Evaluation of genetic diversity indicators for Ontario species

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Abstract

Genetic diversity is essential for maintaining the viability of populations. Despite its importance, genetic diversity has largely been ignored in global biodiversity monitoring due to the cost and expertise required to conduct genetic studies. To address this, new genetic diversity indicators that can be estimated in the absence of genetic data have been developed to allow rapid assessment across many species. Here we apply a genetic indictor approach to assess the genetic health of Ontario's biodiversity. We capitalize on existing estimates of genetic diversity from published studies and calculate proxies of genetic diversity from census data to report on the status of 115 populations spanning 50 species and eight taxonomic groups. We found that 56% of all assessed populations are likely too small to maintain genetic diversity long-term. At the species level, just under half of species (46%) had at least one population in Ontario that that fell below the minimum effective population size needed to maintain genetic diversity. Our results suggests that many Ontario species may be at risk of genetic erosion and highlights the need for genetic diversity monitoring.

Introduction

Biodiversity encompasses the vast array of life on earth, spanning genetic, species, and ecosystem diversity. Genetic diversity reflects the variation in genetic material within and among populations of organisms (DeWoody et al., 2021; Hoban et al., 2023; Mastretta-Yanes et al., 2024a) and it is fundamental to a species' ability to survive and adapt in response to environmental changes (Hoban et al., 2023). Many species are facing population declines due to a myriad of threats, and with decline comes a loss of genetic variation through the stochastic process of genetic drift (Kardos et al., 2021). Low genetic variation in turn increases inbreeding, which can expose harmful mutations that reduce the survival of individuals and subsequently leads to further decreases in population size (Fagan and Holmes, 2006). Populations that are small and have little genetic variation are also unlikely to be able to adapt to environmental change (Frankham, 2005). Therefore, maintaining populations at sizes that are large enough to preserve genetic diversity is crucial for long term viability (DeWoody et al., 2021).

Despite being recognized as one of three key pillars of biodiversity, genetic diversity has been largely ignored in biodiversity reporting and is not included in IUCN Red List status assessments (Schmidt et al., 2023). This has led to recent efforts to better integrate genetics into biodiversity monitoring (Hoban et al., 2021; Laikre et al., 2020). The Kunming-Montreal Global Biodiversity Framework (GBF), adopted in 2022, represents the first global commitment to conserving genetic diversity across all species. Historically, genetic diversity has been overlooked due to the complexity and cost of genetic studies. To address this, the GBF has adopted genetic indicators that can be estimated in the absence of genetic data. Genetic diversity indicators are not meant to replace DNA sequence-based studies, which provide important information on gene flow, inbreeding, and adaptation to inform species management (Hoban et al., 2024). Rather, genetic diversity indicators provide a tractable and repeatable method for estimating proxies of genetic diversity at the scale required for biodiversity reporting and monitoring – i.e. across tens to thousands of species. Indicators provide a first-pass assessment of the genetic health of biodiversity, which can be used to prioritize species or populations that may warrant more detailed genetic studies (Hoban et al., 2024).

The N_e>500 indicator is one of three genetic diversity indicators adopted under the Kunming-Montreal GBF. This indicator reports the number of populations within a species that have effective population sizes greater than 500. Effective population size (N_e) is a key measure of genetic diversity as it determines the rate of genetic drift – i.e. the rate at which genetic diversity is lost in a population due to stochastic processes (Waples, 2022). Small populations experience higher genetic drift and will consequently lose genetic variation much faster than large populations (Kardos et al., 2021). A long-standing guiding principal in conservation genetics is that an effective population size of at least 50 is needed to prevent short-term inbreeding, while 500 is required to ensure long-term ability to adapt to environmental change (Jamieson and Allendorf, 2012). The N_e>500 indicator therefore tracks the proportion of populations within a

species exceeding this critical upper threshold. An N_e>500 indicator value of 0 indicates that all populations are likely too small to maintain the levels of genetic diversity needed to remain viable, while an N_e>500 indicator of 1 indicates the ideal state where all populations are large enough to maintain genetic diversity.

