

A widespread gap in U.S. Endangered Species Act implementation: Risk of genetic erosion within populations

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Impact statement: Many populations of species assessed under the Endangered Species Act are too small to maintain genetic diversity, compromising recovery.

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Abstract:

Loss of genetic diversity reduces fitness and population viability, impeding conservation efforts. Incorporation of genetic diversity into conservation assessments is therefore critical; however these data are rarely included. Here, we use genetic diversity indicators to evaluate the genetic health of 161 species assessed for classification under the U.S. Endangered Species Act (ESA). We found that while most populations are being maintained across species' ranges, many are likely at risk of genetic erosion. Additionally, ESA classification status was not correlated with the genetic indicators, suggesting that genetic health is not being fully considered in extinction risk assessments and/or decision-making. Fortunately, we found that data were widely available to calculate the genetic indicators. Inclusion of affordable and intuitive approaches like genetic indicators in ESA implementation can help ensure protection prior to irreversible losses of genetic diversity. This, in turn, can increase the success of recovery actions, better ensuring the ESA goal of safeguarding biodiversity.

1.1 Introduction

Genetic processes within species impact individual fitness and population viability, yet genetic health is rarely integrated into extinction risk assessments due to limited data availability and the perception that genetic data are too complex to include (Pierson et al. 2016; Neaves et al. 2025; Bail et al. 2026). Here, we define genetic health as maintenance of evolutionary processes that confer population and species-level viability. These processes include high within- and among-population genetic diversity, large effective population sizes, the maintenance of historical patterns of gene flow, and maintaining the distribution of populations across a species' historical range (Kardos et al. 2021). Threats to genetic health include erosion of genetic variation due to genetic drift in small populations, mating among close relatives causing reduced fitness (i.e., inbreeding depression), disrupted connectivity, maladaptation, and extirpation of locally adapted populations. Thus, loss of genome-wide genetic diversity through genetic erosion is driven by diverse mechanisms that reduce the additive genetic variation needed for populations to show an evolutionary response to selection (van Oosterhout et al. 2026). These evolutionary processes have significant implications for conservation and management because low genetic diversity, small population sizes, and population extirpations negatively affect the successful recovery of declining species (Wilcove et al. 1993; Neel et al. 2012; Eberhard et al. 2022).

Inclusion of these genetic concerns in biodiversity assessments was recently improved with the December 2022 adoption of indicators of intraspecific genetic diversity into the Convention on Biological Diversity (CBD) Global Biodiversity Framework – the world's roadmap to halting biodiversity loss by 2030 (Hoban et al. 2023). This policy milestone in genetic diversity conservation reflects a growing acknowledgement that evaluation of genetic health in wild species is critical to biodiversity monitoring and management, even though genetic data are lacking for the majority of species (Torres-Florez et al. 2018; Lawrence et al. 2019; Paz-Vinas et al. 2025). Genetic indicators are useful even in the absence of genetic data because they reflect two major drivers of genetic health: population size, which governs the extent of genetic drift and inbreeding depression, and the maintenance of populations across a species' range, which conserves species-wide genetic diversity and evolutionary potential. Because the evaluation of these processes does not necessarily require DNA-based assessments, genetic indicators can be evaluated rapidly and affordably in many species (Mastretta-Yanes et al. 2024a).

The “proportion of populations with effective population size (N_e) greater than 500” indicator (hereafter the “Ne500 indicator”) assesses if populations are large enough to maintain genetic diversity and evolutionary potential over the long term. It is based on established population genetics theory and empirical data demonstrating that genetic erosion within populations accelerates when the population's N_e is less than 500 (Gilpin and Soulé 1986; Jamieson & Allendorf 2012; Hoban et al. 2020; Willi et al. 2022). By contrast, when N_e is greater than 500, populations show very slow rates of loss of genetic diversity for fitness traits, where losses of genetic diversity to genetic drift are balanced by mutation and the efficiency of selection operating on additive genetic variance (Franklin 1980; Frankham et al. 2014). Since low levels of gene flow among populations can increase genetic diversity and help maintain evolutionary potential, the Ne500 indicator should be evaluated at a metapopulation scale, though the term “population” is used here (Hoban et al. 2021; Mastretta-Yanes et al. 2024b; Waples 2025). The Ne500 indicator can be measured using an estimate of contemporary N_e

(using genetic or demographic methods) or using the population's census size of mature individuals (N_c) and an N_e/N_c ratio to convert N_c to N_e . The N_e/N_c ratio varies across taxonomic groups and even by population, with variability driven by variance in offspring number, breeding strategy, and other life history traits (Waples 2024a). The selection of ratio to apply will depend on data availability and the goals of the assessment, and could range from a species (or population) specific ratio, a taxonomic group average, or a taxon-wide average of 0.1 (Frankham 2021; Hoban et al. 2021). We note that there are some species and populations where application of an N_e/N_c ratio is inappropriate or needs to be carefully considered because census sizes do not reflect underlying genetic processes. These include non-diploid species, clonally reproducing species, and populations known to have undergone a severe bottleneck followed by population expansion (see Frankham 2021; Mastretta-Yanes et al. 2024b). Finally, some have argued that N_e greater than 1,000 is needed to maintain long-term evolutionary potential (Frankham et al. 2014); data collection and analysis could easily be modified to accommodate this change if needed for a given assessment.

The second genetic indicator, the “proportion of populations maintained” (hereafter the “PM indicator”), is based on the principle that environmental heterogeneity and distance drive adaptive divergence among populations, such that genetic composition varies spatially (Wang & Bradburd 2014; Forester et al. 2022a). Thus, extirpation of populations results in genetic erosion at a population scale and a loss of evolutionary potential that cannot be easily recovered. As with the Ne500 indicator, the metapopulation scale is most appropriate for evaluation of the PM indicator, since it is focused on identifying locally adapted populations (Hoban et al. 2024a; Mastretta-Yanes et al. 2024a). The PM indicator is evaluated using estimates of species' historical distributions and pragmatic approaches for delineating populations (reviewed in Mastretta-Yanes et al. 2024b). Historical distributions will ideally reflect the species range prior to anthropogenically mediated fragmentation, though the baseline will by necessity be based on the available data. Population delineation can use a variety of approaches or combinations of available data, including geographic boundaries, ecological or biogeographic proxies for local adaptations, dispersal buffers around occurrence records, genetic studies of population structure, and previously defined evolutionary significant units. Defining populations can be challenging for some species, thus it may be necessary to evaluate species at multiple scales to account for uncertainty (Hoban et al. 2024a).

Genetic indicators are useful not only for monitoring efforts under the CBD, but also in national biodiversity conservation programs and legislation, such as the U.S. Endangered Species Act (ESA). The ESA, signed into law in 1973, is one of the strongest and most effective conservation laws in the world (Greenwald et al. 2019; Fischman et al. 2023), though there remains room for improvement in its implementation (Puckett et al. 2016; Evans et al. 2016; Malcom & Carter 2021; Eberhard et al. 2022). In 2016, the U.S. Fish and Wildlife Service (USFWS) adopted the Species Status Assessment (SSA) framework to improve the scientific rigor, efficiency, consistency, and transparency of extinction risk assessments, while keeping science distinct from the application of policy, which includes the determination of a species' classification status (i.e., threatened, endangered, or not warranted for listing; Smith et al. 2018). SSAs evaluate the capacity of species to withstand environmental and demographic stochasticity and disturbance, catastrophic events, and changes in the biological and physical environment. These assessments consider the best available science on population size, abundance, trend, and distribution as well as genetic, environmental, and phenotypic diversity. Unfortunately, many species assessed under the ESA are data limited (i.e., 36% of species in the 2024-2028 USFWS

National Listing Workplan; USFWS 2016), challenging extinction risk assessment and recovery planning. The inclusion of genetic indicators may help fill some of this data availability gap.

Prior to the SSA framework, deficiencies had been identified in the evaluation and protection of within-species diversity under the ESA. In particular, it has been repeatedly noted that species typically do not receive ESA protections until their populations are very small and the number of extant populations is highly reduced relative to historical conditions, which exacerbates loss of genetic diversity and makes recovery more challenging (Wilcove et al. 1993; Abbutt & Scott 2001; Neel et al. 2012; Eberhard et al. 2022). Although the SSA framework calls for the evaluation of abundance, population trends, population distributions, genetic diversity, and adaptive capacity (including evolutionary potential; Smith et al. 2018; Funk et al. 2019), it is not clear whether the related aspects of genetic health (i.e., maintenance of populations with large effective sizes across species' ranges) are being incorporated into scientific assessments in SSAs and whether they are considered by decision-makers during determinations of classification status.

Here we evaluate the Ne500 and PM indicators for 161 species assessed under the ESA using the SSA framework, more than half of the species with SSAs available at the time of our analysis. Our goals were to (1) evaluate the genetic health of these species using the genetic indicators, (2) determine whether genetic indicator values are correlated with ESA classification status, taxonomic group, or geographic range size, (3) quantify data availability for calculating the indicators, while determining if data availability is influenced by the above covariates, and (4) evaluate the influence of uncertainty on indicator values. If indicators of genetic health are being effectively incorporated into SSAs and that information is being used by decision-makers in their determinations of classification status, we would expect a correlation between status (i.e., endangered, threatened, not warranted) and one or both of the genetic indicators (i.e., 'not warranted for listing' species should have higher genetic indicator values). Lack of a correlation would suggest that genetic health is not being given full consideration in extinction risk assessments, either during SSA production or during status determinations. We examined the additional covariates because taxonomic group may relate to both census and effective sizes, and range size may be positively correlated with larger population sizes (Ellegren & Galtier 2016). Finally, where data were available, we calculated the proportion of populations with N_e less than 50 to identify species with populations at risk of rapid genetic erosion and potential fitness impacts from inbreeding depression (Jamieson & Allendorf 2012).

2.1 Materials and methods

We collected data for species or subspecies (hereafter "species") assessed under the ESA using the SSA framework. We limited data collection to SSAs, given that the SSA informs the classification status decision and we were interested in examining relationships between indicators and ESA status. We downloaded the list of species with SSAs from the Environmental Conservation Online System on March 22, 2023 (<https://ecos.fws.gov/ecp/report/ssa>). We removed SSAs where most of the species' range occurred outside the U.S. or was primarily pelagic, and those that assessed multiple species or focused on a distinct population segment. We selected at random from the remaining SSAs.

We used a previously developed and standardized KoboToolBox to collect data (<https://www.kobotoolbox.org/>; Mastretta-Yanes et al. 2024a, 2024b). We calibrated on a set of

six SSAs to ensure data collection was replicable (i.e., all team members completed the Kobo form for the same six SSAs and results were compared and discussed). Then, smaller groups calibrated on another set of six SSAs before individuals were randomly assigned SSAs. Finally, every Kobo form entry was reviewed and validated by at least one additional team member. We downloaded this verified dataset and processed the file in R version 4.6.1 (R Core Team 2026). We used a modified version of scripts created by Mastretta-Yanes et al. (2024a; available at the Dryad repository <https://doi.org/10.5061/dryad.bk3j9kdkm>) for quality control, data cleaning, and data formatting. Data and code for this analysis have been deposited to Dryad for peer review and will be made public upon publication.

