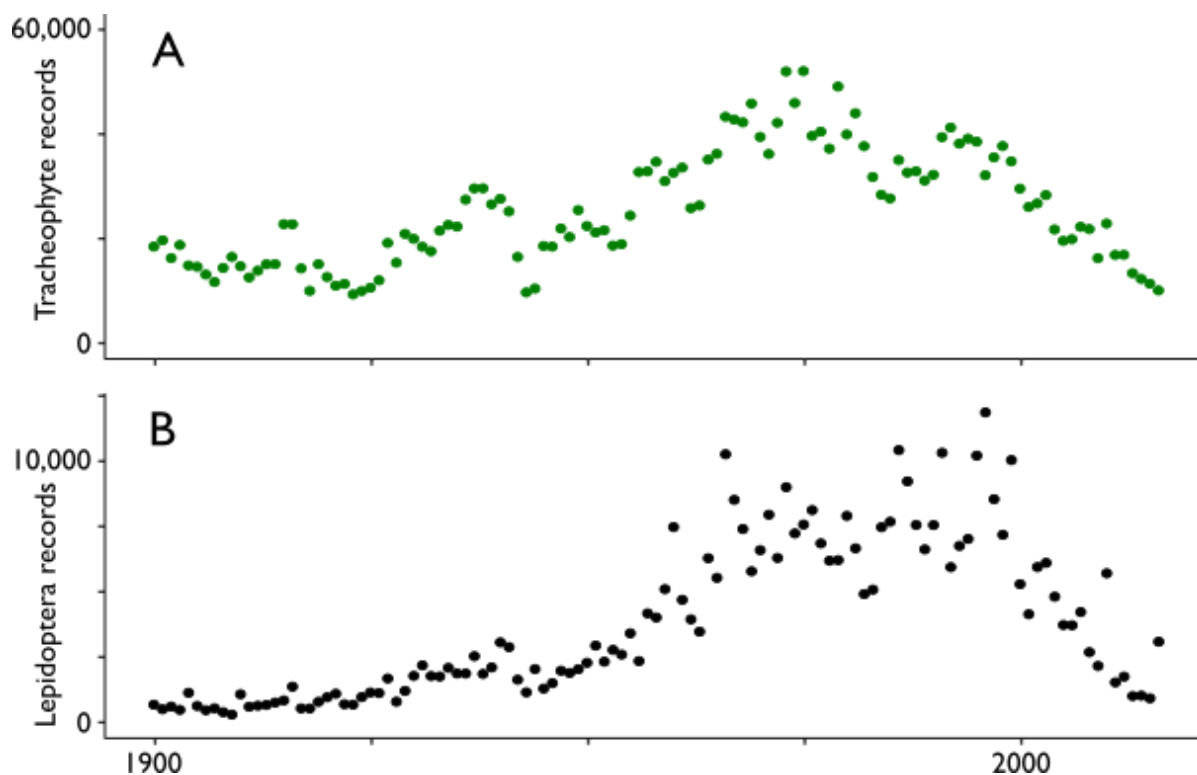**Supporting Information:**

Figure S1: Collection effort varies over time. A) shows the total number of cleaned tracheophyte records from eastern states for each year; B) shows the same for lepidoptera records.

Use of genetically modified crops in the United States

The main genetically modified (GM) crops in the United States are corn, soybeans, and cotton[1]. To estimate the total area of US cropland dedicated to GM crops, we gathered estimates of what proportion of each of these crops were genetically modified to express resistance to herbicide. Our estimates came from four sources: the USDA-NASS report *Acreage*[2] for the period 2000-2016; Fernandez-Cornejo and McBride[3] for cotton and soybeans for the period 1996-1999; Fernandez-Cornejo and McBride[4] for corn 1996-1997; the USDA-NASS report *Crop Production*[5] for corn 1998-1999. We multiplied these to the total area planted for each of these three crops[2] to estimate the total acreage planted with

GM crops, which we compared both to the total acreage planted for corn, soybeans, and cotton, and to the total acreage planted for all crops[2].

The prevalence of genetically modified herbicide resistant crops increased steadily since their introduction in 1996 as shown in Figure S2.
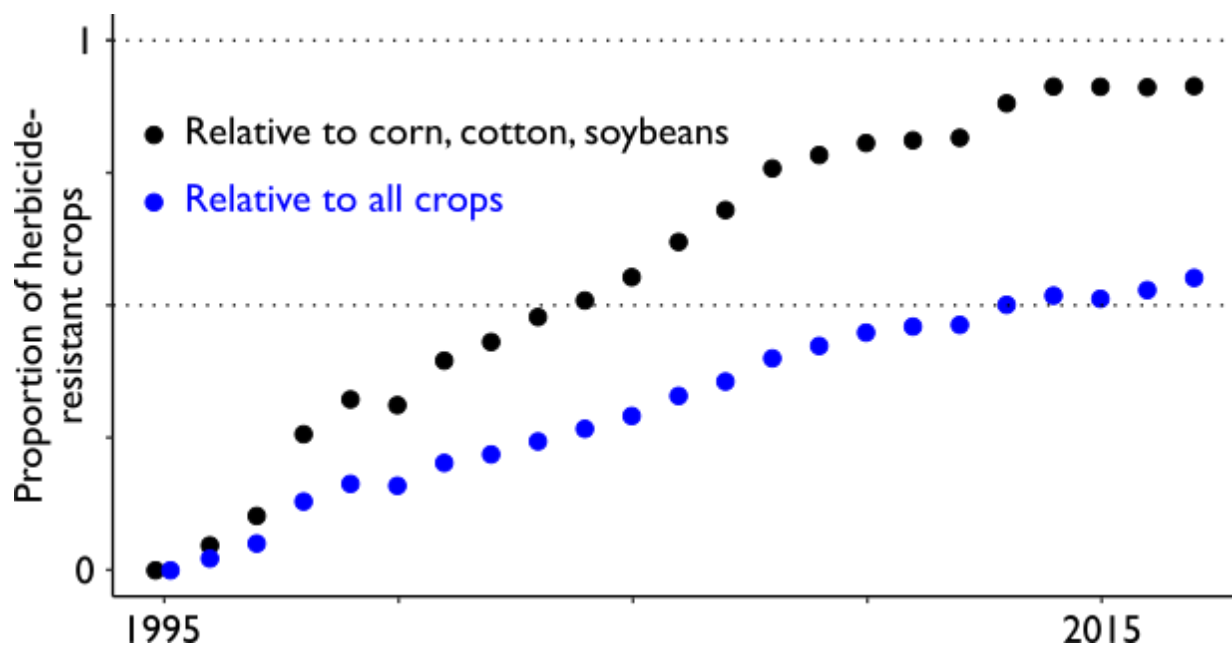

Figure S2: Increase in herbicide-resistant (HR) GM crops in the United States. HR crops were introduced in 1996. Each point shows the proportion of HR GM acreage of corn, cotton, and soybeans as a proportion of all corn, cotton and soybeans acreage (black points), and as a proportion of all crops (blue points). Half of all corn, cotton, and soybeans were HR by 2004; half of all crops by 2013.

Robustness of monarch and milkweed trends

For some years, particularly in the early 1900s, the monarch and milkweed trends displayed in Figure 1 are based on a relatively small number of records. For instance, no monarchs at all were collected in 10 of the years before 1930 (Figure 1). Therefore, we tested whether the trends shown in Figure 1 were artefacts arising from small sample sizes in some years, or if they were robust to some degree of noise added to the underlying data.