Crucially, N_e can be approximated from census population size (N_c, i.e. number of mature individuals in a population) in the absence of genetic data for many species. Effective population size is typically much smaller than census population size, and several studies have examined factors affecting the relative size of N_e to N_c in natural populations (Lee et al., 2011; Waples et al., 2013). Population size fluctuations, variance in family size, the type of population measure, taxonomic group, and unequal sex ratios can all influence expected N_e/N_c ratios (Frankham, 1995). However, on average, most populations have been found to have an Ne/Nc ratio near 0.1 (Hoban et al., 2021). This has been corroborated by multiple studies, covering over a hundred species and thousands of populations (Clarke et al., 2024; Frankham, 1995; Palstra and Fraser, 2012). Therefore, census populations sizes exceeding 5000 individuals can serve as an appropriate benchmark for population viability in the absence of genetic data for many species (Fedorca et al., 2024).

Here we estimate genetic indicators to assess the genetic health of Ontario's biodiversity. We capitalize on existing estimates of N_e from published studies and calculate proxies of Ne from census data to report on the N_e>500 indicator for 50 species spanning eight taxonomic groups. Our aim is to determine if, on average, Ontario species have enough genetic diversity to remain viable in the long-term, and identify those species that fail to meet the N_e>500 threshold and may require further study. To our knowledge this represent the first attempt to assess the genetic status of a large group of species in the province. This work will provide a baseline for future monitoring to track progress towards biodiversity targets.

Methods

We designed our study based on pilot studies and project guidance documents developed by other research groups (Mastretta-Yanes et al., 2024b). These resources provide a standardized framework to align our methods with established principles and objectives. We used a pre-existing questionnaire from KoboToolBox (https://www.kobotoolbox.org/), an open-source platform for data collection and management, to conduct our assessments. In addition to recording data on the number and effective or census size of populations for each species, we recorded standard metadata in Kobo forms such as the species' realm (marine, estuarine, freshwater, or terrestrial), IUCN habitat classification, the proportion of the species' range occurring within Ontario, and whether the species is naturally rare. Additional information, including citations (literature references, expert consultations, or websites) and justifications for decisions about the data used, was documented to support the species' profile. This comprehensive approach ensured a clear and consistent recording of information that can be used

in future re-assessments of the same species. The collected data were then exported as a .csv file and analyzed in R version 4.3.3, using custom functions and a processing pipeline created by the original teams for data quality checks, indicator calculations, and further analyses (Mastretta-Yanes et al., 2024b).

Species Selection

We selected species based on guidelines outlined in the Global Biodiversity Framework guidance document (Mastretta-Yanes et al., 2024b). Selecting only charismatic species, those with economic value, or rare and endangered species could skew the indicator toward reflecting the genetic condition of a specific subset rather than the broader species pool. Our approach aimed to therefore represent a diverse range of taxonomic groups, ecosystems, distributional ranges, conservation statuses, and life history traits. We created an initial list by choosing species across a range of statuses and taxonomic groups from a list of those that have been assessed by the Committee on the Status of Species at Risk in Ontario (COSSARO). We supplemented with additional species that have economic value or are managed in the province or had published or unpublished data available.

Defining extant populations

After compiling the species list, we determined the number of extant populations within Ontario for each species. For the purposes of this analysis, we defined a population as a group of individuals that can mate with each other and has little to no gene flow with other groupings of individuals. This is the most relevant definition for effective population size, since estimates of N_e generally assume that populations are randomly mating with no immigration (Fedorca et al., 2024). Note that the population definition used here differs from that used in provincial and federal species assessments. For example, based on our definition of a population, a single Designatable Unit defined in a provincial or federal status assessment may have been assessed as several distinct populations.

If genetic data were available, populations were defined based on published genetic clusters or clades, which represent genetically distinct groupings of individuals (Pritchard et al., 2000). The number of genetic clusters identified in an analysis is sensitive to the number of individuals and resolution of genetic markers (Pritchard et al., 2000) and the presence of unsampled populations (Puechmaille, 2016). In many cases, genetic structure is not clear-cut and can present as a gradient of admixed individuals or structure can be hierarchical at different spatial scales (Meirmans, 2012). Therefore, not every genetic cluster should be taken as a separate and distinct population. We carefully considered the above scenarios when making decisions and consulted species experts when possible.

In the absence of information on genetic groupings, we defined populations based on species occurrences within Ontario combined with knowledge of dispersal ability, geographic barriers, biogeographic boundaries, and trait differences. Specifically, we grouped species occurrences

that were within a reasonable species-specific dispersal distance into the same population and further considered geographic and anthropogenic barriers that might prevent dispersal and merit population separation. In some cases, populations were defined based on evidence of distinct traits or biogeographic boundaries, which might suggest local adaptation or the presence of significant evolutionary units.

