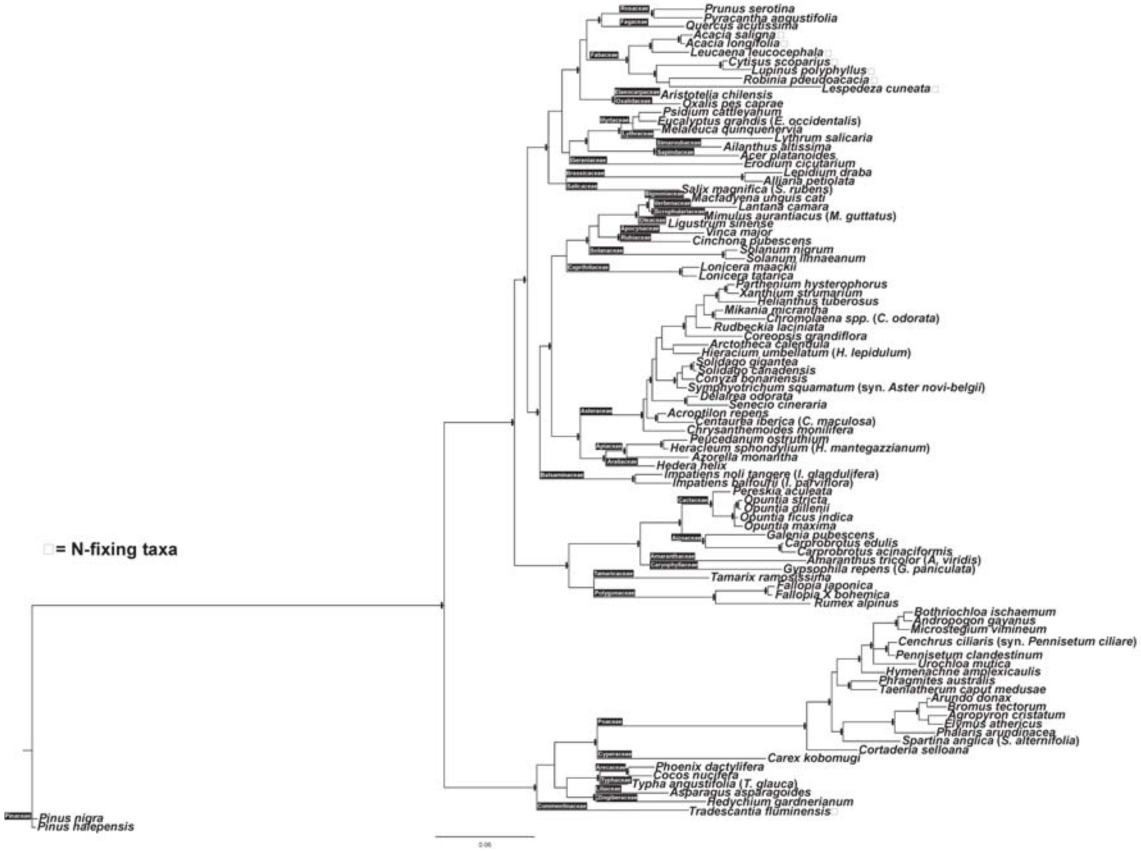
Appendix S1. Bayesian phylogeny based on rbcL DNA sequence data illustrating the phylogenetic relationships among non-native plants included in this study. Species names within brackets are those lacking DNA sequence data and were replaced by taxa within the same genus indicated outside the brackets. Plant families are indicated above branches. High nodal support (posterior probabilities >0.9) is indicated as black rectangular boxes at nodes.



Appendix S2. List of studies for meta-analysis on non-native plant species impact on local plant and animal species richness.

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Appendix S3. R code to test the effect sizes of the impact of non-native plant species on resident plant species richness.