We added noise to our data sets in two different ways. In the first, we randomly selected a single year and data source (GBIF, CMH, OVFW, or MBA for milkweeds; always

SCAN, the only data source, for monarchs). We then made a large change to the number of

monarchs or milkweeds records given in that year and data source, changing it by 50% of

the number of records or by 20 records, whichever was greater. We randomly decided

whether that number of records was either added or subtracted. If the new number of

monarch or milkweed records was less than 0, it was set to 0 instead. If the new number of

monarch or milkweed records was greater than the total number of all lepidoptera or

vascular plant records for that year and data source, then the number of monarch or

milkweed records was set equal to the total number of all lepidoptera or vascular plant

records (i.e., a relative abundance of 1 for that data source and year). If this procedure

resulted in the data set being unchanged (e.g., if we attempted to subtract records from an

entry with 0 records), then we randomly chose a different entry and manipulation instead.

We then removed outliers and plotted these data using the same protocol as for the original

data set. This procedure was repeated 1000 times, beginning from the original data set

each time.

In the second perturbation, we made a small change to every year and data source.

For each year and data source, we changed the number of monarch or milkweed records by

10% or 2 records, whichever was greater, randomly adding or subtracting this number.

The number of monarch or milkweed records was not allowed to go below 0 or above the

total number of lepidoptera or vascular plant records (respectively) for that year and data

source. Outliers were removed, and the perturbed data plotted, with 1000 replicates.

In both cases, we also calculated the point at which the midcentury decline in

monarchs or milkweed began. We calculated this as the maximum point on the smoothed

curve of the mean; if the curve included multiple local maxima, we chose the one closest to

the maximum value of the original curve (1946 for milkweeds, 1956 for monarchs). Our
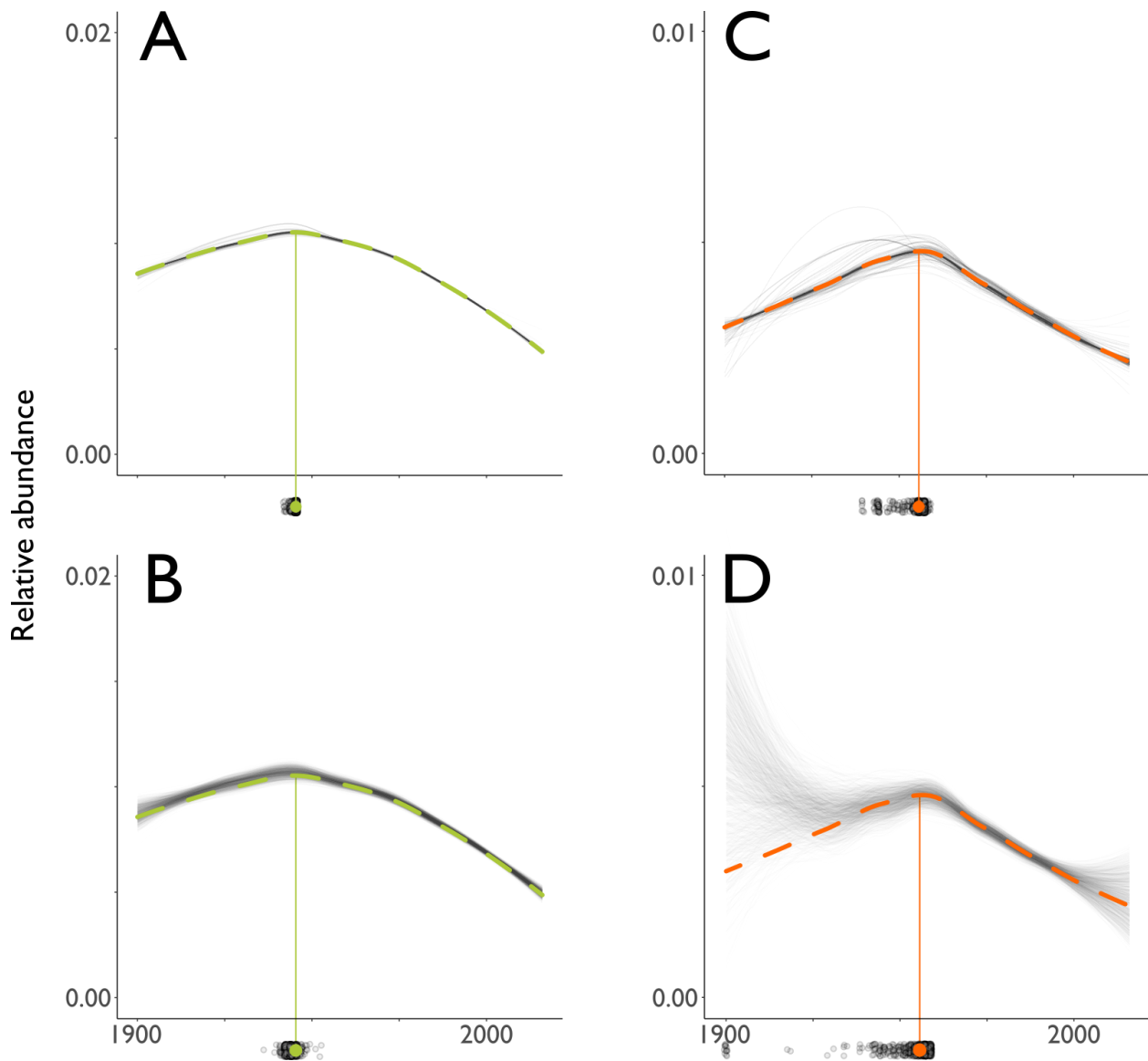
results are shown in Figure S3.

Figure S3: Monarch and milkweed trends are generally robust to the addition of noise. Panels A and B show trends for milkweed, C and D show trends for monarchs. In A and C, a large amount of noise was added to the records for a single year; in B and C, a smaller amount of noise was added to the records for every year. Each trend line in gray represents one of 1000 replicates; the trend line in green or orange represents the original trend for milkweeds and monarchs, respectively. Shown below each graph is the point at which monarch or milkweed decline begins, in gray for each replicate, or in green or orange for the original data. The gray circles have been jittered to improve readability.

As seen above, adding noise to the milkweed data set did not change the overall

trend, with all replicates showing an early-twentieth-century increase followed by a steady

decline. The milkweed decline began slightly earlier in some of the noise-added data sets, but seldom by more than two or three years. For the monarch data set, changing the number of records for a single year by a large amount does not have a strong effect on the overall trend in almost all cases: we still observe the same rise in the early twentieth century and fall in the later twentieth century. Although most of the noise-added data sets begin the decline around 1956, there is more scattering, with some declines beginning a couple of years later, and a handful beginning a decade or more earlier.

When adding a smaller amount of noise to every year, we observed that the monarch data set showed considerable variation in the trend from 1900-1930, which is not surprising considering the relatively small absolute number of monarch records from this period. Most of the trend lines for our 1000 noise-added data sets lie above the trend line for the original data set. This is because many of the years during this period had zero monarch records; since we did not allow the added noise to reduce any records below zero, the noise could only increase the monarch abundance for those years (or leave it unchanged, at zero). Despite the variation, most of the trend lines still showed an increase at some point in the early 1900s, although as with the single-year-noise replicates, the year at which monarch declines began varied. For the most part, we saw declines begin within a year or two of 1956, but a few of the noise-added data sets showed declines that began in the 1930s or 1940s, or even in 1900. There is also a smaller amount of variation in the replicates after 2000. Relatively few records of both monarchs and all lepidoptera have been digitized from this period (Figure S1), possibly because of a decline in collecting or simply because more recently collected specimens have had less time to be digitized. As with the beginning of the trend, in the majority of the cases, the noise-added data sets

showed an increase in monarch abundance after 2000, because records already at zero could not be reduced below zero.

The small number of monarch records from the early twentieth and twenty-first century means that there is some room for change in these trends as more records are digitized in the future. However, the entire trend for milkweeds, and the bulk of the trend for monarchs, including an increase after about 1930 and a later decline, is robust to noise in the underlying data set.

