Monitoring genetic diversity in Sweden with new indicators for the CBD Kunming-Montreal Global Biodiversity Framework

Viktoria Köppä, Henrik Thurfjell, Jessica da Silva, Sean Hoban, Alicia, Mastretta-Yanes, Linda Laikre

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Preface

Genetic diversity (variation within species) is, together with diversity at the ecosystem and species levels, one of the fundamental pillars of biodiversity, as defined by the Convention of Biological Diversity (CBD). At the 15th CBD COP (Kunming-Montreal protocol) the signature parties agreed to include several indicators for genetic diversity in the monitoring framework. As these indicators can be assessed without using genetic data, they are often referred to as proxy-indicators. In this report such proxy-indicators are calculated for a large number of species in Sweden, primarily using data from the red-listing process and species action plans.

The results highlight a general need to increase connectivity and population sizes. For example, 22 % of the populations were found to be too small to maintain long term genetic variation. However, the species evaluated are not fully representative, due to the focus on certain taxonomic groups and species with national action plans. The authors suggest slight modifications to the species assessments for action plans and red listing to include genetic diversity indicators in the future. This would benefit both processes and provide new insights on species´ conservation status.

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Summary

In December 2022 the Fifteenth Conference of the Parties (COP 15) to the Convention on Biological Diversity (CBD) agreed on a new global framework for biological diversity – the Kunming-Montreal Global Biodiversity Framework (GBF). The GBF is associated with a monitoring framework that includes the monitoring of genetic diversity with several indicators including:

- **Headline Indicator A.4:** the proportion of populations within species with an effective population size (N_e) > 500 (hereafter referred to as the *Ne500 indicator*) and a
- **Complementary Indicator A.CY.22:** the proportion of populations maintained within species (hereafter referred to as the *PM indicator*).

Both the Ne500 indicator and the PM indicator were developed through a long and collaborative process, between a large coalition of conservation genetics researchers, conservation biologists, species' managers, and political negotiators, between 2020 and 2022. A third indicator for genetic diversity has also been proposed – the number of species and populations in which genetic diversity is being monitored with DNA-based methods (referred to as the DNA-based monitoring indicator). International efforts are now ongoing to provide guidelines for assessing these indicators at national levels.

Sweden has long taken a leading role in the assessment and monitoring of genetic diversity, and a study has already been carried out focusing on the extent to which Red List data can be used to assess these indicators (Thurfjell et al., 2022). That study indicated that data is available for many species and species groups, but it did not go into detailed assessments.

The purpose of the present study was to

1. Identify and explore sources of information that can be used to assess the indicators for genetic diversity.
2. Use those sources to assess the indicators in more detail than Thurfjell et al. (2022).
3. Assess the indicators for two full taxonomic groups, amphibians and reptiles.
4. Contribute to an initial international effort in nine countries to assess the genetic indicators for c. 100 species per country (Mastretta-Yanes and da Silva et al., 2024), including developing and using assessment protocols, platforms, metadata-instructions, and guidance materials (Mastretta-Yanes et al., 2024a,b).
5. Estimate the effort (time and resources) needed to make assessments and the possibility to assess genetic indicators during the Red List process.
6. Explore views of Red List taxonomic experts on the indicators for genetic diversity and the potential to assess these indicators for species during the Red List process.

Sources explored included National Action Plans (NAPs) for, most often, individual threatened species ("Åtgärdsprogram") where we found a total of 143 plans

covering 319 species. For 70 plans (34 %; covering 108 species) it was possible to assess both the Ne500 and the PM indicator from information available in the NAP.

We recommend a clearer terminology and structure to be incorporated into the NAPs to indicate when separate populations are defined. Furthermore, more details regarding occurrences (population identification), and census sizes within counties are needed.

Other sources explored and used included Red List data, the Swedish national biogeographic survey, citizen science data (particularly Artportalen), scientific articles and reports, and expert consultations. We summarize the potential for using these types of data and include detailed assessments for all amphibian and reptile species in Sweden.

In total, between 3,159 and 3,199 populations were assessed in the study (depending on cases when multiple estimates of number of populations for particular species have been used due to uncertainty).

For the amphibian species, the Ne500 indicator is estimated at 0.46 (i.e., of the 13 species assessed, on average 46 % of each species' populations estimated effective population sizes (N_e) were over 500). The PM indicator is 0.89 (i.e., on average 89 % of each species´ populations are maintained over time), and the DNA-based monitoring indicator is 0.38 (i.e., 38 % of the species have one or more populations being monitored temporally using DNA-based methods). For reptiles (seven taxa: six species, one with two subspecies), indicator values are estimated at 0.57, 0.98 and 0.14 for the Ne500, PM, and DNA-based monitoring indicators, respectively.

We also assessed genetic indicator values for an additional 100 species across several other taxonomic groups, including 20 mammals, 11 birds, 7 fishes, 22 angiosperms, 29 invertebrates, 2 fungi, 5 lichens, 2 mosses, 1 charophyta and 1 pteridophyte. The species were chosen to be assessed based on availability of information in the Red List database, NAPs or through national programs for monitoring of genetic diversity with DNA-based methods. This biases the sample to species that are already threatened, which may inflate the indicator values (see Figure 7 and Table 4 for information on Red List classification of the species assessed in this report).

Taking individual indicator values from each of the 120 species assessed in this study, and averaging provides indicator values for Sweden of 0.22 and 0.78 for the Ne500 and the PM indicator, respectively. Clearly, these values are alarming. On average, a given species has 22 % of its populations above 500 in effective population size, meaning on average 80 % of a given species has populations too small to maintain adaptive potential, and on average, about 20 % of each species populations are lost despite the relatively short monitoring periods (mostly a few decades up to 100 years). Management steps needed include increasing population sizes, as well as increasing and restoring connectivity among populations.

For the DNA-based monitoring indicator, 20 out of the 120 species have one or more populations being temporally monitored using DNA methods. Consequently, this indicator received a value of 0.17.

Overall, we demonstrated how these genetic indicator assessments for CBD reporting can be applied, with the effort to assess a species varying between two working hours to three working days. We compared the present results with those from a previous study based on rapid use of Red List data only (Thurfjell et al., 2022) as well as for species assessed with both Thurfjell et al. (2022) and the present approach (17 herptiles and 20 mammals). We discuss observed discrepancies.

Our dataset of 120 species contributed to the overall development of these indicators internationally (and the accompanying supporting materials) (Hoban et al., 2023; Mastretta-Yanes and da Silva et al., 2024). Through this work, the authors helped inform European Commission knowledge centres and the CBD Ad Hoc Technical Expert Group (AHTEG) on the Kunming-Montreal Monitoring Framework.

Given the utility of the Red List datasets in informing some of the genetic indicator assessments, and the expert coordination needed for both assessments, it would be most efficient and practical to align these processes in Sweden. This may be facilitated by:

- modifying Red List and NAP assessment processes to include the identification of all (sub)populations within a species (or proxies of populations as outlined in this report), and
- evaluate their (approximate) census sizes and corresponding changes over time, as well as
- explicitly reporting any other genetic diversity metrics that could inform the species' conservation and management.
- Further, the tracking of temporal DNA-based monitoring carried out in science-management collaborations or within research should be used as an additional indicator linked to this Red List and NAP work.

It would be relatively easy to incorporate the assessment of genetic diversity indicators in parallel to the Red List assessments because the data required to quantify the genetic diversity indicators is already included to at least some degree in the Red List assessment. Such parallel assessments would be a cost-effective way for Sweden to track progress in its efforts to protect genetic diversity.

To gauge whether the proposed alignment of indicator assessments with Red Listing and NAP processes would be supported, 12 of the 19 expert taxonomic committee leaders for the Red List process were interviewed. All consulted experts supported the idea of genetic diversity indicators. However, two thirds (8 out of 12; 67 %) were supportive of assessing the indicators during the Red List process (at least some species within each taxonomic group), while one third were sceptical of incorporating such assessments. The efforts needed to undertake genetic diversity indicator assessments will vary greatly among taxonomic groups. *For mammals, birds, and angiosperms, assessments are possible based on the information already available (essentially, population sizes and loss of populations over time) and with only slight adjustments to the process* (see section 5). More time, expertise and data may be needed for other groups. For example, for lichens, mosses and fishes, the main challenge is identifying populations and their census sizes in the absence of molecular genetic data. For invertebrates, information is available for only a few species or groups of species, such as butterflies (Rhopalocera; "dagfjärilar" in Swedish), pollinators, and rare species with monitoring programs. Assessing larger sets of species groups will require the collection of more data.

Sammanfattning

I december 2022 enades den femtonde partskonferensen (COP15) till konventionen om biologisk mångfald (CBD) om ett nytt globalt ramverk för biologisk mångfald – Kunming-Montreal Global Biodiversity Framework (GBF). GBF åtföljs av ett uppföljningsramverk som inkluderar övervakning av genetisk mångfald med dessa indikatorer:

- **Huvudindikator A.4:** andelen populationer inom arter med en effektiv populationsstorlek (N_e) > 500 (här kallad Ne500-indikatorn).
- **Kompletterande indikator A.CY.22:** andelen populationer som bibehålls inom arten (hädanefter kallad PM-indikatorn).

Både Ne500-indikatorn och PM-indikatorn utvecklades genom en kollborativ process mellan 2020 och 2022, där en bred koalition av forskare inom bevarandegenetik och, bevarandebiologi, artförvaltare samt politiska förhandlare deltog. En tredje indikator för genetisk mångfald har också föreslagits – antalet arter och populationer där genetisk mångfald övervakas med DNA-baserade metoder (hädanefter DNA-baserad övervakningsindikator). Internationella insatser pågår nu för att ta fram riktlinjer för hur dessa indikatorer ska bedömas på nationell nivå.

Sverige har länge haft en ledande roll i arbetet med att bedöma och övervaka genetisk mångfald, och en tidigare studie har redan undersökt i vilken utsträckning rödlistedata kan användas för att bedöma dessa indikatorer (Thurfjell m.fl. 2022). Den studien visade att data finns tillgängliga för många arter och artgrupper, men innehöll inga detaljerade analyser.

Syftet med föreliggande studie var att:

1. Identifiera och undersöka informationskällor som kan användas för att beräkna indikatorer för genetisk mångfald.
2. Använda dessa källor för att göra mer detaljerade bedömningar än i Thurfjell m.fl. (2022).
3. Ta fram indikatorvärden för två fullständiga taxonomiska grupper, groddjur och kräldjur.
4. Bidra till ett inledande internationellt arbete i nio länder för att skatta genetiska indikatorer för cirka 100 arter per land (Mastretta-Yanes och da Silva m.fl. 2024). Arbetet omfattade utveckling och användning av skattningssprotokoll, plattformar, metadatainstruktioner och vägledningsmaterial (Mastretta-Yanes och da Silva m.fl. 2024; Mastretta-Yanes m.fl. 2024).
5. Uppskatta den arbetsinsats (tid och resurser) som krävs för att genomföra bedömningar samt möjligheten att integrera indikatorerna i rödlistningsprocessen.
6. Undersöka rödlistans taxonomiska experters syn på indikatorerna för genetisk mångfald och möjligheten att bedöma dessa inom rödlistningsarbetet.

De informationskällor som analyserades omfattade bland annat nationella åtgärdsprogram (ÅPG), avseende främst enskilda hotade arter, där totalt 143 program som

omfattar 319 arter identifierades. För 70 program (34 %, omfattande 108 arter) var det möjligt att bedöma både Ne500- och PM-indikatorerna baserat på tillgänglig information.

Vi rekommenderar en tydligare terminologi och struktur i åtgärdsprogrammen för att ange när separata populationer definieras. Vidare behövs mer detaljer anges avseende länsvisa förekomster (identifiering av populationer) och populationsstorlekar.

Andra informationskällor som användes omfattade rödlistedata, den svenska nationella biogeografiska uppföljningen, medborgarforskning (särskilt Artportalen), vetenskapliga artiklar och rapporter samt expertbedömningar. Vi sammanfattar och granskar potentialen i dessa datakällor och presenterar detaljerade analyser för samtliga grod- och kräldjursarter i Sverige.

Totalt bedömdes mellan 3159 och 3199 populationer i studien (beroende på alternativa uppskattningar för vissa arter).

För groddjur (13 arter) uppskattas Ne500-indikatorn till 0,46 (dvs. i genomsnitt har 46 % av en arts populationer en effektiv populationsstorlek över 500). PM-indikatorn uppgår till 0,89 (dvs. i genomsnitt bibehålls 89 % av en arts populationer över tid), och den DNA-baserade övervakningsindikatorn till 0,38 (dvs. 38 % av arterna har minst en population som övervakas över tid med DNA-metoder).

För kräldjur (sju taxa: sex arter, varav en bestående av två underarter) uppskattas indikatorvärdena till 0,57, 0,98 respektive 0,14 för Ne500-, PM- och DNA-indikatorerna.

Vi skattade även genetiska indikatorer för ytterligare 100 arter från flera taxonomiska grupper, inklusive däggdjur, fåglar, fiskar, blomväxter (angiospermer), ryggradslösa djur, svampar, lavar, mossor samt kransalger och ormbunksväxter. Urvalet baserades på tillgången till data i rödlistan, åtgärdsprogram eller nationella övervakningsprogram. Detta kan innebära en viss viktning mot redan hotade arter vilket kan leda till en överskattning av den genetiska hotbilden. Information kring rödliste-klassning av ingående arter redovisas.

Baserat på medelvärden av indikatorerna för de 120 arter som analyserats erhålls nationella indikatorvärden för Sverige på 0,22 för Ne500 och 0,78 för PM. Dessa värden är oroande. I genomsnitt har endast 22 % av en arts populationer en effektiv storlek över 500, vilket innebär att cirka 80 % är för små för att upprätthålla anpassningsförmåga. Samtidigt har omkring 20 % av populationerna försvunnit trots relativt korta uppföljningsperioder. Nödvändiga åtgärder inkluderar att öka populationsstorlekar samt förbättra och återställa konnektiviteten mellan populationer.

För den DNA-baserade övervakningsindikatorn har 20 av 120 arter minst en population som övervakas över tid med DNA-metoder, vilket ger ett indikatorvärde på 0,17.

Sammantaget visar studien hur dessa genetiska indikatorer kan tillämpas i CBD-rapportering, där arbetsinsatsen för en art varierar mellan två timmar och tre arbetsdagar. Resultaten jämfördes med tidigare studier baserade enbart på rödlistedata (Thurfjell m.fl. 2022), särskilt för arter som även inkluderats i denna studie (17 herptiler och 20 däggdjur), och observerade skillnader diskuteras.

Vårt dataset, omfattande 120 arter, bidrog till den internationella utvecklingen av dessa indikatorer samt tillhörande stödmaterial (Hoban m.fl. 2023; Mastretta-Yanes och da Silva m.fl. 2024). Genom detta arbete har författarna även bidragit

med kunskapsunderlag för Europeiska kommissionen och CBD:s tekniska expertgrupp (AHTEG) för indikatorer.

Med tanke på nyttan av rödlistedata för indikatorbedömningar och behovet av expertkoordination vore det mest effektivt att samordna dessa processer i Sverige. Detta kan möjliggöras genom att:

- anpassa rödlistnings- och ÅPG-processer så att alla (sub)populationer identifieras, eller potentiella populationer (proxy) enligt beskrivningen i denna rapport, och
- uppskatta deras populationsstorlekar och förändringar över tid, samt
- tydligt rapportera ytterligare mått på genetisk mångfald som har relevans för förvaltning och övervakning.
- Vidare, bör uppföljning av DNA-baserad övervakning inom forskning och förvaltning användas som en kompletterande indikator kopplad till detta arbete.

Det vore relativt enkelt att integrera skattningen av de genetiska indikatorerna i rödlistningsprocessen, eftersom de nödvändiga uppgifterna redan delvis ingår i rödlistebedömningen. Detta skulle utgöra ett kostnadseffektivt sätt för Sverige att följa upp sina insatser för att bevara genetisk mångfald.

För att undersöka stödet för en sådan samordning intervjuades 12 av 19 experter med ledande roller i rödlistningsarbetet. Samtliga uttryckte stöd för idén med genetiska indikatorer och två tredjedelar var postivt inställda till att inkludera dem i rödlistningsprocessen, medan en tredjedel av experterna var mer tveksamma.

Den arbetsinsats som bedöms krävas för att inkludera genetiska indikatorer i rödlistearbetet skiljer sig mellan experter inom olika artgrupper. För däggdjur, fåglar och blomväxter kan bedömningar i stor utsträckning göras med befintliga data och mindre justeringar. För andra grupper krävs däremot mer data och ytterligare expertis. Exempelvis är det svårt att identifiera populationer och uppskatta deras storlek för lavar, mossor och fiskar utan genetiska data. För ryggradslösa djur finns tillgänliga data endast för vissa grupper, såsom dagfjärilar, pollinatörer och sällsynta arter som omfattas av övervakningsprogram. För att möjliggöra mer heltäckande bedömningar krävs därför ytterligare datainsamling.

1. Introduction

The need to conserve biodiversity has long been recognized and is acknowledged in both international and national legislature such as the Swedish Environmental Goals (Swedish Environmental Protection Agency; SEPA, 2024), the EU Habitats Directive (Council Directive 92/43/EEC), the EU Biodiversity Strategy 2030 (European Commission, 2021), and the UN Convention on Biological Diversity (www.cbd.int). Monitoring is a central aspect of the conservation and maintenance of biological diversity. By systematically and continuously quantifying ecosystems, species and genetic diversity over time, early detection of threats and effects of anthropogenic changes – positive or negative – are possible. Since 1992, the importance of biodiversity monitoring has been highlighted in the UN Convention on Biological Diversity (CBD; https://www.cbd.int).

Genetic diversity refers to biological variation at the DNA-level within species and is expressed as variation within and between populations. Genetic diversity is the foundation for adaptive capacity and is therefore crucial for populations´ long-term survival and evolutionary potential. Consequently, species or populations with low genetic diversity are at increased risk of inbreeding depression, genetic erosion and reduced adaptive capacity (Spielman et al., 2004). Since resilient populations of species are necessary for ecosystem function, maintaining genetic diversity of populations is vital for supporting ecosystem resilience (Reusch et al., 2005). Quantifying and monitoring genetic diversity over time is therefore an essential, proactive measure in the battle against biodiversity loss, which countries should employ to stem overall biodiversity loss.

However, strategies for monitoring genetic diversity have long lagged behind that of species and ecosystems despite scientific knowledge on genetic diversity being available (Laikre et al., 2008, 2010; Hoban et al., 2020) and policy pointing to its need (www.cbd.int). This lag has been repeatedly highlighted by researchers (Laikre et al., 2010; Laikre, 2010; Frankham, 2022) and has been identified as a result of the “conservation genetics gap” – a gap between available scientific knowledge and its use in conservation management and policy implementation (Taylor et al., 2017; Klütsch and Laikre, 2021).

Given that DNA-based monitoring of genetic diversity will, in the near future, only be feasible for a select number of key species due to resource limitations (time, cost, and personnel), there is concern that other species at risk of genetic erosion may go unnoticed. To help address this concern, proxy-based indicators for genetic diversity have been proposed and developed (Hoban et al., 2020; Laikre et al., 2020); thereby allowing for genetic diversity assessments at broader spatial and taxonomic scales at both national and international levels. These proxy indicators are described below and were initially piloted in Sweden through an assessment based on Swedish Red List data (Thurfjell et al., 2022).

1.1 Brief background on proxy-based indicators for genetic diversity

While the CBD highlights the need for biodiversity monitoring, targets and indicators for genetic indicators have been absent for wild species and insufficient for domesticated ones (Laikre et al., 2010; Laikre, 2010). During 2020 – 2022, while the CBD post-2020 Global Biodiversity Framework (GBF) was being elaborated, conservation genetics researchers from around the world worked intensively to communicate the need for stronger and clearer goals and targets, as well as indicators, related to genetic diversity (Hoban et al., 2020; Laikre et al., 2020). This work was initiated by the EU COST Action funded research-practitioner network G-BiKE (Genomic Biodiversity Knowledge for Resilient Ecosystems; https://www.cost.eu/actions/ca18134/), and championed by other research groups, such as GeoBon's Genetic Composition Working Group and IUCN´s Conservation Genetics Working Group, which later came together to form the Coalition for Conservation Genetics (Kershaw et al., 2022; https://www.coalitionforconservationgenetics.org). This coalition published over 15 scientific papers, ran webinars, and provided statements, suggestions, comments to formals requests from the CBD Secretariat, and reviews on the necessary wording for genetic diversity goals and targets, as well as evaluations of suitable indicators for the post-2020 GBF. Three indicators, in particular, were developed, tested and promoted for national and international reporting to the CBD (Laikre et al., 2020; Laikre et al., 2021; Hoban et al., 2020; Hoban et al., 2021a; Hoban et al., 2021b). They focus on the maintenance of genetic diversity within and between populations, and the ultimate importance of using DNA-based techniques to monitor genetic diversity (see Figure 1). The indicators are:

1. The proportion of populations within species with a genetically effective populations size (N_e) > 500 (abbreviated: Ne500 indicator)
2. The proportion of populations maintained within species (abbreviated: PM indicator)
3. The number of species/populations monitored using DNA-based methods (abbreviated: DNA-based monitoring indicator).

The first two indicators are proxy-based (i.e., they infer some aspects of genetic diversity without DNA-based methods). For the Ne500 indicator we use the number of individuals (typically the number of sexually mature individuals; i.e. census size abbreviated N_C) as a proxy for the genetically effective population size (abbreviated N_e; i.e., the size of an ideal population that show the same rate of genetic diversity loss as the actual population at hand; Allendorf et al., 2021). We use the relationship $N_e/N_C \approx 0.1$ which is slightly below the mean and/or the median value observed for many species reported in review articles (Frankham, 1995, 2021; Hoban et al., 2020, 2024) as well as in detailed studies using multigenerational data (e.g. Charlier et al., 2011). This translates into quantifying whether individual populations of species have N_C greater or less than 5,000 individuals (N_C > 5,000 or N_C < 5,000; Ne500 indicator; Figure 1). The PM indicator is looking to quantify how many populations of a species are maintained over time or have been lost (Figure 1). The Ne500 indicator was adopted as a Headline Indicator to address Goal A and Target 4 of the Kunming-Montreal GBF (CBD, 2022a: CBD/COP/DEC/15/4) at the CBD's 15th Conference of the Parties (COP 15); while the PM

indicator was adopted as a Complimentary Indicator for Goal A (CBD, 2022b; CBD/COP/DEC/15/5). These decisions were confirmed by COP 16 in Rome in February 2025 (CBD/COP/CEC/16/31).

Despite the goals, targets and indicators being set at a global level, they are intended to be applied nationally, with Sweden being amongst the first nations to do so in the Swedish environmental objectives from 2005 (https://www.sverigesmiljomal.se; https://www.naturvardsverket.se/en/om-miljoarbetet/swedish-environmental-objectives/). Included in the 16th environmental objective, as well as in the revised specifications of six of the objectives (dnr M2012/1171/Ma), is the explicit objective to maintain sufficient levels of genetic variation within and between populations of plants and animals to assure their long-term survival and adaptive capacity.

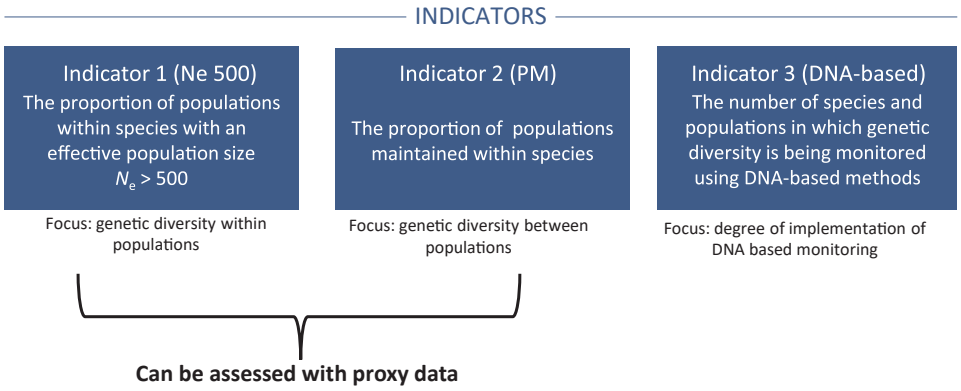


Figure 1. Three pragmatic indicators to monitor trends in genetic diversity proposed by Laikre et al. (2020) and Hoban et al. (2020). The first two indicators can be assessed without genetic data. Illustration modified from Hoban et al. (2020).

Moreover, Sweden was among the first countries to test the proxy indicators using Red List data before their adoption into the GBF and used previously published reviews of knowledge of genetic diversity (Laikre and Ryman, 1997; Wennerström et al., 2016; Laikre et al., 2008; Posledovich et al., 2021a) to quantify the DNA-based monitoring indicator (Thurfjell et al., 2022). That study showed that Red List data can be used to assess the proxy-based indicators, that sufficient information on populations within species is available for many species in Sweden, that the genetic indicators complement the Red List classifications, and that the assessments can be improved to allow for the better assessment of genetic indicators (Thurfjell et al., 2022).

1.2 Brief background on DNA-based indicators applied in Sweden

In parallel to the application of proxy-based indicators for genetic diversity, which is the focus of the present report, DNA-based methods have also been used in Sweden since 2020 (Johannesson and Laikre, 2020, 2022, 2023) to monitor genetic diversity within the framework of environmental monitoring efforts (Andersson et al., 2022). We present that work briefly here since those efforts and the ones of this present report are closely interlinked and have the same focus, which is to understand the extent to which genetic diversity within species is being maintained over time.

Sweden has long been at the forefront of suggesting, developing, and finally, implementing genetic diversity monitoring (Figure 2). Monitoring genetic diversity implies the systematic analyses of genetic diversity measurements in the same population(s) within a particular species over time (Laikre et al., 2008). The need for such monitoring was stressed by Swedish researchers in 1981 (Ryman, 1981) and the first suggestion of a program to monitor genetic diversity was presented by Laikre and Ryman (1997) in a report to the Swedish Environmental Protection Agency (SEPA). The following year, a national review on genetic distinctiveness of natural populations of species in Sweden was presented by Lönn et al. (1998) in another SEPA report. Subsequently, in 2005, the Swedish Parliament adopted a national environmental objective on biological diversity (Swedish Government bill Prop. 2004/05:150) that clearly stated that genetic diversity within and between populations of naturally occurring species shall be maintained to ensure long-term survival. This was followed by updated knowledge reviews and suggestions for monitoring programs in 2008 and 2009 (Laikre et al., 2008; Sjögren-Gulve et al., 2009), which resulted in programs being initiated for aquatic organisms by the Swedish Agency for Marine and Water Management (SwAM) in 2017 (Johannesson and Laikre, 2020, 2022, 2023) and for terrestrial species in 2021 (Posledovich et al., 2021a,b). Since these programs are DNA-based, and thus still quite costly (although costs for genotyping and sequencing are dropping rapidly), only a few key species have been selected for such work based on science-management collaborations including both researchers and managers (Johannesson and Laikre, 2020, 2022, 2023; Posledovich et al., 2021a, b). The selected species monitored using DNA assessments to date include brown trout (Andersson et al., 2022; Kurland et al., 2023), moose (Dussex et al., 2023), salmon, bladderwrack, herring, eelgrass (Johannesson and Laikre, 2023), Arctic char (Saha and Kurland et al., 2024) and mountain bumblebees (Webster and Liu, 2022).

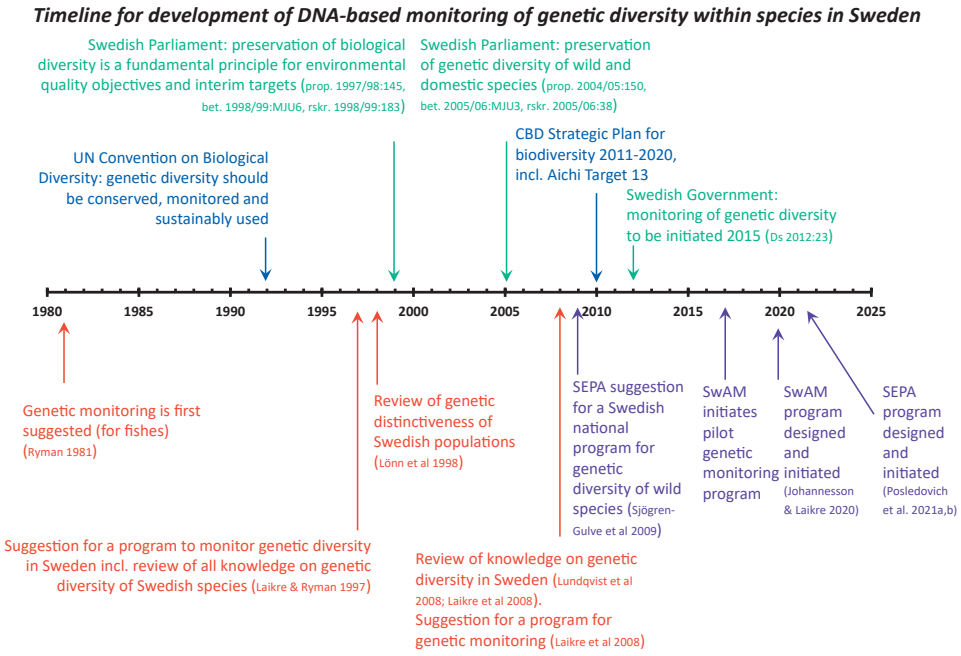


Figure 2. Timeline showing important steps towards DNA-based monitoring of genetic diversity in Sweden. Colors show contributions from different societal actors: red = contributions from science, blue = CBD decisions, green = Swedish Parliament, purple = Swedish national agencies (SEPA = Swedish Environmental Protection Agency, SwAM = Swedish Agency for Marine and Water Management).