We evaluated the following covariates: range size, taxonomic group, and ESA classification status. Range size was categorized as “restricted” or “wide-ranging” based on extent of occurrence ($< 20,000 \text{ km}^2$ for restricted range species), area of occurrence ($< 2,000 \text{ km}^2$ for restricted range species), or descriptions provided in the SSA (e.g., “narrow endemic”). We analyzed taxonomic group at two scales when sufficient sample sizes were available: plants, invertebrates, vertebrates; and bryophytes, gymnosperms, angiosperms, invertebrates, fishes, amphibians, reptiles, birds, mammals. Classification status was categorized as endangered, threatened, delisted, not listed, under review, and candidate. For statistical analysis and data visualizations, “proposed endangered” and “proposed threatened” species were set to “endangered” and “threatened”, respectively; “delisted” was set to “not listed” since both categories mean the species does not meet the definition of threatened or endangered; and singleton categories (i.e., “candidate”) were removed. Statistical analysis of relationships with ESA status were limited to endangered, threatened, and not listed categories, since there was an *a priori* expectation of differences in indicators among these three categories. We also evaluated what types of genetic studies were available for assessed species (i.e., phylogenetic, population genetic, both, or none) based on data reported in the SSA.

Some species were analyzed at multiple spatial scales in the SSAs (i.e., multiple approaches for defining populations) or included multiple assessments of population size or uncertainty about the extinct or extant status of populations. In these cases, we completed multiple Kobo forms reflecting these different approaches or uncertainties, called “multi-assessments”. Where species had multi-assessments for one of the indicators, we averaged the indicator value for statistical analyses and data visualizations. We also assessed the impact of multi-assessments on downstream indicator values.

The PM indicator was calculated as: the number of extant populations / (the number of extant populations + the number of extinct populations). The baseline time period for defining populations was based on historical information in the SSA and generally reflected human-induced changes in species’ ranges from 5-200 years ago. The year or range of years used as a baseline was recorded for each species. Species with populations where the extant or extinct status was unknown were excluded from the PM calculation.

The N_e500 indicator was calculated as: the number of populations with $N_e > 500$ / the number of populations with N_e data. Not all populations had N_e or N_c data; only populations with N_e or N_c data were considered when calculating the N_e500 indicator, so not all populations are included for every species. For N_c data provided as a semi-qualitative measure or as a range, generalized N_c values were assigned to facilitate computation of N_e and the N_e500 indicator. For example, if the N_c range was described as “more than 5,000 by much”, a value of 10,000 was applied for the calculation. When the N_c range was described as “range includes 5,000”, a value

of 5,001 was applied. We used an N_e/N_c conversion ratio of 0.1 to approximate contemporary N_e from N_c . If a species had a reported N_e/N_c ratio, we used that ratio. We evaluated sensitivity of the Ne500 indicator to N_e/N_c ratios of 0.2 and 0.3. To calculate the proportion of populations with N_e less than 50, we used data from populations with N_e or N_c point estimates.

We evaluated relationships among indicator values and covariates using ordered beta regression (Kubinec 2023), which is designed for continuous data with upper and lower bounds (such as the indicator data), using the glmmTMB package v.1.1.14 (Brooks et al. 2017). Ordered beta regression outperforms other options for modeling zero and one inflated data (Kubinec 2023). We evaluated model fit using visual diagnostics and statistical tests (i.e., Kolmogorov–Smirnov test, dispersion test, and outlier test) with the DHARMA package v.0.5.0 (Hartig 2022). Deviations were addressed by fitting dispersion parameters in glmmTMB. We evaluated the relationship between the indicators and range size and taxonomic groupings to determine if species with smaller ranges or specific taxonomic groups were at higher risk of genetic erosion or population extirpation. Similarly, for both indicators and Ne50, we evaluated the relationship between the indicator and ESA status to determine if species with elevated risk status (e.g., threatened or endangered) had lower (i.e., worse) indicator values. For range size and classification status models, we also ran models accounting for phylogeny since shared ancestry may drive patterns of population size and populations maintained across species ranges. We built trees using the rotl package v. 3.1.1 (Michonneau et al. 2016) and ape package v. 5.8-1 (Paradis and Schliep 2019). We first matched species' names to the Open Tree Taxonomy (excluding species that could not be matched) and created a subtree using rotl. We used ape to resolve polytomies, calibrate divergence times, and fit a chronogram using a relaxed model (due to high heterogeneity across the species list). We used TimeTree 5 (Kumar et al. 2022) to estimate divergence times for the calibration. The estimated phylogenetic variance-covariance matrix was fit as a proportional random effect in the ordered beta regression models.

3.1 Results

We assessed 161 species, with angiosperms ($n=48$) and invertebrates ($n=45$) having the highest representation in the data set and gymnosperms and bryophytes the lowest ($n=1$ for both groups; Fig. S1). Most species had restricted ranges ($n=118$), with 43 categorized as wide ranging. For classification status, 59 species were endangered or proposed endangered, 41 were threatened or proposed threatened, 52 were not listed, eight were delisted, and one was a candidate for listing. Most species had data available to estimate the indicators, with 49% of species having sufficient data for the Ne500 indicator (Fig. S2), 74% for the PM indicator (Fig. S3), 39% for both, and 84% for at least one of the indicators. The baseline time period for defining the historical number of populations ranged from 1801 to 2021, with a mean of 1990, median of 2004, and standard deviation of 39 years. Of 161 species, 22% (36/161) had no genetic study available, 17% (27/161) had only a population genetic study, 22% (35/161) had only a phylogenetic study, and 39% (63/161) had both. Invertebrates were less likely to have a population genetic study compared to plants or vertebrates (pairwise Fisher exact test with Holm adjustment for invertebrates and plant comparison $p = 0.008$, estimate and 95% confidence intervals = 0.281 (0.108, 0.701); for invertebrates and vertebrates comparison $p = 0.0006$, estimate and 95% confidence intervals = 0.214 (0.086, 0.512)).

The distribution of the Ne500 indicator skewed low (i.e., Ne500 modal value = 0, Fig. S4) across all categories of ESA classification status and taxonomic groups (Fig. 1a,b), indicating that most populations within any given species may be too small to maintain genetic diversity over the long term. Of the 79 species with data, 47% (37/79) had no populations above the Ne500 threshold, while 18% (14/79) had all populations above. We did not detect a statistically significant relationship between ESA classification status and the Ne500 indicator (Fig. 1a, Table S1; note that sample size is 78 since the “candidate” species was excluded from the analysis). A positive skew in the 95% confidence interval (linear trend ranging from -0.298 – 0.721) supports the non-significant trend that species that are not listed tend to have larger population sizes, though all classification categories span the indicator range from zero to 1 (Fig. 1a, Table S1). We also detected no statistically significant differences in the Ne500 indicator among taxonomic groups (Fig. 1b) or between widespread versus range-restricted species (Tables S2-S3). The estimated divergence time for plants and animals used to calibrate the phylogenetic trees was estimated from 12 studies with a median of 1530 MYA and 95% confidence interval of 1085 - 1671 MYA (Kumar et al. 2022). The phylogenetic tree estimated for species with Ne500 indicator data contained 75/79 species (i.e., four species could not be matched in the Open Tree Taxonomy). Statistical test results for the ESA classification and range size models did not change substantively after correcting for phylogeny (Tables S4-S5).

We assessed the proportion of populations below the Ne50 threshold and found that 14% (8/59) of species with data had all populations below Ne50, 41% (24/59) had half or more populations below Ne50, and 31% (18/59) had all populations above Ne50. As with the Ne500 indicator, we did not detect a statistically significant relationship between ESA classification status and the number of populations with $N_e > 50$ (Table S6); the model correcting for phylogeny did not converge, likely due to smaller sample sizes. Model residuals for Ne500 statistical tests showed some minor underdispersion; fitting dispersion parameters was helpful in some cases, though the deviations were small in all cases (full code, plots, and parameter estimates for these and all other statistical tests can be found at the Dryad peer review URL provided above under 1_data_analysis/4_analysis.html file). For the Ne500 models affected (i.e.,

Tables S2, S3, S5, range size and taxonomic grouping), underdispersion could result in reduced power (Hartig 2022), though plots of the data (e.g., Fig. 1b) show that the Ne500 indicator spans the range of values for all taxonomic groups, pointing to a lack of relationship. However, the large confidence intervals for the invertebrate group (Table S2) reflects the small sample size for this category (Fig. 1b), likely reducing power. The Ne50 test had no misspecification issues.

Unlike the Ne500 indicator, the distribution of the PM indicator skewed high (i.e., PM modal value = 1, Fig. S5) across classification categories and taxonomic groups (Fig. 1c,d), indicating that populations are generally being maintained across species' ranges. Of the 119 species with data, 37% (44/119) had all populations maintained. As with the Ne500 indicator, we detected no statistically significant relationship between ESA classification status and the PM indicator (Fig. 1c; Table S7; note that sample size is 118 since the "candidate" species was excluded from the analysis). There was a positive skew in the 95% confidence interval (linear trend ranging from -0.169 – 0.468), supporting a non-significant trend that species that are not listed tend to maintain more populations, though all classification categories spanned most of the indicator range (Fig. 1c). Invertebrates had significantly lower values for the PM indicator when compared with plants (Fig. 1d; Table S8; $p = 0.028$, estimate and 95% confidence intervals = -0.531 (-1.003, -0.058)). We did not detect a statistically significant difference in the PM indicator for species classified as widespread vs. range-restricted (Table S9). The phylogenetic tree estimated for species with PM indicator data contained 111/119 species (i.e., eight species could not be matched in the Open Tree Taxonomy). Results for the ESA classification and range size models did not change substantively after correcting for phylogeny (Tables S10-S11). Model residuals and diagnostics for the PM indicator statistical tests had no misspecification issues.