Estimating population sizes

Once population boundaries were defined, we gathered population-level data on both effective (N_e) and census (N_c) population size. Existing estimates of contemporary N_e from genetic markers were obtained from scientific publications, graduate theses, and unpublished data held by research teams. Estimates of N_c were derived from counts of mature individuals, estimates from mark-recapture, and extrapolations based on habitat area and known density obtained from scientific publications, provincial (Committee on the Status of Species at Risk in Ontario; COSSARO) and federal (Committee on the Status of Endangered Wildlife in Canada; COSEWIC) species status assessments and management reports. For plants, we only estimated N_c from counts when they were likely to reflect the number of genetic individuals (i.e. genets) rather than the number of stems to avoid counting clones (i.e. ramets). For species that exhibit extreme fluctuations in populations size, we only included estimates of N_c if they reflected a multi-year average. When precise census population size estimates were not available, a quantitative range (e.g. 100-200 individuals) or qualitative estimate (<5000 by much, <5000 but not by much, >5000 but not by much, >5000 by much) was recorded in consultation with taxonomic experts.

Calculating the Ne>500 indicator

For populations that lacked genetic estimates of N_e, we used census population size (N_c) to calculate a proxy of N_e using a standard N_e/N_c ratio of 0.1 (Frankham, 1995). We then calculated the N_e>500 indicator for each species as the proportion of populations that have a N_e greater than 500. The resulting indicator represent the proportion (ranging from 0 to 1) of populations exceeding the threshold, with 1 indicating the ideal state—where all populations have an effective population size above 500. In addition to reporting species and taxonomic group-specific indicator values, we further calculated an Ontario mean value. The Ontario mean genetic indicator was calculated by taking the mean of each taxonomic group's mean (Mastretta-Yanes et al., 2024b). This approach was used to reduce the influence of those groups that are overly represented as we had an uneven number of species in each taxonomic group.

Establishing Baselines for N_e>500 Indicator

For the N_e>500 indicator, we selected a 20-year assessment window (2004–2024) to maximize data availability. Countries, following the CBD's monitoring framework, are advised to choose a baseline that fits their specific context (Mastretta-Yanes et al., 2024b). In most cases, the data used for the N_e>500 indicator came from the past decade. Since population data was often

collected in different years, we recorded the corresponding years separately to ensure a clear and accurate temporal baseline.

Results

Out of an initial list of 67 species, 50 had data to calculate genetic indicators for at least one population. These 50 species spanned eight taxonomic groups—amphibians, reptiles, birds, mammals, fish, insects, molluscs, and plants (Table 1). Birds and mammals were the best represented, each with 12 species included in the final dataset. Insects were least represented, with only two species with enough data to calculate indicators. Final assessments included 15 species listed as endangered by COSSARO, 17 listed as threatened, 12 listed as special concern, and six not at risk. In total 115 populations were assessed (Table 1).

Table 1: Summary of species, populations, and mean Ne>500 indicator values across taxonomic groups in Ontario. The table presents the number of species and populations assessed for each taxonomic group, along with the mean Ne>500 indicator value for each taxon with standard deviation. The Ne>500 indicator reflects the proportion of populations within species with an effective population size exceeding 500, averaged over taxonomic groups.

Taxon	Number of species in each taxon	Number of populations assessed	Mean of Ne>500 indicator
Amphibian	3	5	0
Bird	12	12	0.83 ± 0.39
Fish	3	29	0.41 ± 0.51
Insect	2	2	1
Mammal	12	18	0.54 ± 0.50
Mollusc	6	19	0.98 ± 0.05
Plant	8	21	0.29 ± 0.36
Reptile	4	9	0.56 ± 0.51
	Total = 50	Total = 115	Mean= 0.58 ± 0.35

Census data constituted most of the population size information used to estimate N_e (Appendix 1). Of the 50 species assessed, only 12 (24%) had genetic estimates of effective population size for at least one population. For the remaining 38 (76%) species, we relied on census population size to estimate proxies of N_e. We note that in several cases, genetic N_e estimates were available

for other species but not included in our analysis as they were estimated at spatial scales that were not consistent with our definition of a population. In cases where populations had both census and genetic estimates available, estimates tended to agree with each other except in one population in the eastern foxsnake (*Pantherophis vulpinus*), where genetic estimates of N_e exceeded those extrapolated from census size.