The science-management co-creation process with SwAM also included the development of three DNA-based indicators for genetic diversity with specific thresholds applied to help evaluate rates of change, with the intention of facilitating the translation of these complex patterns for managers (Johannesson and Laikre, 2020, 2022, 2023; Andersson et al., 2022). These DNA-based indicators measure genetic diversity within populations using standard parameters in population genetics such as N_e, heterozygosity, allelic richness, inbreeding and between population genetic diversity using e.g. F_{ST} (Andersson et al., 2020). All these parameters have been identified as Essential Biodiversity Variables (EBVs) for genetic diversity (Hoban et al., 2022; Junker et al., 2023). They provide more detailed information than the proxy-indicators and can also be used for CBD reporting. Complementary work on genetic diversity indicators is being undertaken in, for example, other parts of Europe (e.g., Switzerland; Hvilsom et al., 2022), in USA (California; Hvilsom et al., 2022), and in South Africa (da Silva et al., under review).

1.3 Objectives

The present project aimed at exploring how the proxy-based indicators for genetic diversity adopted by the CBD can be assessed in Sweden. Particularly the focus was to:

1. Explore possible sources of information that can be used to assess the indicators for genetic diversity.
2. Use Red List data, the Species Observation System (Artportalen), National Action Plans (NAPs), scientific literature, and other sources of existing information to assess the indicators in more detail (but still within reasonable time frames) than the previous study (Thurfjell et al., 2022) for two full taxonomic groups namely amphibians (13 species) and reptiles (six species, one subspecies) in Sweden.
3. Contribute to an international effort in nine countries to assess the genetic indicators for c. 100 species per country (Mastretta-Yanes and da Silva et al., 2024), including developing and using assessment protocols, platforms, metadata-instructions, on-line information, and guidance materials (Mastretta-Yanes et al., 2024a,b).
4. Estimate the effort (time and resources) needed to make assessments and the possibility to assess genetic indicators in the Red List process. Through interviews with Red List taxonomic experts explore views on the indicators for genetic diversity and views on the potential to assess these indicators for species in the different taxonomic expert committees.

The assessments in this report were also included in Mastretta-Yanes and da Silva et al. (2024) but more in-depth presentations are provided here, and assessments for 34 of the 120 species have been updated.

2. How to estimate the indicators

The indicators and the basic information needed to assess them are outlined in box below (see also Figure 1).

Indicator Ne500 (Headline A.4 in the Kunming-Montreal Monitoring Framework): This indicator refers to the proportion of populations within species with an effective population size (N_e) above 500. To estimate this indicator, information on the number of populations and how many of the populations per species have an N_e above 500 and how many have an N_e below 500 is ideally needed.

Indicator PM (Complementary Indicator A.CY.22) in the Kunming-Montreal Monitoring Framework): This indicator refers to the proportion of populations maintained within species over time. The information needed includes the number of extinct and extant populations within contemporary time (i.e., approximately no more than 100 – 150 years ago, but most often within a few decades) of a particular species within the country (as the CBD indicators are to be reported nationally).

Indicator DNA-based monitoring; This indicator refers to the proportion of species in which at least one population is being monitored with DNA-based techniques. This indicator is not included in the Kunming-Montreal Monitoring Framework but the indicators is being applied in Swedish national monitoring programs for genetic diversity (see section 1.2; Andersson et al., 2022).

As part of this project, we have contributed to the development of guidance documents on indicator assessments. That work was conducted with collaborators in eight other countries (Australia, Belgium, Colombia, France, Japan, Mexico, South Africa, USA) in an effort co-organized by the Coalition for Conservation Genetics and EU Cost Action G-BiKE. This collaborative effort included a workshop on effective populations size (N_e) in Brasov, Romania organized by G-BiKE. The work initiated during that meeting is reported in Fedorca et al. (2024). The collaborations also included biweekly zoom-meetings where various aspects and questions on data collection and interpretation were carried out, including producing a guidance document on indicator assessments (Mastretta-Yanes et al., 2024a).

We conducted assessments of these indicators aiming for 50 – 100 species from each of the participating countries based on existing detailed information from various national sources during the time available for this project. The process is described in Hoban et al. (2023) and contributed to Mastretta-Yanes and da Silva et al. (2024). The learning outcomes of the collaboration were further published in Mastretta-Yanes et al. (2024a,b) as guidelines for other countries.

The data obtained was recorded using an online data management platform called the KoboToolbox (https://www.kobotoolbox.org/). Part of our work inclu-

ded designing and iteratively testing and modifying the format for data collection using this platform. The information collected per species in the KoboToolbox form is shown in Appendix 1.

2.1 Defining populations

In many cases we found that information on populations of species is poorly known and/or documented. Typically, population genetic assessments have often not been conducted, particularly not across the entire extent of a country. At the same time, defining populations is required for the indicators. When there is no information on population genetic structure or other information defining population occurrences in the literature, other approaches had to be used. Depending on the information available and the taxonomic group, different methods of delimiting populations were applied (Figure 3; sections 2.1.1-2.1.6 below). The general idea was to define populations by identifying potential barriers to gene flow and to estimate what parts of the species range are connected.

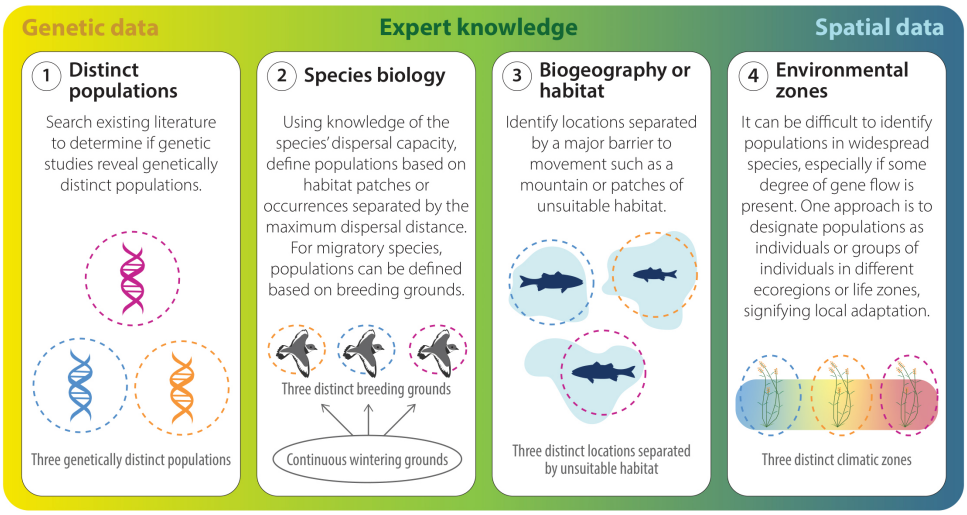


Figure 3. Schematic illustration of different approaches for defining populations based on available data (from Hoban et al., 2024). A combination of approaches is often recommended (see Hoban et al., 2024). Image credit: Robyn Shaw.

In some cases, species may be divided into units based on morphology or phenology (e.g., ecotypes, or ecological or biogeographic proxies, such as habitat zones, or management units). It is also possible to use geographic boundaries (or gaps in distribution) as a method for delimiting populations. The method relies on using the potential dispersal capacity of species to estimate connectivity among observations (sections 2.1.1-2.1.6 below). Often, combinations of approaches are recommended (see Hoban et al., 2024). The designed KoboToolbox form includes several predefined options for identifying and defining populations that have been applied across the species in this study (Figure 4).

2.1.1 Genetic clusters

Studies of population genetic structure is conducted by sampling individuals of a species over a distribution range and then employing molecular genetic techniques to obtain genetic profiles of each individual. These individual data are then analysed jointly to identify patterns of genetic similarity (population identification), levels of variation within populations, patterns of genetic exchange among populations (gene flow) and genetic differences among populations. Such studies may cover the entire geographic range of a species or only selected parts. When only partial information is available this can be used in connection with other methods to estimate an approximate dispersal range and define geographic clusters.

2.1.2 Management units

Species that are subject to managements plans may be divided into management units. These units often represent either dispersal patterns or geographic borders. Here, we used management plans (particularly NAPs) and explored how units are defined. If biological information (genetic and/or ecological studies) suggest that a management unit may consist of several populations, we considered those as populations.

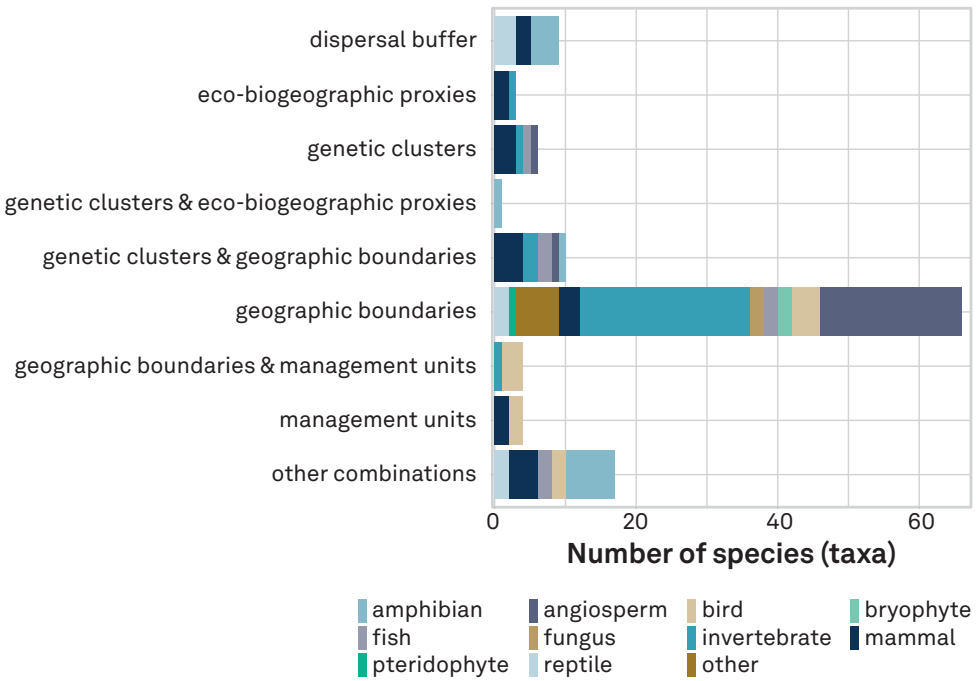


Figure 4. Method used to identify and define the number of populations for the species included in the present study. Labels are based on options available in the KoboToolbox form (Appendix 1). For further details on methods see Mastretta-Yanes and da Silva et al. (2024).

2.1.3 Geographic boundaries

There may be natural barriers in the landscape, such as mountains or waterways, that limit the dispersal of species. In such cases, individuals on either side of a barrier may be considered separate populations. Other barriers in the landscape can

be man-made, such as hydroelectric dams in a river system, roads or railways, and fragmentation due to cities or farmland. Isolated lakes can also be considered as separate populations, as land masses between lakes constitute barriers.

2.1.4 Eco-biogeographic proxies

There may be differences in ecological conditions across the species range, such as seasonality and climate. For example, the EU uses biogeographic regions to aid prioritization of Natura 2000 areas and conservation efforts (European Commission 2021). Biogeographic regions are also used in the EU Habitats Directive to monitor the status of different nature types (European Commission, 2021).

2.1.5 Traits

A species may exhibit differences in behavioural, morphological or physiological traits across its distributional range. These differences can potentially indicate local adaptation or limited genetic exchange among demes. Some examples include differences in bird song dialects or morphological coloration.

2.1.6 Dispersal buffers

When there are no clear barriers to dispersal, it is possible to use an approximate distance of dispersal of the species to estimate geographic clusters. For example, most amphibians have a range of approximately one kilometer (https://www.slu.se/artdatabanken). The method involves mapping known occurrence records and applying a buffer zone around each area of occurrence using the identified dispersal distance per species. Occurrences with overlapping buffer zones are typically considered as the same population. Some species disperse over long distances and therefore the genetic connectivity among occurrences is potentially large, whilst populations of other species may have very narrow home ranges and only move short distances. Thus, the method must be adjusted to fit the species in question. When using citizen science observation data, it is also important to take into consideration that gaps in observation data does not necessarily represent a gap in occurrence. Often, a combination of approaches is recommended as outlined in Hoban et al. (2024).

2.1.7 Other

For most species, it is difficult to find all the information needed from a single source (Figure 3). In many cases the assessment requires piecing together information from different sources and making estimates based on dispersal data and occurrences. For common and widespread species, it may be difficult to assess populations if large scale assessments of genetic population structure have not been conducted. This is the case for some of the amphibians (moor frog, common frog, common toad, smooth newt, great crested newt), and for all the reptiles. For those species, we subdivided the country into units. These units do not represent isolated populations, but rather serve as a proxy for population substructure. The rationale is that we do not expect that the entire country represents one panmictic unit. There is likely a pattern of some isolation by distance, and we base this assumption on assessments of most of these species over restricted areas of

occurrence (e.g. Rödin Mörch, 2019; Johansson et al., 2007; Davis, 2020; Thörn et al., 2021). The main objective of the indicators is to provide information below the species level and to be able to track changes. When subdividing the national population into units, potential declines in a portion of the distribution is more likely to be discovered over time. The subdivision can be done in several ways. One option is to regard the major rivers (Figure 5a) and/or major highways (Figure 5b) as migration barriers. For amphibians and reptiles, busy roads present possible barriers. When available, we have used genetic data to guide the subdivision.

2.1.8 Maps

All maps used in this study were created using QGIS (version 3.22.8; QGIS Development Team, 2020), and observation data were obtained from Artportalen at www.analysisportal.se. (Please note that this resource is no longer available.)

a) b)

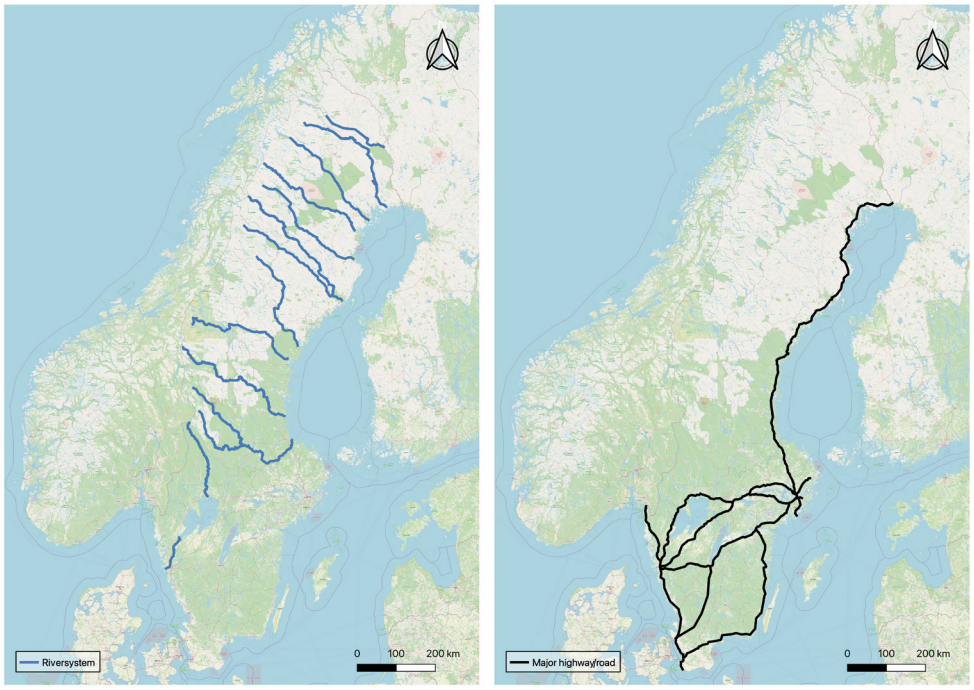


Figure 5. a) Approximate distribution of major river systems in Sweden and b) approximate placement of major highways in Sweden.

2.2 Estimating N_e from N_C

N_e can be estimated from genetic data, but it is also possible to use N_C as a proxy. For some species there is information on the relationship between N_e and N_C (the N_e/N_C ratio; Frankham, 1995; Frankham, 2022; Hoban et al., 2020; Hoban et al., 2024). When the ratio is not known, a conservative estimate of 0.1 is recommended (Hoban et al., 2020; Hoban et al., 2021a; Hoban et al., 2024; Laikre et al., 2021).

Table 1. Species for which we have used a different N_e/N_c ratio than 0.1 based on genetic data (reference in column "Source"). In two cases the ratio from a closely related species was applied.

Species	N_e/N_c ratio	Source	Species *if* the ratio is based on a closely related species
Alces alces	0.28	Ryman et al., 1981	
Canis lupus	0.25	Forslund, 2009; Bruford, 2015	
Cervus elaphus elaphus	0.23	Reed et al., 1986	
Gulo gulo	0.36	Nilsson, 2013	
Pelophylax esculentus	0.82	Sjögren, 1991	*Pelophylax lessonae*
Pelophylax lessonae	0.82	Sjögren, 1991	
Triturus cristatus	0.13-0.24	Jehle et al., 2001; Jehle et al., 2005	*Triturus marmoratus*
Ursus arctos	0.21	Nilsson, 2013	

For this project we have applied a ratio of 0.1 for all species with census data except for eight species (Table 1). In cases where there is only a national census available, we have divided the national census evenly across each population (an important assumption), unless there is an indication that individuals are unevenly distributed across the species' range. To estimate the evenness in distribution we have used distribution maps depicting number of individuals with the help of the SLU Species Observation System (Artportalen; https://www.artportalen.se).

2.3 Estimating population loss

Population loss is primarily estimated through occurrence records and documented loss of distinct populations. During this project, we have used a baseline of no more than 100 years back in time for estimating the number of maintained populations. We found that it is difficult to find records of the disappearance of distinct populations in many cases; however, in some cases there are records of previous occurrence in counties or regions where the species is no longer is present. For Red List species, an estimate of overall decline (if applicable) is often available. We have, however, not used this information unless the decline could be attributed to a defined population. This approach (also used in Mastretta-Yanes and da Silva et al., 2024) results in a conservative estimate of proportion populations maintained (i.e. we classify populations to be maintained even if their distribution range might have decreased).

2.4 DNA-based monitoring

As described earlier (section 1.2), DNA-based monitoring of genetic diversity within and among populations has been initiated in Sweden and several reviews of available knowledge on genetic diversity of naturally occurring species have been carried out since the 1990s (Laikre and Ryman, 1997; Lönn et al., 1998; Laikre et al., 2008; Lundqvist et al., 2008; Wennerström et al., 2016; Posledovich et al., 2021a,b). This data, and other literature information or expert knowledge used for other indicators (see section 3), was used to assess the DNA-based monitoring indicator for each species.

We used two approaches to define the DNA-based indicator:

- **Method 1)** We only regarded "true" genetic monitoring (i.e. samples are collected over time and analysed with DNA-methods to determine temporal trends in genetic essential biodiversity variables). In this case, the indicator value is either "1" or "0". A species is given indicator value "1" if one or more of the species´ populations in Sweden are being monitored with DNA-techniques. If that is not the case, the indicator value is "0".
- **Method 2)** We use a less restrictive approach, which gives values larger than 0 also in cases were genetic studies are available from only a single point in time. If one or more of the species´ populations have been subjected to one or more phylogeographic or phylogenetic studies and no other studies have been carried out the indicator value is "0.25." Species with one or more populations subjected to one or more population genetic assessments at a single time receive an indicator value of "0.5" (regardless of whether phylogeographic studies were carried out). Species in which at least one population is or has been monitored over time with DNA-based methods receives a value of "1" (regardless of whether phylogenetic or population genetic assessments were also carried out).

Finally, we calculate an overall indicator value for a taxonomic group, or for all the assessed species, as a proportion by summing all the values for all assessed species in the group and dividing by the number of species in that group.

3. Sources of information

We explored the following sources of information to assess the three indicators as described in sections 2.2 – 2.4 above:

- National Action Plans (NAPs) from SEPA and SwAM
- Data from Red List assessments provided by the SLU Swedish Species Information Centre
- Data from monitoring schemes and surveys
- Results from the Article 12 reporting (EU Birds Directive)
- Results from the Article 17 reporting (EU Habitats Directive)
- Scientific papers and reports
- Expert consultations

The SLU Swedish Species Information Centre provides a website (artfakta.se) with information about Red List status, taxonomic information and distribution. Observation data is available through Artportalen.se, which is also provided by the SLU Swedish Species Information Centre. Information on the results from the EU Habitats Directive Article 17 reporting is available in a report provided by SEPA (2020) or through https://nature-art17.eionet.europa.eu/article17/species/progress/.

3.1 Action Plans

We located a total of 148 NAPs (Table A2.1) and our work focused on whether the information needed for indicator assessments were readily available in these reports. Of the 148 NAPs, five dealt exclusively with habitats and were thus excluded. The remaining 143 plans concerned a total of 323 species as 35 plans included more than one species (Table 2; A2.1; A2.2). Two species were covered in more than one NAP, and in these cases information in all plans were considered. Seagrass meadows (*Zostera* spp.) were treated as information on a single species because the different seagrass species are not clearly separated in the NAP. Five of the 13 amphibian species in Sweden are currently covered by NAPs, while only one of the six reptile species has a NAP.

To some extent, we found that most of the NAPs can be used for extracting information relevant for the genetic indicator assessments and we summarize this information in Table 2 (see also Table A2.1, A2.2). However, direct information on population size (N_c) is often described in terms of large, small, or viable/non-viable and occurrences are often reported by county with no further details within separate counties. Also, the terms “population”, “site” or “territory” are used in different ways among the NAPs. We recommend a clearer terminology and structure to be implemented in the NAPs to define separate populations. Furthermore, more details regarding occurrences (population identification), and census sizes within counties are needed.

Table 2. Summary from our identification of 143 National Action Plans that concern species (not habitats). The plans cover a total of 319 species, and we explored the potential to use these plans for assessing the three indicators for genetic diversity. Information sought included for Ne500 indicator: number of populations (or sites = geographic area of species occurrence) and their census sizes (or population size estimates), for the PM indicator: number of populations maintained over time (or decreased distribution as well as extinction of populations), and for DNA-based monitoring indicator: clearly provided information on availability of population genetic data. See also Appendix 2: Table A2.1 and A2.2.

Type of information available	Number of species for which this information is available	Proportion of species for which this information is available
Number of populations	77	24%
Number of sites	240	74%
Total census sizes (N_c) at species level	105	33%
Censuses of populations and sites (N_c)	70	22%
Effective population size (N_e) measured with genetic data	1	0.03%
Ne500 indicator assessment possible	**126**	**39%**
Extinct populations/localities	119	37%
Loss of range (but not populations)	28	9%
PM indicator assessment possible	**114**	**35%**
Section on conservation genetics in NAP	167	52%
Genetic studies are reported in NAP (phylogenetic, single-point-in-time, and temporal studies all included here)	31	9.6%
DNA-based monitoring indicator assessment possible	**172**	**53%**
Assessment possible for all 3 indicators	**53**	**16%**
Assessment possible for indicator 1 & 2	**75**	**23%**
NAPs subsequently used for species assessments*	***86****	***27%***

*Number of species for which data from the National Action Plans (NAPs) have been used to fill out a KoboToolbox form that has been used to assess the indicators for the present report as well as for the international assessment in nine countries (Mastretta-Yanes and da Silva et al., 2024).

3.2 Red List data

The Swedish Red List, currently covering approximately 22,000 species, is compiled by the SLU Swedish Species Information Centre (https://www.slu.se/art-databanken/rodlistade-arter), and updated every five years. The Swedish Red List follows the IUCN guidelines with six categories of threat status: Least Concern (LC), Vulnerable (VU), Near Threatened (NT), Endangered (EN), Critically Endangered (CR) or Data Deficient (DD). Each category is based on thresholds for population size, geographical distribution, and decline. This makes the Red List database a good source of information for the proxy-based indicators. The most relevant concepts of relevance in this context can be found in Table 3. We also provide more detailed explanations and discuss how the Red List process could be used to aid genetic diversity indicator assessment in section 5.

We consulted the Red List data in all the indicator assessments reported here. However, the Red List does not seek to identify all individual populations of a species, or estimate their sizes. Instead, the term “population” used by the Red List refers to all individuals of a particular species within the evaluated area (in this case Sweden). Therefore, it is often not straight forward to use Red List “population” data for assessing the genetic indicators.

Table 3. Concepts of relevance for assessing the genetic indicators in the Red List framework. The definitions are from the Guidelines for Red List Categories and Criteria (IUCN, 2012).

Concept	Definition
Population	Total number of individuals of the taxon.
Population size	Number of mature individuals.
Subpopulation	Geographically or otherwise distinct groups in the population between which there is little demographic or genetic exchange (typically one successful migrant individual or gamete per year or less).
Location	The term 'location' defines a geographically or ecologically distinct area in which a single threatening event can rapidly affect all individuals of the taxon present. The size of the location depends on the area covered by the threatening event and may include part of one or many subpopulations.
Severely fragmented	The phrase 'severely fragmented' refers to the situation in which increased extinction risks to the taxon results from the fact that most of its individuals are found in small and relatively isolated subpopulations (in certain circumstances this may be inferred from habitat information). These small subpopulations may go extinct, with a reduced probability of recolonization.
AOO	Area of occupancy (AOO) is a scaled metric that represents the area of suitable habitat currently occupied by the taxon.
EOO	Extent of occurrence (EOO) is defined as "the area contained within the shortest continuous imaginary boundary which can be drawn to encompass all the known, inferred or projected sites of present occurrence of a taxon, excluding cases of vagrancy."

It should be noted that the concept "subpopulations" is defined within the Red List framework as groups of individuals between which there is little to no genetic or demographic exchange (IUCN, 2012). This translates to what we, in this report and elsewhere, consider as "populations" (i.e., populations within species). Therefore, when available, information on subpopulations is directly relevant for assessing the genetic diversity indicators.

The Red List framework also includes a concept called "locations" (Swedish: lokalområde). This does not refer to separated subpopulations but is characterized as a defined area where all individuals of a taxon within that area could be affected by a single outside factor or threat (Table 3). Locations can include several subpopulations or parts of subpopulations (Gärdenfors, 2018). This means that it is not possible to directly translate locations into populations when making species assessments for the genetic diversity indicators.

The Red List assessment identifies three levels of population fragmentation: no fragmentation (0), moderate fragmentation (1) or severe fragmentation (2). Assessing fragmentation includes assessing the number of population fragments which can be used as proxies for populations. However, this information is not available for all species.

In the Red List framework, distribution is described using two types of parameters: Extent of Occurrence (EOO) and Area of Occupancy (AOO). Extent of occurrence is the total size of the geographic range in which the species occur, and area of occupancy is the total size of the geographic area where the species actually occurs (Gärdenfors, 2018).

In some cases, the estimated population size of the largest sub-population is provided, and it is then possible to estimate the minimum number of populations and their approximate sizes based on this information. For example, the sand lizard (*Lacerta agilis*) has an estimated total population size in Sweden of 11,000 individuals and the largest sub-population is estimated to be 500 individuals. This would mean at least 23 populations in Sweden since no population is

larger than 500 individuals. None meet the Ne500 indicator requirement of N_C > 5,000. However, this approach relies on the assumption that the largest sub-population really is a sub-population in a genetic sense and not some other demographic entity (e.g., field site). In Table 4 we summarize available information in the Red List database for the 120 species assessed.

Table 4. Available information from Red List data for amphibians (13 species), angiosperms (22 species), birds (11 species), bryophytes (2 species), fishes (7 species), fungi (2 species), invertebrates (29 species), mammals (20 species), pteridophytes (1 species), reptiles (6 species, one subspecies), and others (6 species). Pop. size = estimated total number of individuals in Sweden. Frag. (fragmentation) degree: 0 = no fragmentation, 1 = moderately fragmented, 2 = severely fragmented. No. loc. = number of locations, which is a geographic division within the Red List framework into separate areas influenced independently by outside factors. The term "location" defines a geographic area where a single threatening event can rapidly affect all individuals of the taxon present (Gärdenfors, 2018). EOO = extent of occurrence, AOO = area of occurrence. NA = information not available.