Uncertainty in assessing the indicators was relatively uncommon and did not have a large impact on downstream estimates. For the Ne500 indicator, 11% of species with data (9/79) required multiple assessments with different Ne500 inputs, but only four of those (5%) resulted in a change in the indicator value (average change of 0.25, Table S9). For the PM indicator, 22% of species with data (26/119) required multiple assessments with different PM inputs, with 19 of those (16%) changing the indicator value (average change of 0.15, Table S12). We also evaluated how the Ne500 indicator was impacted by the N_e/N_c ratio used in cases where a species-specific ratio was unavailable (default ratio = 0.1). As the ratio increased from 0.1 to 0.3, the overall distribution of the Ne500 indicator shifted towards one, since higher ratios translate to larger N_e values (Fig. S6). However, we did not detect statistically significant shifts in the value of the Ne500 indicator as a function of N_e/N_c ratio (Table S13), likely because 54% of species with data (32/59) had no change in their Ne500 indicator across ratios. Only three species had a reported N_e/N_c ratio: Luquillo Mountain babyboot orchid (*Lepanthes eltoroensis*; 0.14), San Francisco garter snake (*Thamnophis sirtalis tetrataenia*; average across population estimates = 0.47), and Gunnison sage-grouse (*Centrocercus minimus*; 0.2). A full list of species assessed is provided in Table S14.

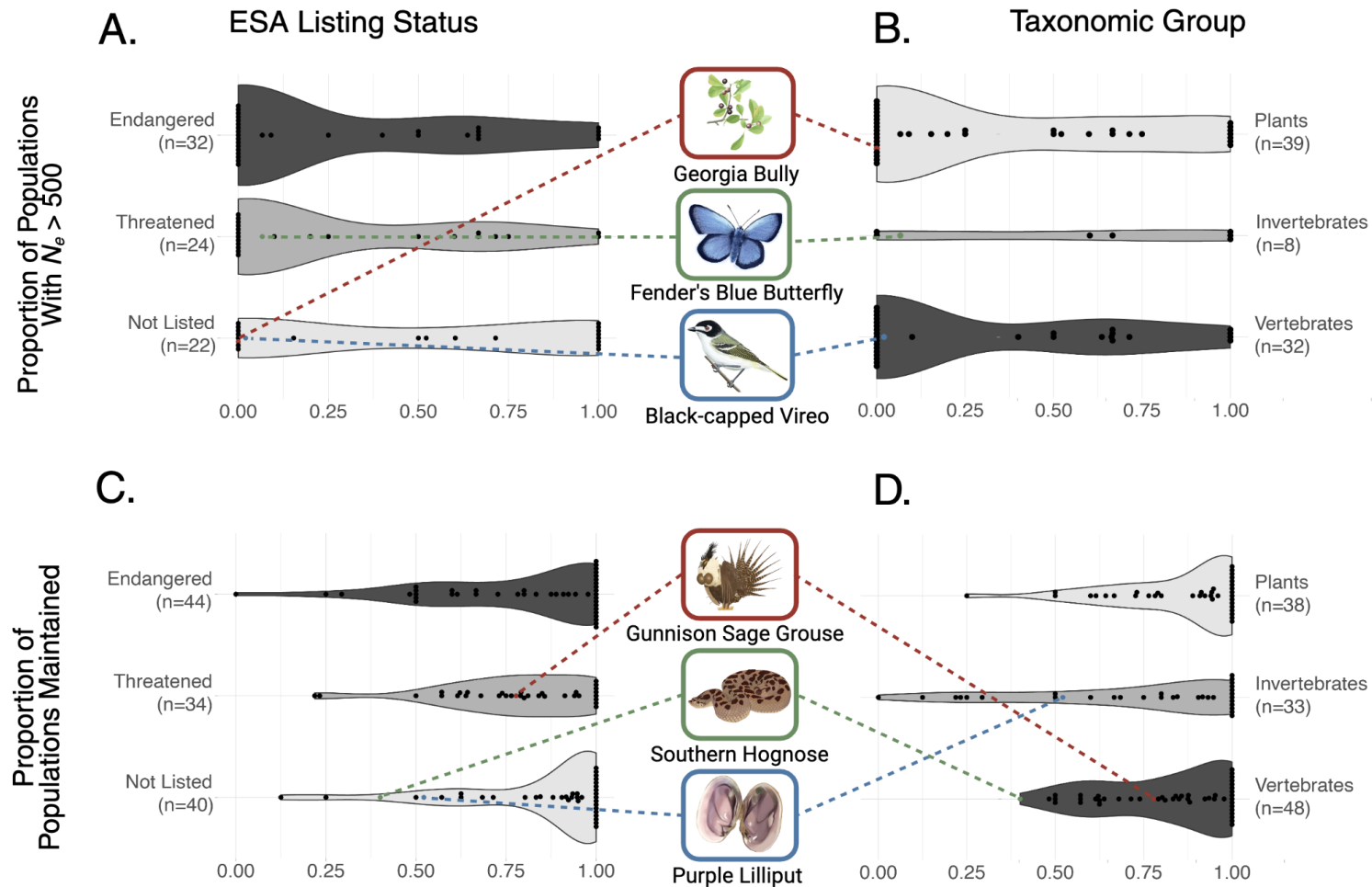


Fig. 1. Genetic indicators by ESA classification status and taxonomic group. Violin plots of the proportion of populations with $N_e > 500$ by (A) ESA classification status and (B) taxonomic group. A value of one means that all assessed populations have an $N_e > 500$, while a value of zero means that all assessed populations have an $N_e < 500$. Violin plots of the proportion of populations maintained within species by (C) ESA classification status and (D) taxonomic group. A value of one means that all populations have been maintained since the species' historical baseline, while a value of zero means that all populations have been extirpated since the historical baseline. Violins are scaled proportionally to the number of observations; some data points are shifted vertically to prevent overplotting. Highlighted species shown at the center of the plots are referenced in the text.

4.1 Discussion

We found that most species recently assessed under the ESA using the SSA framework are likely at risk of genetic erosion within their populations, compromising their ability to maintain genetic diversity and evolutionary potential over the long term. This is particularly concerning given that we did not detect a statistically significant relationship between ESA classification status and the Ne500 indicator, meaning that species that were not listed were just as likely to have Ne500 values of zero as listed species (Fig. 1a). For example, the Georgia bully (*Sideroxylon thornei*, Ne500 = 0, Fig. 1a,b), a flowering plant with a distribution restricted to the southeastern U.S., was classified as not warranted for listing despite 84% (38/45) of its populations having fewer than 50 individuals, and 51% of its populations (23/45) having fewer than 10 individuals (USFWS 2021). Additionally, recruitment has been documented in only 15% (8/54) of element occurrences (a unit smaller than populations). These small population sizes and lack of recruitment point to reduced genetic and demographic viability, and are indicators of elevated extinction risk.

We also did not detect any statistically significant differences in the Ne500 indicator among taxonomic groups (Fig. 1b) or widespread vs. range-restricted species, indicating that reduced effective population sizes and the risk of genetic erosion are likely pervasive problems for at-risk species. One important implication is that wide-ranging species may still experience genetic erosion due to reduced population sizes despite having a larger distribution than range-restricted species. While the distributions of wide-ranging species may offer the benefit of more gene flow due to more available source populations, this should be carefully evaluated since populations cannot be assumed to be in good genetic health just because they are distributed over larger areas. For example, the Purple lilliput (*Toxolasma lividum*), a freshwater mussel, is a wide-ranging species evaluated as not warranted for listing despite all populations falling below the Ne500 metric (Ne500 = 0, using either 64 or 146 populations; USFWS 2020b).

Even more concerning are the 58-63% of populations with data available (representing 36% of species assessed) that had $N_e < 50$, pointing to the importance of this threshold in flagging populations that are at high risk of extirpation. For example, the threatened Fender's blue butterfly (*Icaricia icarioides fenderi*) has nine of its 15 populations falling below the Ne50 threshold (and only one population above Ne500; USFWS 2020a, Fig. 1a,b), increasing the risk of extirpation due to genetic factors. Similarly, the delisted black-capped vireo (*Vireo atricapilla*) has only one of its 49 populations above Ne500, and only four above Ne50 (USFWS 2018, Fig. 1a,b).

While population size may be reduced, we found that most species recently assessed under the ESA are generally maintaining populations across their ranges. Nonetheless, there is a noticeable tail in the distribution of the PM indicator, such that 49% of species have lost at least 1 in 10 populations (indicator value ≤ 0.9) and 32% of species have lost at least 1 in 4 of their populations (indicator value ≤ 0.75). Overall, this is a positive observation for the state of U.S. biodiversity in that some of the distinct elements of genetic diversity found among populations are likely maintained. However, we did not detect a statistically significant relationship between the PM indicator and ESA classification status, suggesting that population losses resulting in reductions in intraspecific diversity may not be sufficiently considered when assessing species viability and conducting status determinations. For example, the southern hognose snake (*Heterodon simus*) was evaluated as not warranted for listing despite a documented range loss of

60% (i.e., $PM = 0.4$, Fig. 1c,d), including extirpation of populations across entire units representing unique elements of adaptive diversity (USFWS 2019a).

Invertebrates had significantly lower values for the PM indicator when compared with plants, suggesting that this group has experienced higher levels of population extirpation. This may be driven by the well-documented high levels of endangerment in freshwater species, including crayfish, mussels, and snails (Lydeard & Mayden 1995; Haag & Williams 2014; Reid et al. 2019; Elkins et al. 2019), which comprised over half of invertebrates we evaluated. Examples include many freshwater mussels, including the purple lilliput discussed above (not listed, with average $PM = 0.52$, Fig. 1c,d), the round hickorynut (*Obovaria subrotunda*, threatened, with average $PM = 0.24$; USFWS 2019c) and the sheepnose mussel (*Plethobasus cyphus*, endangered, $PM = 0.29$; USFWS 2022a). This result is in concordance with previous work that identified higher rates of population extirpation in invertebrates and plants with ESA recovery plans (Leidner & Neel 2011).

Furthermore, when combined with results from the Ne500 indicator, our analysis suggests that although populations of these at-risk species are often being maintained, most are likely too small to prevent genetic erosion and loss of intraspecific diversity that is critical to species viability in both the short and long terms. This points to potential population losses on the horizon for many at-risk species. For example, the Apache trout (*Oncorhynchus apache*) maintains a high PM value (i.e., $PM = 0.90$ - 0.95 depending on the scale of analysis), but has an Ne500 indicator value of zero at both the stream and sub-basin scales (USFWS 2022b). Even more concerning are species whose populations fall below the Ne50 threshold such as the Gunnison sage grouse (*Centrocercus minimus*), a threatened, range-restricted species with a high proportion of populations maintained ($PM = 0.78$, Fig. 1c,d), but with no populations greater than Ne500, and only one of its seven populations greater than Ne50 (USFWS 2019b).

There are cases where species have high values for the genetic indicators but are still listed under the ESA. For example, the Dixie Valley toad (*Anaxyrus williamsi*) is an endemic species with $PM = 1$, yet this species is listed as endangered due to imminent (non-genetic) threats that could result in extinction (USFWS 2023b). Additionally, there may be species with highly restricted habitats that have persisted at population sizes less than Ne500 for long periods with minimal consequences to viability; however, these cases are expected to be infrequent, and monitoring of population sizes over time remains valuable even for these species (Hoban et al. 2024a). These cases clearly underscore the importance of integrating genetic indicators and/or direct measurements of genetic health with other aspects of species' viability and historical, ongoing, and future threats to best inform extinction risk assessments and classification status.

