ONLINE APPENDIX A: Average plant biomass under different treatments

To estimate plant biomass without disruptive sampling of the plots, we first calculated the mean tussock volume per plot by measuring 20 randomly-selected tussocks. We measured basal circumference and height from the ground to the highest leaf, and then calculated the cylinder volume (1). After obtaining the average tussock volume for each plot, we multiplied it by the total count of tussock individuals. To convert plant volume to biomass, we measured the volume of 10 tussock plants from our glasshouse cultures following the same procedure as above. We then clipped them to ground level and dried the leaf material at 60°C for 48 hours. We used a linear regression to test how well volume approximated dry weight, and found a significant relationship ($F_{1,8} = 20.68$, $P = 0.001$, $R^2 = 0.72$).

Table S1: Average dry plant biomass (± standard error) for each treatment combination

	Average Biomass (g)	+/- SE
Control-Control	2036.54	224.63
Control-Nitrogen	3336.00	507.65
Warming-Control	2787.64	406.84
Warming-Nitrogen	3258.41	310.33

Literature cited

1. Laliberte E., Norton D.A., Tylianakis J.M., Scott D. 2010 Comparison of Two Sampling Methods for Quantifying Changes in Vegetation Composition Under Rangeland Development. Rangeland Ecology & Management 63, 537-45.

ONLINE APPENDIX B: Experimental set up and sampling

We generated the warming treatment by installing underground heating cables. We dug a 24m by 19m experimental area in October 2008, to a depth of 20 cm to establish the 20 plots, each separated by a 1m corridor. We then leveled the ground and installed custom-made electric heating cables (Argus Heating Ltd, Christchurch, New Zealand: coiled copper wire on fiberglass core and silicon coating) in half of the plots, and dummy cables in the remaining (unheated) plots. Heating power totaled 940 Watts per plot or a power density of 76W/m^2. Similar power output has been recommended (1) and successfully used in previous underground heating experiments (2).

We paired each warming plot with a control plot to keep the warmed treatments at 3°C above ambient, logging the temperature of all thermocouples every minute using two Campbell CR1000 (Campbell Scientific, USA) data loggers. The average temperature of the thermocouples in the warming plots is used against the control plot to switch the power on and off as required. The warming treatment was first activated in April 2009.

We started the nitrogen treatment application shortly after planting (Jan 2009). We used nitrogen fertilizer in the form of Calcium Ammonium Nitrate granules (Ravensdown LTD, New Zealand). This form of fertilizer combines fast and slower release of biologically available nitrogen, and has been used previously to simulate atmospheric deposition (3). We added a total of 50 Kg ha^{-1} yr^{-1} using evenly-distributed applications

during the rest of the year, with the exception of three winter months, for both 2009 and 2010.

We began sampling insects in January 2010, that is, a full year after plot establishment and planting. Sampling continued at monthly intervals until June 2010 (i.e. mid winter, when snow cover made sampling impractical), and resumed at monthly intervals from September to December 2010, totaling 11 sampling rounds. To minimize disturbance and depletion of caterpillars in the experimental area, we sampled half of each plot during each round, alternating between the two halves. This ensured a time window of at least 8 weeks before re-sampling of the same section. Sampling entailed visually searching for caterpillars on tussock plants, teasing apart the dense vegetation to find any hidden larvae. The standardized plant composition in each plot provided a standardized measure of insect abundance per unit area, unconfounded by differences in host plant availability.

Literature cited:

1. Peterjohn W.T., Melillo J.M., Bowles F.P., Steudler P.A. 1993 Soil Warming and Trace Gas Fluxes - Experimental-Design and Preliminary Flux Results. Oecologia 93, 18-24.
2. Melillo J.M., Steudler P.A., Aber J.D., Newkirk K., Lux H., Bowles F.P., Catricala C., Magill A., Ahrens T., Morrisseau S. 2002 Soil warming and carbon-cycle feedbacks to the climate system. Science 298, 2173-6.
3. Clark C., Tilman D. 2008 Loss of plant species after chronic low-level nitrogen deposition to prairie grasslands. Nature 451, 712-5.

ONLINE APPENDIX C: Calculation of body size estimates

We weighed the caterpillars (Mettler Toledo analytical balance accurate to 0.0001g) directly after collection for all samples. Unlike herbivore mass, parasitoid body mass can only be measured at emergence, and could therefore be strongly determined by the age at which the lepitopteran host was brought into the laboratory for rearing, and the laboratory food provided to the growing caterpillar. Additionally, the host larval mass represents the mass of the individual engaging in the interaction. In contrast, the parasitoid mass represents the offspring of the individual engaging in the interaction, and although parasitoid offspring quality will in part reflect maternal quality, offspring mass could also be influenced by host mass (1). Therefore, to avoid the possibility that these effects could generate spurious differences in the size of individual parasitoids across treatments, we used the average body mass of each parasitoid species. We obtained each species average by weighing 20 randomly selected adult individuals of each species across all treatments, or all individuals for the rarer species (less than 20 individuals).

Literature cited:

1. Cohen J.E., Jonsson T., Muller C.B., Godfray H.C.J., Savage V.M. 2005 Body sizes of hosts and parasitoids in individual feeding relationships. Proceedings of the National Academy of Sciences of the United States of America 102, 684-9.