Scientific name	Common name (Swe)	Common name (En)	Pop. size	Largest sub-pop	Frag. degree	No. loc	EOO (km²)	AOO (km²)
AMPHIBIANS								
Bombina bombina	Klockgroda	Fire-bellied toad	2,600	NA	0	NA	3,900	380
Bufo bufo	Vanlig padda	Common toad	NA	NA	0	NA	545,000	NA
Bufotes viridis	Grönfläckig padda	Green toad	3,000	750	2	4	26,000	250
Epidalea calamita	Strandpadda	Natterjack toad	2,550	NA	1	NA	53,900	600
Hyla arborea	Lövgroda	Tree frog	18,000	NA	0	NA	2,900	1,100
Lissotriton vulgaris	Mindre vatten-salamander	Smooth newt	NA	NA	0	NA	460,000	NA
Pelobates fuscus	Lökgroda	Spadefoot toad	1,530	NA	2	8	3,600	300
Pelophylax esculentus	Ätlig groda	Edible frog	20,000	NA	0	NA	30,000	NA
Pelophylax lessonae	Gölgroda	Pool frog	5,000	NA	0	6	10,190	260
Rana arvalis	Åkergroda	Moor frog	300,000,000	NA	0	NA	500,000	NA
Rana dalmatina	Långbens-groda	Agile frog	46,600	NA	0	8	13,000	1,300
Rana temporaria	Vanlig groda	Common frog	300,000,000	NA	0	NA	575,000	NA
Triturus cristatus	Större vatten-salamander	Great crested newt	200,000	NA	0	NA	29,000	NA
ANGIOSPERMS								
Alisma wahlenbergii	Småsvalting	Baltic water-plantain	150,000	100,000	2	10	NA	120
Chenopodium vulvaria	Stinkmålla	Sinking goosefoot	200,000	50,000	2	2	832,000	16,000
Eryngium maritimum	Martorn	Sea-holly	9,500	6,600	NA	45	NA	184,000
Euphrasia officinalis subsp. officinalis	Finnögontröst	Rostkov's eyebright	50,000	20,000	2	40	NA	240,000
Euphrasia stricta var. suecica	Svensk ögontröst	Drug eyebright	25,000	20,000	2	6	1,016	24
Genista germanica	Tysk ginst	German greenwood	10	10	2	2	16	8
Gentiana pneumonanthe	Klockgentiana	Marsh gentian	300,000	170,000	NA	200	NA	1,500
Gymnadenia nigra	Brunkulla	Black vanilla orchid	1,500	472	1	NA	14,756	284
Jacobaea erucifolia	Flikstånds	Hoary ragwort	800	800	NA	2	292	8
Juncus anceps	Svarttåg	Rush	500	400	2	3	56	12

Scientific name	Common name (Swe)	Common name (En)	Pop. size	Largest sub-pop	Frag. degree	No. loc	EOO (km²)	AOO (km²)
Luronium natans	Flytsvalting	Floating water plantain	60,000	50,000	NA	3	3,500	28
Mertensia maritima	Ostronört	Oyster plant	80	20	2	8	800	36
Myricaria germanica	Klådris	German false tamarisk	50,000	20,000	1	NA	NA	260
Pseudorchis albida	Vityxne	Small white orchid	2,000	180	2	60	NA	500
Pulsatilla patens	Nipsippa	Eastern pasque flower	120,000	107,000	1	45	22,856	196
Pulsatilla vernalis	Mosippa	Spring pasque flower	10,000	2,000	2	NA	NA	2,500
Pulsatilla vulgaris subsp. gotlandica	Gotlandssippa	European pasqueflower	40,600	20,000	0	1	748	48
Ranunculus hederaceus	Murgrönsmöja	Ivy-leaved crowfoot	3,000	400	2	3	387	92
Ranunculus ophioglossifolius	Gotlands-ranunkel	Adder's-tongue spearwort	200	150	NA	2	24	12
Sabulina viscosa	Sandnörel	Sticky sandwort	40	40	NA	1	4	4
Saxifraga osloënsis	Hällebräcka	Saxifrage	400,000	20,000	1	230	NA	1,100
Tephroseris palustris	Kärrnocka	Marsh ragwort	7	7	NA	2	124	4
BIRDS								
Anser erythropus	Fjällgås	Lesser white-fronted goose	NA	24	2	1	100	16
Anthus campestris	Fältpiplärka	Tawny pipit	80	NA	0	5	45,021	150
Calidris alpina schinzii	Sydlig kärrsnäppa	Dunlin	100	70	0	8	130,000	200
Charadrius alexandrinus	Svartbent strandpipare	Kentish plover	NA	NA	NA	NA	NA	NA
Circus pygargus	Ängshök	Montagu's harrier	NA	75	0	NA	170,356	220
Dendrocopos leucotos	Vitryggig hackspett	White-backed woodpecker	14	2	2	4	254,910	50
Emberiza calandra	Kornsparv	Corn bunting	80	50	2	NA	27,892	72
Emberiza hortulana	Ortolansparv	Ortolan bunting	3,000	NA	0	NA	275,987	4,001
Ficedula albicollis	Halsbands-flugsnappare	Collared flycatcher	11,600	NA	0	NA	24,167	4,001
Hydroprogne caspia	Skräntärna	Caspian tern	1,160	NA	0	NA	319,549	440
Limosa limosa	Rödspov	Black-tailed godwit	230	80	0	NA	335,979	230
BRYOPHYTES								
Brachythecium novae-angliae	Brynia	Bryhnia	5,500	20	1	NA	NA	368
Dicranum viride	Barkkvast-mossa	Dicranum moss	400	100	2	NA	NA	250
FISHES								
Coregonus albula	Siklöja	Vendace	NA	NA	0	NA	NA	NA
Gadus morhua	Torsk	Atlantic cod	NA	NA	1	NA	NA	NA
Lampetra fluviatilis	Flodnejonöga	River lamprey	NA	NA	0	NA	NA	NA
Leuciscus aspius	Asp	Aral asp	NA	NA	0	NA	86,000	472
Petromyzon marinus	Havsnejonöga	Sea lamprey	NA	NA	0	NA	24,000	100

Scientific name	Common name (Swe)	Common name (En)	Pop. size	Largest sub-pop	Frag. degree	No. loc	EOO (km^2)	AOO (km^2)
Salmo salar	Lax	Salmon	200,000	6,000	1	35	NA	NA
Silurus glanis	Mal	European catfish	NA	600	2	6	NA	NA
FUNGI								
Geastrum flexuosum	Jordstjärns-tryffel	Earthstar	40	NA	NA	4	8	8
Gomphus clavatus	Violgubbe	Pig's ear	30,000	NA	NA	600	NA	3,000
INVERTEBRATES								
Agonopterix bipunctosa	Ängsskäre-plattmal	Twin-spot flat-body	NA	NA	1	60	NA	240
Anacampsis fuscella	Klöversober-mal	Anacampsis moth	NA	NA	2	25	6,800	100
Anthophora plagiata	Humlepälsbi	Common digger bee	600	600	0	2	6,280	16
Baptria tibiale	Trolldruve-mätare	Tibial or bane-berry moth	NA	NA	1	25	12,000	100
Canthophorus impressus	Spindelört-skinnbagge	Down shield bug	NA	NA	NA	100	9,000	400
Cerambyx cerdo	Större ekbock	Great capri-corn beetle	NA	NA	2	1	4	4
Chalcophora mariana	Jättepraktbagge	Flatheaded pine borer	NA	NA	2	20	NA	80
Depressaria nemolella	Gotländsk säfferots-plattmal	Parsnip moth sp.	NA	NA	2	4	80	16
Dysauxes ancilla	Fönstervinge-spinnare	Handmaid	750	NA	NA	1	16	4
Eresus sandaliatus	Nyckelpige-spindel	Ladybird spider	400	400	NA	1	4	4
Euphydryas aurinia	Väddnätfjäril	Marsh fritillary	15,000	NA	0	NA	NA	1,200
Euphydryas maturna	Asknätfjäril	Scarce fritillary	2,000	NA	2	NA	4,000	156
Harpalus autumnalis	Höstfrölöpare	Autumn ground beetle	NA	NA	2	2	10	8
Harpalus flavescens	Gul frölöpare	Yellowish ground beetle	NA	NA	2	12	1,500	48
Lopinga achine	Dårgräsfjäril	Woodland brown	14,000	NA	0	NA	12,000	480
Lycaena helle	Violett guld-vinge	Violet copper	5,200	NA	2	200	NA	425
Lytta vesicatoria	Spansk fluga	Spanish fly	NA	NA	2	4	80	16
Margaritifera margaritifera	Flodpärl-mussla	Freshwater pearl mussel	NA	NA	NA	1	NA	3,840
Melitaea britomartis	Veronikanät-fjäril	Assmann's fritillary	80	NA	2	2	700	12
Melitta tricincta	Rödtoppebi	Red bartsia blunthorn bee	8,000	7,000	0	15	NA	300
Parnassius mnemosyne	Mnemosyne-fjäril	Clouded apollo	1,800	NA	2	20	NA	200
Pedostrangalia revestita	Almblombock	Black and red longhorn beetle	NA	NA	2	80	NA	320
Phengaris alcon	Alkonblåvinge	Alcon blue	1,500	NA	2	50	13,000	200
Phengaris arion	Svartfläckig blåvinge	Large blue	10,000	NA	0	400	NA	850
Psophus stridulus	Trumgräs-hoppa	Rattle grass-hopper	2,500	500	2	80	NA	450

Scientific name	Common name (Swe)	Common name (En)	Pop. size	Largest sub-pop	Frag. degree	No. loc	EOO (km²)	AOO (km²)
Pytho kolwensis	Större bark-plattbagge	Dead log bark beetle	NA	NA	2	40	NA	160
Scolitantides orion	Fetörtsblå-vinge	Chequered blue butterfly	NA	NA	2	5	15,000	100
Stauroderus scalaris	Skärrande gräshoppa	Large mountain grasshopper	NA	NA	NA	15	160	100
Unio crassus	Tjockskalig målarmussla	Thick-shelled river mussel	NA	NA	2	NA	NA	280
MAMMALS								
Alces alces	Älg	Moose	260,000	NA	0	NA	NA	NA
Barbastella barbastellus	Barbastell	Barbastelle	16,000	NA	0	NA	119,000	3,348
Canis lupus	Eurasiatisk skogsvarg	Grey wolf	210	NA	0	NA	NA	NA
Capreolus capreolus	Rådjur	Roe deer	280,000	NA	0	NA	450,000	200,000
Castor fiber	Bäver	Eurasian beaver	130,000	NA	0	NA	NA	50,000
Cervus elaphus elaphus	Kronhjort	Red deer	5,400	NA	0	NA	12,000	NA
Erinaceus europaeus	Igelkott	Hedgehog	20,001	NA	0	NA	200,000	50,000
Gulo gulo	Järv	Wolverine	287	NA	0	NA	120,000	30,000
Halichoerus grypus	Gråsäl	Grey seal	12,800	NA	0	NA	NA	750
Lepus timidus	Skogshare	Mountain hare	450,000	NA	0	NA	NA	250,000
Lutra lutra	Utter	European otter	4,000	NA	0	NA	NA	15,000
Muscardinus avellanarius	Hasselmus	Hazel dormouse	2,000,000	NA	0	NA	NA	NA
Myotis bechsteinii	Bechsteins fladdermus	Bechstein's bat	200	NA	2	3	2,540	144
Phoca vitulina	Knubbsäl	Harbour seal	8,000	NA	0	NA	15,000	NA
Phoca vitulina (Baltic population)	Knubbsäl (östersjö-populationen)	Harbour seal (Baltic population)	980	NA	1	7	NA	NA
Phocoena phocoena	Tumlare	Harbour porpoise	5,000	NA	0	NA	NA	NA
Phocoena phocoena (Baltic population)	Tumlare (östersjö-populationen)	Harbour porpoise (Baltic population)	98	99	NA	NA	NA	NA
Sicista betulina	Buskmus	Northern birch mouse	128,000	NA	0	NA	5,000	15,000
Sorex isodon	Tajganäbb-mus	Taiga shrew	2,000	NA	1	25	26,000	500
Ursus arctos	Brunbjörn	Brown bear	1,438	NA	0	NA	NA	NA
Vulpes lagopus	Fjällräv	Arctic fox	165	NA	2	3	NA	650
Vulpes vulpes	Rödräv	Red fox	120,000	NA	0	NA	NA	NA
PTERIDOPHYTES								
Botrychium simplex	Dvärglås-bräken	Least moonwort	1,000	300	2	NA	NA	32
REPTILES								
Anguis fragilis	Kopparödla	Slow worm	NA	NA	0	NA	360,000	NA

Scientific name	Common name (Swe)	Common name (En)	Pop. size	Largest sub-pop	Frag. degree	No. loc	EOO (km²)	AOO (km²)
Coronella austriaca	Hasselsnok	Smooth snake	9,000	NA	0	NA	175,000	NA
Lacerta agilis	Sandödla	Sand lizard	11,000	500	0	NA	150,000	NA
Natrix natrix	Snok	Grass snake	NA	NA	0	NA	340,000	1,256
Natrix natrix gotlandica	Gotlandssnok	Grass snake (Gotland)	1,800	NA	0	NA	5,840	NA
Natrix natrix natrix	Snok (fastland)	Grass snake (mainland)	NA	NA	0	NA	330,000	NA
Vipera berus	Huggorm	Viper	NA	NA	0	NA	534,000	500
Zootoca vivipara	Skogsödla	Viviparous lizard	NA	NA	0	NA	583,100	NA
OTHER								
Bryoria nitidula	Glanstagel	Tundra horse-hair lichen	120	NA	0	12	48	32
Bryoria tenuis	Långt broktagel	Pied horse-hair lichen	250	NA	0	60	NA	240
Heterodermia speciosa	Elfenbenslav	Powdered fringe lichen	600	NA	0	60	NA	240
Lamprothamnium papulosum	Axsträfse	Foxtail stone-wort	NA	NA	NA	2	600	12
Leptogium rivulare	Strandskinn-lav	Flooded jelly skin lichen	1,500	NA	0	25	15,848	100
Lobaria hallii	Hårig skrovellav	Gray lung lichen	2,500	NA	2	11	25,000	44

3.3 Biogeographic survey

The biogeographic survey program is a monitoring program aimed at species and habitats included in the EU Habitats Directive (https://www.naturvardsverket.se/om-miljoarbetet/miljoovervakning/programomraden/biogeografisk-uppfoljning-av-naturtyper-och-arter). When available, we have consulted the biogeographic survey reports for information on occurrences and population size. The biogeographic survey is based on occurrence data from the Swedish Species Observation System (Artportalen), and all the occurrence data recorded during surveys are reported into Artportalen. In some cases, the survey is extended to include observations from other reports as well as new search areas.

The biogeographic survey lists the number of localities surveyed, and in how many locations a species was found. For amphibians, localities are categorized into different types depending on whether they represent a basic core water body or a supporting water body in a metapopulation structure. The biogeographic survey reports include information on the general areas of distribution, however, it is mainly divided by county rather than into metapopulation or population units. There are also estimations of population size. Census counts are listed by area or as totals for the entire country, including an estimate for the national census size. It is thus difficult to assess the number of populations and their sizes based solely on the biogeographic survey reports.

3.4 Reports and surveys

Many threatened species are the subjects of monitoring programs or surveys. Swedish law requires that development and construction projects (such as new buildings, roads, bridges, urban areas, parks, etc.) include an evaluation of the effects on wild animal and plant species, ecosystems, and the environment. It is therefore possible to find numerous survey reports for species included in the EU Habitats Directive and for nationally protected species. These reports often cover small areas considered for development or municipality planning. However, the reports can be helpful in combination with other sources to inform on population occurrences and population sizes.

3.5 Literature search

For each species we assessed, we reviewed available literature on genetic diversity for the chosen species. In addition to the available reviews (see section 2.4), we searched for additional literature using search terms “genetic”, “gene flow”, “effective population size”, “population genetics”, “conservation genetics” and “populations” with “Sweden” and the species name or group (e.g., amphibian).

3.6 Expert opinion

During this project, we consulted experts on several occasions. The main issue discussed involved the delimitation of populations, with experts providing information on dispersal capacity in different habitats and knowledge on occurrences. Experts provided up to-date, albeit unpublished, knowledge of areas where the species have disappeared that cannot be gained from reports. This is especially important for species with small populations that may decline rapidly.

3.7 Occurrence data

Occurrence data from databases such as Artportalen (www.artportalen.se), GBIF (www.gbif.se) or the Analysis portal for biodiversity data (http://www.analysisportal.se; please note that this resource is no longer available) are based on observations, both official survey data and citizen science observations. In cases when there is limited information in other sources, occurrence databases are useful sources of information on species distributions and can be used to define populations. However, it is important to keep in mind that gaps in data points do not necessarily mean gaps in species distribution. Observations tend to be higher than expected from the true distribution in and around cities, and lower in rural areas. With citizen science data there are also risks of errors (e.g., species may be misidentified, or location data is incorrectly entered). However, occasional errors are not a huge problem, because they will either occur within clusters of correct observations, or they can often be identified as single outlier observations.

4. Results from assessments of genetic diversity indicators

We conducted genetic diversity indicator assessments for as many species as possible based on existing detailed information from various national sources during the time available for this project. The initial focus was on amphibians (13 species) and reptiles (six species, one with two subspecies assessed) as requested by SEPA (Appendix 3). We then assessed an additional 100 species (Table 4; see also Table A2.3) across eight taxonomic groups (Figure 6). The species were selected based on the following criteria:

a) information available about locations or populations in NAP, the Red List Database, and literature
b) available N_e estimates or ongoing DNA-based monitoring
c) taxonomic group (the goal was to have different groups represented)

Seven species were assessed in two or more alternative ways (detailed in section 4.4 Alternative assessments). Indicator values for species with such multiple assessments were averaged in the analysis of Mastretta-Yanes and da Silva et al. (2024) and we have followed the same procedure.

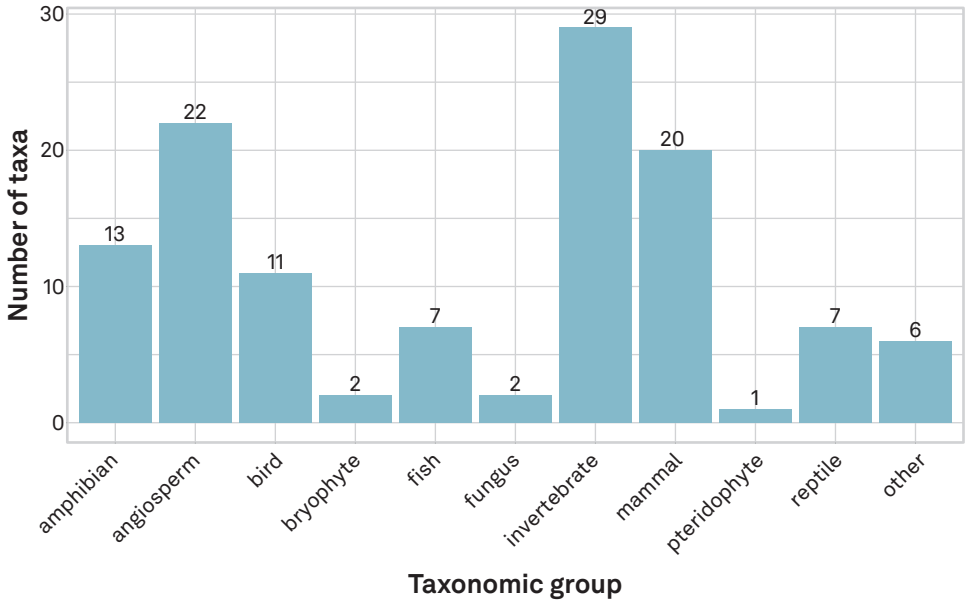


Figure 6. Taxonomic groups of the 120 assessed species, including a few subspecies. The taxonomic groups were identified in the KoboToolbox form (see Appendix 1). The "other" category contains lichens and charophytes.

The dataset includes seven subspecies (*Calidris alpina schinzii, Cervus elaphus elaphus, Euphrasia officinalis officinalis, Euphrasia stricta suecica, Natrix natrix gotlandica, Natrix natrix natrix, Pulsatilla vulgaris gotlandica*), one hybrid species (*Pelophylax esculentus*) and a morphotype (*Coregonus albula* morphotype *trybomi*), which have been assessed as if they are separate species. The term species used throughout this report and the summery statistics thus refer to all assessed taxa regardless of species or subspecies (or morphotype) status.

One priority of the present work was to review the extent to which NAPs could be used for assessing the indicators, and we included 61 species with such plans in our assessment. The NAPs are typically produced for species in need of conservation and thus our dataset is skewed toward species with limited distributions or population sizes. For example, out of the 24,100 Red List taxa (21,700 species plus 2,400 subspecies and other below species taxa) assessed in 2020 2,767 (11.5 %) were categorized as threatened. In contrast, of the 120 assessments included in this report, all of which have a Red List category, 72 (60 %) belong to one of the threatened Red List categories (CR, EN, VU). Only one species is listed as Data Deficient (DD), one is Regionally Extinct (RE) and 46 species (38 %) are Near Threatened or Least Concern (NT, LC; Figure 7).

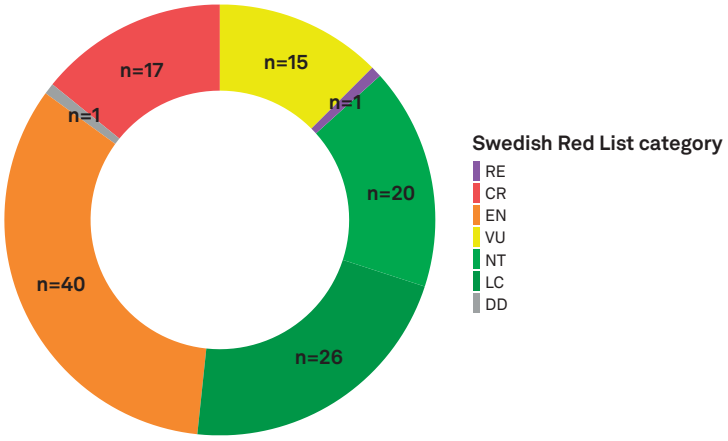


Figure 7. The Swedish Red List categories of the 120 assessed species (including a few subspecies).

Indicator assessments for each of the 120 species are presented in Table 5. We have submitted all assessments using the KoboToolbox form developed by Hoban et al. (2023) and Mastretta-Yanes and da Silva et al. (2024). For two species (*Anacampsis fuscella* and *Lytta vesicatoria*), the population size data is insufficient and therefore there is no Ne500 indicator value for these species. Also, one species has become Regionally Extinct during the monitoring period (Kentish plover) and, since only extant populations are considered for the Ne500 indicator, there is no Ne500 indicator value for this species (while the PM indicator is 0). It should be noted that in these types of cases, it is important to assess both the Ne500 and the PM indicator in parallel (as we do here). If only the Ne500 indicator is used, then the Ne500 value should be 0 in a case like this, in order to more accurately reflect the loss of genetic diversity (see section 4.1). In total, the Ne500 indicator value was quantified for 117 of the 120 species, while the PM indicator and DNA-based monitoring indicators were calculated for all 120 species.

Table 5. Genetic diversity indicator assessments for a total of 120 species in Sweden. For average values per group and overall total, see Table 6. For information about the underlying assessment see Appendix 2: Table A2.3.

Taxa	Common name (Swe)	Common name (En)	N_e > 500	Populations maintained	DNA-based monitoring method 1	DNA-based monitoring method 2	National Red List status
AMPHIBIANS							
*Bombina bombina**	Klockgroda	Fire-bellied toad	0.25	1.00	0.00	0.50	LC
Bufo bufo	Vanlig padda	Common toad	1.00	1.00	1.00	1.00	LC
Bufotes viridis	Grönfläckig padda	Green toad	0.00	0.87	1.00	1.00	VU
Epidalea calamita	Strandpadda	Natterjack toad	0.00	0.92	1.00	1.00	NT
Hyla arborea	Lövgroda	Tree frog	0.50	0.67	0.00	0.50	LC
Lissotriton vulgaris	Mindre vatten-salamander	Smooth newt	1.00	0.98	0.00	0.50	LC
Pelobates fuscus	Lökgroda	Spadefoot toad	0.00	0.75	0.00	0.00	VU
*Pelophylax esculentus***	Ätlig groda	Edible frog	0.50	0.40	0.00	0.50	LC
Pelophylax lessonae	Gölgroda	Pool frog	0.00	1.00	0.00	0.50	VU
Rana arvalis	Åkergroda	Moor frog	1.00	1.00	1.00	1.00	LC
Rana dalmatina[a)]	Långbensgroda	Agile frog	0.56	1.00	0.00	0.00	NT
Rana temporaria	Vanlig groda	Common frog	1.00	1.00	1.00	1.00	LC
Triturus cristatus	Större vatten-salamander	Great crested newt	0.10	0.99	0.00	0.50	LC
ANGIOSPERMS							
Alisma wahlenbergii	Småsvalting	Baltic water-plantain	0.40	0.71	0.00	0.50	NT
Chenopodium vulvaria	Stinkmålla	Sinking goose-foot	0.00	0.60	0.00	0.00	EN
Eryngium maritimum	Martorn	Sea-holly	0.00	0.80	0.00	0.25	VU
Euphrasia officinalis officinalis	Finnögontröst	Rostkov's eyebright	0.15	0.63	0.00	0.25	EN
Euphrasia stricta suecica	Svensk ögontröst	Drug eyebright	0.30	0.33	0.00	0.50	EN
Genista germanica	Tysk ginst	German green-wood	0.00	0.08	0.00	0.00	CR
Gentiana pneumonanthe[a)]	Klockgentiana	Marsh gentian	0.05	1.00	0.00	0.00	EN
Gymnadenia nigra	Brunkulla	Black vanilla orchid	0.00	0.75	0.00	0.25	EN
Jacobaea erucifolia	Flikstånds	Hoary ragwort	0.00	0.67	0.00	0.00	EN
Juncus anceps	Svarttåg	Rush	0.00	0.75	0.00	0.00	CR
Luronium natans	Flytsvalting	Floating water plantain	0.25	0.67	0.00	0.50	EN
Mertensia maritima	Ostronört	Oyster plant	0.00	0.75	0.00	0.00	CR
Myricaria germanica	Klådris	German false tamarisk	0.08	0.65	0.00	0.00	NT
Pseudorchis albida	Vityxne	Small white orchid	0.00	0.63	0.00	0.50	EN
Pulsatilla patens	Nipsippa	Eastern pas-queflower	1.00	0.83	0.00	0.00	NT
Pulsatilla vernalis	Mosippa	Spring pasque flower	0.00	0.75	0.00	0.25	EN
Pulsatilla vulgaris gotlandica	Gotlandsippa	European pas-queflower	0.25	1.00	0.00	0.00	VU
Ranunculus hederaceus	Murgrönsmöja	Ivy-leaved crowfoot	0.00	0.80	0.00	0.00	NT

Taxa	Common name (Swe)	Common name (En)	N_e > 500	Populations maintained	DNA-based monitoring method 1	DNA-based monitoring method 2	National Red List status
Ranunculus ophioglossifolius	Gotlands-ranunkel	Adder's-tongue spearwort	0.00	0.40	0.00	0.25	EN
Sabulina viscosa	Sandnörel	Sticky sandwort	0.00	0.02	0.00	0.00	CR
Saxifraga osloënsis	Hällebräcka	Saxifrage	0.43	0.64	0.00	0.50	VU
Tephroseris palustris	Kärrnocka	Marsh fleawort	0.00	0.25	0.00	0.00	CR
BIRDS							
Anser erythropus	Fjällgås	Lesser white-fronted goose	0.00	0.50	0.00	0.50	CR
Anthus campestris	Fältpiplärka	Tawny pipit	0.00	0.20	0.00	0.00	EN
Calidris alpina schinzii	Sydlig kärrsnäppa	Dunlin	0.00	1.00	1.00	1.00	CR
Charadrius alexandrinus	Svartbent strandpipare	Kentish plover	NA	0.00	0.00	0.00	RE
Circus pygargus	Ångshök	Montagu's harrier	0.00	1.00	0.00	0.00	EN
Dendrocopos leucotos	Vitryggig hackspett	White-backed woodpecker	0.00	0.29	0.00	0.50	CR
Emberiza calandra	Kornsparv	Corn bunting	0.00	1.00	0.00	0.00	EN
Emberiza hortulana	Ortolansparv	Ortolan bunting	0.00	0.67	0.00	0.50	CR
Ficedula albicollis	Halsbands-flugsnappare	Collared fly-catcher	1.00	1.00	1.00	1.00	LC
Hydroprogne caspia[a)]	Skräntärna	Caspian tern	0.00	0.77	0.00	0.00	NT
Limosa limosa	Rödspov	Black-tailed godwit	0.00	1.00	0.00	0.25	EN
BRYOPHYTES							
Brachythecium novae-angliae	Bryhnia	Bryhnia	0.00	0.87	0.00	0.00	LC
Dicranum viride	Barkvastmossa	Dicranum moss	0.00	0.94	0.00	0.00	EN
FISHES							
Coregonus albula morphotype trybomi	Vårlekande siklöja	Spring spawning vendace	0.00	0.25	1.00	1.00	DD
Gadus morhua	Torsk	Atlantic cod	1.00	1.00	1.00	1.00	VU
Lampetra fluviatilis	Flodnejonöga	River lamprey	1.00	1.00	0.00	0.00	LC
Leuciscus aspius	Asp	Aral asp	0.00	1.00	0.00	0.00	NT
Petromyzon marinus	Havsnejonöga	Sea lamprey	0.00	0.74	0.00	0.50	EN
Salmo salar	Lax	Salmon	0.19	0.68	1.00	1.00	LC
Silurus glanis	Mal	European catfish	0.00	0.50	1.00	1.00	NT
FUNGI							
Geastrum flexuosum	Jordstjärns-tryffel	Earthstar	0.00	1.00	0.00	0.00	CR
Gomphus clavatus	Violgubbe	Pig's ear	0.00	0.71	0.00	0.00	VU
INVERTEBRATES							
*Agonopterix bipunctosa****	Ängsskäre-plattmal	Twin-spot flat-body	0.00	0.67	0.00	0.00	VU
Anacampsis fuscella	Klöversobermal	Anacampsis moth	NA	1.00	0.00	0.00	EN
*Anthophora plagiata****	Humplepälsbi	Common digger bee	0.00	0.29	0.00	0.00	EN
*Baptria tibiale****	Trollduve-mätare	Tibial or bane-berry moth	0.00	0.60	0.00	0.00	EN
Canthophorus impressus	Spindelört-skinnbagge	Down shield bug	0.00	1.00	0.00	0.00	NT