We found that integration of genetic indicators into SSAs and downstream decision-making is feasible, given that most species have data available to evaluate one or both indicators. Overall lower data availability for the Ne500 (and Ne50) indicator highlights the need for increased biodiversity inventory work, as well as the importance of estimating contemporary N_e in population genetic studies of at-risk species. Surprisingly, although 56% of species had a population genetic study, only seven (4%) had any genetic estimate of contemporary N_e , suggesting that researchers should give more priority to ensuring that sampling designs and analyses allow for the estimation of this important conservation-relevant parameter (Forester et al. 2022b; Waples 2024b). Unfortunately, population genetic data production does not always translate to accessible conservation-relevant analyses or publications. For example, most population genetic studies sample just a fraction of populations across a species' range, limiting

inference for range-wide extinction risk assessments (e.g., Csilléry et al. 2025, which identified only 1,109 species globally with at least five populations sampled for genetic data). Lack of genetic data and metadata availability is also a common limiting factor for reanalyzing existing data sets to address conservation-relevant questions (Toczydlowski et al. 2021; Crandall et al. 2023). Finally, many published studies do not address questions that are relevant to conservation practice for threatened and endangered species (Jachowski et al. 2024). We thus echo previous calls for enhanced communication and collaboration between conservation practitioners and geneticists (Shafer et al. 2015; Taylor et al. 2017; Neaves et al. 2024; Shaw et al. 2024).

We did identify some striking differences in data availability among taxonomic groups for the Ne500 indicator, with only 18% of invertebrates having sufficient data, compared with 78% of plants and 48% of vertebrates. This is likely due to the difficulty of approximating the census size of many invertebrates due to their small size and/or low detection probability. For example, there are 11 freshwater mussels in our dataset, and surveys often take the form of counting occurrences without an attempt to translate this into modelled N_c . However, estimates were made for some of these species, suggesting there is potential for getting at least rough estimates (and thus, sufficient data) for the Ne500 indicator for other invertebrates in the future. For species with low detection probabilities, genetic approaches for estimating N_e may be easier and more cost-effective than estimating N_c (e.g., Inoue et al. 2015; Smith et al. 2021; Gladstone et al. 2022). Additionally, because calculation of the Ne500 indicator requires only rough population size approximations (e.g., a description such as “population size is much less than 5000 individuals”), qualitative approaches to data collection should be embraced in SSA data calls, such as data collection by local people and integration of indigenous knowledge (e.g., the use of traditional ecological knowledge in the Alexander Archipelago Wolf SSA; USFWS 2023a).

There are a few important considerations that should be addressed when integrating genetic indicators into SSAs. First, we recommend that, when data are available, the Ne50 indicator should be evaluated along with the Ne500 indicator to better inform status determinations (e.g., threatened vs. endangered), since populations with $N_e < 50$ are at elevated risk of extirpation and may contribute to rapid population losses. Second, the scale of gene flow should be carefully considered when assessing the indicators: the Ne500 and PM indicators should be evaluated at a metapopulation scale, since even small amounts of gene flow among populations can increase genetic diversity and help maintain evolutionary potential (Hoban et al. 2020b; Mastretta-Yanes et al. 2024b; Waples 2025). Application of the Ne50 indicator can be complex, though it generally is most appropriately applied to local, isolated populations (Waples 2025). Metapopulations that fall below $N_e < 50$ can clearly be identified as being at high risk of rapid genetic erosion and near-term inbreeding depression. Third, while the genetic indicators can be used to inform extinction risk assessments for any species, conversion of N_c to N_e using an N_e/N_c ratio should be avoided in cases where the census size is unlikely to reflect the genetic status of the population. This includes populations that are known to have undergone severe bottlenecks followed by population expansion, species with asexual (clonal) reproduction, non-diploid species, and heavily managed populations, such as *ex situ* collections (Mastretta-Yanes et al. 2024b). Finally, the genetic indicators do not provide a comprehensive assessment of the genetic health of a species (Hoban et al. 2024b; Allendorf et al. 2024; Hoban et al. 2026). However, when integrated with other data informing species viability, they can provide critical insight into population-level processes that impact extinction risk, in addition to helping guide

recovery planning and providing transparent metrics for tracking recovery progress over time. We also note that use of one or both of the genetic indicators to help inform species viability does not preclude the inclusion of genetic data that can be critical to informing genetic health and management, such as data on introgression and hybridization, inbreeding, changes in allele frequencies, genetic load, and cryptic population structure (Allendorf et al. 2024; Hoban et al. 2024b).

5.1 Conclusions

One of the major findings from this work is that there was no detectable correlation between classification status and indicators of genetic health in species recently assessed under the ESA using the SSA framework (Fig. 1). In particular, species that were not listed or delisted were just as likely to have low genetic indicator values as listed species. This suggests that, at least so far, genetic health is either not being effectively incorporated into many SSAs along with other data informing species' viability, or that the viability impacts of genetic health included in SSAs are not being given full consideration by decision-makers during determinations of classification status. The ongoing lack of integration and/or consideration of genetic health in ESA decisions may have several causes, including the perception that genetic data are only relevant to taxonomic questions or delineating populations, the perception that genetic data are too difficult to incorporate into extinction risk assessments, lack of familiarity with genetic health metrics, and difficulty communicating the relevance of genetic health to extinction risk with decision-makers.

Fortunately, data are available in most species to evaluate one or both of the Ne500 and PM indicators, helping to address this critical gap in assessments of extinction risk under the ESA. The time needed to calculate the indicators from SSA reports was minimal, at approximately three hours per species (Mastretta-Yanes et al. 2024a), which means that inclusion of the indicators is achievable for SSA teams, a critical point given the high USFWS workload, chronically inadequate funding, and the short (12-month) statutory time frame for classification decisions (ESA 1973; Gerber 2016; Malcom & Li 2018; Eberhard et al. 2022). The indicators also provide a useful tool for communicating genetic health in a transparent and standardized manner, facilitating its consideration by decision-makers during classification determinations.

Our work demonstrates that the genetic indicators are a practical and worthwhile addition to the SSA framework, providing actionable information on genetic health that informs all aspects of ESA implementation. Consideration of genetic health in ESA decision-making would support more timely and better-targeted protection of at-risk species prior to irreversible losses of genetic diversity. This, in turn, would increase the success of recovery actions while reducing time to recovery and overall costs, better ensuring the ESA goal of safeguarding biodiversity in the U.S. and globally.

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Supporting Information for:

A widespread gap in U.S. Endangered Species Act implementation: Risk of genetic erosion within populations

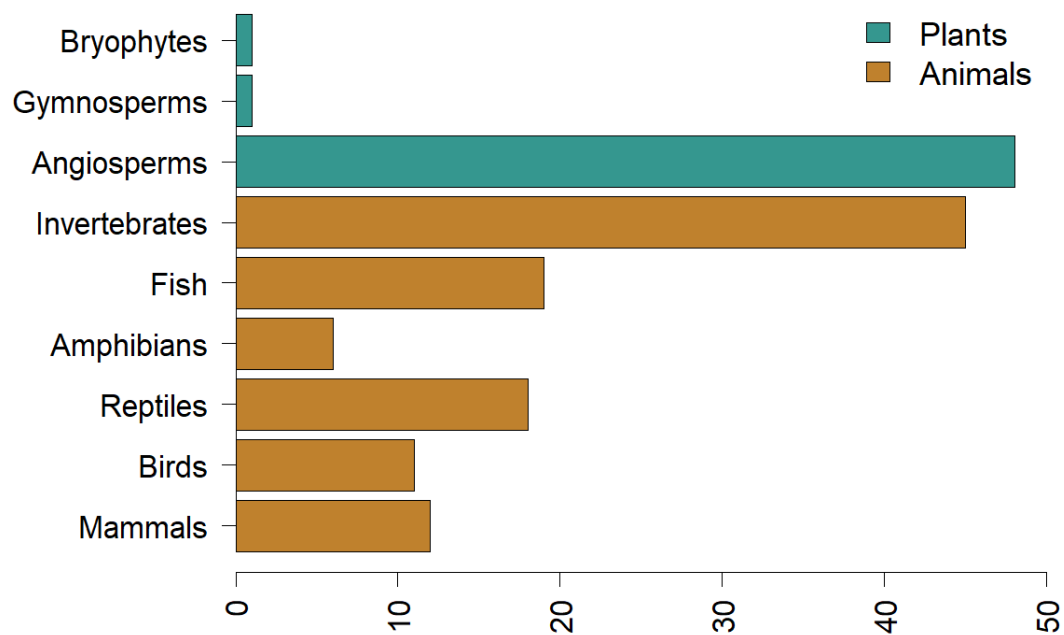


Fig. S1. Taxonomic distribution of 161 species status assessments analyzed.

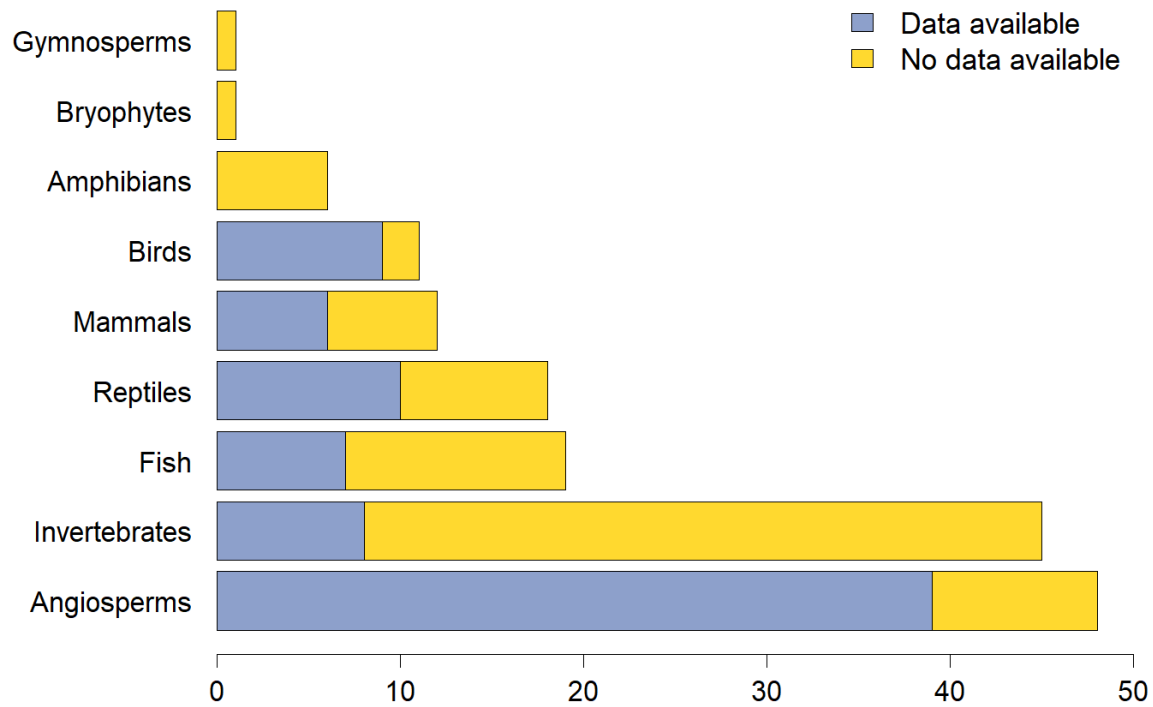


Fig. S2. Data availability for the Ne500 indicator for 161 species across taxonomic groups.