Across all 115 assessed populations, 64 (56%) had estimated effective population sizes below 500, indicating that most assessed populations are not large enough to maintain genetic diversity. At the species-level, the distribution of the N_e>500 indicator was bimodal, with most species either having a value of 0 (i.e. all populations within the species had effective population sizes under 500, n=15, 30%) or 1 (i.e. all populations within the species had effective population sizes over 500, n=27, 54%), with few in between (Figure 1).

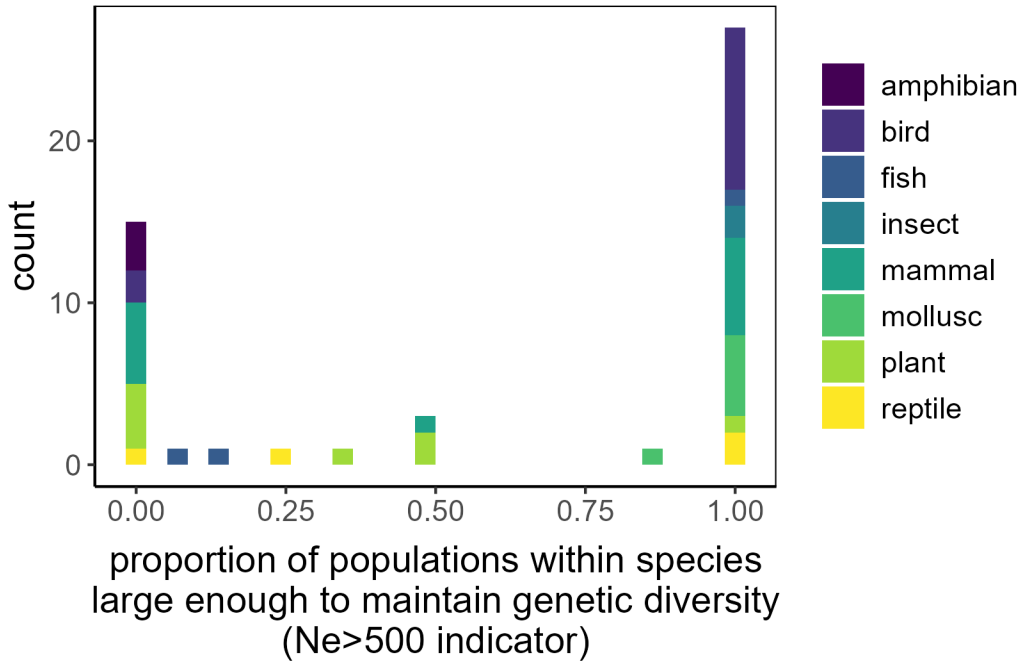

Figure 1. Distribution of species-level Ne>500 genetic diversity indicators. The Ne>500 indicator describes the proportion of populations within a species that exceeds an effective population size of 500. Each bar is color-coded to indicate taxonomic groups.

The values varied across taxonomic groups (Figure 2; Table 1), with insects, birds, and molluscs having mean N_e>500 values at or close to 1 and other groups having mean indicator values under 0.6. Endangered species had on average the lowest N_e>500 indicator values, while species of special concern had the highest (Figure 3). The mean N_e>500 indicator for Ontario (i.e. the average of taxon-averaged indicators) is 0.58 with a standard deviation of 0.35 (Table 1).