Taxa	Common name (Swe)	Common name (En)	N_e > 500	Populations maintained	DNA-based monitoring method 1	DNA-based monitoring method 2	National Red List status
Cerambyx cerdo	Större ekbock	Great capricorn beetle	0.00	0.33	0.00	0.00	CR
Chalcophora mariana	Jätteprakt-bagge	Flatheaded pine borer	0.00	0.25	0.00	0.00	EN
Depressaria nemolella	Gotländsk säfferrot-plattmal	Parsnip moth sp.	0.00	1.00	0.00	0.00	CR
*Dysauxes ancilla****	Fönstervinge-spinnare	Handmaid	0.00	1.00	0.00	0.50	CR
Eresus sandaliatus	Nyckelpige-spindel	Ladybird spider	0.00	1.00	0.00	0.25	VU
*Euphydryas aurinia****	Väddnätsfjäril	Marsh fritillary	0.00	0.80	0.00	0.00	VU
*Euphydryas maturna****	Asknätfjäril	Scarce fritillary	0.00	0.33	0.00	0.00	EN
Harpalus autumnalis	Höstfrölöpare	Autumn ground beetle	0.00	1.00	0.00	0.00	CR
Harpalus flavescens	Gul frölöpare	Yellowish ground beetle	0.00	0.67	0.00	0.00	EN
*Lopinga achine****	Dårgräsfjäril	Woodland brown	1.00	1.00	0.00	0.00	NT
*Lycaena helle****	Violett guldvinge	Violet copper	0.00	0.36	0.00	0.50	EN
Lytta vesicatoria	Spansk fluga	Spanish fly	NA	0.67	0.00	0.00	CR
Margaritifera margaritifera	Flodpärmusla	Freshwater pearl mussel	1.00	0.40	0.00	0.50	EN
*Melitaea britomartis****	Veronikanät-fjäril	Assmann's fritillary	0.00	0.20	0.00	0.00	CR
*Melitta tricincta****	Röddtoppebi	Red bartsia blunthorn bee	0.14	0.78	0.00	0.00	NT
*Parnassius mnemosyne****	Mnemosyne-fjäril	Clouded apollo	0.00	0.29	0.00	0.50	EN
*Pedostrangalia revestita****	Almblombock	Black and red longhorn beetle	0.00	0.61	0.00	0.00	EN
*Phengaris alcon****	Alkonblåvinge	Alcon blue	0.00	1.00	0.00	0.25	EN
*Phengaris arion****	Svartfläckig blåvinge	Large blue	0.13	1.00	0.00	0.50	NT
Psophus stridulus	Trumgräshoppa	Rattle grass-hopper	0.00	1.00	0.00	0.00	EN
Pytho kolwensis	Större bark-plattbagge	Dead log bark beetle	0.00	0.78	0.00	0.25	EN
*Scolitantides orion****	Fetörtsblåvinge	Chequered blue butterfly	0.00	0.63	0.00	0.00	EN
Stauroderus scalaris	Skrärrande gräshoppa	Large mountain grasshopper	0.20	0.63	0.00	0.00	EN
Unio crassus	Tjockskalig målarmussla	Thick-shelled river mussel	0.10	0.27	0.00	0.50	EN
MAMMALS							
Alces alces	Älg	Moose	0.67	1.00	1.00	1.00	LC
Barbastella barbastellus[b)]	Barbastell	Barbastelle	0.39	1.00	0.00	0.00	NT
Canis lupus	Varg	Wolf	0.00	1.00	1.00	1.00	EN
Capreolus capreolus	Rådjur	Roe deer	1.00	1.00	0.00	0.50	LC
Castor fiber	Bäver	Eurasian beaver	1.00	1.00	0.00	0.50	LC
Cervus elaphus elaphus	Kronhjort	Red deer	0.00	1.00	0.00	0.50	NT

Taxa	Common name (Swe)	Common name (En)	N_e > 500	Populations maintained	DNA-based monitoring method 1	DNA-based monitoring method 2	National Red List status
Erinaceus europaeus[a)]	Igelkott	Hedgehog	0.06	1.00	0.00	0.25	NT
Gulo gulo	Järv	Wolverine	0.00	1.00	1.00	1.00	VU
Halichoerus grypus[a)]	Gråsäl	Grey seal	0.35	1.00	0.00	0.50	LC
Lepus timidus	Skogshare	Mountain hare	0.50	1.00	1.00	1.00	NT
Lutra lutra	Utter	European otter	0.00	0.80	1.00	1.00	NT
Muscardinus avellanarius	Hasselmus	Hazel dormouse	1.00	0.92	0.00	0.25	LC
Myotis bechsteinii	Bechsteins fladdermus	Bechstein's bat	0.00	1.00	0.00	0.00	EN
Phoca vitulina	Knubbsäl	Harbour seal	0.20	1.00	0.00	0.50	LC
Phocoena phocoena	Tumlare	Harbour porpoise	0.00	1.00	0.00	0.50	LC
Sicista betulina	Buskmus	Northern birch mouse	1.00	1.00	0.00	0.25	LC
Sorex isodon	Tajganäbbmus	Taiga shrew	0.00	1.00	0.00	0.00	LC
Ursus arctos	Brunbjörn	Brown bear	0.00	1.00	1.00	1.00	NT
Vulpes lagopus	Fjällräv	Arctic fox	0.00	1.00	1.00	1.00	EN
Vulpes vulpes	Rödräv	Red fox	1.00	1.00	1.00	1.00	LC
PTERIDOPHYTES							
Botrychium simplex	Dvärglås-bräken	Least moon-wort	0.00	0.67	0.00	0.25	EN
REPTILES							
Anguis fragilis	Kopparödla	Slow worm	1.00	1.00	0.00	0.25	LC
Coronella austriaca[a)]	Hasselsnok	Smooth snake	0.14	1.00	0.00	0.00	VU
Lacerta agilis	Sandödla	Sand lizard	0.00	0.88	0.00	0.50	VU
Natrix natrix natrix	Snok	Grass snake	1.00	1.00	0.00	0.00	LC
Natrix natrix gotlandica	Gotlandssnok	Gotland grass snake	0.00	1.00	0.00	0.25	NT
Vipera berus	Huggorm	Common viper	0.86	1.00	1.00	1.00	LC
Zootoca vivipara	Skogsödla	Viviparous lizard	1.00	1.00	0.00	0.00	LC
OTHER							
Bryoria nitidula	Glanstagel	Tundra horse-hair lichen	0.00	0.60	0.00	0.25	EN
Bryoria tenuis	Långt broktagel	Pied horsehair lichen	0.00	0.88	0.00	0.25	EN
Heterodermia speciosa	Elfenbenslav	Powdered fringe lichen	0.00	0.67	0.00	0.25	VU
Lamprothamnium papulosum	Axsträfse	Foxtail stone-wort	0.00	1.00	0.00	0.00	EN
Leptogium rivulare	Strandskinnlav	Flooded jellyskin	0.00	0.75	0.00	0.00	EN
Lobaria hallii	Hårig skrovellav	Gray lung lichen	0.00	0.90	0.00	0.25	CR

a) Taxa with average values based on two alternative assessments

b) Taxa with average values based on three alternative assessments

*This is a reintroduced species in Sweden using populations from Denmark

** Hybrid species, most likely introduced in Sweden

*** Pollinating species (defined as pollinating species if the imago form consumes pollen, data from Artfakta https://artfakta.se)

4.1 The Ne500 Indicator

Two species could not be evaluated for the Ne500 indicator due to insufficient information about population size, and one species is regionally extinct, thus 117 species were assessed rather than 120. The overall results for the 117 species, which comprised 3,179 populations, showed an average indicator value 0.22 (Table 6; Figure 8). This means that on average 22 % of populations within species have an effective population size > 500, and the majority (78 %) are below this threshold.

Table 6. Average indicator value per taxonomic group based on the species assessments of Table 5. The DNA-based indicator is assessed as in Table 5 and averaged over taxa (for amphibians five taxa have at least one population subjected to DNA based monitoring so indicator value 5/13 = 0.38). Total values are the average indicator values across all assessed species (± standard deviation; see Table 5). Number of species in each category in parenthesis.

Taxonomic group	Ne500 indicator	PM indicator	DNA-based monitoring indicator, method 1	DNA-based monitoring indicator, method 2
Amphibian	0.46 ± 0.43 (13)	0.89±0.18 (13)	0.38 (13)	0.62 (13)
Angiosperm	0.13 ± 0.24 (22)	0.62 ± 0.26 (22)	0.00 (22)	0.17 (22)
Bird	0.10 ± 0.32 (10)	0.68 ± 0.37 (11)	0.18 (11)	0.34 (11)
Bryophyte	0.00 ± 0.00 (2)	0.90±0.05 (2)	0.00 (2)	0.00 (2)
Fish	0.31 ± 0.47 (7)	0.74 ± 0.29 (7)	0.57 (7)	0.64 (7)
Fungus	0.00 ± 0.00 (2)	0.86 ± 0.21 (2)	0.00 (2)	0.00 (2)
Invertebrate	0.10 ± 0.27 (27)	0.67 ± 0.29 (29)	0.00 (29)	0.11 (29)
Mammal	0.36 ±0.43 (20)	0.99 ± 0.05 (20)	0.40 (20)	0.59 (20)
Pteridophyte	0.00 ± NA (1)	0.67 ± NA (1)	0.00 (1)	0.25 (1)
Reptile	0.57±0.50 (7)	0.98± 0.05 (7)	0.14 (7)	0.29 (7)
Other	0.00 ± 0.00 (6)	0.80 ± 0.15 (6)	0.00 (6)	0.17 (6)
TOTAL	**0.22 ± 0.37 (117)**	**0.78 ± 0.27 (120)**	**0.17 (120)**	**0.32 (120)**

Since we are only considering extant populations for the Ne500 indicator, regionally extinct species are listed as NA rather than receiving a value of 0. The loss of all individuals in a species is instead captured through the PM indicator value (of zero populations maintained). However, should only the Ne500 indicator be assessed, we recommend using a Ne500 indicator value of 0 for this species to showcase that all populations have been lost. Otherwise, a perverse outcome may result, with the loss of populations actually benefiting the Ne500 indicator outcome, when in fact genetic diversity has been lost.

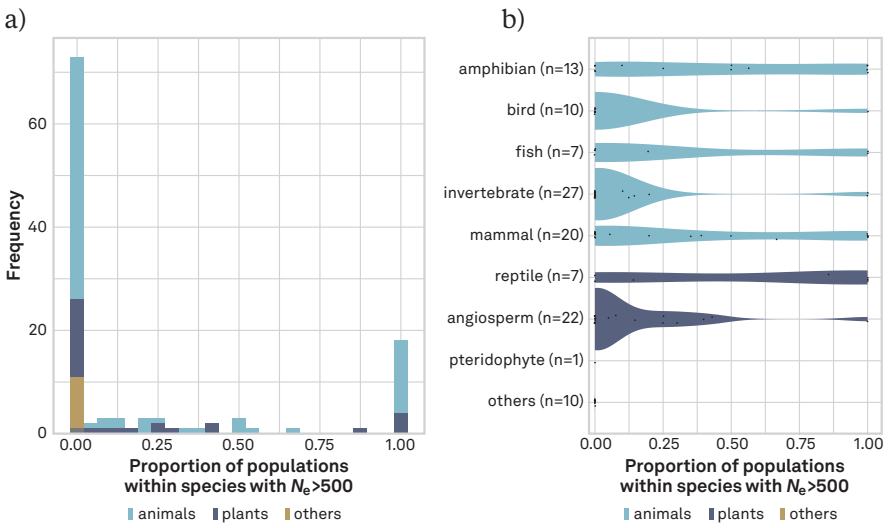


Figure 8. Results for Ne500 indicator assessments: a) Absolut frequency of indicator values across all species and b) distribution of indicator values across taxonomic groups. Species with multiple assessments are averaged (see section 4.4.). Number of species (n) assessed for this indicator is 117.

Of the 3,179 populations assessed, N_e from DNA-based estimates were available for 31 populations representing 11 species (Figure 9). The remaining Ne500 assessments were based on census data (Figure 10), either for each individual population (85 species, 691 populations) or from the national census (35 species, 2,477 populations). It is worth noting that 1,887 (60 %) of the 3,179 populations are represented by only six species (Figure A2.1); two angiosperms, one amphibian, one fish, one fungus, and one invertebrate. Twenty-six percent of these populations (840) belong to the angiosperm *Pulsatilla vernalis*.

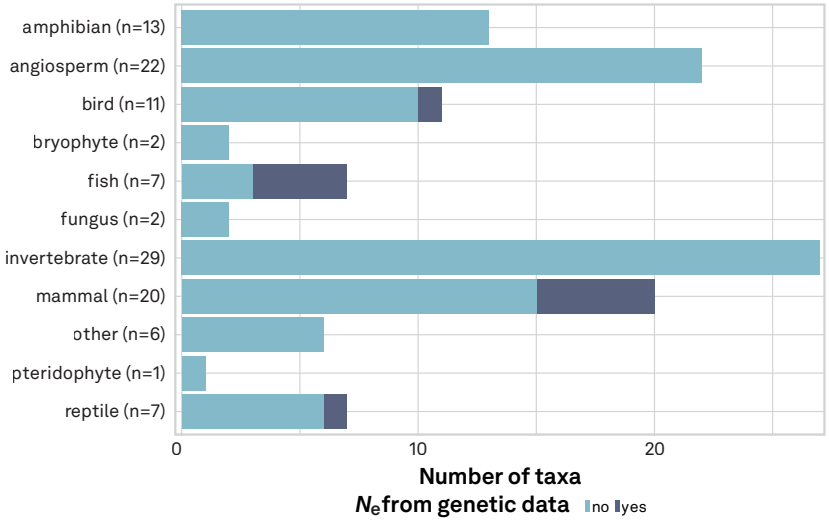


Figure 9. Availability of N_e estimates from genetic data. We found N_e estimates for a few species of reptiles, mammals, fishes, and birds. Most of our dataset consists of N_e estimates based on census data. Information is given per species and includes species assessed more than once. Additional information on taxa assessed more than once is presented under section 4.4 Multiple assessments.

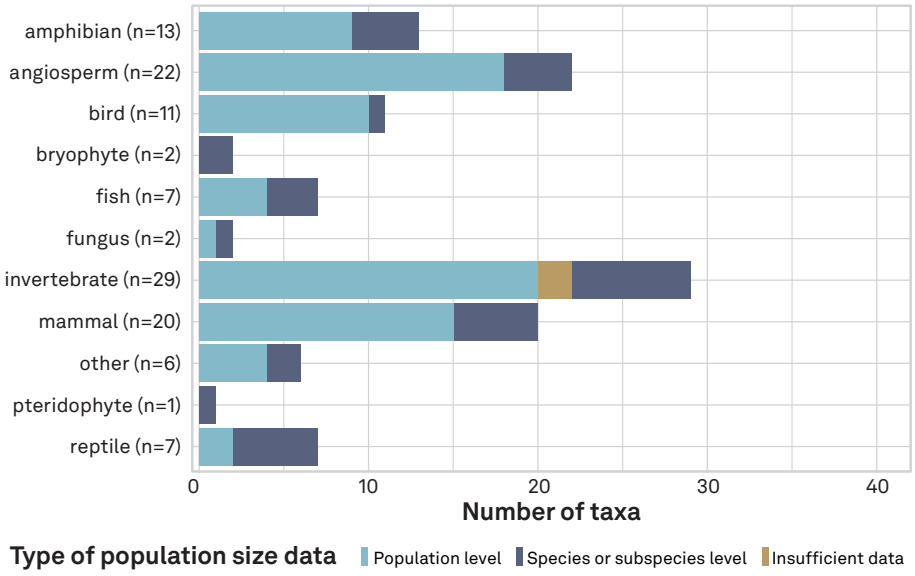


Figure 10. Type of census or N_e data available for the Ne500 indicator assessment. Green indicates that data was available at the population level, blue indicates that data was only available at the national level (species or subspecies level), and grey indicate that there was insufficient data on populations size. The figure displays the number of KoboToolbox forms, which means that it includes multiple data points for species assessed more than once (presented in section 4.4 Multiple assessments).

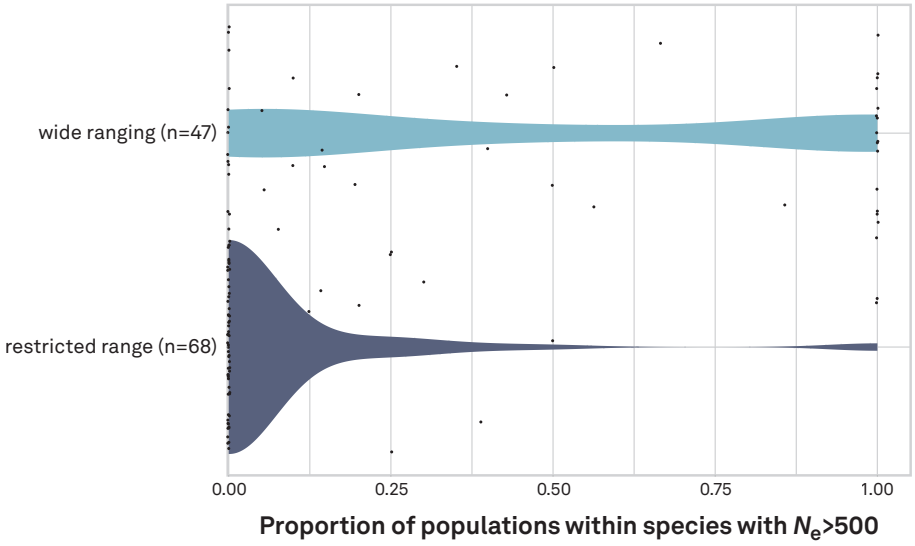


Figure 11. Proportion of populations within species with an N_e below 500 for restricted versus wide-ranging species. The categories (wide ranging and restricted range) were applied based on the Red List framework standard. Total number of species (n) with either of these two classifications = 115.

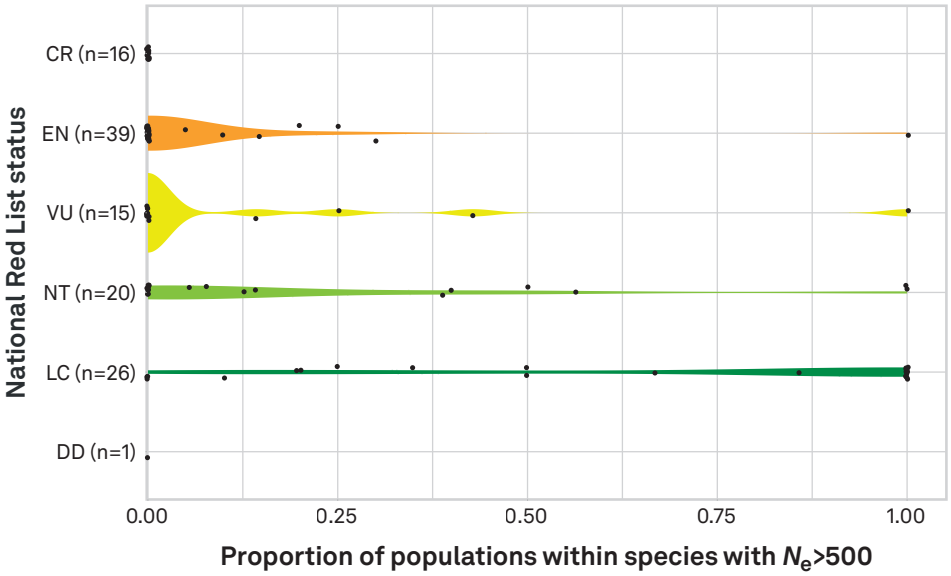


Figure 12. Proportion of populations within species with N_e below 500 for species in the different national Red List categories. The majority of species in the NT-CR categories are found in the lower range. The values for species in the Least Concern category (LC) are distributed across the entire range. Number of species (n) assessed for this indicator is 117.

Comparisons of Ne500 indicator values for wide-ranging versus restricted range species shows that many wide-ranging species have low indicator values (Figure 11). However, on average, Ne500 indicator values are lower for species with a restricted range (Table A2.4, p-value < 0.005). For the different Red List categories, we found a significant difference between different threat status (Tables A2.5; A2.6, p-value < 0.005) Species that are classified as Least Concern (LC) have Ne500 indicator values across the range (0-1; Figure 12). In addition, there is a significant difference in indicator values among taxonomic groups (Table A2.8, p-value < 0.005).

4.2 The PM Indicator

Overall, we identified a total of 1,271 populations that have been lost over the last 50 – 100 years, while 3,179 have survived among the 120 assessed species (but see section 4.4 Multiple assessments). The average indicator value over all 120 species is 0.78 for the PM indicator (Table 6, Figure 13). This implies that, on average, 78 % of populations within the examined species have been maintained.

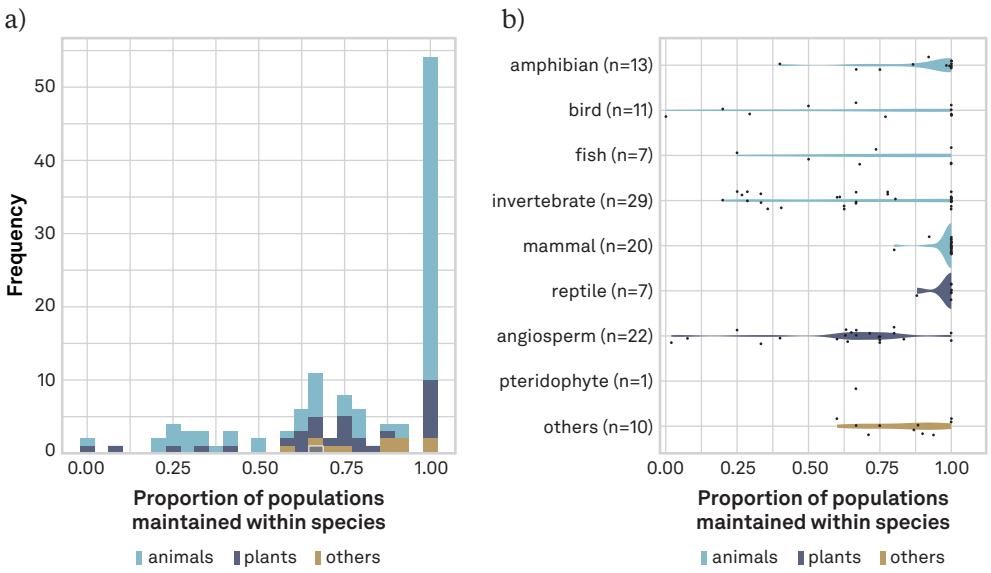


Figure 13. Results for the PM indicator, proportion of populations maintained with a) frequency of indicator values across all species and b) distribution of indicator values across taxonomic groups. Multiple assessments for the same species have been averaged.

It is worth noting that we are using an approach here that likely underestimates the rate of population loss. In some cases, we have indications of a decline in distribution range. This information has been recorded in the KoboToolbox form, however, since this decline cannot be associated to the loss of a whole population, it has not been used in the indicator assessment. In contrast, a different method was applied in Thurfjell et al. (2022). They considered declines in distribution in a way that could affect indicator values. For more details, see section 4.5. It is possible to modify the PM indicator so that a species decline in occurrence range can be used as a proxy for loss of populations.

Different methods of identifying populations (see section 2.1) may yield different results for the number of populations, as shown for alternative assessments (section 4.4). We illustrate the number of populations for different methods in Figure 14 and the PM indicator values in Figure 15. We note that the use of the "genetic clusters" method tends to result in fewer populations and that the "geographic boundaries" method tends to result in a higher number of populations (Mastretta-Yanes and da Silva et al., 2024). The indicator value is slightly lower for methods using some combination of "geographic boundaries." Patterns between methods of identifying populations and resulting values are further examined in Mastretta-Yanes and da Silva et al. (2024).

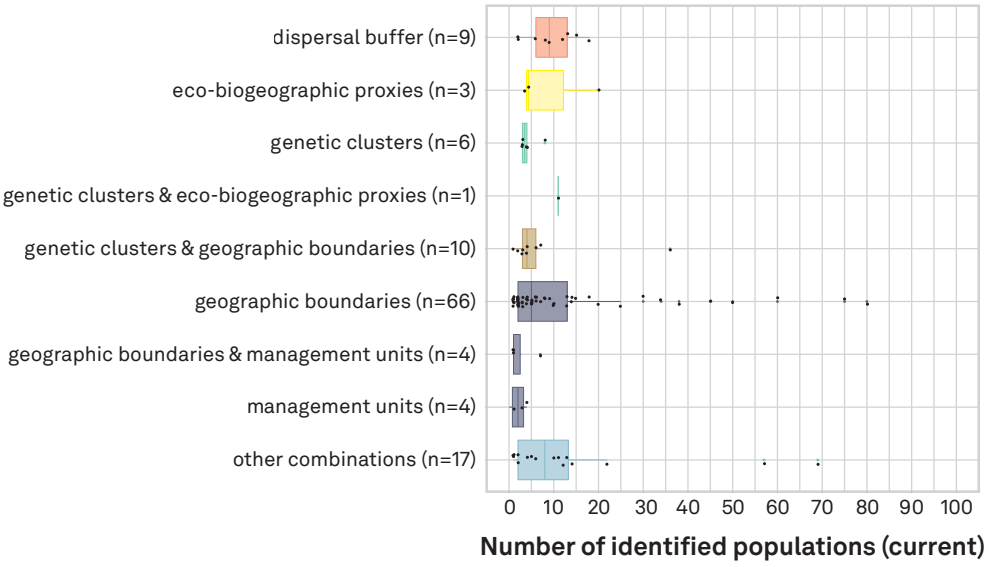


Figure 14. Distribution of populations based on different methods of identifying them. Note that different species are assessed by the different methods, thus, each point is a unique species (total n = 120).

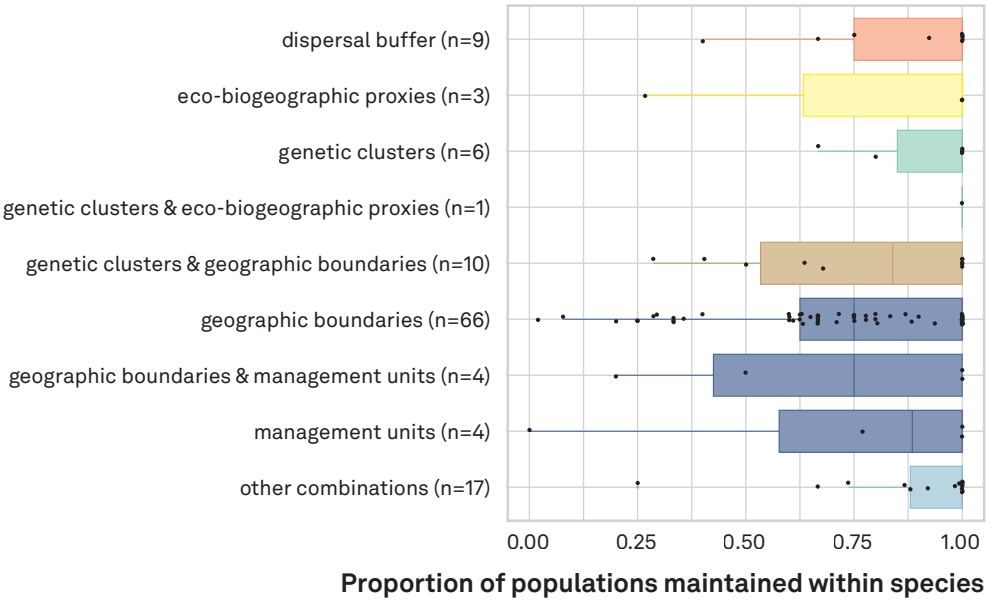


Figure 15. Populations maintained (PM) indicator values using different types of methods to identify populations. Note that different species are assessed by the different methods, thus, each point is a unique species (total n = 120).