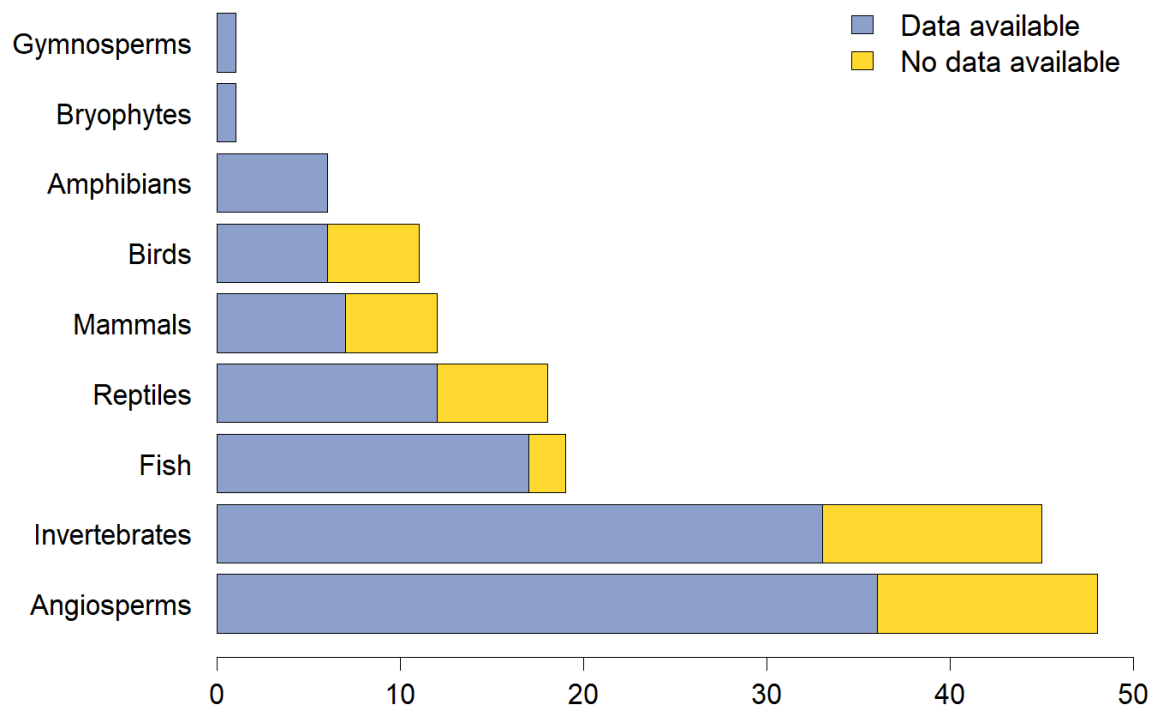


Fig. S3. Data availability for PM indicator for 161 species across taxonomic groups.

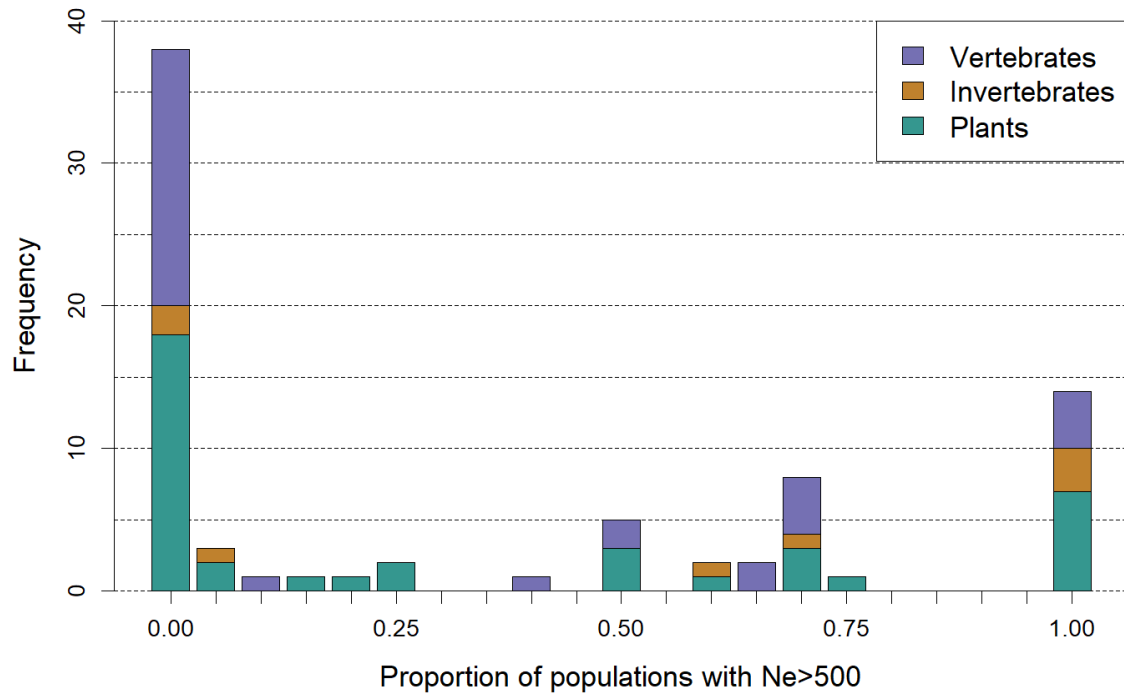


Fig. S4. Proportion of populations with $N_e > 500$ for 79 species. A value of one means that all assessed populations have an $N_e > 500$, while a value of zero means that all assessed populations have an $N_e < 500$.

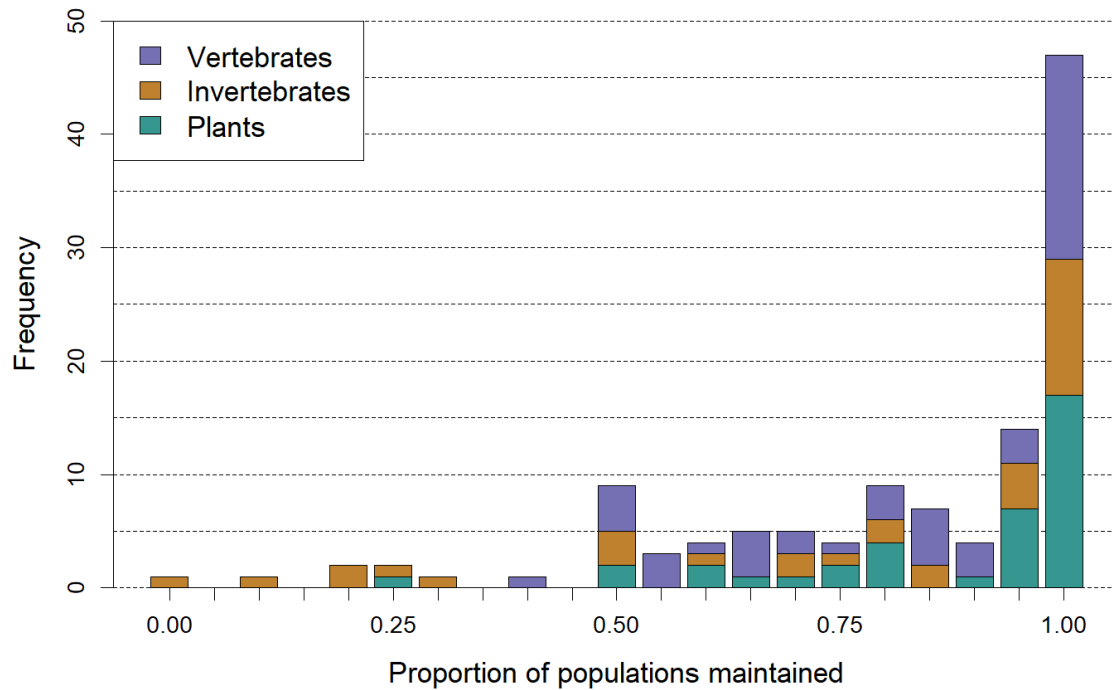


Fig. S5. Proportion of populations maintained for 119 species. A value of one means that all populations have been maintained since the species' historical baseline, while a value of zero means that all populations have been extirpated since the historical baseline.