Abundance trends in other plant species from 1900-2016

To confirm the sensitivity of this analysis to real changes in population size, we did a similar procedure for several species with ongoing invasions of the United States during the time period of this study: garlic mustard, *Alliaria petiolata*[6]; purple loosestrife, *Lythrum salicaria*[7]; Japanese stiltgrass, *Microstegium vimineum*[8]; and kudzu, *Pueraria montana*[9]. *P. montana* is a synonym with *P. lobata*, and some data sets had records for both species names; in this case, we combined *P. lobata* and *P. montana* records. For each invasive species, we compared the total number of records for that species to the total number of tracheophyte records collected within that species' range. Species' ranges were calculated as described for *Asclepias* in the main text.

When visualizing the trends for individual species, we removed some years which were substantial outliers, i.e., falling greater than three standard deviations away from the mean annual abundance (*Alliaria petiolata*: 2002; *L. salicaria*: 2009, 2016; *M. vimineum*: 2001, 2004; *P. montana*: 1966, 1967).

In each case, we detected marked increases in abundance over the course of the twentieth century for these plants known to be invasive in the United States over that period (Figure S4).
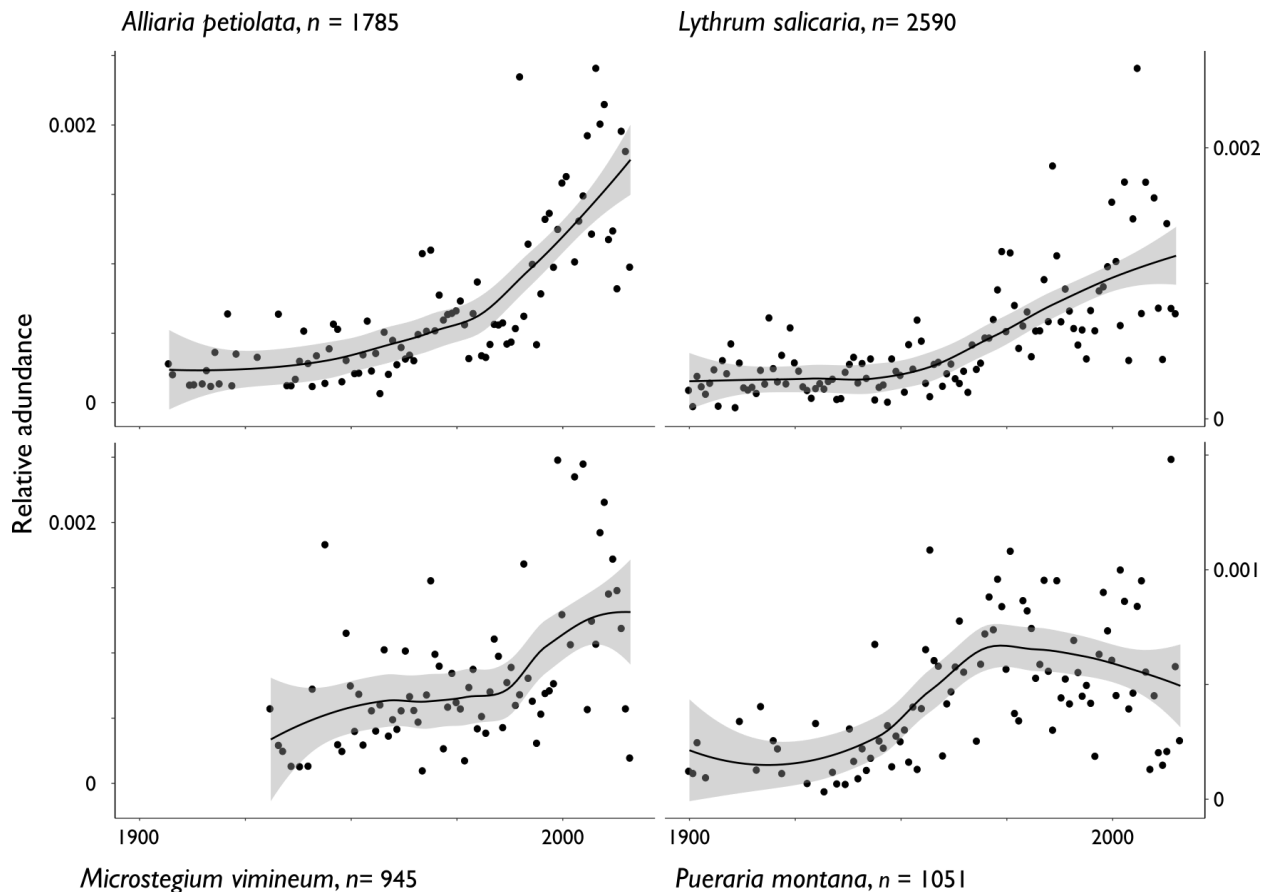

Figure S4: Invasions of the continental United States are apparent from museum specimens. The total number of specimens collected is shown next to each species. Points indicate abundance for each year, lines and shading indicate smoothed mean and 95% confidence intervals. Smoothing was done using the Loess smoothing method implemented in ggplot2[10], with the default smoothing span.

Breaking down abundance trends by land cover category

For each record, we used the associated latitude and longitude to estimate the kind of landscape upon which that specimen was collected. To do this, we consulted the USDA National Agricultural Statistics Service Cropland Data Layer[11]. These data provide estimates of land cover for the continental United States since 2008. We used these data to

categorize specimens as being collected from one of the following categories: developed land (Cropland Data Layer categories 82, 121-124), crop land (CDL categories 1-60, 66-77, 204-254), natural land (CDL categories 63-65, 87, 88, 112, 131-152, 190, 195), grassland (CDL categories 61, 62, 171, 176, 181; this includes both agricultural grasslands such as fallow fields and non-agricultural grasslands), or water (CDL categories 83 and 111). Some points changed cover category over the period since 2008. If land cover information was available for the year in which a specimen was collected, we assigned that specimen that cover category. Otherwise, if one cover category was found at that point during more years than any other cover category, we assigned that specimen that plurality cover category. If there was no plurality cover category, we did not assign a cover category.

Since land cover data only goes back to 2008, these assignments should be viewed as preliminary, as many specimen collection sites no doubt changed land cover between when that specimen was collected and 2008. For instance, some specimens categorized as being collected from "developed" land were likely collected from pasture or agricultural land which has since urbanized.

Shorter-term trends in milkweed decline appear to vary by land cover category; e.g., declines in crop fields land may be much steeper than declines in non-agricultural land, like roadsides[12]. We investigated whether this was the case for our long-term trends.

To calculate abundance on each land cover category, we compared the number of *Asclepias* specimens assigned to that category to the total number of specimens (of all categories) collected in that year, as above. We did not do this for *D. plexippus*, for which there were not enough records to subdivide. To account for the fact that the number of

specimens assigned to a land cover category changes over time (as more specimens are associated with geographic coordinates), we divided this abundance by the proportion of *Asclepias* specimens collected that year which were assigned a land cover category. Finally, we averaged each data source (i.e., GBIF, WIS, etc) separately, weighting them the same as described in the main text methods section, "Abundance trends in the genus Asclepias from 1900-2016". When visualizing the trends for each land cover category, we removed some years which were substantial outliers, i.e., falling greater than three standard deviations away from the mean annual abundance (records from crops: 1971, 1975, 1983; developed land: 1900; grassland: 1929, 1967; natural land: 1939).

