**Supplementary Tables**

**Table S2.** Statistical model of daily average relative humidity.

Family: beta ( logit )  
Formula: hum\_avg ~ total\_biomass.g \* month\_name + (1 | site)  
Data: dat  
  
 AIC BIC logLik deviance df.resid   
 -749.4 -718.7 384.7 -769.4 150   
  
Random effects:  
  
Conditional model:  
 Groups Name Variance Std.Dev.  
 site (Intercept) 0.0752 0.2742   
Number of obs: 160, groups: site, 4  
  
Overdispersion parameter for beta family (): 260   
  
Conditional model:  
 Estimate Std. Error z value Pr(>|z|)  
(Intercept) 1.924e+00 1.454e-01 13.226 < 2e-16  
total\_biomass.g 5.863e-04 2.967e-04 1.976 0.0481  
month\_nameLate August -5.127e-02 6.773e-02 -0.757 0.4491  
month\_nameSeptember -1.005e-01 6.728e-02 -1.494 0.1351  
month\_nameOctober -3.885e-01 6.398e-02 -6.073 1.26e-09  
total\_biomass.g:month\_nameLate August 1.563e-04 4.167e-04 0.375 0.7076  
total\_biomass.g:month\_nameSeptember 2.314e-04 4.149e-04 0.558 0.5771  
total\_biomass.g:month\_nameOctober 4.873e-05 3.911e-04 0.125 0.9008  
   
(Intercept) \*\*\*  
total\_biomass.g \*   
month\_nameLate August   
month\_nameSeptember   
month\_nameOctober \*\*\*  
total\_biomass.g:month\_nameLate August   
total\_biomass.g:month\_nameSeptember   
total\_biomass.g:month\_nameOctober   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Table S3.** Statistical model of disease severity (proportion leaf area without green) on *Microstegium* in control treatment plots in September.

Family: beta ( logit )  
Formula: plant\_severity\_adjusted ~ hum\_avg + (1 | site/plot)  
Data: sep\_mv\_water\_dat  
  
 AIC BIC logLik deviance df.resid   
 -79.2 -68.7 44.6 -89.2 55   
  
Random effects:  
  
Conditional model:  
 Groups Name Variance Std.Dev.   
 plot:site (Intercept) 1.527e-01 3.908e-01  
 site (Intercept) 5.959e-11 7.719e-06  
Number of obs: 60, groups: plot:site, 20; site, 2  
  
Overdispersion parameter for beta family (): 2.3   
  
Conditional model:  
 Estimate Std. Error z value Pr(>|z|)   
(Intercept) -29.261 4.508 -6.492 8.50e-11 \*\*\*  
hum\_avg 34.345 5.340 6.431 1.27e-10 \*\*\*  
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Table S4.** Statistical model of total *Microstegium* biomass.

Family: gaussian   
 Links: mu = identity; sigma = identity   
Formula: Mv\_biomass.g ~ (asym \* fung) \* (1 - exp(-exp(lrc) \* Mv\_density))   
 asym ~ fungicide + (1 | site)  
 fung ~ fungicide  
 lrc ~ fungicide  
 Data: mv\_dat (Number of observations: 32)   
Samples: 3 chains, each with iter = 6000; warmup = 1000; thin = 1;  
 total post-warmup samples = 15000  
  
Group-Level Effects:   
~site (Number of levels: 4)   
 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
sd(asym\_Intercept) 3.27 8.92 0.04 24.29 1.00 13534 8332  
  
Population-Level Effects:   
 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
asym\_Intercept 377.41 43.62 299.40 471.03 1.00 9422 8993  
asym\_fungicide 110.27 57.27 -4.06 220.77 1.00 9928 10045  
fung\_Intercept 1.00 0.00 1.00 1.00 1.00 15839 9233  
fung\_fungicide -0.12 0.00 -0.12 -0.12 1.00 16235 9287  
lrc\_Intercept -2.84 0.32 -3.50 -2.21 1.00 9082 9033  
lrc\_fungicide 0.05 0.38 -0.69 0.81 1.00 8973 9673  
  
Family Specific Parameters:   
 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
sigma 84.48 11.55 65.41 110.40 1.00 13607 10170  
  
Samples were drawn using sampling(NUTS). For each parameter, Bulk\_ESS  
and Tail\_ESS are effective sample size measures, and Rhat is the potential  
scale reduction factor on split chains (at convergence, Rhat = 1).

**Table S5.** Statistical model of total *Elymus* biomass.

Family: gaussian   
 Links: mu = identity; sigma = identity   
Formula: Ev\_biomass.g ~ (asym \* fung) \* (1 - exp(-exp(lrc) \* Ev\_density))   
 asym ~ fungicide + (1 | site)  
 fung ~ fungicide  
 lrc ~ fungicide  
 Data: ev\_dat (Number of observations: 56)   
Samples: 3 chains, each with iter = 6000; warmup = 1000; thin = 1;  
 total post-warmup samples = 15000  
  
Group-Level Effects:   
~site (Number of levels: 4)   
 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
sd(asym\_Intercept) 8.09 10.83 0.07 35.05 1.00 2836 7366  
  
Population-Level Effects:   
 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
asym\_Intercept 58.60 8.41 42.70 75.55 1.00 8517 9973  
asym\_fungicide 1.84 8.56 -14.53 18.93 1.00 9565 10576  
fung\_Intercept 1.00 0.00 1.00 1.00 1.00 17342 8782  
fung\_fungicide 0.03 0.00 0.03 0.03 1.00 17463 8708  
lrc\_Intercept -2.46 0.34 -3.09 -1.75 1.00 6988 8556  
lrc\_fungicide 0.44 0.41 -0.33 1.30 1.00 7724 7655  
  
Family Specific Parameters:   
 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
sigma 25.39 2.72 20.68 31.32 1.00 6552 9152  
  
Samples were drawn using sampling(NUTS). For each parameter, Bulk\_ESS  
and Tail\_ESS are effective sample size measures, and Rhat is the potential  
scale reduction factor on split chains (at convergence, Rhat = 1).