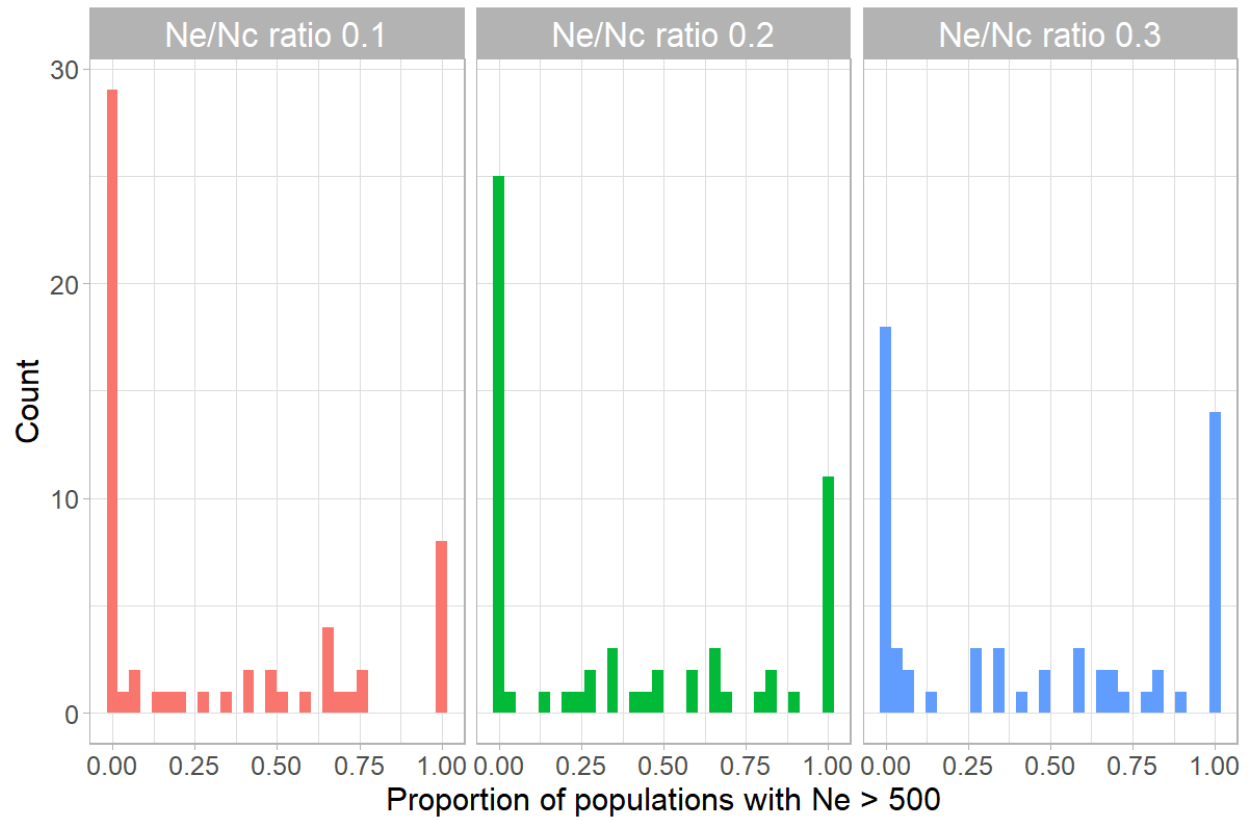


Fig. S6. Proportion of populations maintained for 59 species with Nc count data using different default Ne/Nc ratios of 0.1, 0.2, and 0.3. A value of one means that all assessed populations have an Ne > 500, while a value of zero means that all assessed populations have an Ne < 500.

Table S1. Ordered beta regression with ESA classification status evaluated as an ordered factor (levels = endangered, threatened, not listed): Does the number of populations with Ne>500 vary by ESA classification status? CI = confidence interval.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	-0.256	0.193	-1.323	-0.634	0.123	0.186
ESA status (linear trend)	0.211	0.260	0.813	-0.298	0.721	0.416
ESA status (quadratic trend)	0.128	0.246	0.519	-0.354	0.609	0.603

Table S2. Ordered beta regression: Does the number of populations with Ne>500 vary by taxonomic group (3 groups represented)? CI = confidence interval; plants are the reference category.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	-0.300	0.222	-1.351	-0.734	0.135	0.177
Invertebrates	0.491	0.529	0.928	-0.546	1.529	0.353
Vertebrates	-0.021	0.294	-0.070	-0.596	0.555	0.944

Table S3. Ordered beta regression: Does the number of populations with Ne>500 vary by species range size? CI = confidence interval; restricted is the reference category.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	-0.235	0.205	-1.145	-0.637	0.167	0.252
Wide ranging	-0.086	0.301	-0.286	-0.677	0.505	0.775

Table S4. Ordered beta regression with ESA classification status evaluated as an ordered factor (levels = endangered, threatened, not listed) correcting for phylogeny: Does the number of populations with Ne>500 vary by ESA classification status after accounting for phylogeny? CI = confidence interval.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	-0.247	0.195	-1.267	-0.628	0.135	0.205

ESA status (linear trend)	0.283	0.266	1.064	-0.238	0.803	0.287
ESA status (quadratic trend)	0.110	0.248	0.441	-0.377	0.596	0.659

Table S5. Ordered beta regression: Does the number of populations with $N_e > 500$ vary by species range size after accounting for phylogeny? CI = confidence interval; restricted is the reference category.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	-0.228	0.207	-1.103	-0.633	0.177	0.270
Wide ranging	-0.210	0.317	-0.660	-0.832	0.412	0.509

Table S6. Ordered beta regression with ESA classification status evaluated as an ordered factor (levels = endangered, threatened, not listed): Does the number of populations with $N_e > 50$ vary by ESA classification status? CI = confidence interval.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	-0.034	0.204	-0.168	-0.435	0.366	0.867
ESA status (linear trend)	-0.024	0.293	-0.083	-0.599	0.551	0.934
ESA status (quadratic trend)	0.022	0.277	0.081	-0.520	0.565	0.935

Table S7. Ordered beta regression with ESA classification status evaluated as an ordered factor (levels = endangered, threatened, not listed): Does the number of maintained populations vary by ESA classification status? CI = confidence interval.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	0.855	0.111	7.715	0.638	1.072	<0.001
ESA status (linear trend)	0.150	0.163	0.921	-0.169	0.468	0.357
ESA status (quadratic trend)	0.160	0.158	1.010	-0.150	0.469	0.312

Table S8. Ordered beta regression: Does the number of maintained populations vary by taxonomic group (3 groups represented)? CI = confidence interval; plants are the reference category.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	1.098	0.179	6.118	0.746	1.450	<0.001
Invertebrates	-0.531	0.241	-2.201	-1.003	-0.058	0.028
Vertebrates	-0.210	0.216	-0.976	-0.633	0.212	0.329

Table S9. Ordered beta regression: Does the number of maintained populations vary by species range size? CI = confidence interval; restricted is the reference category.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	0.904	0.127	7.094	0.654	1.154	<0.001
Wide ranging	-0.151	0.200	-0.757	-0.543	0.240	0.449

Table S10. Ordered beta regression with ESA classification status evaluated as an ordered factor (levels = endangered, threatened, not listed) correcting for phylogeny: Does the number of maintained populations vary by ESA classification status after accounting for phylogeny? CI = confidence interval.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	0.943	0.181	5.209	0.588	1.298	<0.001
ESA status (linear trend)	0.167	0.174	0.958	-0.174	0.508	0.338
ESA status (quadratic trend)	0.192	0.180	1.063	-0.162	0.545	0.288

Table S11. Ordered beta regression: Does the number of maintained populations vary by species range size after accounting for phylogeny? CI = confidence interval; restricted is the reference category.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	0.911	0.179	5.080	0.559	1.262	<0.001
Wide ranging	-0.009	0.226	-0.041	-0.451	0.433	0.968

Table S12. Species with multiple assessments (i.e., different values for calculating a given indicator: Ne500, PM, or both) and resulting indicator values. NA = no data (shaded in gray).

Species	Taxonomic group	# pops	# pops with Ne	# pops > 500	Ne500	# extant pops	# extinct pops	PM	Different inputs	Different value
<i>Aphelocoma coerulescens</i>	bird	10	10	1	0.10	10	0	1.00	Both	Both
		NA	NA	NA	NA	19	2	0.90		
<i>Oncorhynchus clarkii virginalis</i>	fish	122	122	40	0.33	122	6	0.95	Both	Both
		4	4	4	1.00	4	1	0.80		
<i>Alasmodontia varicosa</i>	invertebrate	241	171	35	0.20	241	NA	NA	Both	Ne500
		4	4	4	1.00	4	NA	NA		
<i>Etheostoma chienense</i>	fish	1	1	0	0.00	1	0	1.00	Both	Ne500
		2	1	1	1.00	2	0	1.00		
<i>Mustela nigripes</i>	mammal	14	14	0	0.00	14	15	0.48	Both	PM
		1	1	0	0.00	1	NA	NA		
<i>Oncorhynchus apache</i>	fish	30	30	0	0.00	30	14	0.68	Both	PM
		7	7	0	0.00	7	0	1.00		
<i>Plestiodon egregius egregius</i>	reptile	15	15	0	0.00	15	8	0.65	Both	PM
		19	15	0	0.00	19	4	0.83		
<i>Toxolasma lividum</i>	invertebrate	64	64	0	0.00	65	67	0.49	Both	PM
		146	146	0	0.00	146	119	0.55		
<i>Pseudemys rubriventris</i>	reptile	1	1	0	0.00	1	0	1.00	Both	No
		43	21	0	0.00	43	0	1.00		
<i>Cambarus elkensis</i>	invertebrate	NA	NA	NA	NA	1	0	1.00	PM	No
		NA	NA	NA	NA	6	0	1.00		
<i>Necturus lewisi</i>	amphibian	NA	NA	NA	NA	9	0	1.00	PM	No
		NA	NA	NA	NA	3	0	1.00		

Species	Taxonomic group	# pops	# pops with Ne	# pops > 500	Ne500	# extant pops	# extinct pops	PM	Different inputs	Different value
<i>Notropis mekistocholas</i>	fish	NA	NA	NA	NA	1	0	1.00	PM	No
		NA	NA	NA	NA	8	0	1.00		
<i>Thoburnia atripinnis</i>	fish	NA	NA	NA	NA	24	0	1.00	PM	No
		NA	NA	NA	NA	9	0	1.00		
<i>Ambystoma cingulatum</i>	amphibian	NA	NA	NA	NA	9	16	0.36	PM	PM
		NA	NA	NA	NA	4	0	1.00		
<i>Bombus terricola</i>	invertebrate	NA	NA	NA	NA	15	3	0.83	PM	PM
		NA	NA	NA	NA	47364	7908	0.86		
<i>Cryptobranchus alleganiensis alleganiensis</i>	amphibian	NA	NA	NA	NA	345	225	0.61	PM	PM
		NA	NA	NA	NA	4	0	1.00		
<i>Erimystax harrisi</i>	fish	NA	NA	NA	NA	21	2	0.91	PM	PM
		NA	NA	NA	NA	22	1	0.96		
<i>Etheostoma osburni</i>	fish	NA	NA	NA	NA	18	17	0.51	PM	PM
		NA	NA	NA	NA	5	2	0.71		
<i>Heterelmis stephani</i>	invertebrate	NA	NA	NA	NA	0	2	0.00	PM	PM
		NA	NA	NA	NA	1	1	0.50		
<i>Lavinia exilicauda chi</i>	fish	NA	NA	NA	NA	2	2	0.50	PM	PM
		NA	NA	NA	NA	3	1	0.75		
<i>Notophthalmus perstriatus</i>	amphibian	NA	NA	NA	NA	116	74	0.61	PM	PM
		NA	NA	NA	NA	173	17	0.91		
		NA	NA	NA	NA	2	0	1.00		
<i>Noturus munitus</i>	fish	NA	NA	NA	NA	12	4	0.75	PM	PM
		NA	NA	NA	NA	5	1	0.83		

Species	Taxonomic group	# pops	# pops with N_e	# pops > 500	Ne500	# extant pops	# extinct pops	PM	Different inputs	Different value
<i>Obovaria subrotunda</i>	invertebrate	NA	NA	NA	NA	65	232	0.22	PM	PM
		NA	NA	NA	NA	34	104	0.25		
<i>Pleurobema rubrum</i>	invertebrate	NA	NA	NA	NA	28	108	0.21	PM	PM
		NA	NA	NA	NA	35	116	0.23		
<i>Rhynchospora crinipes</i>	angiosperm	39	19	0	0.00	35	4	0.90	PM	PM
		39	19	0	0.00	37	2	0.95		
<i>Streptanthus bracteatus</i>	angiosperm	16	16	0	0.00	16	2	0.89	PM	PM
		3	3	0	0.00	3	0	1.00		

Table S13. Ordered beta regression: Does the value of the Ne500 indicator significantly vary with the N_e/N_c ratio used? CI = confidence interval; reference group is N_e/N_c ratio = 0.1.

