INDICATOR: Changes in status of Species at Risk

Startegic Direction: Enhanced Resilience

Target: 11 By 2030, the conservation of species and ecosystems in Ontario is improved.

Theme: State of Ecosystems and Species

Background Information

Biodiversity is the variety of life on earth and exists at three levels — ecosystems, species and genetics. Genetic diversity reflects the variation in genetic material within and among populations and organisms (DeWoody et al., 2021; Hoban et al., 2023; Mastretta-Yanes et al., 2024a) and is fundamental to a species' ability to survive and adapt in response to environmental changes (Hoban et al., 2023; Jalilvand et al. 2025). A reduction in genetic diversity can occur when species populations decline; smaller populations have little genetic variation and are unlikely to be able to adapt to environmental change (Frankham, 2005). Maintaining populations at sizes large enough to preserve genetic diversity is crucial for long-term viability (DeWoody et al. 2021).

Despite being recognized as one of the three key pillars of biodiversity, genetic diversity has largely been ignored in global biodiversity monitoring due to the cost and expertise required to conduct genetic studies. Recent efforts have been made to better integrate genetic information into biodiversity monitoring (Hoban et al. 2021). The Kunming-Montreal Global Biodiversity Framework (GBF), adopted in 2022, represents the first global commitment to conserving genetic diversity across all species. To address this, the GBF has adopted genetic indicators that can also 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 Ne>500 indicator is one of three genetic diversity indicators adopted under the Kunming-Montreal GBF. It measures the proportion of populations within a species which are of sufficient size to maintain genetic diversity and adaptive potential (GEOBON 2025). Effective population size (Ne) describes the 'genetic size' of a population. When a population is below a threshold of approximately Ne=500, genetic diversity loss starts to occur. Small populations will lose genetic variation much faster than large populations (Kardos et al., 2021). A long-standing guiding principle 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). Crucially, Ne can be approximated from census population size (Nc i.e. number of mature individuals in a population) in the absence of genetic data for many species. This is known as the 50/500 Rule. This approach has been applied across taxa, however, it is important to note that the likelihood of achieving this threshold is not necessarily equal across different taxonomic groups, and awareness is required when interpreting the results.

This report estimates genetic indicators to assess the genetic health of Ontario's biodiversity based on analysis completed by the MNR. See the full report, including a full list of species, here.

Data Analysis

In this report, genetic indicators are estimated to assess the genetic health of Ontario's biodiversity. Ne>500 indicators for 50 species spanning eight taxonomic groups are calculated from existing estimates of effective population size (Ne) from published studies, and calculating proxies of Ne from census data. The 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 Ne>500 threshold and may require further study.

Assessments were conducted using a pre-existing questionnaire from KoboToolBox, an open-source platform for data collection and management.

A step-by-step process was used to define the species, populations, estimate their effective (Ne) size, and compare those to the Ne500 threshold:

1. Selecting species – species were selected based on guidelines outlined in the GBF guidance document (Mastretta-Yanes et al., 2024b), representing a diverse range of taxonomic groups, ecosystems, distributional ranges, conservation status, and life history traits. The initial list was created from species assessed by the Committee on the Status of Species at Risk in Ontario (COSSARO), by choosing species across a range of statuses and taxonomic groups, and additional species were added that have economic value, are managed in the province or, had published or unpublished data available.
2. Defining extant populations — The number of existing populations[1] were determined within Ontario for each species. If genetic data were available, populations were defined based on published genetic clusters or clades[2] , which represent genetically distinct groupings of individuals (Pritchard et al., 2000). In many cases, genetic structure is not clear cut, and in the absence of information about genetic groupings, populations are based on species occurrences within Ontario combined with information of dispersal ability, geographic barriers, biogeographic boundaries, and trait differences. 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.
3. Estimating population sizes — population-level data on both effective (Ne) and census (Nc) population size were gathered. Existing estimates of contemporary Ne from genetic markers were obtained from scientific publications, graduate theses, and unpublished data held by research teams. Estimates of Nc were obtained from counts of mature individuals, estimates from mark-recapture, and estimates based on habitat area and known density obtained from scientific publications, provincial and federal species status assessments and management reports.