```
rm(list=ls())

#load needed libraries
library(ape)
library(nlme)
library(MASS)

#functions for the Meta-Analysis

model_fit <- function(formula,tree,d){
  #fit of a Meta-Anyalsis based on phylogenetic regression

  mint <- gls(formula,
correlation=corGrafen(0.5,tree,fixed=FALSE),method='ML',weights=varFixed(~w),data
=d)

  r <- d$y - fitted(mint)
  Q <- sum(d$w*r^2)
  df <- length(r) - 1
  C <- sum(d$w) - sum(d$w^2) / sum(d$w)
  T2 <- (Q - df)/C
  new_w <- 1/(1/d$w + T2)
  d$new_w <- new_w

  m <- gls(formula,
correlation=corGrafen(0.5,tree,fixed=FALSE),method='ML',weights=varFixed(~new_w)
,data=d)
}


#load phylogenetic tree
tr_plant <- read.tree(file='tree_plant.txt')


#load data set
d_plant <- read.table(file='dataset_plant.txt',header=TRUE)


#compute effect size and the weight
y <- log(d_plant$mean_control / d_plant$mean_invaded)
```

```
names(y) <- rownames(d_plant)
sdy <- (d_plant$SD_control / d_plant$mean_control + d_plant$SD_invaded / d_plant$mean_invaded)
w <- 1/sdy^2

#covariables
x1 <- factor(d_plant$Life_form)
x2 <- factor(d_plant$N_fixing)
x3 <- factor(d_plant$Clonal)
x4 <- factor(d_plant$Biogeographical_region)
x5 <- factor(d_plant$Insularity.)
x6 <- factor(d_plant$Habitat_type)

#creat the data frame made of response variable, cavariables, and weights
d2 <- as.data.frame(x = y)
d2$x1 <- x1
d2$x2 <- x2
d2$x3 <- x3
d2$x4 <- x4
d2$x5 <- x5
d2$x6 <- x6
d2$w <- w


#full model
formula = y ~ -1 + x1 + x2 + x3 + x4 + x5 + x6
m <- model_fit(formula,tr_plant,d2)
AIC(m)

#model selection procedure

#first step
#model without x1
formula = y ~ -1 + x2 + x3 + x4 + x5 + x6
m_x1 <- model_fit(formula,tr_plant,d2)
AIC(m_x1)
#model without x2
formula = y ~ -1 + x1 + x3 + x4 + x5 + x6
m_x2 <- model_fit(formula,tr_plant,d2)
AIC(m_x2)
#model without x3
formula = y ~ -1 + x1 + x2 + x4 + x5 + x6
m_x3 <- model_fit(formula,tr_plant,d2)
AIC(m_x3)
```

```
#model without x4
formula = y ~ -1 + x1 + x2 + x3 + x5 + x6
m_x4 <- model_fit(formula,tr_plant,d2)
AIC(m_x4)
#model without x5
formula = y ~ -1 + x1 + x2 + x3 + x4 + x6
m_x5 <- model_fit(formula,tr_plant,d2)
AIC(m_x5)
#model without x6
formula = y ~ -1 + x1 + x2 + x3 + x4 + x5
m_x6 <- model_fit(formula,tr_plant,d2)
AIC(m_x6)

AIC(m,m_x1,m_x2,m_x3,m_x4,m_x5,m_x6)

#based on AIC, we remove the covariable x4
formula = y ~ -1 + x1 + x2 + x3 + x5 + x6
m <- model_fit(formula,tr_plant,d2)
AIC(m)


#second step
#model without x1
formula = y ~ -1 + x2 + x3 + x5 + x6
m_x1 <- model_fit(formula,tr_plant,d2)
AIC(m_x1)
#model without x2
formula = y ~ -1 + x1 + x3 + x5 + x6
m_x2 <- model_fit(formula,tr_plant,d2)
AIC(m_x2)
#model without x3
formula = y ~ -1 + x1 + x2 + x5 + x6
m_x3 <- model_fit(formula,tr_plant,d2)
AIC(m_x3)
#model without x5
formula = y ~ -1 + x1 + x2 + x3 + x6
m_x5 <- model_fit(formula,tr_plant,d2)
AIC(m_x5)
#model without x6

formula = y ~ -1 + x1 + x2 + x3 + x5

m_x6 <- model_fit(formula,tr_plant,d2)
AIC(m_x6)
```

```
AIC(m,m_x1,m_x2,m_x3,m_x5,m_x6)



#based on AIC, we remove the covariable x1
formula = y ~ -1 + x2 + x3 + x5 + x6
m <- model_fit(formula,tr_plant,d2)
AIC(m)

#third step
#model without x2
formula = y ~ -1 + x3 + x5 + x6
m_x2 <- model_fit(formula,tr_plant,d2)
AIC(m_x2)
#model without x3
formula = y ~ -1 + x2 + x5 + x6
m_x3 <- model_fit(formula,tr_plant,d2)
AIC(m_x3)
#model without x5
formula = y ~ -1 + x2 + x3 + x6
m_x5 <- model_fit(formula,tr_plant,d2)
AIC(m_x5)
#model without x6
formula = y ~ -1 + x2 + x3 + x5