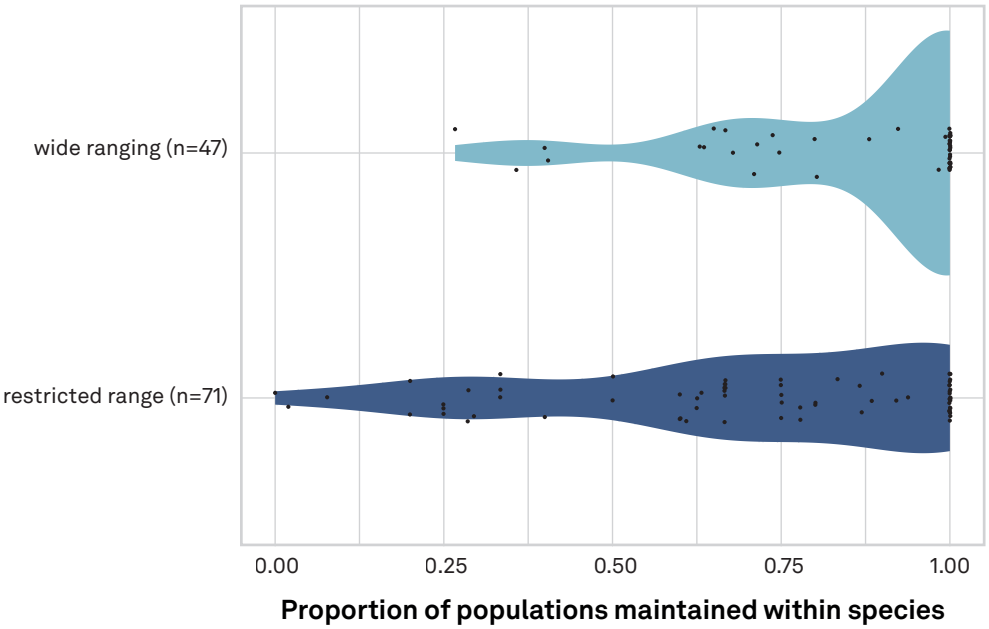


Figure 16. Proportion of populations maintained (PM) indicator, for wide ranging and restricted range species. A total of 118 species were classified into either of these two distribution categories using the Red List framework standards (Gärdenfors, 2018).

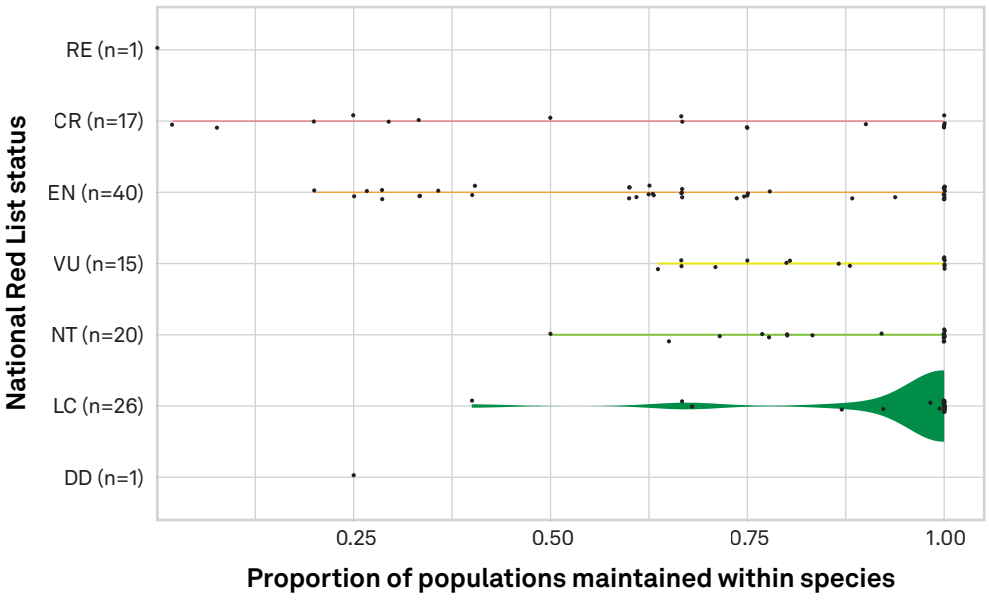


Figure 17. Proportion of populations maintained (PM) indicator for each of the six IUCN Red List categories, as well as RE (Regionally Extinct). Total number of species and subspecies (n) = 120.

We found a significant difference in indicator values between wide-ranging and restricted range species (Figure 16, Table A2.4, p-value < 0.005). We also found a difference between the Red List category in average indicator values (Figure 17, Table A2.5; A2.7, p-value < 0.005). In addition, there is a significant difference in indicator values among taxonomic groups (Table A2.9, p-value < 0.005).

4.3 The DNA-based monitoring indicator

We applied two methods for assessing the DNA-based monitoring indicator. For the first method, a value of 1 was assigned to species for which at least one population is being genetically monitored over time with DNA-methods (see sections 1.2, 2.4). This was the case for 20 species (17 %), while for the other 100 species, the indicator value was 0 since no such temporal monitoring approach was conducted (Table 5, Figure 18). The overall indicator value with this approach is 0.17 (Table 6).

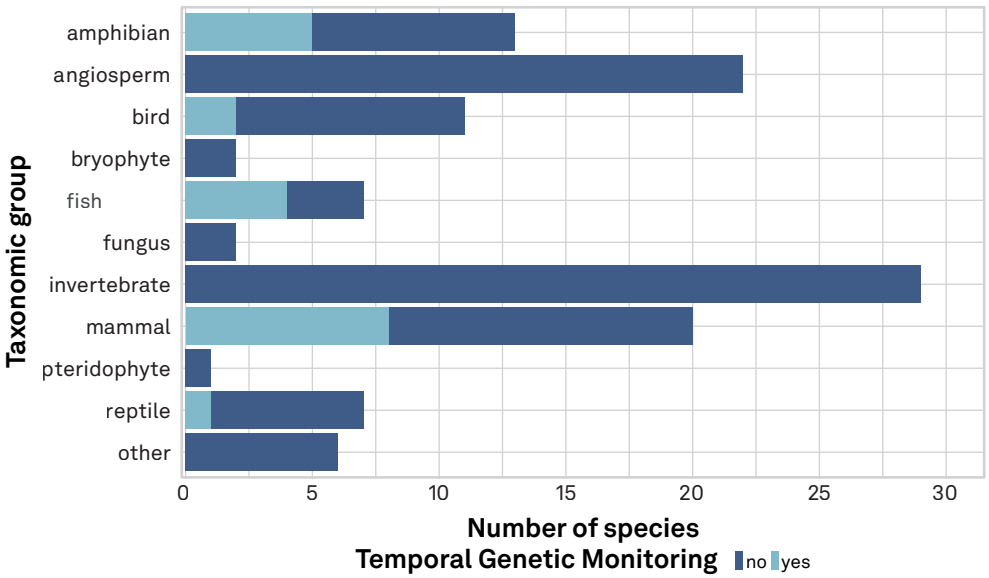


Figure 18. The extent to which DNA-based monitoring occurs in separate taxonomic groups. Yes = temporal genetic monitoring using DNA-based methods is conducted for one or more populations of a species; see Tables 4, 5, 6.

Using the second approach, for which the score assigned to species varied based on the kind of DNA-data or studied undertaken, the overall indicator value was 0.32 (Tables 5-6, Figure 19).

Table 7 provides more detailed information per species. Method 1 is generally recommended since it addresses monitoring of changes in genetic composition over time. Method 2 has the advantage of highlighting the importance and value of population genetic and phylogenetic information, which can act as critical baselines for future studies to assess temporal trends (Posledovich et al., 2021).

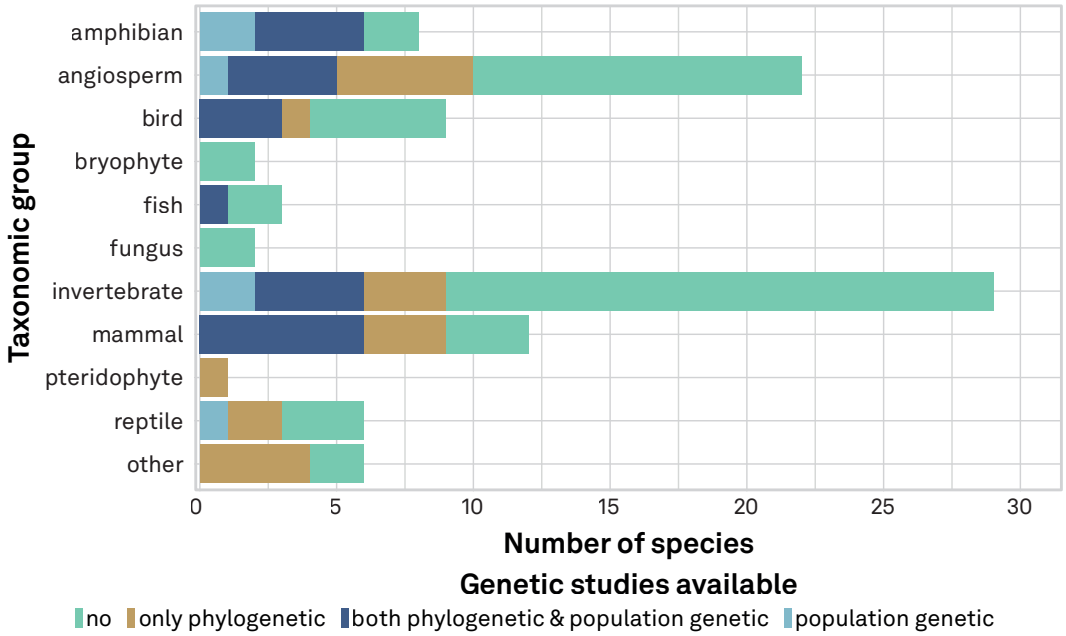


Figure 19. The extent to which genetic studies are available for species in different taxonomic groups. The values refer to the complementary information which can be used to evaluate the DNA based monitoring indicator using method 2 (Table 7). Population genetic studies include studies with temporal monitoring. The number of species with temporal monitoring is shown in Figure 18.

Table 7. Assessment of the DNA-based monitoring indicator using two different methods. Method 1 for assessing the DNA-based monitoring indicator gives value 0 for all species that have no population being monitored with DNA-based methods (those with values 0, 0.25 and 0.5 with method 2) and 1 for those who has ongoing DNA-monitoring (also value 1 with method 2). In method 2, several types of DNA-based information are taken into consideration (see section 2.4). Species receive an indicator value of 0 if no genetic study has been conducted for the species, the value 0.25 for one or more phylogenetic/phylogeographic study(s) alone, 0.5 for one or more population genetic studies (regardless if phylogenetic/phylogeographic studies are available or not), and the value 1 is provided if temporal genetic monitoring is conducted for one or more populations of the species (value 1 regardless if phylogenetic/phylogeographic and/or population genetic studies are also available). Indicator value 1 is marked with bold.

Taxon	Common name (Swe)	Common name (En)	Phylo-genetic studies	Pop. genetic studies	Temporal monitoring of genetic diversity	DNA-based monitoring indicator method 1	DNA-based monitoring indicator method 2
Bombina bombina	Klockgroda	Fire-bellied toad	Yes	Yes	No	0.00	0.50
Bufo bufo	Vanlig padda	Common toad	Yes	Yes	Yes	1.00	1.00
Bufotes viridis	Grönfläckig padda	Green toad	Yes	Yes	Yes	1.00	1.00
Epidalea calamita	Strandpadda	Natterjack toad	Yes	Yes	Yes	1.00	1.00
Hyla arborea	Lövgroda	Tree frog	Yes	Yes	No	0.00	0.50
Lissotriton vulgaris	Mindre vatten-salamander	Smooth newt	No	Yes	No	0.00	0.50
Pelobates fuscus	Lökgroda	Spadefoot toad	No	No	No	0.00	0.00
Pelophylax esculentus	Ätlig groda	Edible frog	Yes	Yes	No	0.00	0.50
Pelophylax lessonae	Gölgroda	Pool frog	Yes	Yes	No	0.00	0.50
Rana arvalis	Åkergroda	Moor frog	Yes	Yes	Yes	1.00	1.00

Taxon	Common name (Swe)	Common name (En)	Phylo-genetic studies	Pop. genetic studies	Temporal monitoring of genetic diversity	DNA-based monitoring indicator method 1	DNA-based monitoring indicator method 2
Rana dalmatina	Långbens-groda	Agile frog	No	No	No	0.00	0.00
Rana temporaria	Vanlig groda	Common frog	Yes	Yes	Yes	1.00	1.00
Triturus cristatus	Större vatten-salamander	Great crested newt	No	Yes	No	0.00	0.50
Alisma wahlenbergii	Småsvalting	Baltic water-plantain	Yes	Yes	No	0.00	0.50
Chenopodium vulvaria	Stinkmålla	Sinking goose-foot	No	No	No	0.00	0.00
Eryngium maritimum	Martorn	Sea-holly	Yes	No	No	0.00	0.25
Euphrasia officinalis officinalis	Finnögontröst	Rostkov's eyebright	Yes	No	No	0.00	0.25
Euphrasia stricta suecica	Svensk ögon-tröst	Drug eyebright	Yes	Yes	No	0.00	0.50
Genista germanica	Tysk ginst	German green-wood	No	No	No	0.00	0.00
Gentiana pneumo nanthe	Klockgentiana	Marsh gentian	No	No	No	0.00	0.00
Gymnadenia nigra	Brunkulla	Black vanilla orchid	Yes	No	No	0.00	0.25
Jacobaea erucifolia	Flikstånds	Hoary ragwort	No	No	No	0.00	0.00
Juncus anceps	Svarttåg	Rush	No	No	No	0.00	0.00
Luronium natans	Flytsvalting	Floating water plantain	No	Yes	No	0.00	0.50
Mertensia maritima	Ostronört	Oyster plant	No	No	No	0.00	0.00
Myricaria germanica	Klådris	German false tamarisk	No	No	No	0.00	0.00
Pseudorchis albida	Vityxne	Small white orchid	Yes	Yes	No	0.00	0.50
Pulsatilla patens	Nipsippa	Eastern pasque flower	No	No	No	0.00	0.00
Pulsatilla vernalis	Mosippa	Spring pasque flower	Yes	No	No	0.00	0.25
Pulsatilla vulgaris gotlandica	Gotlandsippa	European pasque flower	No	No	No	0.00	0.00
Ranunculus hederaceus	Murgrönsmöja	Ivy-leaved crowfoot	No	No	No	0.00	0.00
Ranunculus ophioglossi-folius	Gotlands ranunkel	Adder's-tongue spearwort	Yes	No	No	0.00	0.25
Sabulina viscosa	Sandnörel	Sticky sandwort	No	No	No	0.00	0.00
Saxifraga osloënsis	Hällebräcka	Saxifrage	Yes	Yes	No	0.00	0.50
Tephroseris palustris	Kärrnocka	Marsh fleawort	No	No	No	0.00	0.00
Anser erythropus	Fjällgås	Lesser white-fronted goose	Yes	Yes	No	0.00	0.50

Taxon	Common name (Swe)	Common name (En)	Phylo-genetic studies	Pop. genetic studies	Temporal monitoring of genetic diversity	DNA-based monitoring indicator method 1	DNA-based monitoring indicator method 2
Anthus campestris	Fältpiplärka	Tawny pipit	No	No	No	0.00	0.00
Calidris alpina schinzii	Sydlig kärrsnäppa	Dunlin	Yes	Yes	Yes	1.00	1.00
Charadrius alexandrinus	Svartbent strandpipare	Kentish plover	No	No	No	0.00	0.00
Circus pygargus	Ängshök	Montagu's harrier	No	No	No	0.00	0.00
Dendrocopos leucotos	Vitryggig hackspett	White-backed woodpecker	Yes	Yes	No	0.00	0.50
Emberiza calandra	Kornsparv	Corn bunting	No	No	No	0.00	0.00
Emberiza hortulana	Ortolansparv	Ortolan bunting	Yes	Yes	No	0.00	0.50
Ficedula albicollis	Halsbands-flugsnappare	Collared flycatcher	Yes	Yes	Yes	1.00	1.00
Hydroprogne caspia	Skräntärna	Caspian tern	No	No	No	0.00	0.00
Limosa limosa	Rödspov	Black-tailed godwit	Yes	No	No	0.00	0.25
Brachythecium novae-angliae	Bryhnia	Bryhnia	No	No	No	0.00	0.00
Dicranum viride	Barkvast-mossa	Dicranum moss	No	No	No	0.00	0.00
Coregonus albula morphotype trybomi	Vårlekande siklöja	Spring spawning vendace	Yes	Yes	Yes	1.00	1.00
Gadus morhua	Torsk	Atlantic cod	No	Yes	Yes	1.00	1.00
Lampetra fluviatilis	Flodnejonöga	River lamprey	No	No	No	0.00	0.00
Leuciscus aspius	Asp	Aral asp	No	No	No	0.00	0.00
Petromyzon marinus	Havsnejonöga	Sea lamprey	Yes	Yes	No	0.00	0.50
Salmo salar	Lax	Salmon	Yes	Yes	Yes	1.00	1.00
Silurus glanis	Mal	European catfish	Yes	Yes	Yes	1.00	1.00
Geastrum flexuosum	Jordstjärns-tryffel	Earthstar	No	No	No	0.00	0.00
Gomphus clavatus	Violgubbe	Pig's ear	No	No	No	0.00	0.00
*Agonopterix bipunctosa***	Änskäreplatt-mal	Twin-spot flat-body	No	No	No	0.00	0.00
Anacampsis fuscella	Klöversober-mal	Anacampsis moth	No	No	No	0.00	0.00
*Anthophora plagiata****	Humplepälsbi	Common digger bee	No	No	No	0.00	0.00
*Baptria tibiale****	Trollduve-mätare	Tibial or baneberry moth	No	No	No	0.00	0.00
Canthophorus impressus	Spindelört-skinnbagge	Down shield bug	No	No	No	0.00	0.00
Cerambyx cerdo	Större ekbock	Great capricorn beetle	No	No	No	0.00	0.00

Taxon	Common name (Swe)	Common name (En)	Phylo-genetic studies	Pop. genetic studies	Temporal monitoring of genetic diversity	DNA-based monitoring indicator method 1	DNA-based monitoring indicator method 2
Chalcophora mariana	Jätteprakt-bagge	Flatheaded pine borer	No	No	No	0.00	0.00
Depressaria nemolella	Gotländsk säfferrotplatt-mal	Parsnip moth sp.	No	No	No	0.00	0.00
Dysauxes ancilla	Fönstervinge-spinnare	Handmaid	No	Yes	No	0.00	0.50
Eresus sandaliatus	Nyckelpige-spindel	Ladybird spider	Yes	No	No	0.00	0.25
*Euphydryas aurinia****	Väddnätsfjäril	Marsh fritillary	No	No	No	0.00	0.00
*Euphydryas maturna****	Asknätfjäril	Scarce fritillary	No	No	No	0.00	0.00
Harpalus autumnalis	Höstfrölöpare	Autumn ground beetle	No	No	No	0.00	0.00
Harpalus flavescens	Gul frölöpare	Yellowish ground beetle	No	No	No	0.00	0.00
Lopinga achine	Dårgräsfjäril	Woodland brown	No	No	No	0.00	0.00
Lycaena helle	Violett guld-vinge	Violet copper	Yes	Yes	No	0.00	0.50
Lytta vesicatoria	Spansk fluga	Spanish fly	No	No	No	0.00	0.00
Margaritifera margaritifera	Flodpärmusla	Freshwater pearl mussel	Yes	Yes	No	0.00	0.50
*Melitaea britomartis ****	Veronikanät-fjäril	Assmann's fritillary	No	No	No	0.00	0.00
*Melitta tricincta****	Röddtoppebi	Red bartsia blunthorn bee	No	No	No	0.00	0.00
Parnassius mnemosyne	Mnemosyne-fjäril	Clouded apollo	No	Yes	No	0.00	0.50
*Pedostrangalia revestita****	Almblombock	Black and red longhorn beetle	No	No	No	0.00	0.00
Phengaris alcon	Alkonblåvinge	Alcon blue	Yes	No	No	0.00	0.25
Phengaris arion	Svartfläckig blåvinge	Large blue	Yes	Yes	No	0.00	0.50
Psophus stridulus	Trumgräs-hoppa	Rattle grasshopper	No	No	No	0.00	0.00
Pytho kolwensis	Större bark-plattbagge	Dead log bark beetle	Yes	No	No	0.00	0.25
*Scolitantides orion ****	Fetörtsblå-vinge	Chequered blue butterfly	No	No	No	0.00	0.00
Stauroderus scalaris	Skrärrande gräshoppa	Large mountain grasshopper	No	No	No	0.00	0.00
Unio crassus	Tjockskalig målarmussla	Thick-shelled river mussel	Yes	Yes	No	0.00	0.50
Alces alces	Älg	Moose	No	Yes	Yes	1.00	1.00
Barbastella barbastellus	Barbastell	Barbastelle	No	No	No	0.00	0.00
Canis lupus	Varg	Wolf	Yes	Yes	Yes	1.00	1.00
Capreolus capreolus	Rådjur	Roe deer	Yes	Yes	No	0.00	0.50
Castor fiber	Bäver	Eurasian beaver	Yes	Yes	No	0.00	0.50

Taxon	Common name (Swe)	Common name (En)	Phylo-genetic studies	Pop. genetic studies	Temporal monitoring of genetic diversity	DNA-based monitoring indicator method 1	DNA-based monitoring indicator method 2
Cervus elaphus elaphus	Kronhjort	Red deer	Yes	Yes	No	0.00	0.50
Erinaceus europaeus	Igelkott	Hedgehog	Yes	No	No	0.00	0.25
Gulo gulo	Järv	Wolverine	Yes	Yes	Yes	1.00	1.00
Halichoerus grypus	Gråsäl	Grey seal	Yes	Yes	No	0.00	0.50
Lepus timidus	Skogshare	Mountain hare	Yes	Yes	Yes	1.00	1.00
Lutra lutra	Utter	European otter	Yes	Yes	Yes	1.00	1.00
Muscardinus avellanarius	Hasselmus	Hazel dormouse	Yes	No	No	0.00	0.25
Myotis bechsteinii	Bechsteins fladdermus	Bechstein's bat	No	No	No	0.00	0.00
Phoca vitulina	Knubbsäl	Harbour seal	Yes	Yes	No	0.00	0.50
Phocoena phocoena	Tumlare	Harbour porpoise	Yes	Yes	No	0.00	0.50
Sicista betulina	Buskmus	Northern birch mouse	Yes	No	No	0.00	0.25
Sorex isodon	Tajganäbbmus	Taiga shrew	No	No	No	0.00	0.00
Ursus arctos	Brunbjörn	Brown bear	Yes	Yes	Yes	1.00	1.00
Vulpes lagopus	Fjällräv	Arctic fox	Yes	Yes	Yes	1.00	1.00
Vulpes vulpes	Rödräv	Red fox	Yes	Yes	Yes	1.00	1.00
Bryoria nitidula	Glanstagel	Horsehair lichen	Yes	No	No	0.00	0.25
Bryoria tenuis	Långt broktagel	Pied horsehair lichen	Yes	No	No	0.00	0.25
Heterodermia speciosa	Elfenbenslav	Powdered fringe lichen	Yes	No	No	0.00	0.25
Lamprot-hamnium papulosum	Axsträfse	Foxtail stonewort	No	No	No	0.00	0.00
Leptogium rivulare	Strandskinn-lav	Flooded jellyskin	No	No	No	0.00	0.00
Lobaria hallii	Hårig skrovellav	Gray lung lichen	Yes	No	No	0.00	0.25
Botrychium simplex	Dvärglås-bräken	Least moonwort	Yes	No	No	0.00	0.25
Anguis fragilis	Kopparödla	Slow worm	Yes	No	No	0.00	0.25
Coronella austriaca	Hasselsnok	Smooth snake	No	No	No	0.00	0.00
Lacerta agilis	Sandödla	Sand lizard	No	Yes	No	0.00	0.50
Natrix natrix gotlandica	Gotlandssnok	Gotland grass snake	Yes	No	No	0.00	0.25
Natrix natrix natrix	Snok	Grass snake	No	No	No	0.00	0.00
Vipera berus	Huggorm	European viper	Yes	Yes	Yes	1.00	1.00
Zootoca vivipara	Skogsödla	Viviparous lizard	No	No	No	0.00	0.00

4.4 Alternative assessments

We conducted more than one assessment for seven species. Six of these included two assessments and in one case, three alternative assessments (Tables 8, 9). This was done since population definitions differed, or there was conflicting information on population occurrences or sizes. For each of these species we performed an assessment in KoboToolbox for each of the alternative ways to define population occurrence and size. We then calculated the indicator value for each of these species by averaging over the assessments (Mastretta-Yanes and da Silva et al., 2024). We subsequently used these average indicator values in this report.

Table 8. Alternative assessments for seven species and the Ne500 average indicator value applied in this report. National N_c = total census size in Sweden, Pops = number of extant populations, > 500 = number of extant populations with N_e > 500, < 500 = number of extant populations with N_e < 500. Ne500 = Ne500 indicator value.

			Assessment 1			
Species	**National N_c**	**Pops**	**> 500**	**< 500**	**Ne500**	**Average Ne500 over assessments**
Barbastella barbastellus	16,000	6	1	5	0.17	0.39
Coronella austriaca	9,000	7	2	5	0.29	0.14
Erinaceus europaeus	20,001	18	0	18	0.00	0.06
Gentiana pneumonanthe	300,000	200	0	200	0.00	0.05
Halichoerus grypus	12,800	5	1	4	0.20	0.35
Hydroprogne caspia	1,160	7	0	7	0.00	0.00
Rana dalmatina	46,600	8	3	5	0.38	0.56
			Assessment 2			
Species	**National N_c**	**Pops**	**> 500**	**< 500**	**Ne500**	**Average Ne500 over assessments**
Barbastella barbastellus	16,000	6	0	6	0.00	0.39
Coronella austriaca	9,000	11	0	11	0.00	0.14
Erinaceus europaeus	20,001	18	2	16	0.11	0.06
Gentiana pneumonanthe	300,000	200	20	180	0.10	0.05
Halichoerus grypus	12,800	2	1	1	0.50	0.35
Hydroprogne caspia	1,160	1	0	1	0.00	0.00
Rana dalmatina	46,600	4	3	1	0.75	0.56
			Assessment 3			
Species	**National N_c**	**Pops**	**> 500**	**< 500**	**Ne500**	**Average Ne500 over assessments**
Barbastella barbastellus	16,000	1	1	0	1.00	0.39
Coronella austriaca	9,000	-	-	-	-	0.14
Erinaceus europaeus	20,001	-	-	-	-	0.06
Gentiana pneumonanthe	300,000	-	-	-	-	0.05
Halichoerus grypus	12,800	-	-	-	-	0.35
Hydroprogne caspia	1,160	-	-	-	-	0.00
Rana dalmatina	46,600	-	-	-	-	0.56

For five species (*Barbastella barbastellus, Coronella austriaca, Halichoerus grypus, Hydroprogne caspia, Rana dalmatina*), a second or third assessment was needed because the number of extant populations could be identified in different ways. In *Hydroprogne caspia*, we could define number of populations either as one single population for the whole country or based on number of colonies. If we define populations based on num-

ber of colonies, the PM indicator will be assessed as seven maintained populations out of 13 historical ones (six colonies have gone extinct) and PM = 0.54. If we consider the distribution as a single population for the entire country, we have not lost any populations and the PM indicator is 1.0 (Table 9). For *Barbastella barbastellus*, three alternative assessments were needed; the species is found in six clusters but with unclear information on the amount of exchange among them. Therefore, we chose to include an alternative with the entire country being considered as a single population. A third alternative assessment was needed for this species since it is unclear how many individuals of the total national census is found in each of the six clusters, and one cluster could potentially include more than 5,000 individuals.

Table 9. Alternative assessments of five species and the average PM indicator value applied in this report. No. extant pops = number of extant populations. No. extinct pops = number of extinct populations. PM = PM indicator value (proportion of populations maintained).

	Assessment 1			Assessment 2			Assessment 3			
Species	**No. extant pops**	**No. extinct pops**	**PM**	**No. extant pops**	**No. extinct pops**	**PM**	**No. extant pops**	**No. extinct pops**	**PM**	**Average PM**
Barbastella barbastellus	6	0	1.00	1	0	1.00	1	0	1.00	1.00
Coronella austriaca	7	0	1.00	11	0	1.00				1.00
Halichoerus grypus	5	0	1.00	2	0	1.00	-	-	-	1.00
Hydroprogne caspia	7	6	0.54	1	0	1.00	-	-	-	0.77
Rana dalmatina	8	0	1.00	4	0	1.00	-	-	-	1.00

For two species (*Erinaceus europaeus, Gentiana pneumonanthe*) the alternative assessments only involved a change in the number of populations above $N_e > 500$. Again, the alternatives depend on how existing populations are defined. The alternative assessments resulted in a change in Ne500 indicator value for six species (Table 8; Figure 20a) and a change in PM indicator value for one species (Table 9; Figure 20b).