We found declines in milkweed abundance in all four categories of land cover (Figure S5). In the case of cropland, grassland, and natural land, we saw an increase in the early twentieth century that predated the decline in the second half of the century. In the case of developed land, we saw a steady decline, although this could be because many sites that are currently developed were in fact in another land cover category before urbanization. Thus, the count of records from developed land is likely inflated in the early part of the twentieth century.
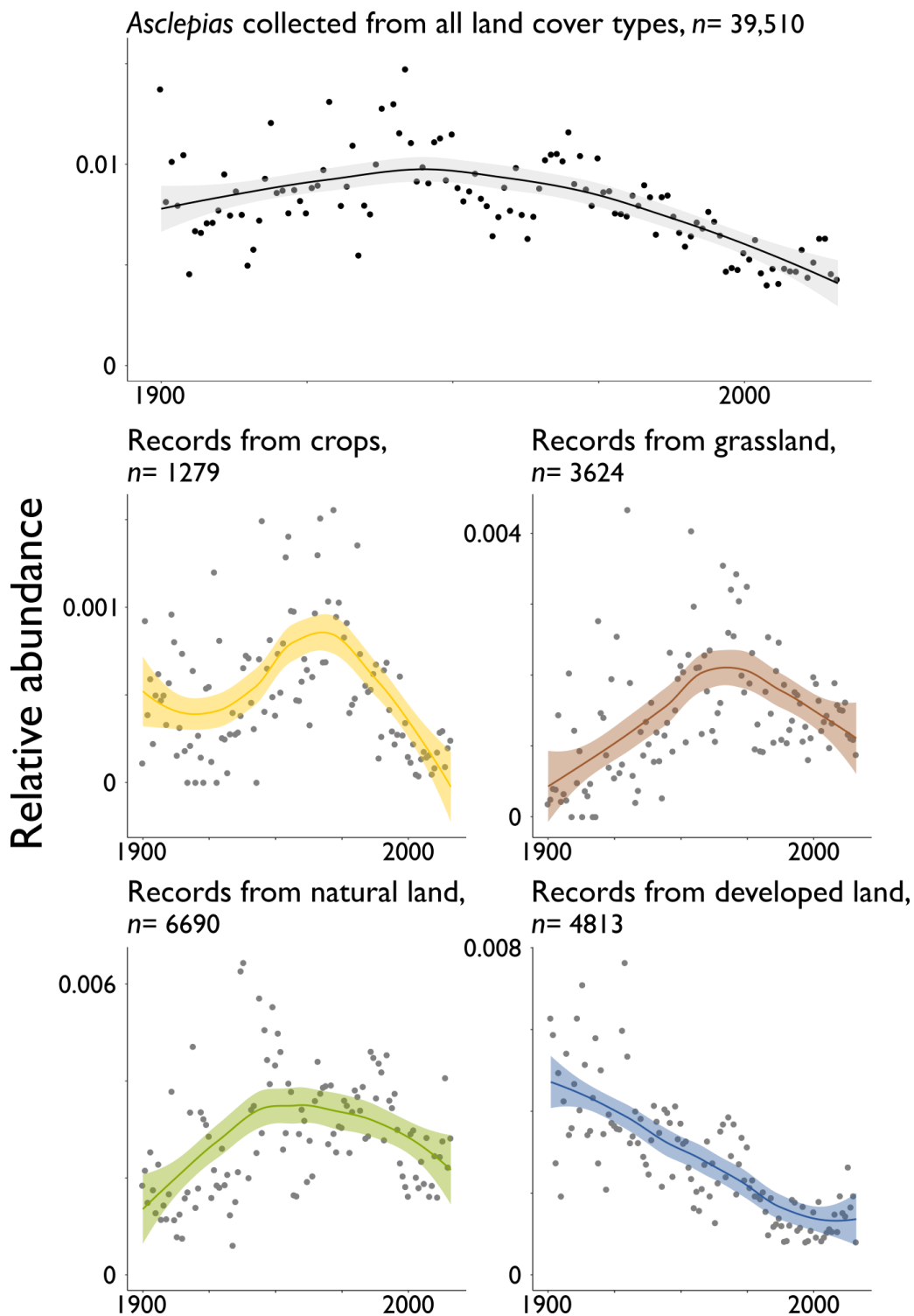
Figure S5: Milkweed decline over the twentieth century is seen across land use types. The total number of specimens collected on that land cover type is shown above each graph. Points indicate abundance for each year, lines and shading indicate smoothed mean and 95% confidence intervals. Smoothing was done using the Loess smoothing method implemented in ggplot2[10], with the default smoothing span. Because land cover was not determined for all records, the abundances for each land cover type do not add up to the abundance for the genus as a whole.

Abundance trends for individual Asclepias *species from 1900-2016*

We examined species level trends for *A. incarnata*, *A. tuberosa*, *A. verticillata*, *A. syriaca*, *A. viridiflora*, *A. speciosa*, *A. amplexicaulis*, *A. viridis*, *A. quadrifolia*, and *A. asperula*. Records of these 10 species combined made up 63% of the total data set. For each species, we calculated its range and abundance as described in the main text for the *Asclepias* genus. When visualizing the trends for individual species, we removed some years which were substantial outliers, i.e., falling greater than three standard deviations away from the mean annual abundance (*A. amplexicaulis*: 1903, 1909, 1988; *A. asperula*: 1936, 1940; *A. quadrifolia*: 1924; *A. speciosa*: 1943, 1970; *A. tuberosa*: 1937; *A. verticillata*, 1921; *A. viridiflora*; 1904; *A. viridis*, 1904, 1918, 1994). These trends are visualized in Figure 2. We also divided the *Asclepias* records into 10-year bins, and calculated the relative proportion of each species over time (we did not identify or remove outliers in this part of the analysis). As noted in the main text, the relatively slow declines in these two species mean that these species now account for a greater proportion of the total milkweed records than they did at the beginning of our study period. This change in the makeup of the community of milkweeds is visualized in Figure S6.
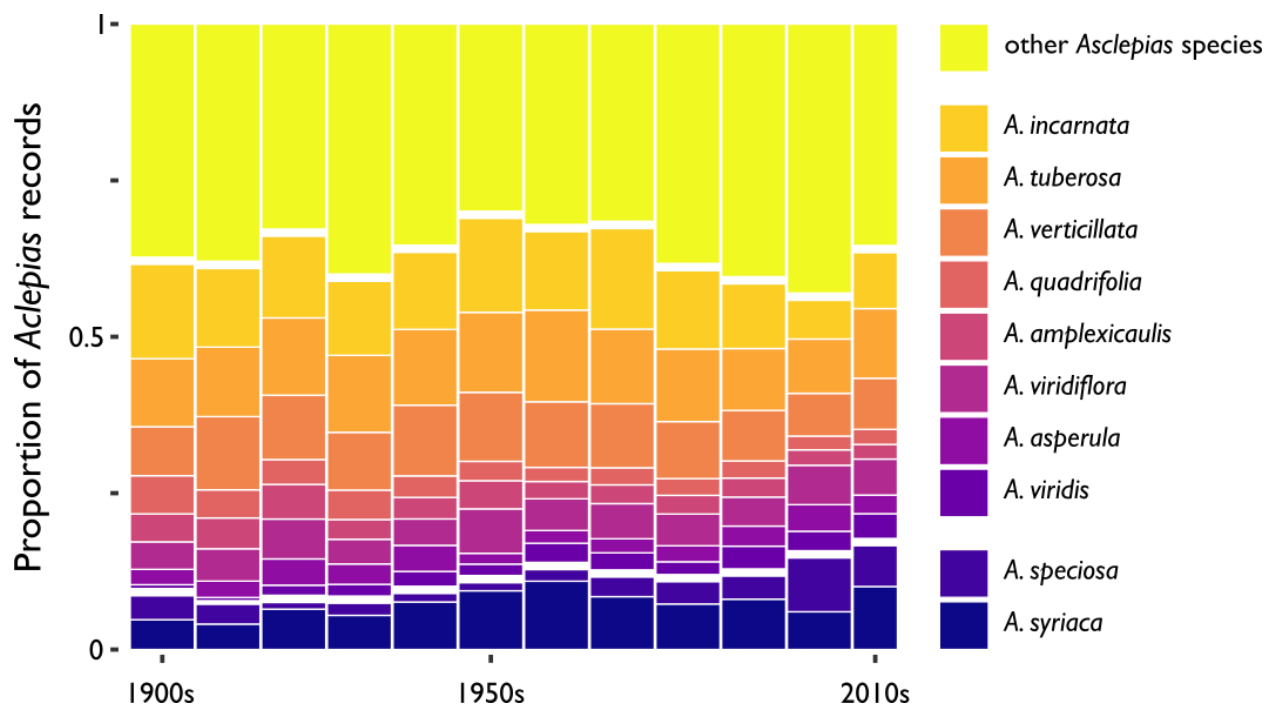
Figure S6: Changes in composition of *Asclepias* records over time. *A. syriaca* and *A. speciosa* make up a greater proportion of *Asclepias* records in the past few decades than early in the twentieth century.