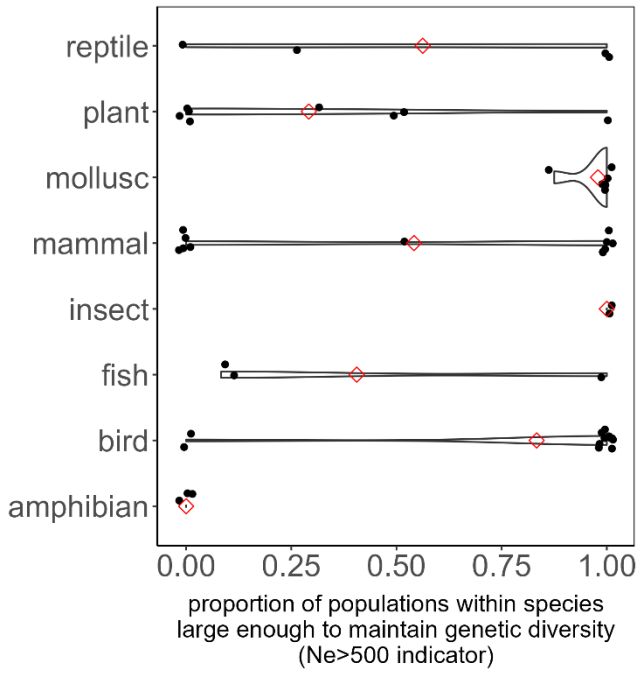

Figure 2. Violin plots showing the distribution of species-level Ne>500 genetic diversity indicators across taxonomic groups. Red diamonds show mean Ne>500 per taxonomic group.

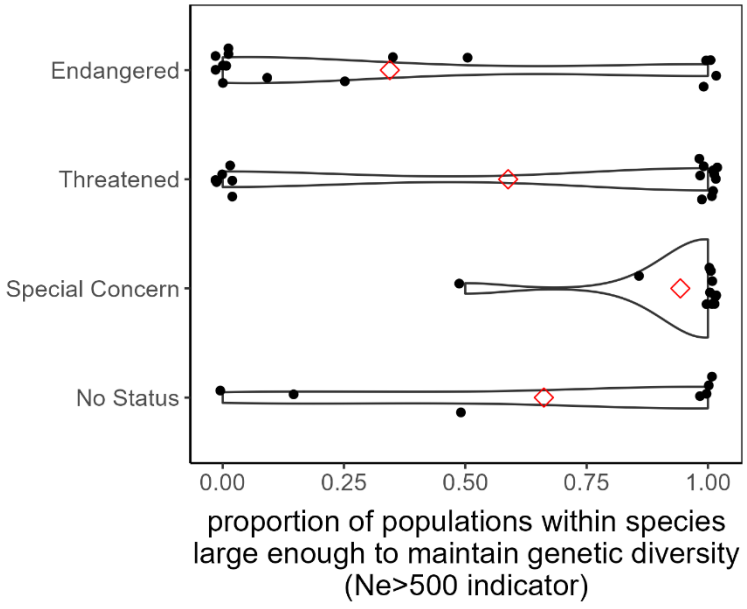

Figure 3. Violin plots showing the distribution of species-level Ne>500 genetic diversity indicators for species with different conservation statuses according to the Committee on the Status of Species at Risk in Ontario (COSSARO). Species assessed by COSSARO as 'not at risk' were lumped with species that have not been assessed in the 'no status' category.

Discussion

Bias in the species pool

We aimed to assess genetic diversity indicators in a representative group of Ontario species. Ultimately, we estimated indicators for 50 species from an initial list of 67. The resulting data is not without biases – several taxonomic groups were under-represented, and most of the species assessed are species-at-risk. Therefore, averaged results should be interpreted with caution as they likely do not represent the true diversity of Ontario's estimated 30,000 species. Nevertheless, these first efforts are necessary to establish infrastructure and methods for data collection and analysis and highlight areas for improvement. Current guidelines (Mastretta-Yanes et al., 2024b) suggest assessing 100 species to achieve a representative sample, and this target is likely achievable in the future for Ontario species.

Insects and plants make up most of Ontario's biodiversity, yet these groups were represented by only 2 and 8 species in our dataset, respectively. The lack of representation of these groups is not an Ontario-specific problem. For described species globally, only 1.3% of insects and 18% of plants have been assessed by the International Union for Conservation of Nature (IUCN) for the Red List of Threatened Species (IUCN 2025). In contrast, 78-100% of all described mammals, birds, reptiles, amphibians, and fishes have been assessed by IUCN. In part, this discrepancy in biodiversity reporting for insects and plants reflects a general lack of appropriate knowledge and census data. Many insect populations are large and fluctuate widely across years (Fox et al., 2019) and therefore single year censuses are not useful for describing the effective size of populations. For plants, we had to exclude many species in our original list due to their clonality, as counts of individual reproductive stems do not reflect the number of genetic individuals. Other plant species were excluded due to a lack of knowledge of population structure across Ontario. Plant gene flow is complicated as seeds and pollen can be carried by multiple abiotic or biotic vectors (Auffret et al., 2017), and due to their sessile nature, many plant populations are also locally adapted to their environment (Flood and Hancock, 2017). This means that defining the number of extant populations based on distributions alone may not be an appropriate method for many plant species. Given these challenges, greater investment in genetic studies may be warranted to improve genetic indicator estimates for insects and plants in Ontario.