ONLINE APPENDIX D: R code for ZIP model

Example *R* code for the Zero-Inflated Poisson (ZIP) model. The function *jags2* (part of the *R2jags* library written by Yu-Sung Su and Masanao Yajima) calls an MCMC routine in *JAGS 2.2.0*, which can be downloaded from http://www-ice.iarc.fr/~martyn/software/jags/. In this example, interaction data are stored as a text file listing separate vectors for the response variable and each explanatory variable, with each row corresponding to a single observation (e.g., Count <- c(0,0,1,2) HostDensity <- c(8,6,23,20) ParasitoidDensity <- c(5,3,1,8)). The data are ordered such that all zero entries in the vector "Count" come before all non-zero entries; this is necessary because we are using an arbitrary sampling distribution (the ZIP model), which requires use of the "zeros trick" in *JAGS 2.2.0*. Results are output in a specified folder, here "Results", located in the working directory.

Explanatory comments are preceded by the #-symbol and are ignored by the software.

```
# Required library
library(R2jags)

# CREATE OUTPUTS (including a pdf of posterior distributions)
MyOutputs<-function(MyModel,HABITATNAME,ModelName,NUMPARS,MyCoda,N){
  # Write table with intervals
  print("Printing Parameters summary")
  write.table(MyModel$summary[1:NUMPARS,],
              paste("Results/ParamEstDev_",HABITATNAME,"_",ModelName,".csv",sep=""))
  print("Printing DIC")
  # Write DIC, pD
  DicTab<-matrix(0,1,2)
  colnames(DicTab)<-c("DIC","pD")
  DicTab[1,1]<-MyModel$DIC
  DicTab[1,2]<-MyModel$pD
  write.table(DicTab,paste("Results/DIC_",HABITATNAME,"-",ModelName,".csv",sep=""))
  print("Plotting Parameters estimates")
  # Plot estimates of parameters for various chains and deviance
  pdf(paste("Results/Pardens_",HABITATNAME,"_",ModelName,".pdf",sep=""))
  plot(MyCoda[,1:NUMPARS,])
  dev.off()
    return(0)
}

# Load data file “All_dat.txt”
HABITATNAME<-"All"
source(paste(HABITATNAME,"_dat.txt",sep=""))
# Preparation for “zeros trick”, which allows arbitrary sampling distributions to be used
N<-length(Count)
Nz<-length(Count[Count==0])
zeros<-rep(0,N)
y<-Count[(Nz+1):N]

# Prepare the call to JAGS 2.2.0
# Set run length, burn-in length, number of chains, thinning, and number of parameters
NITER=100000
BURNIN=NITER/2
NCHAINS=3
NTHIN=20
NPARAM=7

# Set data and parameters to pass to JAGS 2.2.0
data<-
list("N","Nz","zeros","y","HostBodySize","HostDensity","ParasitoidBodySize","ParasitoidDe
nsity")
params<-c("alpha00","alpha","beta00","beta")
# Call JAGS 2.2.0 (see Appendix 2)
model1<-
jags2(data=data,inits=NULL,parameters.to.save=params,model.file="JAGS_model.txt",n.iter=N
ITER,n.thin=NTHIN,n.burnin=BURNIN,n.chains=NCHAINS)
coda1<-as.mcmc.list(model1)

# Run output code
MyOutputs(model1,HABITATNAME,"MODEL_NAME",NPARAM,coda1,N)
ModelSelection<-c(model1$DIC,model1$pD)
write.table(t(ModelSelection),"MODEL_NAME.R",row.names=F,col.names=F)
```

ONLINE APPENDIX E: JAGS code for ZIP model definition

Example Zero-Inflated Poisson model definition in *JAGS 2.2.0* syntax. This should be saved in the working directory and included as a variable in the call to *jags2* (if the code in Appendix S1 is used then the file should be saved as "JAGS_model.txt"). *JAGS 2.2.0* uses similar but not identical syntax and nomenclature to the popular WinBUGS software (http://www.mrc-bsu.cam.ac.uk/bugs/winbugs/contents.shtml).

Uninformative priors are set to be normal distributions with extremely large variance.

```
model{
   for(i in 1:Nz){
      zeros[i]~dpois(mu[i])
      mu[i]<--log(1-p[i]+p[i]*exp(-lambda[i]))
      logit(p[i])<-alpha00+alpha[1]*HostDensity[i]
      log(lambda[i])<-
beta00+beta[1]*HostDensity[i]+beta[2]*ParasitoidDensity[i]+beta[3]*Host
BodySize[i]+beta[4]*ParasitoidBodySize[i]
   }
   for(i in (Nz+1):N){
      zeros[i]~dpois(mu[i])
      mu[i]<--(log(p[i])-lambda[i]+y[i-Nz]*log(lambda[i])-logfact(y[i-
Nz]))
      logit(p[i])<-alpha00+alpha[1]*HostDensity[i]
      log(lambda[i])<-
beta00+beta[1]*HostDensity[i]+beta[2]*ParasitoidDensity[i]+beta[3]*Host
BodySize[i]+beta[4]*ParasitoidBodySize[i]
   }
   for(j in 1:1){
      alpha[j]~dnorm(0,0.000001)
   }
   for(k in 1:4){
      beta[k]~dnorm(0,0.000001)
   }
   alpha00~dnorm(0,0.000001)
   beta00~dnorm(0,0.000001)
}
```