Comparison of our trends from museum specimens to other data sets

Using Pearson's correlation coefficient, we compared the abundance of milkweeds and monarchs from our museum data both to each other, and also to estimates of monarch and milkweed abundance from other datasets. We examined three other data sets: estimates of the size of the monarch overwintering population from 1994-2014[13], Monarch Larva Monitoring Project (MLMP) estimates of immature (egg stage) monarch population sizes in the summer breeding grounds from 1999-2014[14], and North American Butterfly Association (NABA) estimates of adult monarch population sizes in the summer breeding grounds from 1993-2014[15]. For the latter two data sets, we also employed the corrections for changes in land cover described by Pleasants *et al.*[14].

A relatively small number of states contribute disproportionately to the eastern migratory population[16]. Therefore, we also calculated milkweed abundance in these states

alone, using the methods described above, but including only records from Texas, Oklahoma, Missouri, Illinois, Indiana, and Ohio. We compared these estimates of milkweed abundance from the core area to the size of the overwintering population.

We found no correlation between our estimate of milkweed abundance with our estimate of monarch abundance. However, there was substantial year-to-year variation, which may have obscured the overall trend. To test this hypothesis, we grouped monarch and milkweed abundance into five-year bins, taking the median abundance for each bin, and measured the correlation between these two data sets.

There is little correlation between our *D. plexippus* abundance and NABA citizen-science counts of adult butterflies (r = 0.11, *p* = 0.6, Figure S7A). However, Pleasants *et al.*[14] point out that these metrics may be biased because few citizen-science records are made from agricultural land, and they provide corrected NABA counts for the period 1999-2014. If we use these corrected counts, there is a much stronger (while not "statistically significant") correlation between *D. plexippus* abundance and NABA counts (r = 0.48, *p* = 0.06, Figure S7B).

There was a strong correlation between our *D. plexippus* abundance and MLMP citizen-science counts of monarch eggs over the period 1999-2014, whether (r = 0.65, *p* < 0.01, Figure S7C) or not (r = 0.66, *p* < 0.01) we used the collection-bias corrections of Pleasants *et al.*[14].

There was a reasonable (if not significant) correlation between our *D. plexippus* abundance and estimates of monarch population sizes during the following winter over the period 1994-2014 (r = 0.40, *p* = 0.07, Figure S7D).

Our estimates of *A. syriaca* abundance had a slightly negative correlation with the estimates of *A. syriaca* abundance of Pleasants *et al.*[14] over the period 1999-2014 (r = -0.35, p = 0.2, Figure S7E). However, Pleasants *et al.*[14] estimated *A. syriaca* abundances from Iowa data alone, while we include *A. syriaca* from across its range in the continental United States. We did not have enough *A. syriaca* records from Iowa during the 1999-2014 period (n = 3) to compare our results more directly.

Overall, previously published data from purpose-built citizen science initiatives predict the size of monarch overwintering populations better than do our data: corrected NABA estimates vs overwintering population size, r = 0.74, p < 0.01; MLMP estimates vs overwintering population size, r = 0.55, p < 0.05. However, our data are reasonable predictive, supporting their use for the period before 1993 when no other published data sets on monarch or milkweed abundance are available.

We also tested whether our metrics of *Asclepias* spp. abundance predicted monarch abundance. Our milkweed abundance did not predict monarch abundance over the period 1900-2016 (r = 0.16, p = 0.08, Figure S7F). This was still the case when looked at over 5-year bins (r = 0.18, p = 0.4, Figure S7G). Additionally, we tested whether the lack of correlation between the two was due to a temporal mismatch between monarch and milkweed trends. We thus tested for a correlation between milkweed abundance and monarch abundance 10 years later, choosing 10 years as our temporal lag because this was the period between the beginning of the milkweed decline and the beginning of the monarch decline (as quantified by taking the maxima of the best fit splines shown in Figure 1). Adding this lag did not improve the correlation of these data sets (r = 0.08, p = 0.4).

Our milkweed abundance had some mild ability to predict the size of the monarch overwintering population the following winter from 1994-2014 (r = 0.34, *p* = 0.14, Figure S7H). However, the milkweed abundance metric includes many records from states that contribute relatively little to the monarch population[16]. Therefore, we subsequently calculated milkweed abundance in only those states that contribute the most to the monarch population. We found that milkweed abundance in these states does indeed predict the size of the subsequent overwintering population from 1994-2014 (r = 0.45, *p* < 0.05, Figure S7I), albeit not as well as did the purpose-collected data of Pleasants *et al.*[14] during the period 1999-2014 (r = 0.70, *p* < 0.01). Core state milkweed abundances did not improve our ability to predict museum-specimen based monarch abundances, either throughout the eastern United States (r = 0.08, *p* = 0.4) or in the core states specifically (r = 0.13, *p* = 0.2).

In general, our abundance metrics had some, if weak, power to predict other, previous measurements of monarch and milkweed abundance. This is likely a combination of error in our data set, error in others' data sets, and natural variability in monarch and milkweed populations across time and space.

Likewise, the weakness of the relationship between abundance of milkweed and monarchs is perhaps not surprising, as both data sets are relatively noisy at the year-to-year, and even 5-year-to-5-year level, particularly the abundance of *D. plexippus.* This is likely a combination of sampling error introduced by the method of examining museum collections with natural variation in insect population sizes, as all other metrics of monarch abundance have great amounts of year-to-year variation[15,17]. Furthermore, factors beyond milkweed abundance, particularly weather, are known to effect monarch population