Variable	Estimate	Standard error	z value	Lower 95% CI	Upper 95% CI	Pr(> z)
Intercept	-0.431	0.176	-2.443	-0.776	-0.085	0.015
N_e/N_c ratio = 0.2	0.219	0.222	0.986	-0.216	0.654	0.324
N_e/N_c ratio = 0.3	0.329	0.223	1.472	-0.109	0.766	0.141

Table S14. Scientific and common names of 161 species assessed; includes range size, taxonomic group (by 9 and 3 groupings), and ESA classification status.

Scientific name	Common name	Range size	Taxonomic group (9 grps)	Taxonomic group (3 grps)	ESA status
<i>Donrichardsia macroneuron</i>	South Llano Springs Moss	restricted	bryophyte	Plants	Endangered
<i>Pinus albicaulis</i>	Whitebark Pine	wide-ranging	gymnosperm	Plants	Threatened
<i>Diplacus vandenbergensis</i>	Vandenberg Monkeyflower	restricted	angiosperm	Plants	Endangered
<i>Phacelia formosula</i>	North Park Phacelia	restricted	angiosperm	Plants	Endangered
<i>Spiranthes delitescens</i>	Canelo Hills ladies-tresses	restricted	angiosperm	Plants	Endangered
<i>Chrysopsis floridana</i>	Florida golden aster	restricted	angiosperm	Plants	Endangered
<i>Eriogonum tiehmii</i>	Tiehm's buckwheat	restricted	angiosperm	Plants	Endangered
<i>Cirsium scariosum loncholepis</i>	La Graciosa thistle	restricted	angiosperm	Plants	Endangered
<i>Scirpus ancistrochaetus</i>	Northeastern bulrush	wide-ranging	angiosperm	Plants	Endangered

Scientific name	Common name	Range size	Taxonomic group (9 grps)	Taxonomic group (3 grps)	ESA status
<i>Asclepias prostrata</i>	Prostrate Milkweed	restricted	angiosperm	Plants	Endangered
<i>Ipomopsis polyantha</i>	Pagosa Skyrocket	restricted	angiosperm	Plants	Endangered
<i>Leavenworthia texana</i>	Texas golden glade cress	restricted	angiosperm	Plants	Endangered
<i>Eryngium sparganophyllum</i>	Arizona Eryngo	restricted	angiosperm	Plants	Endangered
<i>Solanum conocarpum</i>	Marron Bacora	restricted	angiosperm	Plants	Endangered
<i>Pedicularis furbishiae</i>	Furbish's Lousewort	restricted	angiosperm	Plants	Endangered
<i>Enchinomastus erectocentrus acunensis</i>	Acuña Cactus	restricted	angiosperm	Plants	Endangered
<i>Plagiobothrys hirtus</i>	Rough Popcornflower	restricted	angiosperm	Plants	Endangered
<i>Styrax platanifolius texanus</i>	Texas snowbells	restricted	angiosperm	Plants	Endangered
<i>Lupinus constancei</i>	Lassics Lupine	restricted	angiosperm	Plants	Endangered
<i>Sclerocactus brevihamatus tobuschii</i>	Tobusch fishhook cactus	wide-ranging	angiosperm	Plants	Threatened
<i>Eriogonum gypsophilum</i>	Gypsum Wild Buckwheat	restricted	angiosperm	Plants	Threatened
<i>Graptopetalum bartramii</i>	Bartram's stonecrop	wide-ranging	angiosperm	Plants	Threatened
<i>Layia carnosa</i>	Beach layia	restricted	angiosperm	Plants	Threatened
<i>Scutellaria ocmulgee</i>	Ocmulgee skullcap	restricted	angiosperm	Plants	Threatened
<i>Lespedeza leptostachya</i>	Prairie Bush-Clover	restricted	angiosperm	Plants	Threatened
<i>Streptanthus bracteatus</i>	Bracted Twistflower	restricted	angiosperm	Plants	Threatened
<i>Lepidium papilliferum</i>	Slickspot Peppergrass	restricted	angiosperm	Plants	Threatened
<i>Arabis georgiana</i>	Georgia rockcress	restricted	angiosperm	Plants	Threatened
<i>Phacelia submutica</i>	DeBuque Phacelia	restricted	angiosperm	Plants	Threatened
<i>Cirsium wrightii</i>	Wright's marsh thistle	restricted	angiosperm	Plants	Threatened
<i>Yermo xanthocephalus</i>	Desert yellowhead	restricted	angiosperm	Plants	Threatened
<i>Castilleja levisecta</i>	golden paintbrush	wide-ranging	angiosperm	Plants	Threatened
<i>Acmispon dendroideus traskiae</i>	San Clemente Island Lotus	restricted	angiosperm	Plants	Delisted
<i>Castilleja grisea</i>	San Clemente Island Paintbrush	restricted	angiosperm	Plants	Delisted
<i>Delphinium variegatum kinkiense</i>	San Clemente Island larkspur	restricted	angiosperm	Plants	Delisted
<i>Lomatium bradshawii</i>	Bradshaw's lomatium	restricted	angiosperm	Plants	Delisted
<i>Lepanthes eltoroensis</i>	Luquillo Mountain babyboot orchid	restricted	angiosperm	Plants	Delisted
<i>Malacothamnus clementinus</i>	San Clemente Island Bushmallow	restricted	angiosperm	Plants	Delisted
<i>Astragalus schmolliae</i>	Chapin Mesa Milkvetch	restricted	angiosperm	Plants	Not Listed
<i>Trichocentrum undulatum</i>	Cape Sable orchid	restricted	angiosperm	Plants	Not Listed
<i>Astragalus microcymbus</i>	Skiff milkvetch	restricted	angiosperm	Plants	Not Listed
<i>Boechera pusilla</i>	Fremont County Rockcress	restricted	angiosperm	Plants	Not Listed
<i>Sideroxylon thornei</i>	Georgia Bully	wide-ranging	angiosperm	Plants	Not Listed

Scientific name	Common name	Range size	Taxonomic group (9 grps)	Taxonomic group (3 grps)	ESA status
<i>Mimulus gemmiparus</i>	Rocky Mountain monkeyflower	restricted	angiosperm	Plants	Not Listed
<i>Alnus maritima</i>	Seaside Alder	restricted	angiosperm	Plants	Not Listed
<i>Alnus maritima maritima</i>	Delmarva alder	restricted	angiosperm	Plants	Not Listed
<i>Alnus maritima georgiensis</i>	Georgia Alder	restricted	angiosperm	Plants	Not Listed
<i>Alnus maritima oklahomensis</i>	Oklahoma alder	restricted	angiosperm	Plants	Not Listed
<i>Rhynchospora crinipes</i>	Hairy-peduncled beaked-rush	wide-ranging	angiosperm	Plants	Not Listed
<i>Sisyrinchium sarmentosum</i>	Mountain blue-eyed grass	restricted	angiosperm	Plants	Not Listed
<i>Elliptio spinosa</i>	Altamaha spinymussel	restricted	invertebrate	Invertebrates	Endangered
<i>Euphilotes enoptes smithi</i>	Smith's Blue Butterfly	restricted	invertebrate	Invertebrates	Endangered
<i>Villosa fabalis</i>	Rayed bean	restricted	invertebrate	Invertebrates	Endangered
<i>Plethobasus cyphus</i>	Sheepnose Mussel	restricted	invertebrate	Invertebrates	Endangered
<i>Epioblasma triquetra</i>	Snuffbox	wide-ranging	invertebrate	Invertebrates	Endangered
<i>Orconectes shoupi</i>	Nashville crayfish	restricted	invertebrate	Invertebrates	Endangered
<i>Planorbella magnifica</i>	Magnificent Ramshorn	restricted	invertebrate	Invertebrates	Endangered
<i>Speyeria callippe callippe</i>	Callippe Silverspot Butterfly	restricted	invertebrate	Invertebrates	Endangered
<i>Euphydryas anicia cloudcrofti</i>	Sacramento Mountains Checkerspot Butterfly	restricted	invertebrate	Invertebrates	Endangered
<i>Bombus franklini</i>	Franklin's Bumblebee	restricted	invertebrate	Invertebrates	Endangered
<i>Ptychobranhus subtentum</i>	Fluted kidneyshell	wide-ranging	invertebrate	Invertebrates	Endangered
<i>Popenaias popeii</i>	Texas Hornshell	restricted	invertebrate	Invertebrates	Endangered
<i>Pleurobema athearni</i>	Canoe Creek Clubshell	restricted	invertebrate	Invertebrates	Endangered
<i>Cambarus cracens</i>	Slenderclaw Crayfish	restricted	invertebrate	Invertebrates	Endangered
<i>Texella reyesi</i>	Bone Cave Harvestman	restricted	invertebrate	Invertebrates	Endangered
<i>Pleurobema rubrum</i>	Pyramid Pigtoe	wide-ranging	invertebrate	Invertebrates	Threatened
<i>Obovaria subrotunda</i>	Round Hickorynut Mussel	wide-ranging	invertebrate	Invertebrates	Threatened
<i>Icaricia icarioides fenderi</i>	Fender's Blue Butterfly	restricted	invertebrate	Invertebrates	Threatened
<i>Procambarus econfinae</i>	Panama City Crayfish	restricted	invertebrate	Invertebrates	Threatened
<i>Nicrophorus americanus</i>	American Burying Beetle	wide-ranging	invertebrate	Invertebrates	Threatened
<i>Speyeria nokomis nokomis</i>	Silverspot butterfly	restricted	invertebrate	Invertebrates	Threatened
<i>Hesperia dacotae</i>	Dakota skipper	wide-ranging	invertebrate	Invertebrates	Threatened
<i>Faxonius marchandi</i>	Mammoth Spring Crayfish	restricted	invertebrate	Invertebrates	Not Listed
<i>Papaipema eryngii</i>	Rattlesnake-Master Borer Moth	restricted	invertebrate	Invertebrates	Not Listed
<i>Stygobromus indentatus</i>	Tidewater Amphipod	restricted	invertebrate	Invertebrates	Not Listed
<i>Toxolasma lividum</i>	Purple Lilliput	wide-ranging	invertebrate	Invertebrates	Not Listed
<i>Monadenia fidelis minor</i>	Dalles sideband	restricted	invertebrate	Invertebrates	Not Listed