Our species list was primarily based on the availability of data from conservation reports (COSSARO and COSEWIC reports) and relevant publications in Ontario, which resulted in a bias toward species-at-risk. Based on our experiences gathering census data from these reports, we see an opportunity to expand to other, non-listed species in the future. For example, most of the species-at-risk bird population size estimates reported in COSSARO and COSEWIC came from extrapolations of Ontario Breeding Bird Atlas counts. The Ontario Breeding Bird Atlas contains point count data for 124 Ontario bird species, and thus future efforts might focus on

collaborating with an expert to estimate population sizes for a more representative group. Similar data is available for butterflies from the North American Butterfly Association butterfly counts.

N_e>500 Indicator

Across all 115 assessed populations, 56% (n=64) had estimated effective population sizes under 500, suggesting that most are likely too small to maintain genetic diversity in the long term. At the species-level, 46% (n=23) had N_e>500 values under 1, meaning that at least one of their populations in Ontario failed to meet the threshold needed to maintain genetic diversity. The overall N_e>500 genetic indicator for Ontario was 0.58; this is higher than published indicators from nine countries, which ranged from 0.08-0.42 (Mastretta-Yanes et al., 2024a). Given certain biases in the species pool for our analysis, it remains to be seen if this is reflective of the actual state of Ontario species. Nevertheless, our work provides a baseline for future monitoring.

Birds, insects, and molluscs had the highest average indicators, ranging from 0.83-1 (Table 1), suggesting that these groups support populations large enough to maintain genetic diversity. This is not surprising considering that many of the birds (e.g. barn swallow, evening grosbeak) and both insects (monarch and yellow-banded bumblebee) that we assessed have relatively continuous distributions across large parts of Ontario. Molluscs also had consistently high estimates of N_e>500, despite several of the included mussel species experiencing drastic population declines. For example, the kidneyshell (*Ptychobranchus fasciolaris*) is estimated to have declined by 50% in Ontario over the last three generations (COSSARO, 2013). Our results suggest that populations may not have yet declined to the point where the ability to maintain genetic diversity is compromised. However, failure to address ongoing threats and continued declines are expected to lead to genetic diversity loss eventually (DiLeo et al., 2024; Kardos et al., 2021). Furthermore, because genetic responses are lagged in response to disturbance, genetic diversity can continue to decline even after populations stabilize, particularly in species with long generation times (Gargiulo et al., 2025). This highlights that genetic indicators should not be used in isolation to assess species conservation status.

Thirty percent of species had N_e>500 values of zero, meaning that none of their populations meet the threshold needed to maintain genetic diversity in the long-term. Of the eight taxonomic groups assessed, amphibians had the lowest average genetic diversity indicator value (Table 1). This is in line with results from a recent global meta-analysis of genetically-derived N_e estimates which found that amphibians were the least likely taxonomic group to exceed the N_e>500 threshold (Clarke et al., 2024). However, we only assessed three amphibian species, all of which are endangered and have extremely restricted ranges. A more representative sample is likely to reveal more optimistic genetic diversity indicator values for this group as many amphibian species have extensive ranges within the province.

As expected, species listed as endangered in Ontario by COSSARO had the lowest average N_e>500 indicators. In addition to ecological threats, our results suggest these species are also at

risk of experiencing negative impacts associated with low genetic diversity (Fagan and Holmes 2006). As recovery efforts proceed, the genetic status of these species may need to be considered. While localized efforts to protect populations and reduce threats may increase census population size, genetic diversity can only be recovered if gene flow among population is restored or genetic variation is introduced through other interventions (e.g. translocations or re-introduction from ex situ populations; Whiteley et al., 2015).