sizes[18]. The effect of such other factors on long term trends in monarch population size certainly merits further investigation. However, when views on a decades-to-century time scale, the correspondence between milkweed and monarch abundance remains striking (Figure 1A).
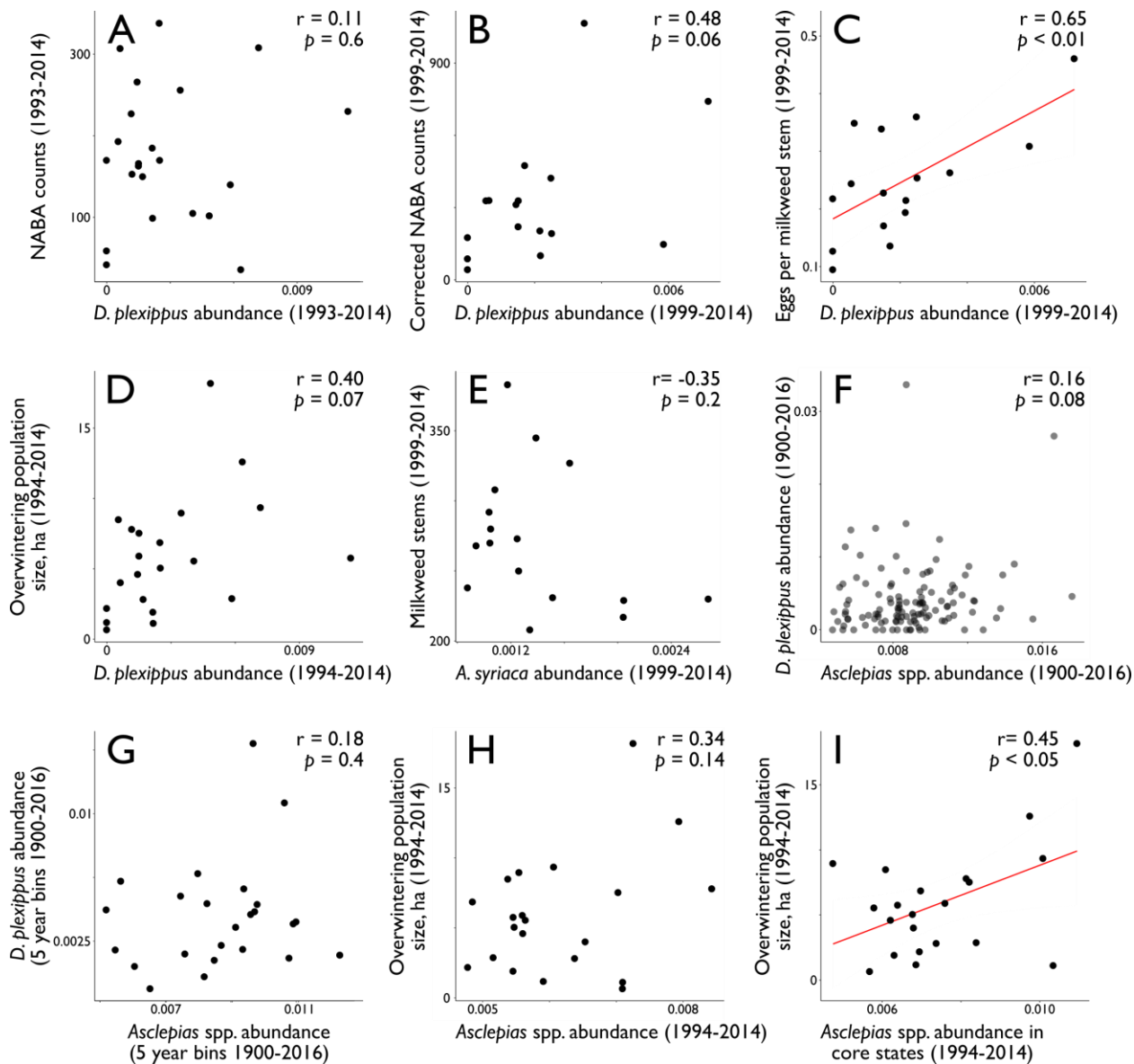

Figure S7: Correlations between various metrics of monarch and milkweed abundance.

Agricultural data

We gathered data on selected agricultural practices in the United States, namely, the

number of farms and other agricultural operations such as ranches and tree nurseries[19],

the total area of farmland[20], the amount of nitrogen and phosphorus fertilizers used[21,22],

and the amount of glyphosate herbicide used[23]. Nitrogen and phosphorus fertilizer use

were highly correlated with each other (Figure S8), and so we combined them into a single

variable by scaling both variables to have a mean of zero and a standard deviation of 1,

then adding the scaled variables to produce a metric of total nitrogen-plus-phosphorus

fertilizer used. The remaining variables were much less strongly correlated with each

other. The correlation coefficients between predictor variables and/or *A. syriaca*

abundance are shown in Table S1 (after binning by region and five year period as described

below).

Data on glyphosate use were only available at the national level; data on the other

three factors, however, were available at the state level. We divided the states into six

regions (Figure S9) with relatively homogenous agricultural practices, combining the data

for each state. We divided the *A. syriaca* and tracheophyte records gathered above by

region, then used these to calculate the relative abundance of *A. syriaca* within each region.

Since there was some degree of variation from year to year, we pooled the regional

data into five year bins. As the year-to-year data for *A. syriaca* contained several outlying

data points, we took the median value for *A. syriaca* abundance in each five year bin, as this

greatly lessened the ability of outlier data points to effect the model compared to year-to-

year data or calculating occurrence across the five year period (i.e., roughly a weighted

mean). Using the median rather than mean or single-year bins accordingly increased the

predictive power of the global model and increased our ability to distinguish different

models using AIC (Table S3). We averaged the agricultural data across the five year period

(or the two year period, in the case of the 2005-2006 bin). The agricultural data was then

standardized so that within each factor, the mean was zero and the standard deviation was

one.

The nationwide trends for each chosen agricultural variable are shown in Figure

S10. We then used state-by-state variation in these characteristics to divide the *A. syriaca*

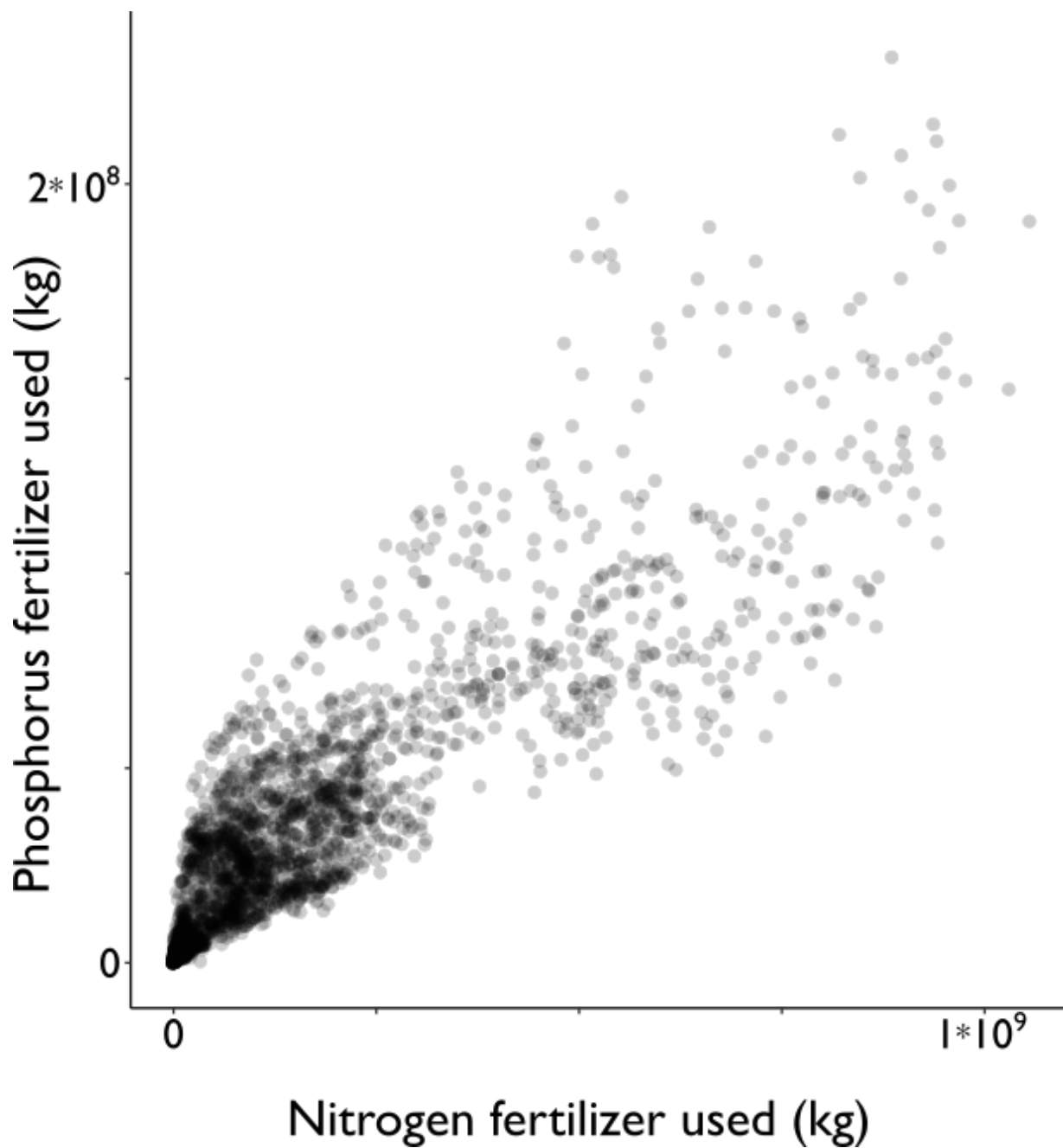range into six, relatively homogenous regions (Figure S11).