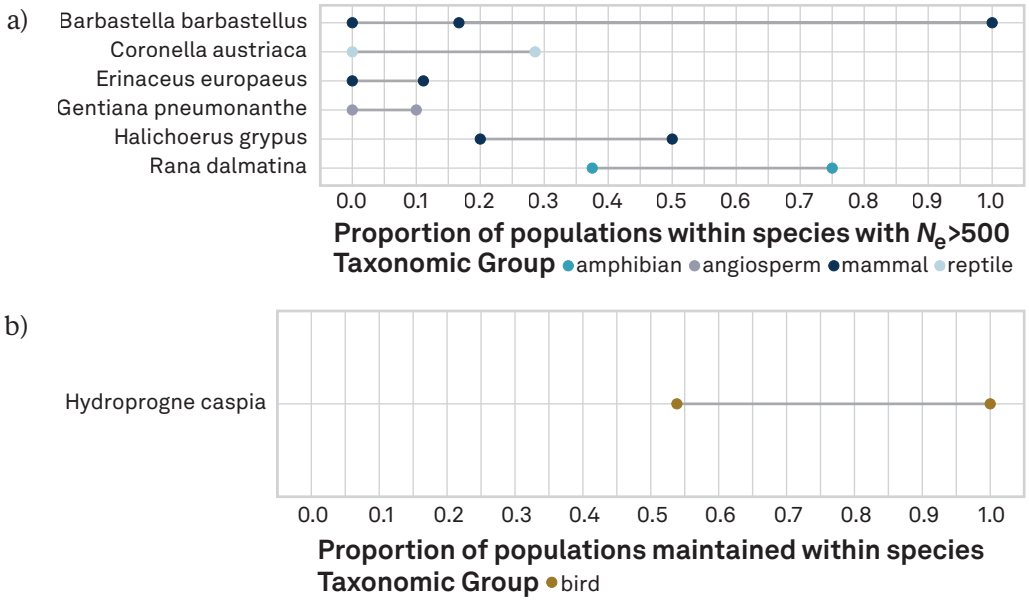


Figure 20. Differences in indicator values for species with alternative assessment for a) the Ne500 indicator and b) the PM indicator. For six species out of seven, the Ne500 indicator differed, while one out of five species had a different PM indicator value. Species with identical indicator values have been excluded from the figure (one species had an identical value for the Ne500 indicator, four were identical for the PM indicator).

The alternative assessments of the number of populations affect the total number of populations considered in this report (Table 10). For simplification we have calculated an average number of populations (for the five species) to use for comparisons across the 120 species.

Table 10. The total number of populations across all 120 species is different when using alternative assessments. We have used an average for the seven species with multiple definitions when reporting the number of populations assessed (sections 4.1 and 4.2) and for figures. For example: *Rana dalmatina* is assessed as either four or eight extant populations, with the average of six. Only assessments 1 and 2 are included in the table as assessment three does not include any change in the number of populations. Pops. = number of extant populations. Extinct = number of extinct populations.

Taxonomic group	Pops. assessment 1	Pops. assessment 2	Average Pops.	Extinct assessment 1	Extinct assessment 2	Average Extinct
Amphibians	354	358	356	19	19	19
Angiosperms	1,284	1,284	1,284	476	476	476
Birds	29	35	32	21	27	24
Bryophytes	50	50	50	5	5	5
Fishes	202	202	202	31	31	31
Fungus	285	285	285	116	116	116
Invertebrates	704	704	704	570	570	570
Mammals	77	85	82	2	2	2
Pteridophytes	8	8	8	4	4	4
Reptiles	76	80	78	3	3	3
Other	83	83	83	21	21	21
TOTAL	3,152	3,174	3,154	1,268	1,274	1,271

4.5 Comparison with Thurfjell et al. 2022

The study by Thurfjell et al. (2022) used only Red List data to assess the genetic diversity indicators for amphibians, reptiles, and mammals. Here, we compare the results of that study to the present results of more detailed assessment of all 13 amphibians and six reptiles, as well as 20 mammals, based on multiple sources of data In total, 37 species (20 mammals, 13 amphibians and 4 reptiles) were assessed by both Thurfjell et al. (2022) and the present study (see Table 11).

For the Ne500 indicator, 14 of the 37 species received the same indicator values in both studies, while 23 species differed (Table 11; Figure 21). The largest difference was observed for the 20 mammal species (Ne500 = 0.54 in the Thurfjell et al. (2022) study; Ne500 = 0.37 in the present study; Table 12). These differences were found to be significant for mammals ($p = 0.0135$) and for all species ($p = 0.0143$) based on Wilcoxon matched pairs test (Table A2.8). The lower values obtained in the present study likely reflect the incorporation of additional data sources and more detailed information on population structure and population sizes, which allowed for a more refined assessment of effective population sizes.

For the PM indicator, 14 of the 37 species differed, while 23 species had the same indicator values (Table 11; Figure 22). For 11 species, the PM values were not comparable due to the way the data was captured by Thurfjell et al. (2022). The present study only accounted for the loss of distinct populations, whilst Thurfjell et al. (2022) also accounted for a loss in range (see section 2.3). These detected differences were however not significant based on the Wilcoxon matched pairs test (Table A2.10).

Overall, the comparison highlights that assessments based solely on Red List data can provide a useful first approximation of genetic diversity indicators, but may overestimate indicator values when detailed information on population sizes and population structure is lacking. Incorporating additional data sources can therefore improve the accuracy and resolution of genetic indicator assessments.

It is important to note that the primary purpose of Red List assessments is to evaluate extinction risk rather than the genetic health of species or populations. It is therefore not surprising that additional sources of information are required to assess genetic diversity indicators in more detail. In the present study, much of this information was compiled after the Red List assessments had already been completed. Closer coordination between Red List assessments and genetic indicator assessments could therefore be beneficial for both processes. Integrating considerations of population structure and population size during Red List assessments could facilitate more efficient evaluation of genetic indicators, while also providing additional context relevant to long-term species viability.

Table 11. Comparison of reported indicator values in Thurfjell et al. (2022) and indicator values in this study for a total of 37 species; 20 mammals, 13 amphibians and 4 reptiles. The PM indicator is not comparable for 14 species due to how data was captured in Thurfjell et al. (2022) in which they used "Yes" or "No" for maintained range. All these 14 species were classified as "No" in Thurfjell et al. (2022).

	Ne500 indicator		PM indicator		
Species	**This study**	**Thurfjell et al. 2022**	**This study**	**Thurfjell et al. 2022**	**Comments**
MAMMALS					
Alces alces, Moose	0.67	1.00	1.00	1.00	*Ne500:* Since Thurfjell et al. 2022 new information became available from genetic monitoring showing an N_e value below 500 for one of the three genetic clusters.
Barbastella barbastellus, Barbastelle	0.39	1.00	1.00	1.00	*Ne500:* Thurfjell et al. 2022 assumes one continuous population with national N_e > 500. Here, we identify six populations; one with N_e > 500, the other five are below 500.
Canis lupus, Wolf	0.00	0.00	1.00	1.00	
Capreolus capreolus, Roe deer	1.00	1.00	1.00	1.00	
Castor fiber, Eurasian beaver	1.00	1.00	1.00	1.00	
Cervus elaphus elaphus, Red deer	0.00	0.50	1.00	1.00	*Ne500:* This species occurs in two populations. Thurfjell et al. 2022 estimates one with N_e > 500, the other below 500. The present study estimates that both populations are below 500. This is due to a DNA based assessment, available for one for these populations (Zachos et al., 2016), that was not considered in Thurfjell et al. (2022).
Erinaceus europaeus, Hedgehog	0.06	0.90	1.00	0.90	*Ne500:* Thurfjell et al. 2022 accounts for the possibility of small, isolated populations in valleys and on islands, otherwise assuming a large and continuous population. In this study we have mapped occurrences and buffer zones, approximating 18 populations, with two populations estimated N_e above 500. The national census is likely above 20,000.
Gulo gulo, Wolverine	0.00	0.00	1.00	1.00	
Halichoerus grypus, Grey seal	0.35	0.50	1.00	0.50	*Ne500*: Differences are due to how populations are defined. In Thurfjell et al. 2022 the Baltic Sea is considered as one unit. In the present study, we have used two alternative approaches where the Baltic Sea is either one unit or divided into four populations. There are more than 5,000 seals in the Baltic Sea, and therefore the N_e will be above 500 for this unit as a whole. Since most of the stock is concentrated around the Stockholm archipelago, that population is estimated as having N_e > 500, while the other three populations are below 500 for that approach. There is also a small population on the west coast of Sweden, which is included in both assessments. *PM*: Thurfjell et al. 2022 accounts for a decline in range for the west coast population while in the present study we assumed all populations are maintained since there is no information on any population losses.

	Ne500 indicator		PM indicator		
Species	**This study**	**Thurfjell et al. 2022**	**This study**	**Thurfjell et al. 2022**	**Comments**
Lepus timidus, Mountain hare	0.50	0.90	1.00	Non-comparable	*Ne500:* In the present study we mapped the occurrences and divided the mainland in three large populations. We also separated the islands of Gotland and Öland, and considered the subspecies *Lepus timidus sylvaticus* in Skåne as a separate population. Skåne, Gotland and Öland are each assumed to be below N_e = 500, while the other three mainland populations are above. Thurfjell et al. 2022 assumes a more or less continuous population but accounts for the possibility of small and isolated populations on islands.
Lutra lutra, European otter	0.00	0.00	0.80	1.00	*PM:* The Thurfjell et al. 2022 assessment is based on a general increase of the species in the entire country. In this study, the assessment is based on four current genetic clusters and the disappearance of a distinct genetic cluster from Småland.
Muscardinus avellanarius, Hazel dormouse	1.00	0.90	0.92	0.90	*Ne500*: Thurfjell et al. 2022 accounts for the possibility of small and isolated populations. In this study we divided the range into 12 units and estimated that all populations are more than 5,000 individuals. *PM*: Thurfjell et al. 2022 accounts for a general decline. In this study the assessment is based on the loss of the species from one county.
Myotis bechsteinii, Bechstein's bat	0.00	0.00	1.00	0.90	*PM*: Thurfjell et al. 2022 accounts for a general decline. In this study we have not found any information on the loss of distinct populations.
Phoca vitulina, Harbour seal	0.20	0.50	1.00	0.50	*Ne500*: Thurfjell et al. 2022 is based on two populations, one small and isolated in the Baltic Sea, and a larger population along the west coast. In this study, we divided the west coast stock into four management units based on Olsen et al. (2014), thus five populations in total. *PM*: Thurfjell et al. 2022 is based on a decline in range for one (Baltic Sea) of two populations. Here, we have not found any information about the loss of distinct populations.
Phocoena phocoena, Harbour porpoise	0.00	0.67	1.00	0.67	*Ne500*: Both studies use the same number of populations, based on three management units. There is a small and isolated population in the Baltic Sea, and two larger populations on the west coast and Belt Sea. Thurfjell et al. 2022 assumes N_e > 500 for both west coast populations due to connectivity within a larger transboundary area. Here, we assessed all populations as below 5,000 based on the number of reproductive individuals within Swedish waters. *PM*: Thurfjell et al. 2022 is based on a decline in one (Baltic) of three populations. Here, we have not found any information on the loss of subpopulations.

	Ne500 indicator		PM indicator		
Species	**This study**	**Thurfjell et al. 2022**	**This study**	**Thurfjell et al. 2022**	**Comments**
Sicista betulina, Northern birch mouse	1.00	0.90	1.00	0.90	*Ne500:* Thurfjell et al. 2022 accounts for the possibility of some small and isolated populations but assumes most of the distribution as continuous. *PM*: Thurfjell et al. 2022 accounts for a general decline. In this study we have not found any information on the loss of distinct populations.
Sorex isodon, Taiga shrew	0.00	0.00	1.00	Non-comparable	
Ursus arctos, Brown bear	0.00	0.00	1.00	1.00	
Vulpes lagopus, Arctic fox	0.00	0.00	1.00	Non-comparable	*PM:* Thurfjell et al. 2022 assumes one population, for which the range has declined. In this study, we divided the species into several populations based on genetic data (Keeling Hemphill et al., 2020) and we have not found any information about the loss of a distinct subpopulation.
Vulpes vulpes, Red fox	1.00	1.00	1.00	1.00	
AMPHIBIANS					
Bombina bombina, Fire-bellied toad	0.25	0.00	1.00	Non-comparable	*Ne500:* Thurfjell et al. 2022 is based on a reintroduction using a small group of individuals from Denmark and that the species then expanded. We have not taken the reintroduction bottleneck into account when estimating population size. The census is currently above 5,000 for one of four populations, and that estimate is used in the present study.
Bufo bufo, Common toad	1.00	0.90	1.00	0.90	*Ne500:* Thurfjell et al. 2022 accounts for the possibility of some small and isolated populations but assumes most of the distribution as continuous. *PM*: The Thurfjell et al. 2022 assessment is based on a general decline across the total distribution. We have not identified the loss of any distinct population in this study.
Bufotes viridis, Green toad	0.00	0.00	0.87	Non-comparable	*PM*: The Thurfjell et al. 2022 assessment is based on a general decline across the total distribution. The species is fragmented and we identified the loss of two distinct populations with 13 remaining in this study.
Epidalea calamita, Natterjack toad	0.00	0.00	0.92	Non-comparable	*PM:* The Thurfjell et al. 2022 assessment is based on a general decline across the total distribution. In this study, we identified six distinct populations that have disappeared. The current distribution is highly divided, and the species is found on a large number of islands on the west coast.
Hyla arborea, Tree frog	0.50	0.00	0.67	Non-comparable	*Ne500:* The Thurfjell et al. 2022 assessment is based on the distribution consisting of a number of smaller populations, most likely none above 5,000. In this study, we defined one separate small population in Halland, but considered the entire distribution in Skåne as one unit of approximately 18,000 individuals. *PM*: The Thurfjell et al. 2022 assessment is based on a general decline across the entire distribution. In this study, we identified two extant populations and the loss of one distinct population.

	Ne500 indicator		PM indicator		
Species	**This study**	**Thurfjell et al. 2022**	**This study**	**Thurfjell et al. 2022**	**Comments**
Lissotriton vulgaris, Smooth newt	1.00	0.90	0.98	0.90	*Ne500:* Thurfjell et al. 2022 accounts for the possibility of some small and isolated populations but assumes most of the distribution as continuous. *PM:* The Thurfjell et al. 2022 assessment is based on a general decline in range. In this study, we divided the distribution into 57 extant populations and identified the loss of the species in one area.
Pelobates fuscus, Spadefoot toad	0.00	0.00	0.75	Non-comparable	*Ne500:* The Thurfjell et al. 2022 assessment is based on a general decline across all of the distribution. In this study we identified 15 extant populations and identified the loss of five populations.
Pelophylax esculentus, Edible frog	0.50	0.90	0.40	0.90	*Ne500:* The Thurfjell et al. 2022 assessment is based on an expanding continuous population and a few small and isolated populations. In this study, we assumed one large expanding population in Skåne and one small population in Östergötland. *PM:* We identified two extant populations and the loss of three distinct populations in this study. In Thurfjell et al. 2022 the assessment considers both that a few small populations have likely been lost and that the species is expanding.
Pelophylax lessonae, Pool frog	0.00	0.00	1.00	Non-comparable	*PM:* The species was most likely more common in the past but was not discovered until recently. A loss of range is assumed across the distribution in Thurfjell et al. 2022. We have not identified the loss of any distinct populations in this study.
Rana arvalis, Moor frog	1.00	0.90	1.00	0.90	
Rana dalmatina, Agile frog	0.56	0.90	1.00	Non-comparable	*Ne500:* The Thurfjell et al. 2022 assessment is based on two large populations, and possibly some small and isolated populations. We have assessed the species in two alternative ways, either using four populations based on map analysis or eight populations based on information in NAP. Individuals are not evenly distributed across their range but most individuals are found on the island of Öland.
Rana temporaria, Common frog	1.00	0.90	1.00	0.90	
Triturus cristatus, Great crested newt	0.10	0.50	0.99	Non-comparable	*Ne500:* The Thurfjell et al. 2022 assessment is based on a more or less continuous distribution in southern Sweden. In this study, we assumed a large number of populations across Sweden with the majority of them being small and isolated.

Species	Ne500 indicator		PM indicator		Comments
	This study	Thurfjell et al. 2022	This study	Thurfjell et al. 2022	
REPTILES					
Coronella austriaca, Smooth snake	0.14	0.50	1.00	Non-comparable	*Ne500:* Thurfjell et al. 2022 assumes a continuous distribution in the southern part of the range and more isolated populations in the north. In this study, we have assessed the species in two ways by mapping the occurrences and dividing the distribution into either 7 or 11 clusters, with two or no populations with an assumed N_e > 500 respectively. *PM:* The Thurfjell et al. 2022 assessment is based on a loss of range and historical localities in a more or less continuous distribution. We have not identified the disappearance of any distinct populations in this study.
Lacerta agilis, Sand lizard	0.00	0.10	0.88	Non-comparable	*Ne500:* Thurfjell et al. 2022 assumes one continuous population accompanied by many small and isolated populations. In this study we have we have based the assessment of many small populations, none above 5,000 individuals.
Natrix natrix, Grass snake	0.50	0.90	1.00	Non-comparable	*Ne500:* Thurfjell et al. 2022 accounts for the possibility of some small and isolated populations but assumes most of the distribution as continuous. In this study, we separated the subspecies for assessment. The subspecies only found on Gotland has a total of 1,800 reproductive individuals. For the mainland grass snake, we divided the distribution into several clusters, all N_e > 500. The combined indicator value is therefore 50 %.
Vipera berus, Common viper	0.86	0.90	1.00	0.90	*Ne500:* Thurfjell et al. 2022 accounts for the possibility of some small and isolated populations but assumes most of the distribution as continuous. In this study, we included two small and isolated populations found in literature, and divided the rest of the distribution into several large clusters each N_e > 500. *PM:* The Thurfjell et al. 2022 assessment is based on a decline across its range. In this study, we have not identified the loss of any distinct populations.

Table 12. Average indicator values by class for 37 species assessed by both Thurfjell et al. 2022 and the present study, with n = number of species assessed. Note that for the PM indicator only 23 species were possible to compare due to divergent approaches for assessment (see Table 11).

Taxon	Ne500 indicator			PM indicator		
	n	Thurfjell et al. 2022	Present study	n	Thurfjell et al. 2022	Present study
Amphibian	13	0.454 ± 0.45	0.455 ± 0.43	5	0.900 ± 0.00	0.877 ± 0.27
Mammal	20	0.538 ± 0.44	0.358 ± 0.43*	17	0.898 ± 0.17	0.984 ± 0.05
Reptile	4	0.600 ± 0.38	0.374 ± 0.39	1	0.900 ± NA	1.000 ± NA
TOTAL	37	0.515 ± 0.43	0.394 ± 0.41*	23	0.899 ± 0.15	0.961 ± 0.13

*Significant difference with Wilcoxon-matched pairs test.

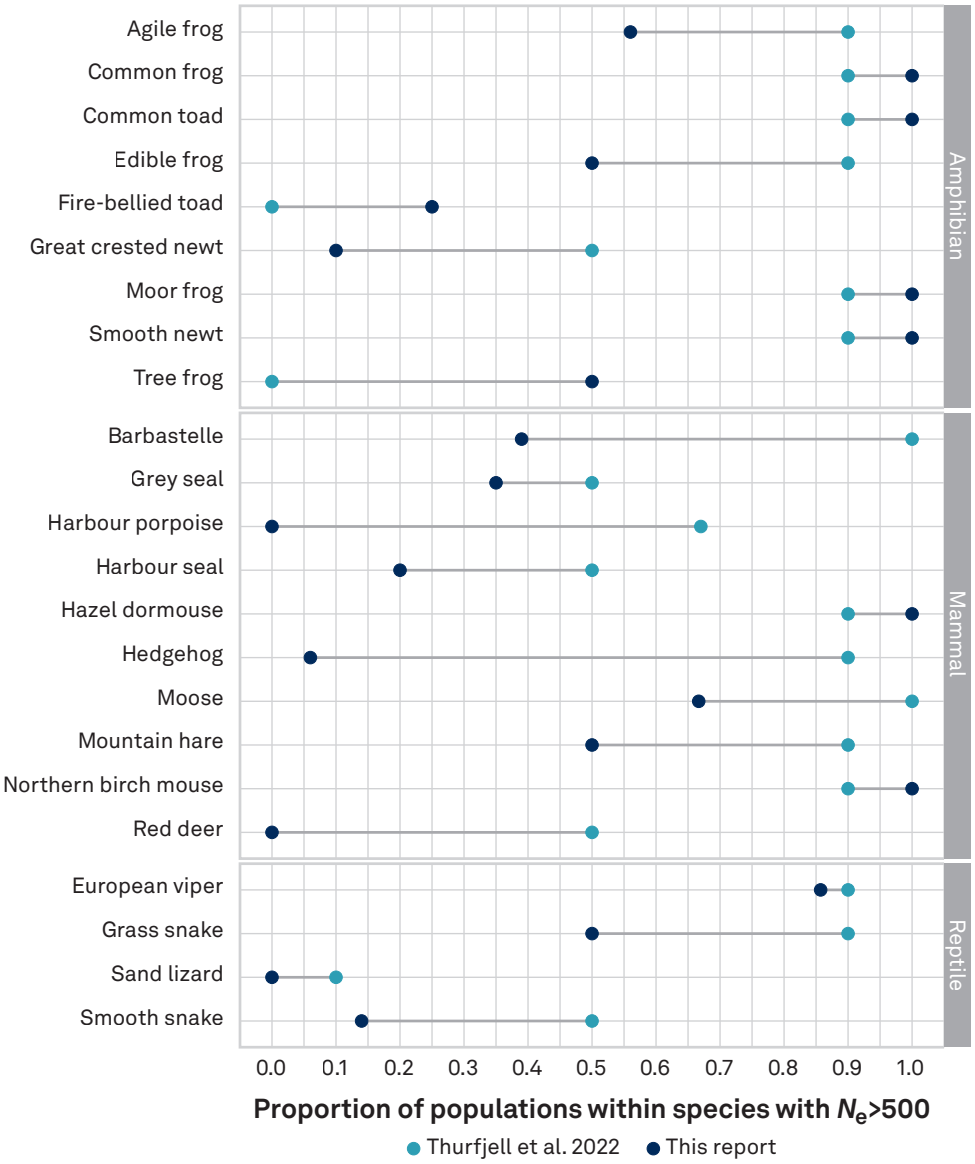


Figure 21. Comparison with Thurfjell et al. (2022) of the Ne500 indicator for 23 species (out of 37), for which the indicator values differed between the two assessments. The Ne500 indicator value was the same in both assessments for 14 species not shown here (Table 11). In the present study the Ne500 indicator value is lower for 13 species and higher for 10 species compared to Thurfjell et al. (2022).

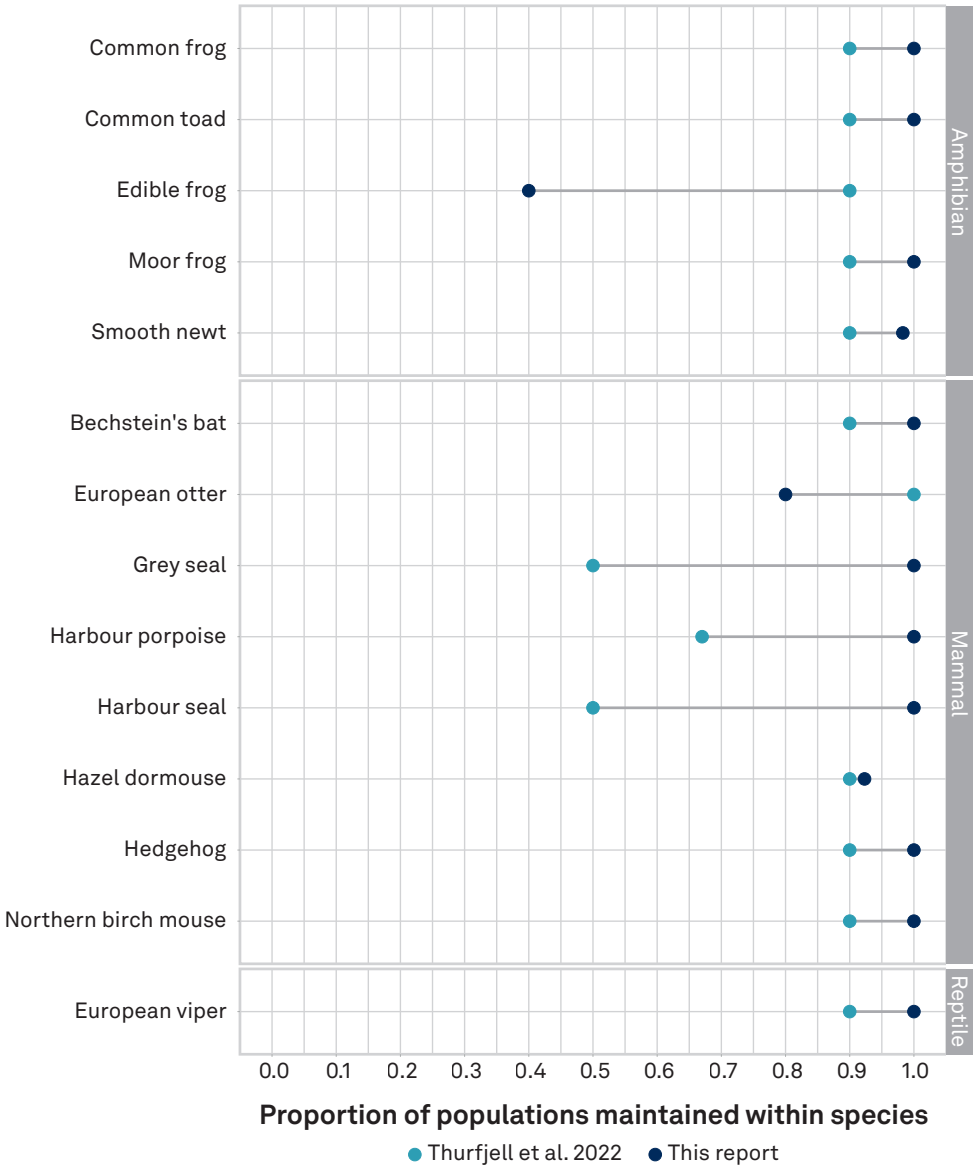


Figure 22. Comparison of PM indicator values for 14 species assessed both in the present study and in Thurfjell et al. (2022) for which the indicator value differed between the two assessments. Please note that for 14 species the indicator values are not comparable due to the way the data is captured in the Thurfjell et al. (2022) study (whether the species maintains its range = Yes or No; see Table 11). Thus, the PM indicator values could only be compared for 23 species. Of these, nine species had the same indicator value in both assessments (not shown here, see. Table 11).

5. Potential for national implementation of the CBD indicators in Sweden in connection to the Red List process

Thurfjell et al. (2022) suggested that the CBD indicators could be assessed in parallel with the Swedish Red List classifications, which are updated every five years. This is because much of the information needed to calculate the CBD indicators is, or could be, available in Red List databases. If the Red List process is modified to always include the number of subpopulations within species and their census sizes were recorded in parallel with other data, indicators for genetic diversity could be assessed from the Red List data. To better understand whether experts leading and coordinating the Red List assessments in Sweden would support this strategy, we carried out an interview study. Before going into the details of the study (sections 5.3 and 5.4), we first describe the organization of Red List process in Sweden (5.1) and important concepts of the Red List that are of relevance for genetic indicator assessments (5.2).

5.1 The Red List expert committees

The SLU Species Information Centre is responsible for producing national Red List assessments in Sweden and the EU Habitats Directive Article 17 reporting. The assessments are carried out by 16 expert committees each dedicated to a particular taxonomic group (see Table 13).

The Red List committees consist of experts from different backgrounds and professions, including consultants, researchers, and skilled amateurs. The committee's expertise needs to cover different species and different parts of the country, and potentially different types of habitats. Skills regarding nature conservation are also important. For some taxonomic groups, there are only a limited number of people who have sufficient knowledge on the species within the group. In some cases, committee members have a very broad knowledge of species and know almost all the species in their taxonomic group(s), while others are more specialized to certain sub-groups. Also, committee members who have good knowledge in management of the database systems or are involved in species-specific projects are of importance for the committee work.

The assessment process varies greatly between committees depending on the taxonomic group and the type of data available. For some groups, the coordinator of the committee compiles the data and presents a preliminary assessment to the committee members. Other committees divide the compilation of work among

committee members, with each member focusing on particular species. Yet other groups have workshops to undertake the assessments collaboratively.