Low N_e>500 indicators were not restricted to endangered species; notably, even among some wide-ranging taxa, the N_e>500 indicator tends to be skewed toward lower values, as seen in species like the black bear, caribou, and muskellenge. Species with broad ranges are generally considered to be at lower conservation risk (Staude et al., 2020). For example, the black bear is classified as Least Concern on the IUCN Red List, yet certain populations within the species face significant threats. For other species like muskellunge, low contemporary N_e might reflect naturally low historical population sizes. Many species reach their northern range limit in Ontario and populations at range edges tend to be smaller, more isolated, and subject to increased genetic drift and reduced gene flow than populations at the center of their range (Eckert et al., 2008; Hengeveld and Haeck, 1982; Vucetich and Waite, 2003). This is exacerbated in regions that experience glaciation such as Ontario, where post-glacial recolonization causes repeated founded events and bottlenecks as species expanded north from southern refugia (Eckert et al., 2008; Hewitt, 2000; Hoffmann and Blows, 1994).

Caveats

Most of the data used in this study came from census population size proxies of N_e. The lack of available genetic estimates of N_e highlights that a proxy approach is needed for any meaningful genetic biodiversity reporting (Hoban et al., 2024). However, results should be interpreted cautiously as N_c does not always accurately reflect N_e and N_e/N_c cannot always be assumed to be 0.1 (Clarke et al., 2024). Genetic estimates of effective population size and N_e/N_c ratios are sensitive to factors such as spatial structure, life history traits, and whether generations overlap (Falconer, 1981; Frankham, 1995; Wright, 1984). Future work should consider taxon- or species-specific ratios, and test if our results are robust to different assumptions.

Another challenge we faced was defining the number of extant populations for species. This is a critical step, as it determines the spatial scale at which population size is estimated (Fedorca et al., 2024). For species with highly disjunct populations and low dispersal ability this was a relatively straight forward exercise. However, many species show complex spatial population structures, and defining populations involved a degree of subjectivity. For example, both existing census population size and genetic effective population size estimates for the eastern foxsnake (*Pantherophis vulpinus*) come from three disjunct populations in Ontario (COSSARO, 2022; Row et al., 2011). However, genetic studies suggest that one of these populations is further subdivided into several genetic clusters over small spatial scales (DiLeo et al., 2010; Row et al., 2010). We lumped these on the basis that there are no obvious barriers to dispersal that would

prevent gene flow among these clusters. However, future work can account for this uncertainty by averaging indicators over alternative assessment for the same species. For other species such as birds, information on population structure was completely lacking. We assigned all but one bird species to a single population in Ontario based on the best available data suggesting ranges are continuous and dispersal ability large. However, despite continuous ranges, birds can exhibit genetic and trait divergence over small spatial scales (Garrido-Bautista et al., 2024; Garroway et al., 2013). The degree to which this applies to Ontario bird species is unknown and highlights the need for genetic studies to clarify population structure.

Conclusions

Our study demonstrates that calculating genetic diversity indicators is feasible for monitoring a previously overlooked aspect of biodiversity. Our assessment reveals that while many species in Ontario maintain most of their populations at sufficient size to protect genetic diversity, a similar number are at risk of losing genetic diversity due to small population size. Our results suggests that many Ontario species may be at risk of genetic erosion and highlights the need for genetic diversity monitoring. This work will provide a baseline for future monitoring to track progress towards biodiversity targets.

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Appendix

Appendix 1. Percentage of species within each taxonomic group that had genetic estimates of effective population size (Ne) available, census population size (Nc), or both.

Taxonomic Group	Total Count	% with Ne Data	% with Nc Data	% with Both
Amphibian	3	0.00%	100.00%	0.00%
Bird	12	0.00%	100.00%	0.00%
Fish	3	100.00%	33.33%	33.33%
Insect	2	50.00%	50.00%	0.00%
Mammal	12	33.33%	91.67%	25.00%
Mollusc	6	33.33%	66.67%	0.00%
Plant	8	0.00%	100.00%	0.00%
Reptile	4	50.00%	100.00%	50.00%

Appendix 2. Ne>500 genetic indicators for 50 species. COSSARO status, the number of populations within species with either Ne or Nc data, the number of populations within species that had effective population sizes over 500, and the species Ne>500 indicator (proportion of populations within species with Ne over 500) are shown.