Figure S8: Nitrogen and phosphorus use are tightly correlated (r = 0.88, p << 0.001). Each point represents the fertilizer use for a single state (including all 48 states in the continental United States) in a single year from 1950-2006.
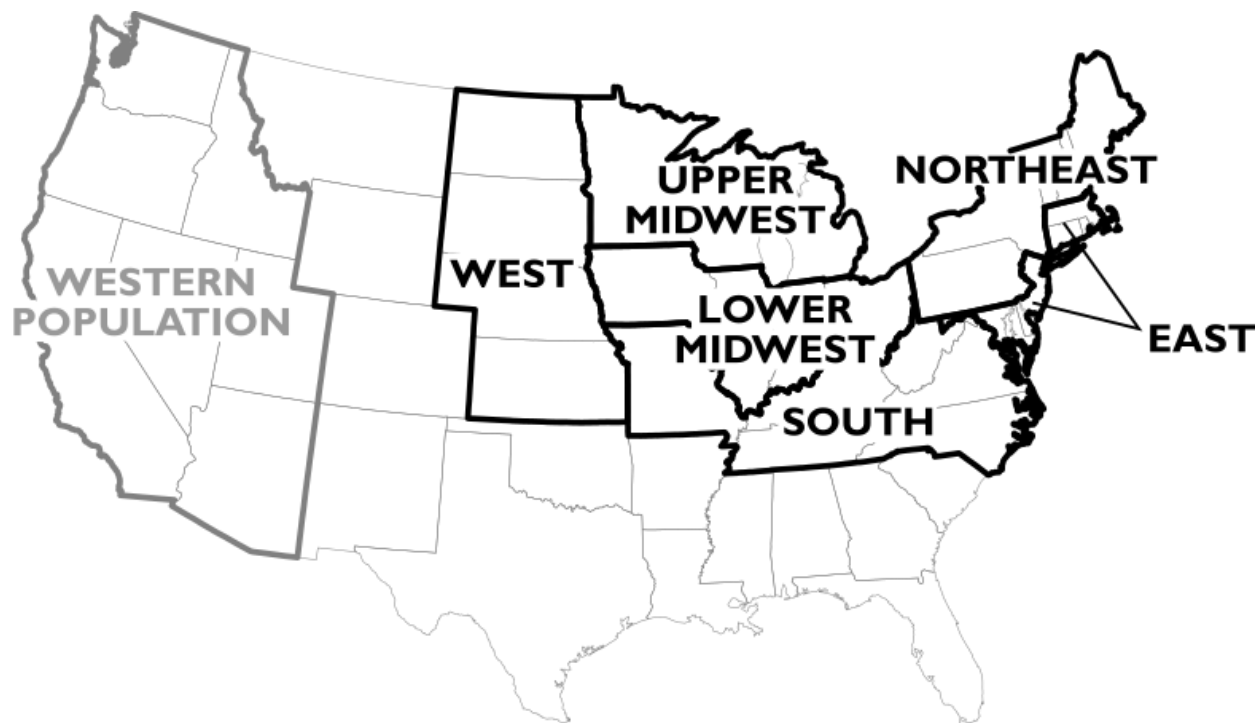
Figure S9: The six agricultural regions used in the *A. syriaca* model. The six regions are outlined in black. States home to the western population of *D. plexippus* are also indicated.
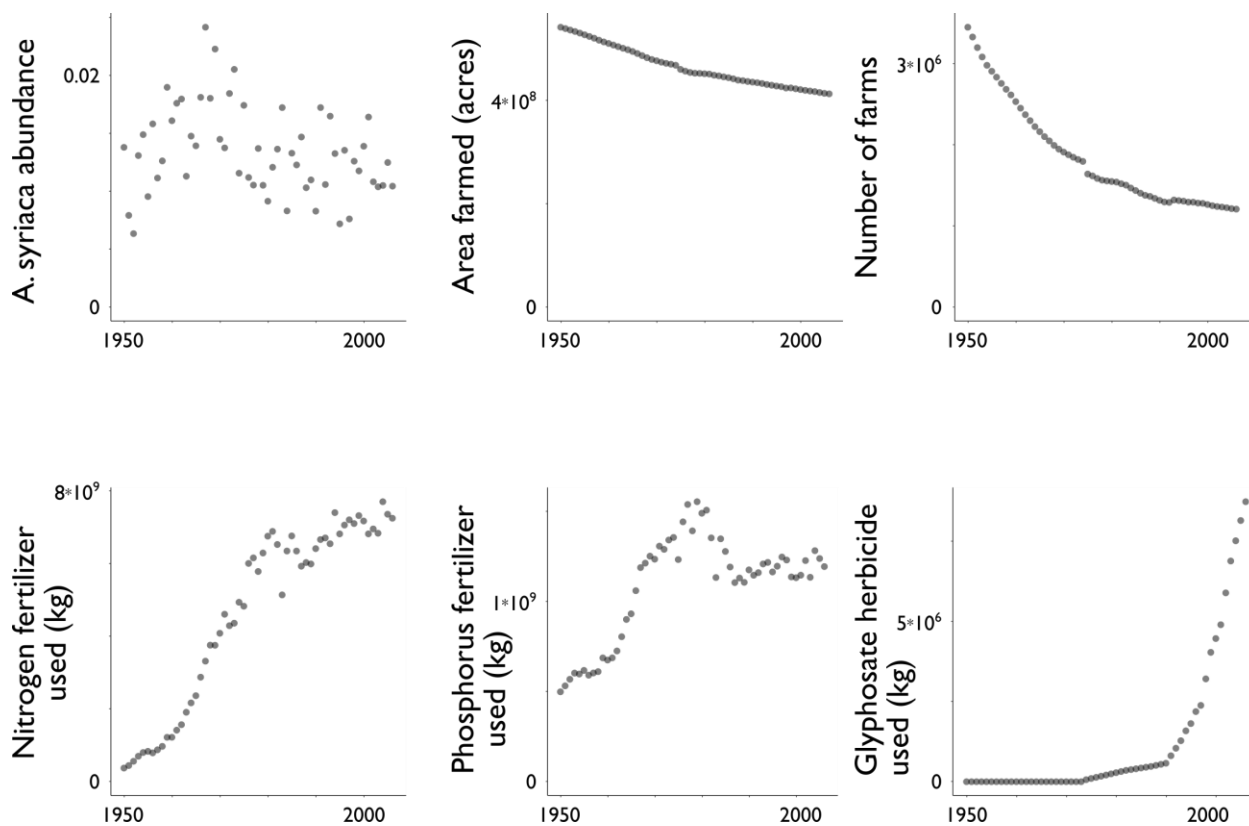
Figure S10: Nationwide trends for chosen agricultural variables. Each point shows the total for all states within the area of our model (see Figure S4) for a single year.
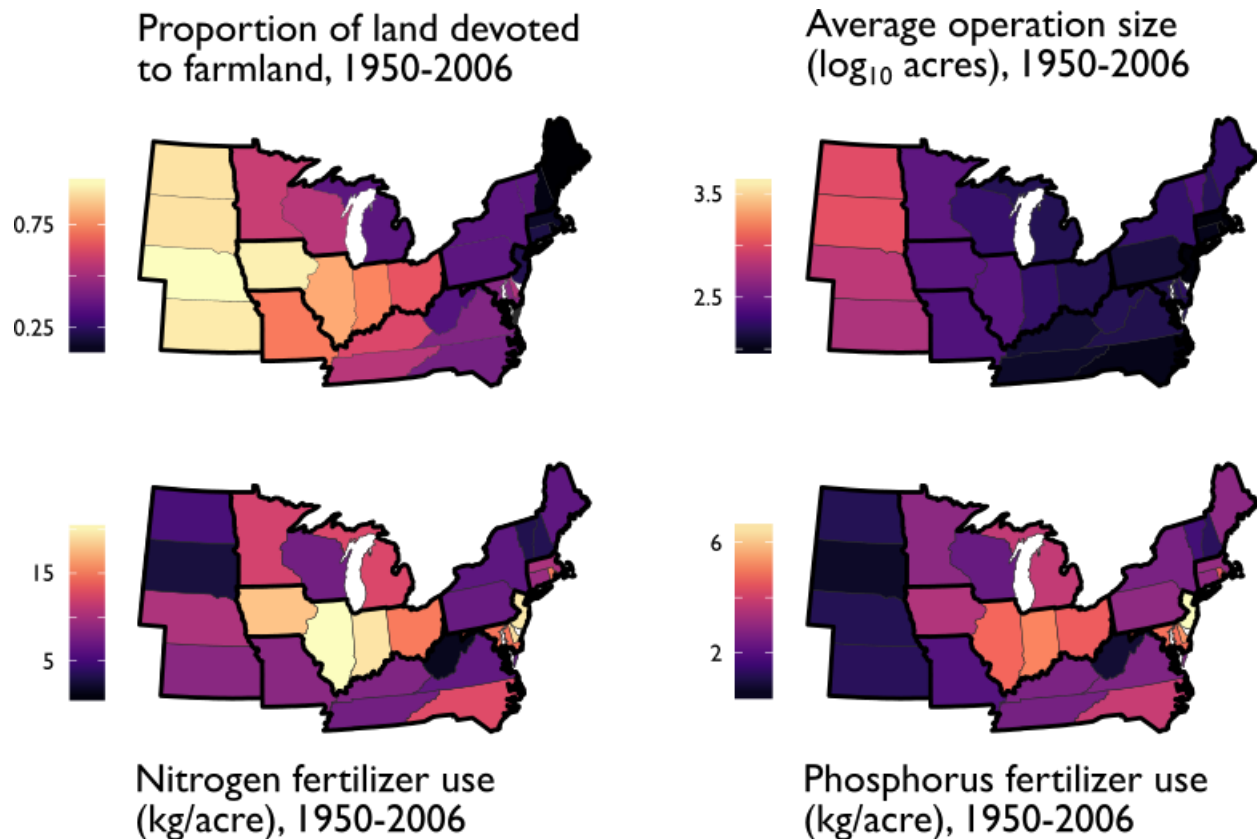
Figure S11: States were grouped into regions (thick black lines) with relatively homogenous agricultural practices.

