonis2(com.ds ~ Light...average + Litter..., data = l.dat,
                    strata = l.dat[, "Tree.pairs"],
                    by = "margin", nperm = 100000)
xtable(ptab.env)
```

```
## % latex table generated in R 3.6.2 by xtable 1.8-4 package
## % Tue Apr 7 18:10:36 2020
## \begin{table}[ht]
## \centering
## \begin{tabular}{lrrrrr}
## \hline
## & Df & SumOfSqs & R2 & F & Pr(>F) \\
## \hline
## Light...average & 1 & 0.41 & 0.02 & 1.23 & 0.2400 \\
## Litter.. & 1 & 1.01 & 0.05 & 3.01 & 0.0070 \\
## Residual & 57 & 19.14 & 0.90 & & \\
## Total & 59 & 21.27 & 1.00 & & \\
## \hline
## \end{tabular}
## \end{table}
```

```
nm.ds.out <- nm.ds(vegdist(com.ds), 2, 2)
ord <- nm.ds.min(nm.ds.out, dims = 2)
```

```
## Minimum stress for given dimensionality: 0.2164016
## r^2 for minimum stress configuration: 0.6474944
```

```
ord.pch <- c("R", "S")[(l.dat[, "Moth"] + 1)]
plot(X2~ X1, data = ord, pch = ord.pch)
```



litter not light was correlated with large rocks (dist cor, in text)

```
cor.test(tapply(l.dat[, "Big.rocks.."], l.dat[, "Tree.pairs"], diff),
         tapply(l.dat[, "Litter.."], l.dat[, "Tree.pairs"], diff))
```

```
##
## Pearson's product-moment correlation
##
## data:  tapply(l.dat[, "Big.rocks.."], l.dat[, "Tree.pairs"], diff) and tapply(l.dat[, "Litter.."], l
## t = -11.106, df = 28, p-value = 9.054e-12
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.9530598 -0.8039735
## sample estimates:
##      cor
## -0.9027609
```

```
cor.test(tapply(l.dat[, "Big.rocks.."], l.dat[, "Tree.pairs"], diff),
         tapply(l.dat[, "Light...average"], l.dat[, "Tree.pairs"], diff))
```

```
##
## Pearson's product-moment correlation
##
## data:  tapply(l.dat[, "Big.rocks.."], l.dat[, "Tree.pairs"], diff) and tapply(l.dat[, "Light...average"], l
## t = 0.71624, df = 28, p-value = 0.4798
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.2376184 0.4716125
## sample estimates:
##      cor
## 0.1341335
```