4. Calculating the Ne>500 indicator — For populations that lacked genetic estimates of Ne, census population size (Nc) was used to calculate a proxy of Ne using a standard Ne/Nc ratio of 0.1 (Frankham, 1995). The Ne>500 indicator was then calculated for each species as the proportion of populations that have a Ne greater than 500. The resulting indicator represents 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, the Ontario mean value was calculated. 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.
5. Establishing Baselines for Ne>500 Indicator — For the Ne>500 indicator, a 20-year assessment window (2004-2024) was selected to maximize data availability. In most cases, the data used for the Ne>500 indicator came from the past decade.

The information presented in this indicator represents a summary of the technical report: Evaluation of genetic diversity indicators for Ontario Species – March 2025, prepared by the MNR (Jalilvand et al. 2025).

See full report.

Results

Trend: Baseline	**Data Confidence:** Medium	**Geographic Extent:** Provincial

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).

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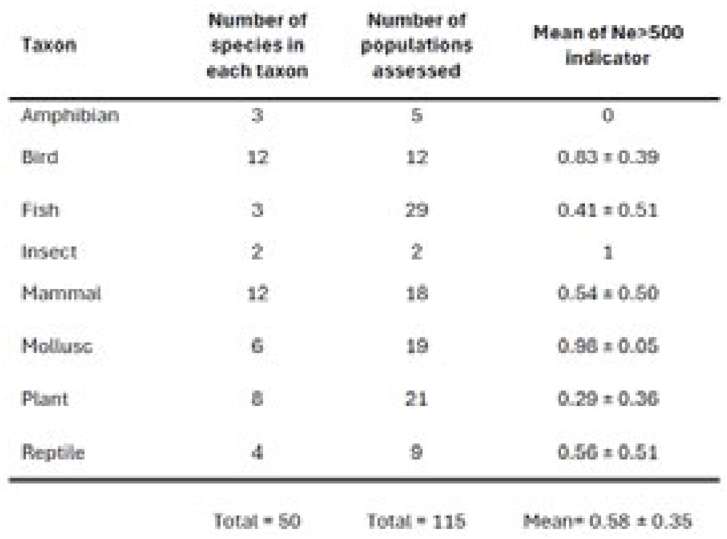
[1] For this analysis population is defined as a group of individuals that can mate with each other and has little to no gene flow with other groupings of individuals, the population definition used here differs from that used in provincial and federal species assessments

[2] A group of organisms believed to have evolved from a common ancestor, according to the principles of cladistics.

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. Note: range is 0-1 with 1 indicating the ideal state.



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 Ne. 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, census population size (Nc) was used to estimate proxies of Ne. 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 Ne 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 Ne>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).

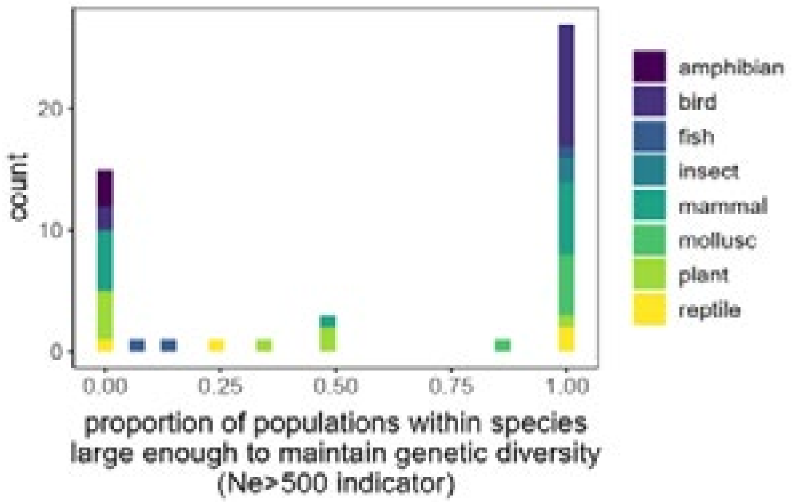


Figure 1. Distribution of species-level Ne>500 genetic diversity indicators. The Ne>500 indicator describes the proportion of populations within a species that exceeds an effective population size of 500. Each bar is color-coded to indicate taxonomic groups.