Scientific name	Common name	Range size	Taxonomic group (9 grps)	Taxonomic group (3 grps)	ESA status
<i>Leptoxis arkansensis</i>	Arkansas Mudalia	restricted	invertebrate	Invertebrates	Not Listed
<i>Optioservus phaeus</i>	Scott riffle beetle	restricted	invertebrate	Invertebrates	Not Listed
<i>Cambarus elkensis</i>	Elk River crayfish	restricted	invertebrate	Invertebrates	Not Listed
<i>Faxonius roberti</i>	Spring River Crayfish	restricted	invertebrate	Invertebrates	Not Listed
<i>Cicindela theatina</i>	Great Sand Dunes Tiger Beetle	restricted	invertebrate	Invertebrates	Not Listed
<i>Pyrgulopsis morrisoni</i>	Page springsnail	restricted	invertebrate	Invertebrates	Not Listed
<i>Procambarus orcinus</i>	Woodville Karst Cave Crayfish	restricted	invertebrate	Invertebrates	Not Listed
<i>Cryptomastix devia</i>	Puget Oregonian	wide-ranging	invertebrate	Invertebrates	Not Listed
<i>Rhaphiomidas trochilus</i>	San Joaquin Valley Giant Flower-Loving Fly	restricted	invertebrate	Invertebrates	Not Listed
<i>Euphilotes ancilla cryptica</i>	Spring Mountains dark blue butterfly late form	restricted	invertebrate	Invertebrates	Not Listed
<i>Euphilotes ancilla purpura</i>	The Spring Mountains dark blue butterfly early form	restricted	invertebrate	Invertebrates	Not Listed
<i>Heterelmis stephani</i>	Stephan's Riffle Beetle	restricted	invertebrate	Invertebrates	Not Listed
<i>Procambarus pictus</i>	Black Creek Crayfish	restricted	invertebrate	Invertebrates	Not Listed
<i>Pyrgulopsis thompsoni</i>	Huachuca springsnail	restricted	invertebrate	Invertebrates	Not Listed
<i>Alasmidonta varicosa</i>	Brook floater	wide-ranging	invertebrate	Invertebrates	Not Listed
<i>Pyrgulopsis turbatrix</i>	Southwest Nevada Pyrg	restricted	invertebrate	Invertebrates	Not Listed
<i>Bombus terricola</i>	Yellow Banded Bumble Bee	wide-ranging	invertebrate	Invertebrates	Not Listed
<i>Hemphillia burringtoni</i>	Burrington Jumping Slug	wide-ranging	invertebrate	Invertebrates	Not Listed
<i>Oncorhynchus clarkii virginalis</i>	Rio Grande Cutthroat Trout	wide-ranging	fish	Vertebrates	Candidate
<i>Percina antesella</i>	Amber Darter	restricted	fish	Vertebrates	Endangered
<i>Fundulus julisia</i>	Barrens Topminnow	restricted	fish	Vertebrates	Endangered
<i>Ptychocheilus lucius</i>	Colorado Pikeminnow	wide-ranging	fish	Vertebrates	Endangered
<i>Xyrauchen texanus</i>	Razorback Sucker	restricted	fish	Vertebrates	Endangered
<i>Notropis topeka</i>	Topeka shiner	wide-ranging	fish	Vertebrates	Endangered
<i>Etheostoma chienense</i>	Relict Darter	restricted	fish	Vertebrates	Endangered
<i>Etheostoma osburni</i>	Candy Darter	restricted	fish	Vertebrates	Endangered
<i>Notropis mekistocholas</i>	Cape Fear shiner	restricted	fish	Vertebrates	Endangered
<i>Percina rex</i>	Roanoke Logperch	restricted	fish	Vertebrates	Endangered
<i>Oncorhynchus apache</i>	Apache trout	restricted	fish	Vertebrates	Threatened
<i>Etheostoma trisella</i>	Trispot Darter	restricted	fish	Vertebrates	Threatened
<i>Noturus munitus</i>	Frecklebelly Madtom	restricted	fish	Vertebrates	Threatened
<i>Etheostoma forbesi</i>	Barrens Darter	restricted	fish	Vertebrates	Not Listed
<i>Lavinia exilicauda chi</i>	Clear Lake Hitch	restricted	fish	Vertebrates	Not Listed
<i>Etheostoma cinereum</i>	Ashy Darter	restricted	fish	Vertebrates	Not Listed
<i>Erimystax harryi</i>	Ozark Chub	wide-ranging	fish	Vertebrates	Not Listed

Scientific name	Common name	Range size	Taxonomic group (9 grps)	Taxonomic group (3 grps)	ESA status
<i>Etheostoma maydeni</i>	Redlips Darter	restricted	fish	Vertebrates	Not Listed
<i>Thoburnia atripinnis</i>	Blackfin Sucker	restricted	fish	Vertebrates	Not Listed
<i>Anaxyrus williamsi</i>	Dixie Valley Toad	restricted	amphibian	Vertebrates	Endangered
<i>Ambystoma cingulatum</i>	frosted flatwoods salamander	restricted	amphibian	Vertebrates	Threatened
<i>Necturus lewisi</i>	Neuse River Waterdog	wide-ranging	amphibian	Vertebrates	Threatened
<i>Cryptobranchus alleganiensis alleganiensis</i>	Eastern hellbender	wide-ranging	amphibian	Vertebrates	Not Listed
<i>Plethodon hubrichti</i>	Peaks of Otter Salamander	restricted	amphibian	Vertebrates	Not Listed
<i>Notophthalmus perstriatus</i>	Striped Newt	wide-ranging	amphibian	Vertebrates	Not Listed
<i>Tantilla oolitica</i>	Rim Rock Crowned Snake	restricted	reptile	Vertebrates	Endangered
<i>Chilabothrus granti</i>	Virgin Islands tree boa	restricted	reptile	Vertebrates	Endangered
<i>Gambelia sila</i>	Blunt-nosed Leopard Lizard	restricted	reptile	Vertebrates	Endangered
<i>Pseudemys rubriventris</i>	Northern Red-bellied Cooter	restricted	reptile	Vertebrates	Endangered
<i>Thamnophis sirtalis tetrataenia</i>	San Francisco gartersnake	restricted	reptile	Vertebrates	Endangered
<i>Drymarchon couperi</i>	Eastern indigo snake	wide-ranging	reptile	Vertebrates	Threatened
<i>Glyptemys muhlenbergii</i>	Northern Population of the Bog Turtle	restricted	reptile	Vertebrates	Threatened
<i>Macrochelys suwanniensis</i>	Suwannee alligator snapping turtle	restricted	reptile	Vertebrates	Threatened
<i>Graptemys pearlensis</i>	Pearl River Map Turtle	restricted	reptile	Vertebrates	Threatened
<i>Macrochelys temminckii</i>	Alligator Snapping Turtle	wide-ranging	reptile	Vertebrates	Threatened
<i>Plestiodon egregius egregius</i>	Florida Keys mole skink	restricted	reptile	Vertebrates	Threatened
<i>Sistrurus catenatus</i>	Eastern Massassauga rattlesnake	wide-ranging	reptile	Vertebrates	Threatened
<i>Pseudemys gorzugi</i>	Rio Grande Cooter	wide-ranging	reptile	Vertebrates	Not Listed
<i>Elgaria panamintina</i>	Panamint Alligator Lizard	restricted	reptile	Vertebrates	Not Listed
<i>Gopherus morafkai</i>	Sonoran Desert Tortoise	wide-ranging	reptile	Vertebrates	Not Listed
<i>Charina umbratica</i>	Southern Rubber Boa	restricted	reptile	Vertebrates	Not Listed
<i>Clonophis kirtlandii</i>	Kirtland's snake	wide-ranging	reptile	Vertebrates	Not Listed
<i>Heterodon simus</i>	Southern Hognose Snake	wide-ranging	reptile	Vertebrates	Not Listed
<i>Picoides borealis</i>	Red-cockaded woodpecker	wide-ranging	bird	Vertebrates	Endangered
<i>Strix occidentalis occidentalis</i>	California Spotted Owl	wide-ranging	bird	Vertebrates	Endangered
<i>Lagopus leucura rainierensis</i>	Mount Rainier White-tailed Ptarmigan	wide-ranging	bird	Vertebrates	Threatened
<i>Centrocercus minimus</i>	Gunnison Sage-Grouse	restricted	bird	Vertebrates	Threatened
<i>Aphelocoma coerulescens</i>	Florida Scrub Jay	wide-ranging	bird	Vertebrates	Threatened

Scientific name	Common name	Range size	Taxonomic group (9 grps)	Taxonomic group (3 grps)	ESA status
<i>Drepanis coccinea</i>	ʻIiwi	wide-ranging	bird	Vertebrates	Threatened
<i>Laterallus jamaicensis jamaicensis</i>	Eastern black rail	wide-ranging	bird	Vertebrates	Threatened
<i>Eremophila alpestris strigata</i>	Streaked Horned Lark	restricted	bird	Vertebrates	Threatened
<i>Artemisiospiza belli clementeae</i>	San Clemente Bell's Sparrow	restricted	bird	Vertebrates	Delisted
<i>Vireo atricapilla</i>	Black-capped vireo	wide-ranging	bird	Vertebrates	Delisted
<i>Ammodramus maritimus macgillivraii</i>	MacGillivray's Seaside Sparrow	restricted	bird	Vertebrates	Not Listed
<i>Odocoileus virginianus clavium</i>	Key deer	restricted	mammal	Vertebrates	Endangered
<i>Sorex ornatus relictus</i>	Buena Vista Lake ornate shrew	restricted	mammal	Vertebrates	Endangered
<i>Myotis septentrionalis</i>	Northern long-eared bat	wide-ranging	mammal	Vertebrates	Endangered
<i>Perimyotis subflavus</i>	Tricolored Bat	wide-ranging	mammal	Vertebrates	Endangered
<i>Zapus hudsonius luteus</i>	New Mexico meadow jumping mouse	restricted	mammal	Vertebrates	Endangered
<i>Dipodomys ingens</i>	Giant Kangaroo Rat	restricted	mammal	Vertebrates	Endangered
<i>Neotamias minimus atristriatus</i>	Penasco least chipmunk	restricted	mammal	Vertebrates	Endangered
<i>Sylvilagus bachmani riparius</i>	Riparian Brush Rabbit	restricted	mammal	Vertebrates	Endangered
<i>Mustela nigripes</i>	Black-footed Ferret	wide-ranging	mammal	Vertebrates	Endangered
<i>Martes caurina</i>	Coastal marten	restricted	mammal	Vertebrates	Threatened
<i>Dipodomys stephensi</i>	Stephens' Kangaroo Rat	restricted	mammal	Vertebrates	Threatened
<i>Cynomys leucurus</i>	White-tailed prairie dog	wide-ranging	mammal	Vertebrates	Not Listed