At the start of each Red List process every five years, a preliminary list of candidate species to assess is identified. This list includes already listed species and species that are thought to be at risk. In general, the start of the assessment process is focused on identifying new information, validating occurrences in the species portal or discussing focal areas for the assessment period. In particular, new provincial findings that indicate some type of decrease or increase need to be validated, which may mean studying information in the Swedish Species Observation System (Artportalen) or contacting the person who have provided the information in the system. There may be changes in taxonomy to consider and even species that are newly discovered/described in the country.

For each species, the expert committee collects data on national census size (sometimes also regional or subpopulation sizes), distribution, trends and fragmentation, and enter this information into the Red List database. The Red List classification for that species is generated based on the applied criteria and thresholds (IUCN, 2012). How the underlying data is collected varies greatly depending on the sources of information available for the species in question. For some groups such as birds, fishes, and some mammals, the challenge is to manage large amounts of data on occurrences to compile, interpret, and put into a proper context. For other groups, such as mosses, insects and fungi, for which there is limited information, the problem is rather to obtain data. This means that some taxonomic committees work more with proxies than other groups.

In many cases the individual experts and their knowledge play a decisive role in the assessment. There are also experts outside of the committee that are consulted and who can provide essential information and knowledge. Some committees send out the preliminary Red List assessments to experts outside of the committee for feedback before submission. There is also a process for an internal review at the Swedish Species Information Centre before the obligatory external reviews.

5.2 Red List concepts of relevance for the genetic diversity indicators

Five concepts from the Red List framework are relevant for estimating the number of populations that can be used for the genetic indicator assessments: fragmentation, number of subpopulations, number of locations, extent of occurrence (EOO) and area of occurrence (AOO; see Table 3). These concepts are considered in one or more of the five criteria applied to classify the threat status of a species (IUCN, 2012). With limited extra effort, assessments of these concepts can improve the possibility to address the genetic diversity indicators using Red List data.

The assessment of potential fragmentation (natural as well as human induced fragmentation) and number of fragments according to IUCN includes investigating the spatial distribution of the fragments and the distances between fragments. For species that are classified as fragmented, the number of fragments/subpopulations is available. As per the definition of subpopulation, there should be limited exchange between sites of occurrence (fragments). Thus, the information from the fragmentation criterion could be used to estimate the number of populations for the genetic diversity indicators.

Under Red List criteria B and C, the number and size of subpopulations are considered (Red List Criteria A-D; IUCN 2012). This factor is only taken into consideration if 1) there is a suspicion of decrease in number of subpopulations, 2) the number of subpopulations is expected to be small, or 3) if a large proportion of the individuals (> 90 %) occur in one single subpopulation. However, it is not customary to quantify the number of subpopulations more than what is required within the threat assessment criterion used (Red List Criteria A-D; IUCN 2012). It would improve the assessment of the genetic diversity indicators should it be standard to quantify this factor regardless of the threshold considerations.

The term location is used to define areas subject to risks, and may or may not include several subpopulations. Therefore, the number of locations cannot be translated directly into number of subpopulations. However, the criteria "number of locations" and the information evaluated in order to assess this criterion can be useful for getting an idea of the spatial distribution of the species.

Extent of occurrence (EOO) and area of occurrence (AOO) are two concepts that are used within the Red List framework to assess and quantify the distribution of species. EOO refers to the extent of the species range and encircles the entire distribution area. AOO in contrast refers to where the species is located and excludes all empty areas within the range. A large difference between EOO and AOO suggests that the species is divided into several separate areas. The AOO defined areas could be used to aid in assessing the number of populations for the genetic diversity indicators. This method is already used today when assessing the number of locations and subpopulations for the Red List assessment. By combining the information from the AOO assessment with known dispersal distances, it may also be possible to assess the number of populations for the genetic diversity indicators.

Within the Red List framework, the number of reproductive individuals is assessed for the entire population (as per IUCN definition) and referred to as population size. There are also criteria for the size of subpopulations and portion of the population found in a single location/subpopulation, however, it is not customary to quantify the number or size of the individual subpopulations, more than is required within the assessment criterion.

It is important to note that many of the factors within the Red List, such as geographical isolation and population sizes, focus on processes that would also affect genetic variation, even if this is not explicitly investigated. There are species for which the phenotypic response of genetic problems is noted. However, genetic diversity cannot be assumed to be captured by these criteria alone (and that was not the explicit intent of the criteria). Inbreeding depression and other bottleneck effects may go undetected.

5.3 Interviews with the Red List expert committee coordinators

We invited the 19 coordinators for the 16 taxonomic committees (Table 13) to participate in individual interviews to get their views on assessing the genetic indicators for their taxonomic group during the Red List process to aid in the calculation of the indicators for CBD and national reporting. We also wanted to find out what the potential challenges would be for the different taxonomic groups.

Twelve of the 19 coordinators agreed to be interviewed, representing 13 of the 16 taxonomic committees (Table 13). The interviews were carried out between April and September 2023. Ten interviews were conducted via video conference (Zoom). In one case the interview was conducted over the phone, and in another the respondent answered the questions via email. The video interviews lasted between 35 and 75 minutes and were recorded and transcribed for qualitative analysis. The interview over the phone lasted ten minutes. This interview was much shorter because it focused solely on the genetic diversity indicators and the potential for applying the genetic diversity indicators to this taxonomic group is so limited that each question took less than a minute to answer. The interviews were based on a series of questions that had been provided to the respondents beforehand (Appendix 4).

The interview questions (14 in total) centred around four topics:

1. Background on the committees and their work process.
2. The potential for assessing the genetic diversity indicators within the Red List process.
3. How the workflow within the committee would have to be modified, and how much added time and work it would involve.
4. How genetic variation is currently considered during the Red List assessment.

Table 13. Expert taxon committees and their coordinators. Coordinators marked in bold were included in the present interview study (12 out of a total of 19 coordinators). Arachnids, Hemiptera, Diptera, and Myriapods are grouped under other terrestrial invertebrates and share the same coordinator (coordinator L). Birds and Bats are sub-committees to the committee Vertebrates (excl. Fish) and each have a sub-coordinator.

Committee/subcommittee	Number of leads	Coordinator
Angiosperm	1	Coordinator A
Fish	1	Coordinator B
Fungi	3	**Coordinator C**, D, E
Hymenoptera	1	Coordinator F
Lepidoptera	1	Coordinator G
Limnic invertebrates	1	Coordinator H
Marine invertebrates	1	Coordinator I
Moss	2	**Coordinator J**, K
Other terrestrial invertebrates:	1	Coordinator L
Arachnids		
Hemiptera		
Diptera		
Myriapods		
Vertebrates (excl Fish)	1	Coordinator M (main)
Bats	1	Coordinator N (sub)
Birds	1	Coordinator O (sub)
Taxonomic committees not represented in the interview study:		
Algae	1	Coordinator P
Beetles	2	Coordinator Q, R
Lichen	1	Coordinator S

5.4 Results from interviews

Of the 12 interviewed coordinators, eight expressed an overall positive attitude toward the genetic diversity indicators and in including them into the Red List process (Table 14). However, many of them stressed the need for more detailed information on how this would be carried out. Several experts highlighted the need for selecting a subset of species to assess rather than the entire species group, exemplified by this comment (translated from Swedish):

> *"Achieving the same level of detail as for the Article 17 (EU Habitats Directive) reporting for all the species in the Red List is utopian."*

When asked how many species would be considered feasible to assess for the genetic diversity indicators, answers ranged from a handful to most species within a taxonomic group (Table 14). The estimated added effort needed for the assessment ranged from 30 minutes per species to several months for the entire species group (Table 14). Time requirements are thought to depend on the level of detail required. Several experts suggested using simplified versions of the indicators for which not all individual populations have to be identified and assessed individually. The simplifications were suggested to include estimating a rough proportion of populations with $N_e > 500$ without identifying individual populations. Such simplification was thought to reduce the time needed. However, they potentially risk missing cases of genetic erosion.

Table 14. Summary of answers describing general attitude to assessing genetic diversity indicators in the Red List context, what proportion of species in the taxonomic group that would be possible to asses with respect to currently available information or analysis based on already available information. Added work effort refers to how long the assessment would take as well as potential additional resources that are necessary. The interviewees' responses have been translated from Swedish.

Interviewee	General attitude	Possible proportion of species	Added work effort needed
Coordinator A (Angiosperm)	Positive	Majority	Detailed assessments for several species would take months to complete and would require someone dedicated to it.
Coordinator B (Fish)	Positive	60 %	Rough estimates are manageable and possibly easily. This differs from the Red List work, in which you do not produce your own data, but only use the data that is available.
Coordinator C (Fungi)	Positive	50 %	Fits well into the current workflow. There are good methods and standards for estimating census, fragmentation and dispersal.
Coordinator F (Hymenoptera)	Negative	A handful	Require more data to be possible, such as more surveys and information about dispersal distances and habitat preferences of species.
Coordinator G (Lepidoptera)	Positive	Few, well studied species	1-2 months for a limited set, for some species more surveys are needed. But if you establish a system for assessing butterflies, you may be able to add additional groups gradually.
Coordinator H (Limnic invertebrates)	Negative	Few charismatic	For most species there is limited information. There are a few species that are being monitored and surveyed, but otherwise data is too scarse.

Interviewee	General attitude	Possible proportion of species	Added work effort needed
Coordinator I (Marine invertebrates)	Negative	None	There is no available data. Extensive surveys would be needed to estimate distribution and census.
Coordinator K (Mosses)	Positive	Unsure	It may be possible to do using the currents standards but uncertain if they can be applied to estimate the indicators.
Coordinator L (Other terrestrial invertebrates)	Negative	Very few	Much more information needed about distribution, population sizes.
Coordinator M (Vertebrates)	Positive	All but, 10-20 % good	30 minutes to a few hours per species.
Coordinator N (Bats)	Positive	30 %	Depends on level of accuracy. In general, more data is needed but rough estimates are possible for some species.
Coordinator O (Birds)	Positive	Most	Given immigration history, migration strategy, and population size, it is possible to identify populations that are genetically vulnerable. For the most endangered species, we can see signs of what is likely genetic problems that would show up in genetic screenings.

Even though several of the experts highlighted the need for additional information to be able to assess the genetic indicators, they also point out that when something is implemented it will force a change. Demands for reporting create more focus on the species in question and highlight the need for monitoring programs or the development of detection methods adapted to that particular species. Currently, many methods are used to detect presence or absence of each species. There is limited time to spend on following up on historical or semi-optimal sites, or to conduct detailed surveys. This means that the committees do not assess sites previously documented to be unoccupied. Also, sites not regarded as optimal for the species are not assessed. When additional information is needed for reporting, such as for the Habitats Directive, concerted efforts are made to collect the required information, and this could lead to funding for biogeographic survey programs by county administrative boards. At the same time, other experts point out that they can make use of the already available information as a starting point. One voice on this topic (translated from Swedish):

> *"It is an important point that the conditions look different for different groups, but at the same time you can make assessments even if you have insufficient data. It is important that the debate does not just become that the data is too poor. It's still the best foundation we have. If you know which habitats species thrive in or can't handle."*

5.4.1 Results from interviews with respect to estimating the number of populations

Seven of twelve lead coordinators responded that estimating the number of populations would require gathering additional information than what is currently available or needed for the Red List assessments. Additional knowledge on ecology and dispersal behaviour, and for some species an assessment, would require some type of survey to get a better idea of occurrences or population sizes (Table 15).

Table 15. Responses to the question on estimated added work effort to estimate the number of populations within species. The responses have been summarized and translated from Swedish.

Committee	Work effort to estimate populations	Comment
Coordinator A (Angiosperm)	To assess the number of subpopulations, one can use AOO as a proxy. This is already being used today when assessing the number of locations. But the best thing would probably be to use GIS maps and look at dispersal distances under different conditions, make buffer zones and calculate from there.	Requires assessing the dispersal capacity of species and whether they are outcrossing or not. The committee can provide information but the GIS analysis should be performed by someone else.
Coordinator B (Fish)	For marine species it is very difficult to know what is a population and what is not. It is easier with well-defined watercourses where you know that they cannot come into contact with each other. Different stocks are usually considered, and they can be extremely large, but there are also small populations along the coast. There are some small species that are basically everywhere, and without any type of targeted studies, it is impossible to know how many there are and how big they are.	It is not customary to quantify the number of subpopulations or the size of the individual subpopulations, more than is required within the subpopulation criterion.
Coordinator C (Fungi)	It would be possible to produce maps for the fungi and look at dispersal distances and habitats. Much of it can be incorporated into what is already being done today.	
Coordinator F (Hymenoptera)	In order to delimit populations, one would need to know more about the dispersal capacity of individual species and the types of environments that lead to fragmentation.	
Coordinator G (Lepidoptera)	For those species that have Action Plans with details on distribution, it would not be too difficult to estimate the amount of exchange between localities. Some species have genetic studies as well. It is more difficult with species that are found in a relatively large number of localities. However, information from the fragmentation criterion could be used.	There are available estimates of how dispersal prone different species are.
Coordinator H (Limnic invertebrates)	Cannot say	There is too limited data on where populations are located and there are no genetic studies, except for high-profile species.
Coordinator I (Marine invertebrates)	Not possible	It is challenging enough to just assess if the species exist in the country.
Coordinator K (Mosses)	Would require little extra work as there is already a good system in place for assessing subpopulations as part of the fragmentation criteria.	When assessing high fragmentation according to IUCN, you look at distances between subpopulations and how divided the distribution is. It is something that is often discussed, but it is not easy to assess.
Coordinator L (Other terrestrial Invertebrates)	It may be possible to make rough estimates of populations based on knowledge about the species' habitat and substrate preferences. This also requires estimating likely dispersal capacity. However, it might be challenging to interpret missing data and blank spaces in occurrence maps.	For a more detailed assessment of number of populations more information is needed. Environmental monitoring data is generally not performed at the scale needed to provide information on a species level.

Committee	Work effort to estimate populations	Comment
Coordinator M (Vertebrates)	It depends on the level of detail. It is possible to make rough estimates based on dispersal distances and distribution fairly quickly for most species. Making maps and applying MaxEnt models based on dispersal capacity, habitat preferences and resilience is more complicated and takes more time.	
Coordinator N (Bats)	To estimate the number of populations would require more knowledge about breeding behaviour, site fidelity and dispersal. The colonies, wintering grounds and breeding grounds are not the same and it is unclear to what degree individuals return to the same site. Some species exhibit a swarming behaviour and others claim mating territory.	Few colonies and overwintering sites are actually known. There are some species that are very difficult to find and to identify, and there is very little data to work with.
Coordinator O (Birds)	Most stationary species are spread across the country and it is more a matter of clines rather than isolation. Among the migratory species one has to consider the degree of philopatry. There are species that are extremely philopatric and then there are systems, like the geese, for which philopatry is sex-linked. Generally, there is a high degree of breeding site fidelity but it doesn't take that much to achieve one effective migrant per generation.	In the Red List assessment today, the amount of isolation between occurrences within a local area is not taken into account. And then number of subpopulations and local areas are only counted up to the threshold value for the different criteria.

All interviewees listed the Swedish Species Portal (Artportalen) as their main source of occurrence data underlying the Red List assessment. However, there are considerable challenges with survey and occurrence data for some species, such as those that are difficult to identify and discover. Therefore, the quality of distribution maps differs between species groups. For example, for fishes, distribution maps become very coarse because of the nature of the habitat. For rare species the distribution may be so uncertain that it is difficult to determine a range and therefore only occurrences are mapped.

The interviews show that species with limited information on occurrences are evaluated based on potential locations that are extrapolated from environmental data on habitats, or specific hosts/substrates that the species is associated together with an expectation on the species commonness. This is mainly evaluated based on how difficult the species is to identify and the propensity for citizens to report on that particular species. The interviewees express that the same type of methods can be used to delimit populations for the genetic diversity indicators when the estimated dispersal between locations could be evaluated based on suitable environments or unfavourable habitats. One possible approach is to use GIS and apply dispersal distances under different conditions and make buffer zones to calculate the number of populations (Figure 23).

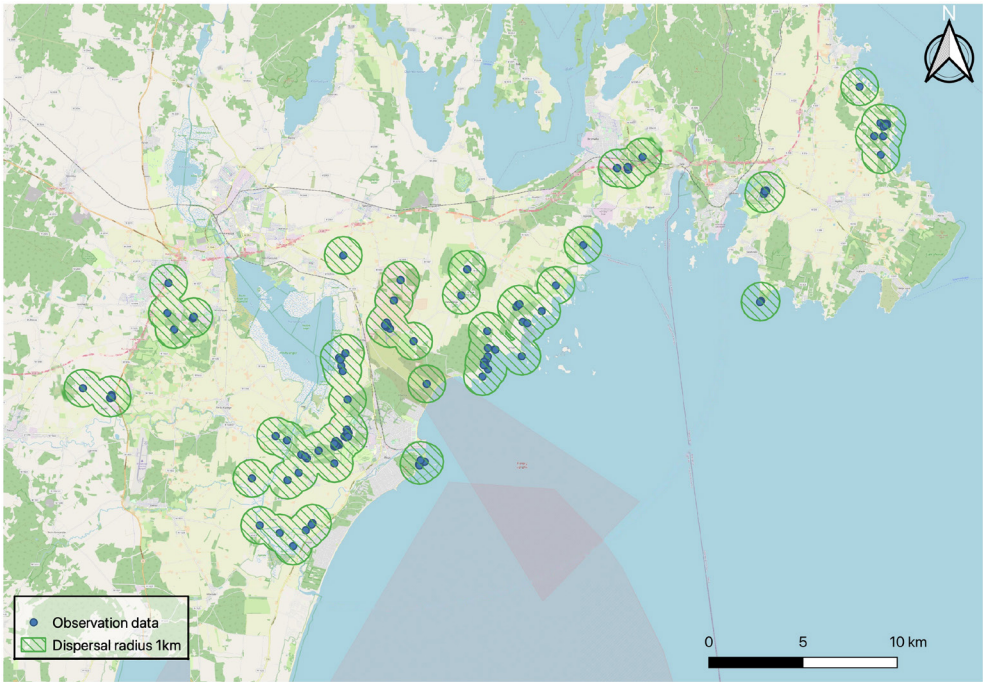


Figure 23. Example of GIS map with buffer zones (in green) around each point of recorded species occurrence. Populations are defined based on overlapping buffer zones. In the present example, 16 populations are identified.

However, the Red List process generally only uses readily available information, rather than collecting and processing data. Producing GIS maps with dispersal buffers and spatial analysis (MaxEnt) would require additional time and work. The monitoring tool *Genes from Space* can be an option that does not require expertise (https://teams.issibern.ch/genesfromspace/).
One manager suggested that these tasks could preferably be performed by individuals outside of the committee with expertise in GIS and mapping. The committee would then function in an advisory capacity and provide input on dispersal, environmental tolerability and other necessary factors. This approach requires good estimations of the dispersal capacity of individual species, which interviewees point out are lacking in many cases. The breeding behaviour is especially important in highly mobile and migratory species. For that type of species, one needs to ascertain if individuals return to the same breeding grounds across years and to what degree the young disperse into new areas.

5.4.2 Results from interviews with respect to assessing population size

We asked the coordinators about the estimated work effort needed to assess the census size of individual population within each species. The answers are summarized in Table 15. Eight out of twelve interviewees responded that estimating the populations sizes for the genetic diversity indicators is possible to do using the data available today, or with minimal added effort. Five interviewees answered that such estimations are very difficult, or impossible due to lack of information or other factors such as high variability (Table 16).

The number of reproductive individuals may be estimated from a density index or from actual counts. Other species are assessed schematically. For example, both fungi and mosses have standards for calculating number of individuals. For more well-known groups, existing census data can be used, or extrapolations based on environmental data. For the more poorly known species, there may be many unreported occurrences, and data has to be based upon estimation of how frequent the species is expected to be. To estimate this, the interviewees describe that they take into consideration how difficult species detection is, and how likely people are to report the species, as well as the amount of suitable habitat.

The interviewed coordinators expressed that the general focus of the Red List is on the location of species and whether they are increasing or decreasing. Population size is only relevant when the number is below 20,000 for the Red List, unless it concerns the size of individual subpopulations (Criteria D 2.a.i and D 2.a.ii; IUCN, 2012). It is often necessary to account for the lack of information and include a margin of error. Sometimes the uncertainty is so high that population size is not estimated.

Estimating effective population size will be very difficult for groups when there is a large degree of uncertainty and the interval includes the threshold. For species that likely have a very large number of populations (in the thousands) the indicator will be very difficult to assess because it is impossible to estimate the size of all populations. Even though most populations may be large in size, there can be small unidentified populations with fewer individuals. In that case, it was suggested better to use fixed intervals for population sizes (e.g. 0-10, 11-20, etc) instead, and estimate that the majority (95 %) is above the threshold.

Table 16. Responses to the question about added work effort to estimate sizes of individual populations (N_c) and associated challenges. The responses have been translated from Swedish.

Committee	Work effort to estimate population size	Comment
Coordinator A (Angiosperm)	To estimate population sizes, there is good data for those species when there is "flora guardian data" (Floraväktarna, https://svenskbotanik.se/engagera-dig/floravaktarna/).	
Coordinator B (Fish)	Effective population size is rarely known but estimating whether it is over or under 5,000 individuals can probably be done for some species.	It is impossible to know all the populations for some species, and how large they are. Even though the majority are likely above 5,000, some smaller populations may exist. It would be easier to provide an estimate in terms of percentages or proportions.
Coordinator C (Fungi)	To estimate the number of individuals, there are already good templates for and how to use unreported figures.	
Coordinator F (Hymenoptera)	There is a lot of uncertainty in estimates of population sizes. The estimates are rough estimates of sometimes hundreds of thousands. It would be very difficult to distinguish between 3,000 or 7,000 and therefore, impossible to say whether it is above or below 5,000 except for species that are extremely limited, with the populations being well below 5,000 individuals.	
Coordinator G (Lepidoptera)	For species with action plans and monitoring programs there may be estimates of population size. Otherwise, it is usually not assessed. Instead, number of sites are counted and it may be possible to use that and extrapolate based on the expected number of individuals per site.	Insects are difficult, as the number of individuals can fluctuate greatly.
Coordinator H (Limnic invertebrates)	Cannot say	The main focus is on locating populations and assessing if they are increasing or decreasing.
Coordinator I (Marine invertebrates)	Not possible	
Coordinator K (Mosses)	For the number of individuals, there are good templates that are based on area and density, which makes it consistent and straightforward to estimate population sizes.	
Coordinator L (Other terrestrial Invertebrates)	The number of individuals is impossible to assess, because the number of individuals varies so greatly. But for the vast majority of species in this group, the census size for all populations is above 5,000. Only extremely rare species in this group have N_c per population < 5,000.	
Coordinator M (Vertebrates)	Estimating populations sizes is fairly quick. Because of the uncertainty in the data, it is mostly guesswork.	
Coordinator N (Bats)	Population size is based on monitoring data, occurrence data, and extrapolations based on the amount of suitable habitat.	
Coordinator O (Birds)	There are a lot of bird species that do not reach population sizes of 5,000. About 1/3 have a national population size less than the general standard for N_e = 500.	

5.4.3 Results from interviews with respect to estimating population loss

We asked for views on how estimates of loss of populations could be carried out for the PM indicator assessment and the results are summarized in Table 17. Some potential sources for information on such loss were brought up during the interviews. These sources include historical records, museum collections and old distribution maps. The species portal (Artportalen) provides data from 1980 and onwards. There is more uncertainty prior to that time. Information about occurrence for example for NAP is often captured by county, and committees usually note if a species disappear from a county. This information could potentially be used to estimate population loss, using county as a proxy for populations.

Information is generally more scarce for species that are not identified as threatened or not previously Red Listed, for species that are less easy to find and identify, as well as species that are less charismatic or commercially important. It is also difficult to estimate trends or identify losses for species with high fluctuations or for plants with long lived seed banks. It is not uncommon that species disappear from an area only to reappear after several years.

Several of the interviewees refer to the inability of the Red List to capture species that are declining very slowly, are no longer declining, or remain at a comparatively small population size. In the Red List framework, decline is measured for three generations or ten years, whichever is the longest. The indicator value would in most cases account for a longer time period and this would potentially capture species that are not considered Endangered by the Red List standards.

Table 17. Responses to questions regarding work effort needed to estimate loss of populations. The responses have been translated from Swedish.

Committee	Work effort to estimate population loss	Comment
Coordinator A (Angiosperm)	When it comes to loss of populations, there is some old inventory data, but in the species portal there is only data from 1980 onwards. It can be difficult to estimate whether a population has really disappeared because some plants are very difficult to find or have long-lived seed banks. There are species that have suddenly reappeared after several years without findings.	
Coordinator B (Fish)	It is possible to assess extinction over time for certain species, such as freshwater and anadromous species, when there are lists of occupied bodies of water. But for most fishes, that data doesn't exist. It's very hard to see a decrease or increase by 100 populations here or there, if the total number is in the thousands. However, it would be possible to obtain information about genetic variation over time with the help of historical samples and genetic analyses.	
Coordinator C (Fungi)	There are methods for making projections and these could be used to look back in time. There is also an ongoing project on mapping rediscoveries and lost populations in Dalarna. The knowledge that comes out of that project can be applied to such analyses.	

Committee	Work effort to estimate population loss	Comment
Coordinator F (Hymenoptera)	Trends can be assigned to species that have gone extinct but otherwise, it is difficult because of the lack of information. There are not that many old museum collections of the order because historically they were not as popular among private collectors. Therefore, we have little knowledge on historical distribution.	Species that stopped declining and stabilized at a lower level are not captured by the Red List. The assessment takes place over 10-20 years. The population may be 20 % of what it was 50 years ago, but there is no way to highlight that in the Red List.
Coordinator G (Lepidoptera)	Based on Swedish butterfly monitoring, there are data on trends (decrease, increase, or stable) for some species since the start in 2010. It is difficult to see trends in insect population size at all because they vary so much from year to year. But if you want to identify lost populations, there are few species with that kind of information. It is possible for those species for which you follow the populations and have action programs. For some species, there is information about provincial occurrences further back in time, and it is known that they have disappeared from several of the provinces where they previously existed. But it can be difficult to determine when they disappeared.	
Coordinator H (Limnic invertebrates)	Cannot say	Most species are assessed for a 10-year period, as they are short-lived. This is a much smaller time frame than for the indicators.
Coordinator I (Marine invertebrates)	Not possible	
Coordinator K (Mosses)		
Coordinator L (Other terrestrial Invertebrates)	Presently, loss assessments are made at the county level, with a species being considered extirpated if there were previous findings but not anymore. It may be possible to use this as a proxy for a lost population.	
Coordinator M (Vertebrates)	The best way is to look up old literature with distribution maps and systematically go through species by species.	
Coordinator N (Bats)	The validation group started in 2020, which means that most occurrence data from earlier than that has not been validated. For the common species there is some data emerging now, but for the rare species that are not captured in monitoring programs there is not enough data to say anything about trends and losses.	
Coordinator O (Birds)	Population loss is not the most relevant indicator for birds because they're so mobile. Some colony-nesting species may suddenly abandon colony sites and move. There are local extinctions, but it is usually more relevant to measure them at the national level. If the habitat changes, the birds disappear, but they have not become extinct, they moved.	The Red List does not pick up on slight decreases, such as reductions of 10 % a year, until the population is below 2,000 individuals.

5.4.4 Comments from interviewees on genetic considerations in the Red List process

In general, all experts are supportive of the idea of genetic diversity indicators, even if all of them do not find it possible to apply within their taxonomic group due to data constraints. Overall, genetic variation is given very little consideration in the Red List process today. When studies are available that indicate genetic differences, this information can be included in the Red List process and it is also possible to note if a subpopulation is considered particularly vulnerable. The same suggestion has been made in South Africa (da Silva et al., under review). Sometimes subspecies or distinct subpopulations are assessed separately and receive their own Red List category. Conversely, a species can be considered less vulnerable if there is immigration from a nearby region. This is accounted for during the Red List process and can lead to a downgrading of the species' threat status.

Genetics is more often used in taxonomic contexts for less well-known groups. That is, to separate morphologically similar species to make sure that you do not misinterpret sister species as different subpopulations of the same species or to confirm that two ecotypes belong to the same species.

Three different coordinators comment (translated from Swedish):

> *"Genetics should not be a separate interest. It is important with that connection, that based on what we know about population development and the occurrence of the species, we can predict genetic problems with a high probability. The Red List concerns extinction processes for which genetics is extremely important. But it is important to remember that the Red List measures extinction risk and not an erosion risk."*

> *"There is a benefit to using genetic indicators or genetic data for species that are difficult to monitor, and that do not leave faeces or other traces behind. Genetic indices are a great complement, and it can inform which initiatives to prioritise. This is not only relevant for the Red List but for practical nature conservation in general."*

> *"It's great that this aspect is included, that we should also preserve the genetic variation and not just the number of individuals. That is something that has been missing in CBD and also in the Red List."*

6. Conclusions

We applied three proxy-based indicators to assess genetic diversity of species using multiple sources of information. Another priority was to review the extent National Action Plans (NAPs) could be used for assessing the indicators. Furthermore, we surveyed the opinions of committee members responsible for Red List assessments in Sweden on their views on the feasibility of assessing genetic indicators for their taxonomic groups in parallel to the Red List assessments.