m_x6 <- model_fit(formula,tr_plant,d2)
AIC(m_x6)

AIC(m,m_x2,m_x3,m_x5,m_x6)



#based on AIC, we remove the covariable x6
formula = y ~ -1 + x2 + x3 + x5
m <- model_fit(formula,tr_plant,d2)
AIC(m)

#fourth step
#model without x2
formula = y ~ -1 + x3 + x5
m_x2 <- model_fit(formula,tr_plant,d2)
AIC(m_x2)
#model without x3
formula = y ~ -1 + x2 + x5
m_x3 <- model_fit(formula,tr_plant,d2)
```

```
AIC(m_x3)
#model without x5
formula = y ~ -1 + x2 + x3
m_x5 <- model_fit(formula,tr_plant,d2)
AIC(m_x5)

AIC(m,m_x2,m_x3,m_x5)

#based on AIC, we remove the covariable x5
formula = y ~ -1 + x2 + x3
m <- model_fit(formula,tr_plant,d2)
AIC(m)

#fifth step
#model without x2
formula = y ~ -1 + x3
m_x2 <- model_fit(formula,tr_plant,d2)
AIC(m_x2)
#model without x3
formula = y ~ -1 + x2
m_x3 <- model_fit(formula,tr_plant,d2)
AIC(m_x3)

AIC(m,m_x2,m_x3)
#based on AIC, the procedure has converged
#############################################
## compute the delta AIC

formula = y ~ -1 + x2 + x3
mfull <- model_fit(formula,tr_plant,d2)
AIC(mfull)
summary(mfull)

#-x2
formula = y ~ -1 + x3
mfull_x2 <- model_fit(formula,tr_plant,d2)
AIC(mfull_x2)

#-x3
formula = y ~ -1 + x2
mfull_x3 <- model_fit(formula,tr_plant,d2)
AIC(mfull_x3)

#-phylo
```

```
mfull_phylo <- gls(y ~ -1 + x2 + x3,
correlation=corPagel(0,tr_plant,fixed=TRUE),method='ML',weights=varFixed(~w))
r <- y - fitted(mfull_phylo)
Q <- sum(w*r^2)
df <- length(r) - 1
C <- sum(w) - sum(w^2) / sum(w)
T2 <- (Q - df)/C
new_w <- 1/(1/w + T2)
mfull_phylo <- gls(y ~ -1 + x1 + x3 + x2 + x6,
correlation=corPagel(0,tr_plant,fixed=TRUE),method='ML',weights=varFixed(~new_w)
)
AIC(mfull_phylo)

AIC(mfull_x2,mfull_x3,mfull_phylo)-AIC(mfull)
```

Appendix S4. R code to test the effect sizes of the impact of non-native plant species on resident animal species richness.

```
rm(list=ls())

#load needed libraries
library(ape)
library(nlme)
library(MASS)

#functions for the Meta-Analysis

model_fit <- function(formula,tree,d){
  #fit of a Meta-Anyalsis based on phylogenetic regression

  mint <- gls(formula,
correlation=corGrafen(0.5,tree,fixed=FALSE),method='ML',weights=varFixed(~w),data
=d)

  r <- d$y - fitted(mint)
  Q <- sum(d$w*r^2)
  df <- length(r) - 1
  C <- sum(d$w) - sum(d$w^2) / sum(d$w)
  T2 <- (Q - df)/C
  new_w <- 1/(1/d$w + T2)
  d$new_w <- new_w

  m <- gls(formula,
correlation=corGrafen(0.5,tree,fixed=FALSE),method='ML',weights=varFixed(~new_w)
,data=d)

}

model_fit_no_phylo <- function(formula,d){
  #fit of a Meta-Anyalsis based with a standard linear regression

  mint <- gls(formula,method='ML',weights=varFixed(~w),data=d)

  r <- d$y - fitted(mint)
  Q <- sum(d$w*r^2)
  df <- length(r) - 1
  C <- sum(d$w) - sum(d$w^2) / sum(d$w)
```

```
  T2 <- (Q - df)/C
  new_w <- 1/(1/d$w + T2)
  d$new_w <- new_w

  m <- gls(formula,method='ML',weights=varFixed(~new_w),data=d)

}

#load phylogenetic tree
tr_animal <- read.tree(file='tree_animal.txt')


#load data set
d_animal <- read.table(file='dataset_animal.txt',header=TRUE)


#compute effect size and the weight
y <- log(d_animal$mean_control / d_animal$mean_invaded)
names(y) <- rownames(d_animal)
sdy <- (d_animal$SD_control / d_animal$mean_control + d_animal$SD_invaded /
d_animal$mean_invaded)
w <- 1/sdy^2

#covariables
x1 <- factor(d_animal$Life_form)
x2 <- factor(d_animal$N_fixing)
x3 <- factor(d_animal$Clonal)
x4 <- factor(d_animal$Biogeographical_region)
x5 <- factor(d_animal$Insularity.)