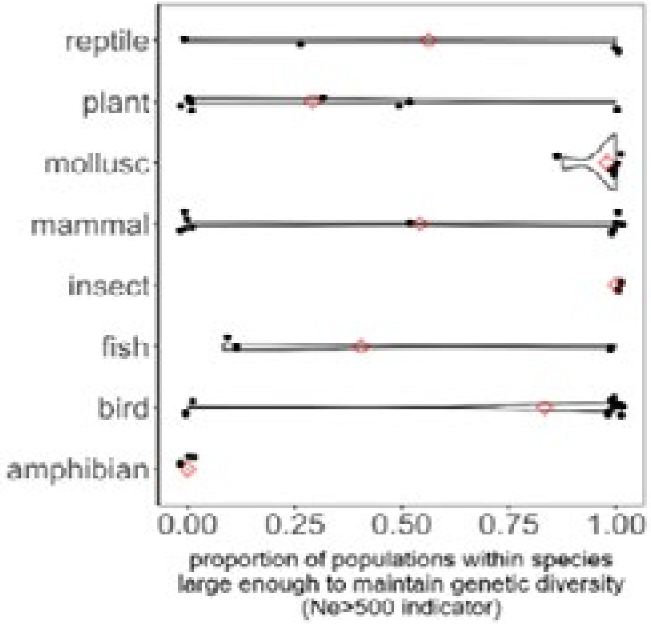


Figure 2. Violin plots showing the distribution of species-level Ne>500 genetic diversity indicators across taxonomic groups. Red diamonds show mean Ne>500 per taxonomic group.

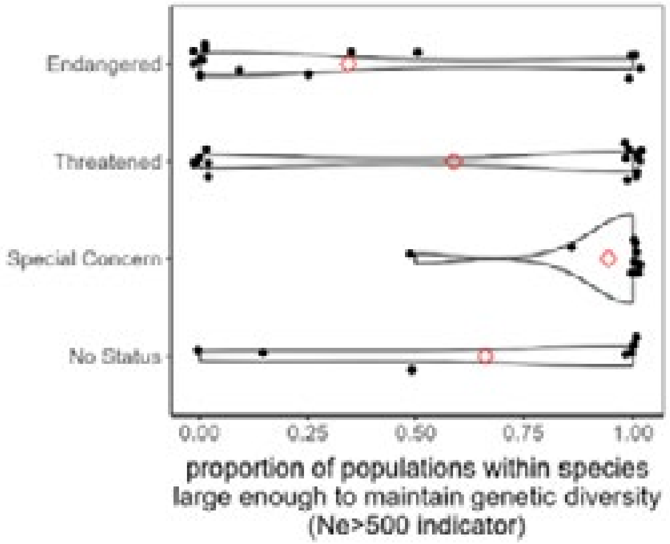


Figure 3. Violin plots showing the distribution of species-level Ne>500 genetic diversity indicators for species with different conservation statuses according to the Committee on the Status of Species at Risk in Ontario (COSSARO). Species assessed by COSSARO as 'not at risk' were lumped with species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

Status

- Out of an initial list of 67 species, 50 species across eight taxonomic groups had data to calculate genetic indicators for at least one population. 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 genetic indicators.
- Of the 50 species assessed, 15 are listed as endangered by COSSARO, 17 listed as threatened, 12 listed as special concern, and six were not at risk. In total 115 populations were assessed (Table 1).
- 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 Ne>500 indicator showed that 30% (n=15) had a value of 0 (i.e. all populations within the species had effective population sizes under 500) and 54% (n=27) had a value of 1 (i.e. all populations within the species had effective population sizes over 500), with (8?) species falling between 0 and 1 (Figure 1).
- Endangered species had on average the lowest Ne>500 indicator values, while species of special concern had the highest (Figure 3). The mean Ne>500 indicator for Ontario (i.e. the average of taxon-averaged indicators) is 0.58 with a standard deviation of 0.35 (Table 1).
- There are limitations to this approach (as identified in the technical report). Efforts will continue to increase the number of species included in the indicator and to address some of the limitations for 2030.

Links

Related Targets: N/A

Related Themes: N/A

Web Links

COSEWIC – Committee on the status of endangered wildlife in Canada https://cosewic.ca/index.php/en/

COSSARO – Committee on the status of species at risk in Ontario http://cossaroagency.ca/species/

GeoBon Genetic Diversity Indicator – Proportion of populations with Ne>500 - https://geobon.org/genetic-diversity-indicator-proportion-of-populations-with-ne-500/

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