Robustness of multimodel inference

As above, we tested whether the results of our multi-model inference were robust to some degree of noise added to the underlying data. We added noise to our data sets in two different ways. In the first, we randomly selected a single year, region (as shown in Figure S11) and data source (GBIF, CMH, OVFW, or MBA). We then made a large change to the number of common milkweed records given in that data source for that year and region, changing it by 50% of the number of records or by 20 records, whichever was greater. We randomly decided whether that number of records was either added or subtracted. If the new number of milkweed records was less than 0, it was set to 0 instead. If the new number of milkweed records was greater than the total number of all vascular plant

records for that year, region, and data source, then the number of milkweed records was set equal to the total number of all vascular plant records (i.e., a relative abundance of 1). If this procedure resulted in the data set being unchanged (e.g., if we attempted to subtract records from an entry with 0 records), then we randomly chose a different entry and manipulation instead. We then used this data set for multi-model inference using the same protocol as for the original data set. This procedure was repeated 1000 times, beginning from the original data set each time.

In the second perturbation, we made a small change to every year and data source. For each year and data source, we changed the number of common milkweed records by 10% or 2 records, whichever was greater, randomly adding or subtracting this number. The number of milkweed records was not allowed to go below 0 or above the total number of vascular plant records (respectively) for that year and data source. This data set was then used for multi-model inference, with 1000 replicates.

In both cases, we determined the average importance of each variable (i.e., the relative weight of the models containing that variable from among the selected models) across all 1000 replicates. Within each replicate, the effect (i.e., coefficient of that variable in the linear model) of each variable on *A. syriaca* abundance was averaged across all the retained models, weighting by the relative likelihood of each model. When a variable was not found in a model, it was considered to have an effect of zero. These estimates of effect size were then averaged across all 1000 replicates. Importances and estimates are shown in Table S2.

Making a large change to a single entry had very little effect on either the average importance or estimate of the effect of any of the four variables. Making small changes to

every entry had the effect of lessening the difference in importance among the variables:

number of farms and area farmed are now similarly important (found in 79% of all models,

by model weight), and have similar effect size estimates, while the importance of fertilizer

use and glyphosate use are raised, but still less than the other factors (found in less than

half of all models, by model weight), and with smaller effect size estimates, although the

gap between effect sizes has narrowed somewhat. These results suggest that our multi-

model inference procedure is robust to errors, even large errors, that affect single entries

in our data set, but if there is widespread error in these data sets, it may reduce our ability

to distinguish between the importance of various agricultural factors in predicting *A.*

syriaca abundance.

Table S1: Correlation of variables used in multi-model inference

	A. syriaca abundance	Glyphosate use	Fertilizer use	Area farmed
Number of farms	-0.37	-0.25	0.24	0.40
Area farmed	0.01	-0.08	0.48	
Fertilizer use	-0.08	0.19		
Glyphosate use	0.12			

Each cell shows the correlation coefficient between the values of each pair of predictor and/or response variables from multi-model inference. Each predictor variable was first scaled as described above. Individual data points for the correlations are values for multi-state regions over a five year period, as described above.

Table S2: Effects of noise on multi-model inference

	Importance: original data	Importance: with noise I	Importance: with noise II	Estimate: original data	Estimate: with noise I	Estimate: with noise II
Number of farms	1.00	0.995	0.79	-4.04	-4.02	-13.5
Area farmed	0.55	0.55	0.79	1.10	1.10	13.9
Fertilizer use	0.21	0.21	0.47	-0.09	-0.09	-2.90
Glyphosate use	0.19	0.19	0.38	0.04	0.04	1.53

"Importance" gives the relative weight of the models containing that variable, averaged across 1000 replicates. "Estimate" gives the mean effect of each agricultural variable. The estimate for each predictor variable is first averaged within each replicate across all selected models according to their model weight, then these values are averaged across 1000 replicates. All "estimates" are multiplied by 10^4 for readability. Two kinds of replicate additions of noise were performed. In Type I, we changed the number of *A. syriaca* records for a single region and five-year period by a large amount. In Type II, we changed the number of *A. syriaca* records by a small amount across all regions and five-year periods.

Table S3: Effects of alternative methods of calculating occurrence on model selection

ΔAIC of model:	1	2	3	4	5	6	Additional models	Pseudo-R^2
Median	0	0.38	1.93	2.36	2.65	2.68	0	0.18
Mean	0	0.30	1.03	0.80	3.44	-	7	0.16
Annual	1.02	1.92	0	2.53	3.91	3.99	7	0.06

We took three approaches to modelling *A. syriaca* occurrence, using the median milkweed occurrence in 5-year bins ("Median"), calculating occurrence using the combined records across each 5-year bin ("Mean"), or modelling the annual occurrences against the annual values for each agricultural variable. Presented here are the ΔAIC values for each of models 1-6 (corresponding to the model numbers given in Table 2), as well as the number of additional models within 4 ΔAIC units of the best model. We also present the marginal Pseudo-R^2 of the global model, which represents the variance explained by the fixed factors in a mixed model. Model 6 was not within 4 ΔAIC units of the best model in the "Mean" treatment.

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