x6 <- factor(d_animal$Habitat_type)

#creat the data frame made of response variable, cavariables, and weights
d2 <- as.data.frame(x = y)
d2$x1 <- x1
d2$x2 <- x2
d2$x3 <- x3
d2$x4 <- x4
d2$x5 <- x5
d2$x6 <- x6
d2$w <- w
```

```
#null model
#-phylo
mnull <- gls(y ~ 1, method='ML',weights=varFixed(~w))
r <- y - fitted(mnull)
Q <- sum(w*r^2)
df <- length(r) - 1
C <- sum(w) - sum(w^2) / sum(w)
T2 <- (Q - df)/C
new_w <- 1/(1/w + T2)
mnull <- gls(y ~ 1, method='ML',weights=varFixed(~new_w))
AIC(mnull)

#model selection procedure

#first step
#model with phylogeny only
formula = y ~ 1
m <- model_fit(formula,tr_animal,d2)
AIC(m)
#model with x1
formula = y ~ -1 + x1
m_x1 <- model_fit_no_phylo(formula,d2)
AIC(m_x1)
#model with x2
formula = y ~ -1 + x2
m_x2 <- model_fit_no_phylo(formula,d2)
AIC(m_x2)
#model with x3
formula = y ~ -1 + x3
m_x3 <- model_fit_no_phylo(formula,d2)
AIC(m_x3)
#model with x4
formula = y ~ -1 + x4
m_x4 <- model_fit_no_phylo(formula,d2)
AIC(m_x4)
#model with x5
formula = y ~ -1 + x5
m_x5 <- model_fit_no_phylo(formula,d2)
AIC(m_x5)
#model with x6
formula = y ~ -1 + x6
m_x6 <- model_fit_no_phylo(formula,d2)
AIC(m_x6)
```

```
AIC(mnull,m,m_x1,m_x2,m_x3,m_x4,m_x5,m_x6)

#based on AIC, we add x5
formula = y ~ -1 + x5
m2 <- model_fit_no_phylo(formula,d2)

#second step
#with x1
formula = y ~ -1 + x5 + x1
m2_x1 <- model_fit_no_phylo(formula,d2)
#with x2
formula = y ~ -1 + x5 + x2
m2_x2 <- model_fit_no_phylo(formula,d2)
#with x3
formula = y ~ -1 + x5 + x3
m2_x3 <- model_fit_no_phylo(formula,d2)
#with x4
formula = y ~ -1 + x5 + x4
m2_x4 <- model_fit_no_phylo(formula,d2)
#with x6
formula = y ~ -1 + x5 + x6
m2_x6 <- model_fit_no_phylo(formula,d2)
#with phylo
formula = y ~ -1 + x5
m2_phylo <- model_fit(formula,tr_animal,d2)

AIC(m2,m2_x1,m2_x2,m2_x3,m2_x4,m2_x6,m2_phylo)

#based on AIC, we add the phylogeny
formula = y ~ -1 + x5
m3 <- model_fit(formula,tr_animal,d2)

#third step
#with x1
formula = y ~ -1 + x5 + x1
m3_x1 <- model_fit(formula,tr_animal,d2)
#with x2
formula = y ~ -1 + x5 + x2
m3_x2 <- model_fit(formula,tr_animal,d2)
#with x3
formula = y ~ -1 + x5 + x3
m3_x3 <- model_fit(formula,tr_animal,d2)
#with x4
formula = y ~ -1 + x5 + x4
```

```
m3_x4 <- model_fit(formula,tr_animal,d2)
#with x6
formula = y ~ -1 + x5 + x6
m3_x6 <- model_fit(formula,tr_animal,d2)

AIC(m3,m3_x1,m3_x2,m3_x3,m3_x4,m3_x6)
#based on AIC, the procedure has converged

##################################################
 compte the delta AIC

#full model
formula = y ~ 1 + x5
mfull <- model_fit(formula,tr_animal,d2)

#-x5
formula = y ~ 1
mfull_x5 <- model_fit(formula,tr_animal,d2)

#-phylo
formula = y ~ -1 + x5
mfull_phylo <- model_fit_no_phylo(formula,d2)

AIC(mfull_phylo,mfull_x5)-AIC(mfull)
```