Common Name	Scientific Name	Taxonomic Group	COSSARO status	Number of populations with data	Number of populations over Ne500	Proportion of populations over Ne500 (Ne>500)
Fowler's toad	Anaxyrus fowleri	amphibian	Endangered	3	0	0
Northern Dusky Salamander	Desmognathus fuscus	amphibian	Endangered	1	0	0
Allegheny Mountain Dusky Salamander	Desmognathus ochrophaeus	amphibian	Endangered	1	0	0
Barn owl	Tyto alba	bird	Endangered	1	0	0
Louisiana Waterthrush	Parkesia motacilla	bird	Threatened	1	0	0
Eastern-Whip-poor-will	Antrostomus vociferus	bird	Special Concern	1	1	1
Common Nighthawk	Chordeiles minor	bird	Special Concern	1	1	1
Olive-sided Flycatcher	Contopus cooperi	bird	Special Concern	1	1	1
Rusty Blackbird	Euphagus carolinus	bird	Special Concern	1	1	1
Barn Swallow	Hirundo rustica	bird	Special Concern	1	1	1
Chimney Swift	Chaetura pelagica	bird	Threatened	1	1	1
Evening Grosbeak	Coccothraustes vespertinus	bird	Threatened	1	1	1
Bobolink	Dolichonyx oryzivorus	bird	Threatened	1	1	1
Hudsonian Godwit	Limosa haemastica	bird	Threatened	1	1	1
Lesser Yellowlegs	Tringa flavipes	bird	Threatened	1	1	1
Redside Dace	Clinostomus elongatus	fish	Endangered	12	1	0.08
Muskellunge	Esox masquinongy	fish	No Status	15	2	0.13
Deepwater Sculpin	Myoxocephalus thompsonii	fish	Not at risk	2	2	1
Yellow-banded Bumble Bee	Bombus terricola	insect	Special Concern	1	1	1
monarch	Danaus plexippus	insect	Special Concern	1	1	1
American Badger	Taxidea taxus	mammal	Endangered	2	0	0
Grey fox	Urocyon cinereoargenteus	mammal	Endangered	2	0	0
Elk (Red deer)	Cervus elaphus	mammal	No Status	4	0	0

Eastern wolf	Canis lycaon	mammal	Threatened	1	0	0
Polar bear	Ursus maritimus	mammal	Threatened	1	0	0
Black bear	Ursus americanus	mammal	No Status	2	1	0.5
Little brown myotis	Myotis lucifugus	mammal	Endangered	1	1	1
Moose	Alces alces	mammal	No Status	1	1	1
White tailed deer	Odocoileus virginianus	mammal	No Status	1	1	1
Beluga whale	Delphinapterus leucas	mammal	Not at risk	1	1	1
Grey wolf	Canis lupus	mammal	Threatened	1	1	1
Caribou	Rangifer tarandus	mammal	Threatened	1	1	1
Rainbow	Villosa iris	mollusc	Special Concern	8	7	0.88
Eastern Banded Tigersnail	Anguispira kochi kochi	mollusc	Endangered	4	4	1
Kidneyshell	Ptychobranchus fasciolaris	mollusc	Endangered	1	1	1
Mapleleaf	Quadrula quadrula	mollusc	Special Concern	1	1	1
Purple Wartyback	Cyclonaias tuberculata	mollusc	Threatened	3	3	1
Wavy-rayed lampmussel	Lampsilis fasciola	mollusc	Threatened	2	2	1
Downy Yellow False Foxglove	Aureolaria virginica	plant	Endangered	3	0	0
Spotted Wintergreen	Chimaphila maculata	plant	Threatened	4	0	0
Deerberry	Vaccinium stamineum	plant	Threatened	3	0	0
Hairy Valerian	Valeriana edulis ssp. ciliata	plant	Threatened	3	0	0
Colicroot	Aletris farinosa	plant	Endangered	3	1	0.33
Small White Lady slipper	Cypripedium candidum	plant	Endangered	2	1	0.5
Lakeside Daisy	Tetraneuris herbacea	plant	Special Concern	2	1	0.5
Common Hoptree	Ptelea trifoliata	plant	Special Concern	1	1	1
Eastern Hog-nosed Snake	Heterodon platirhinos	reptile	Threatened	1	0	0
Massasauga rattlesnake	Sistrurus catenatus	reptile	Endangered	4	1	0.25
Eastern Foxsnake	Pantherophis vulpinus	reptile	Endangered	3	3	1
Blanding's turtle	Emys blandingii	reptile	Threatened	1	1	1