The indicators highlight the need to increase population sizes and connectivity for many of the species assessed. Of the 117 species assessed for the Ne500 indicator, on average a given species had 22 % of its populations too small to maintain genetic diversity.

Species with NAPs are more likely to have conservation needs, making the dataset biased and potentially deflating the average indicator value. However, 40 % of LC (Least Concern) species in our dataset have an N_e indicator value below 0.50, meaning that 50 % of LC species populations are too small to retain genetic diversity and adaptive potential, even though they are not considered at risk. The 120 species assessed for the PM indicator have maintained 78 % of their populations. Only 20 out of 120 species had been temporally monitored with DNA-based methods in our dataset.

We assessed all species found in Sweden of two taxonomic groups (amphibians and reptiles), which would not bias the dataset towards species with conservation needs as all were included. They showed the same pattern for the overall indicator values. Most populations are maintained (89 % for amphibians and 98 % for reptiles), although many populations are too small (44 % for amphibians and 59 % for reptiles). All LC reptile species have sufficient population sizes, (except for a few viper populations), however 50 % of the LC amphibian species have indicator values below 0.50. Because so many populations are so small, we are on the edge of a cliff, looking at likely many more lost populations and a rapidly decreasing PM indicator soon.

There is a complication when populations have been extirpated during the assessment period. We used the example of the Kentish plover *Charadrius alexandrinus,* which became regionally extinct. When both indicators are used together, they complement each other. However, if only the Ne500 indicator is used we recommend including lost populations in the evaluation as zero, so that the loss is captured in the indicator value instead of improving it.

One of the main challenges for indicator assessments that we identified is how a “population” is defined by different sources. Biologically meaningful identification based on genetic relationships (population genetic analyses or proxies thereof) are often not used. In IUCN Red List context, “population” refers to the entire national or global occurrence of a species (i.e., its full distribution), whilst the “location” or “area” refers to defined geographic regions. Other definitions are used in reports, NAPs or scientific papers. In some cases, this makes it difficult to combine different sources of information. It is especially problematic when the term is not clearly described.

The Red List taxonomic experts indicated that assessments during the Red List process would be possible with relatively limited extra work, at least for most organism groups, and we conclude that an important next step would be to initiate such implementation among those groups. Several ideas for improvements of the Red List were identified in our interviews with the taxonomic group coordinators. Many of the factors necessary to assess the indicators are part of the red listing process already, such as details of range fragmentation, but they are not quantified for all species. The degree of isolation between sites within a geographic area is also not addressed. Quantifying subpopulations and assessing genetic isolation would not require substantial changes in the procedure. However, there are already considerable challenges to deliver the assessments within the available time frame when compiling the Red List. To assess the indicators as part of the Red List process on a larger scale, procedures need to be developed to generate good assessments reasonably fast. Several of the experts mentioned the possibility of using categories or ranges instead of entering values for populations.

Each taxonomic group comes with its own set of challenges. For many species the data needed is unavailable and would require a large inventory effort to produce the underlying occurrence and census data. Such efforts have been implemented for species included in the Habitat Directive (Article 17), but it would not be possible with that level of detail for all the species on the Red List. There are three broad types of species categories: i) those that have Action Programs or monitoring programs with well documented occurrences, ii) those that have a relatively large number of localities or continuous distribution, making it challenging to delimit populations, and iii) those with a largely unknown degree of occurrence, making it difficult to define populations.

We found that the indicators for genetic diversity can be assessed within reasonable time frames (2 – 24 working hours per species) using already available information. We also note that it would be possible to modify species' assessments for NAPs and the Red List to include genetic diversity indicators. This would benefit both of these processes given that the information provided by the genetic indicators could provide new insights on species´ conservation status.

After demonstrating how these genetic indicator assessments for CBD reporting can be implemented, we consider the actual results alarming. Nearly 80 % of the species have too small populations to secure adaptive potential, and almost 20 % of populations have been lost over the relatively short monitoring periods. It will be important to increase population sizes as well as securing connectivity among populations to sustain Sweden's natural resources into the future. Including genetic diversity indicators when assessing conservation status is an imperative action.

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Appendix 1: KoboToolbox form

The following pages outlines the interactive form, co-created within our international collaborations, that was used to collect data from the assessments. The form was created through the platform KoboToolbox (www.kobotoolbox.org), which allows users to create data collection forms, makes the form available online for data collection, and stores the collected data on the server. More details can be found in Hoban et al. (2023), Mastretta-Yanes and da Silva et al. (2024) , and Mastretta-Yanes et al. (2024a,b), as well as through our online guidelines at: https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/

International Genetic Indicator testing V 4.0

Section 1: Assessor and Country information

EMAIL ADDRESS OF ASSESSOR *

NAME OF ASSESSOR *

COUNTRY OF ASSESSMENT *
Because this study is trying to showcase how individual countries will report to the CBD on the proposed genetic diversity indicators, please list the country for this specific assessment. .

Section 2: Species Taxonomy

GENUS *

SPECIES *
Only type the epithet, e.g. "sapiens" instead of "Homo sapiens". Do NOT include Taxonomic Authority or year of description. That will be provided below.

SUBSPECIES OR VARIETY
Only type the infraspecific epithet. Leave blank if the assessment is not being done below the species level.

TAXONOMIC AUTHORITY
Please include the Taxonomic Authority and year for the species (or subspecies/variety) being assessed. E.g., For Mellivora capensis, type (Schreber, 1776). If Unknown, please leave blank.

COMMON NAME *
Please provide the most widely used common name for the species, followed by the language in brackets. For example, the common names for Taxus baccata are Common yew in English and If commun in French. If more than one widely used common name exists, please separate them with a semicolon. E.g. Common yew (EN); If commun (FR).

TAXONOMIC GROUP *

- ◯ Angiosperm
- ◯ Gymnosperm
- ◯ Pteridophytes (e.g., ferns)
- ◯ Bryophyte
- ◯ Fungus
- ◯ Invertebrate
- ◯ Fish
- ◯ Amphibian
- ◯ Reptile
- ◯ Bird
- ◯ Mammal
- ◯ Other

IF AVAILABLE, ADD THE GBIF TAXONID FOR THIS SPECIES
e.g. 2684495 for Juniperus blancoi as shown here https://www.gbif.org/species/2684495 (scroll down to the end "Taxon identifiers" section)

IF AVAILABLE, ADD THE NCBI TAXONID FOR THIS SPECIES
e.g. 698470 for Juniperus blancoi as shown here https://www.ncbi.nlm.nih.gov/search/all/?term=juniperus%20blancoi

IF AVAILABLE, ADD THE TAXONID FOR THIS SPECIES FROM ANY INFORMATION SYSTEM OR LOCAL DATABASE IN THE COUNTRY OF ASSESSMENT.

Section 3: Indicator 2

QUESTIONS IN THIS SECTION DIRECTLY HELP IN QUANTIFYING INDICATOR 2, AND WILL INFORM THE SECTION ON INDICATOR 1 BY STIPULATING THE NUMBER OF POPULATIONS YOU WILL BE ASKED TO COMPLETE WITH RESPECT TO POPULATION NAME AND SIZE.

NUMBER OF EXTINCT (KNOWN) POPULATIONS WITHIN THE COUNTRY OF ASSESSMENT *
Type -999 if unknown

TYPE THE NAME OR REGION OF THE EXTINCT POPULATIONS, SEPARATED BY A SEMICOLON (";")

NUMBER OF EXTANT (KNOWN) POPULATIONS WITHIN THE COUNTRY OF ASSESSMENT *
Type -999 if unknown

COULD OTHER POPULATIONS EXIST IN THE COUNTRY OF ASSESSMENT?
I.e., Does the number of known populations cover the entire range of the species within the country of assessment?

- ◯ It is highly likely that no other populations exists in the country (e.g., extensive surveys have been conducted and/or habitat expected to be unsuitable)
- ◯ It is possible that other populations exist but these have not been clearly defined
- ◯ Unknown

PLEASE PROVIDE AN EXPLANATION AS TO WHY THIS OPTION WAS CHOSEN. *

WHAT YEAR OR TIME PERIOD IS THIS POPULATION STRUCTURE BASED ON? *

BROADLY, WHICH OF THE FOLLOWING CATEGORIES BETTER DEFINES HOW POPULATIONS ARE DEFINED FOR THIS SPECIES? *
Refer to Guidance Document and Kobo User Manual for examples of each option.

- ☐ Genetic clusters/clades
- ☐ Geographic boundaries
- ☐ Ecological or Biogeographic proxies
- ☐ Traits (e.g., behavioural, morphological, physiological)
- ☐ Management Units (demography/ migration)
- ☐ Other

PLEASE PROVIDE A BRIEF BUT CLEAR EXPLANATION (METHOD) ON HOW POPULATIONS WERE DEFINED.
For example if a buffer zone among occurrence points was used, specify the source of the occurrence points and the size of the buffer: or if geographic layers (e.g. basins, biogeographic regions, etc) were used to crop the distribution range, please explain how was this done: or if it was based on expert consultation, please explain how (e.g. workshop, interview) and provide name of expert(s).

IF A MAP ILLUSTRATING THE EXTANT POPULATIONS EXISTS, PLEASE UPLOAD IT HERE, ENSURING THAT EACH POPULATION IS CLEARLY MARKED. A MULTIPAGE DOCUMENT (EG PDF) CAN BE INCLUDED TO "ZOOM IN" INTO DIFFERENT POPULATIONS, IF REQUIRED..
Accepted files: pdf, png, jpg. Please be reasonable with file size.

Click here to upload file. (< 10MB)

IF AVAILABLE, PLEASE RECORD THE OVERALL DECLINE IN SPECIES' HABITAT AREA OR, IF RELEVANT, IN CENSUS SIZE (NC)
This information may act as a proxy for population loss and hence genetic diversity, should the number of historical population be unknown.

SOURCE OF SPECIES POPULATION INFORMATION (LITERATURE REFERENCE, WEBSITE LINK, EXPERT CONSULTATION) *
Please list all relevant sources used in acquiring the species information separated by a semicolon (;). It is advised that all referenced documents are saved to a species specific folder in your personal records in case further consultation is required. If information was based on expert consultation, please provide name of expert(s).

Section 4: Preface to Indicator 1

IS THERE ANY DATA ON POPULATION SIZES (E.G. NE, NC) FOR AT LEAST ONE POPULATION FOR THIS SPECIES? *

- ◯ Yes
- ◯ No, but Census size data does exist for the species as a whole.
- ◯ No, the species has insufficient data.

EFFECTIVE SIZE - ARE THERE EFFECTIVE SIZE ESTIMATES (NE) FOR AT LEAST ONE OF THE EXTANT POPULATIONS? *

- ◯ Yes
- ◯ No, but other genetic diversity information does exist (e.g., allelic richness, heterozygosity, inbreeding)
- ◯ No

CENSUS SIZE - ARE THERE CENSUS SIZE ESTIMATES (NC) FOR AT LEAST ONE OF THE EXTANT POPULATIONS? *

- ◯ Yes
- ◯ No

IS THERE A KNOWN EFFECTIVE POPULATION SIZE TO CENSUS SIZE (NE/NC) RATIO FOR THIS SPECIES OR A HIGHLY SIMILAR/CLOSELY RELATED SPECIES (E.G. WITHIN THE SAME GENUS AND HAVING THE SAME LIFE HISTORY TRAITS)? *
Try conducting a quick Google Search (or similar) using the search terms "Ne" AND "effective population size" AND [the genus name].

- ◯ Yes, a ratio exists for this species.
- ◯ Yes, a ratio exists for a highly similar species.
- ◯ No

IF YES (AT THE SPECIES LEVEL), PLEASE PROVIDE THE RATIO.
Use decimals (".") instead of ":". NOTE: A single value per species is recommended; however, if there is some uncertainty in this ratio, a range may be provided.

IN WHAT YEAR WAS THE RATIO ESTABLISHED (SAMPLING, NOT PUBLICATION)? *

WHAT CLOSELY RELATED/HIGHLY SIMILAR SPECIES IS THE RATIO BASED ON?
Please write the scientific name.

IF YES (AT THE SPECIES LEVEL), PLEASE PROVIDE THE RATIO.
Use decimals (".") instead of ":". NOTE: A single value per species is recommended; however, if there is some uncertainty in this ratio, a range may be provided.

ANY ADDITIONAL COMMENTS OR NOTES REGARDING THE INFORMATION THAT HAS BEEN PROVIDED ABOVE.

Section 5: Indicator 1 (per population)

QUESTIONS IN THIS SECTION ARE DIRECTLY ASSOCIATED WITH CALCULATING INDICATOR 1. THE NUMBER OF POPULATIONS YOU WILL BE REQUIRED TO ANSWER QUESTIONS IS DIRECTLY RELATED TO THE NUMBER OF EXTANT POPULATIONS THAT WERE ENTERED IN SECTION 3. DATA FOR NO MORE THAN 25 POPULATIONS CAN BE ENTERED (UNLESS REQUESTED) IN THE KOBO FORM, BUT MORE CAN BE ADDED IN THE TEMPLATE.

» Population 1

POPULATION 1 NAME *
If a name has not been assigned to this population in literature, please provide your own unique name here.

WHAT IS THE ORIGIN OF POPULATION 1?
You can provide details in the comments section for this population, if needed.

- ○ historically natural
- ○ introduced
- ○ re-introduced
- ○ reinforced (assisted gene flow)

WHEN WAS THE POPULATION TRANSLOCATED (INTRODUCED, RE-INTRODUCED OR REINFORCED)?

WHAT IS THE EFFECTIVE POPULATION SIZE (NE) FOR POPULATION 1? (POINT ESTIMATE) *
If you have a confidence interval include it in next questions. If Ne is not known for this population, type -999

IF AVAILABLE, WHICH IS THE LOWER LIMIT OF THE NE CONFIDENCE INTERVAL FOR POPULATION 1?
If not available, type -999

IF AVAILABLE, WHICH IS THE UPPER LIMIT OF THE NE CONFIDENCE INTERVAL FOR POPULATION 1?
If not available, type -999. If infinite, type 999 999 999
▸ *more details*

IN WHAT YEAR WAS THE DATA USED TO ESTIMATE NE COLLECTED FOR POPULATION 1? *
Please state the year when the sampling was done, not when it was published.

WHAT GENETIC MARKERS WERE USED TO ESTIMATE NE FOR THIS POPULATION? *

- ○ Whole Genome Sequence data
- ○ SNPs (single nucleotide polymorphisms)
- ○ Microsatellites
- ○ Chloroplast/Mitodondrial DNA
- ○ Other
- ○ Unknown

IF 'OTHER', PLEASE EXPLAIN.

WHAT METHOD WAS USED IN CALCULATING NE FOR THIS POPULATION? *

- ○ Linkage disequilibrium (e.g., LDNE, NeEstimator, SNeP)
- ○ Heterozygosity excess (e.g., NeEstimator)
- ○ Temporal changes in allele frequency (e.g., MLNE, NeEstimator, TempoFS)
- ○ Genetic relatedness [sibship/parentage] (e.g., Colony, NeEstimator)
- ○ Approximate Bayesian Computation (e.g., ONESAMP)
- ○ Other
- ○ Unknown

PLEASE LIST ALL RELEVANT SOURCES REPORTING ON EFFECTIVE POPULATION SIZE FOR THIS POPULATION *
Please separate each source using a semicolon (;).

IF THERE IS A CENSUS POPULATION SIZE (NC) AVAILABLE, IS THIS A RANGE OR POINT ESTIMATE? *

- ◯ quantitative range or qualitative data (e.g. "1,000 to 2,000" or "expert says few hundreds")
- ◯ point estimate (quantitative data with or without confidence intervals, as well as round estimates e.g. "expert says around 3,000)
- ◯ unknown (no Nc available for this population)

IN WHAT YEAR WAS THE NC ESTIMATED FOR POPULATION 1?
Please state the year when the sampling was done, not when it was published

HOW WAS NC CALCULATED IN THIS POPULATION? *

- ◯ Count
- ◯ Extrapolated based on habitat area and known density
- ◯ Other (please specify in the comments)
- ◯ Unknown

WHATS THE RANGE OF THE NC FOR POPULATION 1? *

- ◯ < 5,000 by much
- ◯ < 5,000 but not by much (tens or a few hundred less)
- ◯ > 5,000 but not by much (tens or a few hundred more)
- ◯ > 5,000 by much
- ◯ estimate is a range including both less and greather than 5,000 (e.g. "3,000 to 10,000")

IF A MORE DETAILED RANGE IS AVAILABLE PLEASE ENTER IT HERE.

IF KNOWN, WHAT IS THE CENSUS POPULATION SIZE (NC) FOR POPULATION 1? (POINT ESTIMATE) *
If you have a confidence interval include it in next questions.

IF AVAILABLE, WHICH IS THE LOWER LIMIT OF THE NC CONFIDENCE INTERVAL FOR POPULATION 1?
This should be the lower value of the 95% Confidence Interval. If that is unavailable, leave this question blank and please record the confidence interval used (e.g. 90%) in the 'ANY ADDITIONAL COMMENTS OR NOTES' question at the end of the Section.

IF AVAILABLE, WHICH IS THE UPPER LIMIT OF THE NC CONFIDENCE INTERVAL FOR POPULATION 1?
This should be the upper value of the 95% Confidence Interval. If that is unavailable, please record the confidence interval used (e.g. 90%) in the 'ANY ADDITIONAL COMMENTS OR NOTES' question at the end of the Section.

PLEASE LIST ALL RELEVANT SOURCES OF CENSUS SIZE INFORMATION (LITERATURE REFERENCE, WEBSITE LINK, EXPERT CONSULTATION) FOR THIS POPULATION *
Please separate sources using a semicolon (;)

ANY ADDITIONAL COMMENTS OR NOTES REGARDING THE INFORMATION THAT HAS BEEN PROVIDED OR WHY IT COULD NOT BE FOR POPULATION 1?

Section 6: Modified Indicator 1 for the Entire Species Within the Country of Assessment

THIS SECTION SHOULD ONLY BE COMPLETED IF THERE IS DATA ON THE NUMBER OF INDIVIDUALS FOR THE ENTIRE SPECIES; AND SHOULD NOT BE COMPLETED IF INDIVIDUAL POPULATION SIZE DATA EXISTS.

CENSUS SIZE - IS THIS A RANGE OR POINT ESTIMATE? *

- ◯ quantitative range or qualitative data (e.g. "1,000 to 2,000" or "expert says few hundreds")
- ◯ point estimate (quantitative data with or without confidence intervals, as well as round estimates e.g. "expert says around 3,000)
- ◯ unknown (no Nc available for this population)

WHAT IS THE RANGE OF NC FOR THE SPECIES? *

- ◯ < 5,000 by much
- ◯ < 5,000 but not by much (tens or a few hundred less)
- ◯ > 5,000 but not by much (tens or a few hundred more)
- ◯ > 5,000 by much
- ◯ estimate is a range including both less and greather than 5,000 (e.g. "3,000 to 10,000")

IF A MORE DETAILED RANGE IS AVAILABLE, PLEASE ENTER IT HERE.

WHAT IS THE CENSUS SIZE (NC) FOR THE SPECIES? (POINT ESTIMATE) *
If you have a confidence interval include it in next questions. Leave blank if Nc was not quantitatively estimated.

IF AVAILABLE, WHICH IS THE LOWER LIMIT OF THE NC CONFIDENCE INTERVAL FOR THE SPECIES?
This should be the lower value of the 95% Confidence Interval. If that is unavailable, please record the confidence interval used (e.g. 90%) in the 'ANY ADDITIONAL COMMENTS OR NOTES' question at the end of the Section.

IF AVAILABLE, WHICH IS THE UPPER LIMIT OF THE NC CONFIDENCE INTERVAL FOR THE SPECIES?
This should be the upper value of the 95% Confidence Interval. If that is unavailable, please record the confidence interval used (e.g. 90%) in the 'ANY ADDITIONAL COMMENTS OR NOTES' question at the end of the Section.

IN WHAT YEAR WAS NC ESTIMATED FOR THE SPECIES? *
Please state the year when the sampling was done, not when it was published

SOURCE OF SPECIES CENSUS SIZE INFORMATION (LITERATURE REFERENCE, WEBSITE LINK, EXPERT CONSULTATION) *
Please list all relevant sources used in acquiring the species information separated by a semi-colon (;). It is advised that all referenced documents are saved to a species specific folder in your personal records in case further consultation is required. If information was based on expert consultation, please provide name of expert(s).

ANY ADDITIONAL COMMENTS OR NOTES WITH RESPECT TO THE INFORMATION PROVIDED IN THIS SECTION.
E.g., record the confidence interval used for the point estimate if not 95%.

Section 7: Indicator 3

QUESTIONS IN THIS SECTION WILL CONTRIBUTE TOWARDS QUANTIFYING INDICATOR 3 - NUMBER OF SPECIES AND POPULATIONS IN WHICH GENETIC DIVERSITY IS BEING MONITORED USING DNA BASED METHODS

HAVE GENETIC STUDIES BEEN CONDUCTED INVOLVING THE SPECIES? *

- ◯ Yes, but only phylogenetic/phylogeographic studies.
- ◯ Yes, but only population-level studies.
- ◯ Yes, both phylogenetic and population studies.
- ◯ No

HAS TEMPORAL GENETIC MONITORING BEEN CONDUCTED FOR ONE OR MORE POPULATIONS OF THIS SPECIES? *
A temporal comparison using at least two time points of various genetic diversity metrics for the species.

- ◯ Yes
- ◯ No
- ◯ Unknown

IF YES, WHAT YEARS DID THIS TAKE PLACE? *

PLEASE CITE ALL DATA SOURCES FOR THE GENETIC STUDIES (LITERATURE REFERENCE, WEBSITE LINK, EXPERT CONSULTATION) SEPARATED BY A SEMI-COLON (;). IT IS ADVISED THAT ALL REFERENCED DOCUMENTS ARE SAVED TO A SPECIES SPECIFIC FOLDER IN YOUR PERSONAL RECORDS IN CASE FURTHER CONSULTATION IS REQUIRED. *

Section 8: Other Species Information

WHILE THE ANSWERS TO THE QUESTIONS IN THIS SECTION WILL NOT DIRECTLY CONTRIBUTE TO QUANTIFYING ANY OF THE GENETIC DIVERSITY INDICATORS BEING INVESTIGATED, THEY WILL HELP REFINE METRICS, SUCH AS THE NE:NC RATIO, AND PROVIDE CONTEXTUAL INFORMATION ON THE TYPE OF SPECIES BEING ASSESSED (E.G., THREATENED STATUS, LIFE HISTORY CLASSIFICATIONS) WHICH COULD BE INFORMATIVE TO COUNTRIES IN THEIR NATIONAL REPORTING. THESE DATA CAN ALSO HELP DEVELOP NEW AND REFINE EXISTING NE:NC RATIOS FOR SPECIES. AS SUCH THESE VAST MAJORITY OF THE QUESTIONS IN THIS SECTION ARE MANDATORY. IF THE REQUIRED INFORMATION IS NOT AVAILABLE DURING THE TIME OF ASSESSMENT, FOR WHATEVER REASON, PLEASE MARK THE QUESTIONS AS UNKNOWN, BUT PLEASE ENSURE THESE ARE FOLLOWED UP TO ALLOW FOR FUTURE DOWNSTREAM ANALYSES

REALM *
Select all that apply

- ☐ Marine
- ☐ Estuarine
- ☐ Freshwater
- ☐ Terrestrial

IUCN HABITAT CLASSIFICATION *
IUCN (2012) IUCN Habitat Classification Scheme. https://www.iucnredlist.org/resources/habitat-classification-scheme. Select all that apply.

- ☐ Artificial - terrestial
- ☐ Artificial - aquatic
- ☐ Caves & Subterranean habitat
- ☐ Desert
- ☐ Forest & Woodland
- ☐ Grassland
- ☐ Marine-Neritic
- ☐ Marine-Oceanic
- ☐ Marine-Deep Ocean Floor
- ☐ Marine-Intertidal
- ☐ Marine-Coastal/Supratidal
- ☐ Rocky Area
- ☐ Savanna
- ☐ Shrubland
- ☐ Wetland
- ☐ Unknown/Other

OTHER HABITAT DATA
Please feel free to elaborate further on the habitat (sub-types) of the species. E.g., Wetland may be broken down further into streams/rivers, and lakes,. Beaches fall under Marine Intertidal.

IS THIS SPECIES A NATIONAL ENDEMIC? *

- ◯ Yes
- ◯ No

IF NO, PLEASE SELECT THE TRANSBOUNDARY NATURE OF THE SPECIES. *
Select all that apply.

- ☐ Present in more than 1 country
- ☐ Migratory
- ☐ Oceanic
- ☐ Other

IF OTHER, PLEASE EXPLAIN. *

WHAT PROPORTION OF THE SPECIES RANGE OCCURS WITHIN THE ASSESSMENT COUNTRY? *
Note: Occurs refers to where a species breds and/or spends most of its time.

- ◯ Less than 10%
- ◯ 10-25%
- ◯ 25-50%
- ◯ 50-75%
- ◯ 75-99%
- ◯ Unknown

SPECIES RANGE *
Wide-ranging: an EOO greater than 20 000 km2 (based on IUCN Criterion B1) or present in more than one-third of a country's 20-km grid squares (following Katayama et al. 2014 PLoSOne study). Restricted: an EOO < 20 000 km2 or an AOO < 2 000 km2. A list of restricted species compiled using KBA criteria (i.e.IUCN Criteria B2) can be found online from https://www.keybiodiversityareas.org/working-with-kbas/proposing-updating/criteria-tools; however, it is recognized that not all restricted species will be included in this list.

- ◯ Wide-ranging
- ◯ Restricted (i.e., narrow)
- ◯ Unknown

IS THE SPECIES RARE? *
Rare: Low densities of individuals: Species always occurs as single individuals or very small subpopulations (typically fewer than 50 mature individuals) scattered over a wide area

- ◯ Yes - naturally rare
- ◯ Yes - recently rare (anthropogenic effect)
- ◯ No

EXTENT OF OCCURRENCE (EOO) IN KM2
If a point estimate is not available, please enter a range value.

AREA OF OCCURRENCE (AOO) IN KM2
If a point estimate is not available, please enter a range value.

LEVEL OF POPULATION FRAGMENTATION *
As per IUCN definition, severely fragmented means that more than half of the species' total Area of Ocurrence is in habitat patches that are (1) smaller than would be required to support a viable population, and (2) separated from other habitat patches by a large distance. Moderately fragmented refers to a species with less than half of its area of occurrece in habitat patches.

- ◯ Severely fragmented
- ◯ Moderately fragmented
- ◯ None (continuous population)
- ◯ Unknown

ADDITIONAL INFORMATION ON SPECIES RANGE.
Feel free to include other specific information on the range of the species.

GLOBAL RED LIST CATEGORY (IUCN) *
For transboundary species, this will assessment will cover the entire known range of the species, not just the country of assessment.

- ◯ Critically Endangered (CR)
- ◯ Endangered (EN)
- ◯ Vulnerable (VU)
- ◯ Near Threatened (NT)
- ◯ Least Concern (LC)
- ◯ Data Deficient (DD)
- ◯ Not assessed
- ◯ Unknown
- ◯ Regionally extinct (RE). Select only for National Redlists.

NATIONAL RED LIST CATEGORY *

- ◯ Critically Endangered (CR)
- ◯ Endangered (EN)
- ◯ Vulnerable (VU)
- ◯ Near Threatened (NT)
- ◯ Least Concern (LC)
- ◯ Data Deficient (DD)
- ◯ Not assessed
- ◯ Unknown
- ◯ Regionally extinct (RE). Select only for National Redlists.

OTHER SPECIES STATUS ASSESSMENT(S)
Please write the species conservation status as recognized by all other assessments or the status range in instances where different classifications are provided for different regions, states, provinces or a country. Please separate all entries with a semicolon (;).

SOURCE OF SPECIES STATUS AND DISTRIBUTION (LITERATURE REFERENCE, WEBSITE LINK, EXPERT CONSULTATION) *
Please list all relevant sources used in acquiring the species information separated by a semicolon (;). It is advised that all referenced documents are saved to a species specific folder in your personal records in case further consultation is required. If information was based on expert consultation, please provide name of expert(s).

LIFE HISTORY TRAITS - THE NEXT FEW QUESTIONS RELATE TO LIFE HISTORY TRAITS WHICH CAN BE USED TO INFORM AND REFINE NE:NC RATIOS. IF LIFE HISTORY DATA DOES NOT EXIST FOR THE SPECIES BEING ASSESSED, BUT DOES EXIST FOR A CLOSELY RELATED SPECIES BELIEVED OR KNOWN TO HAVE A SIMILAR LIFESTYLE, PLEASE ANSWER THE LIFE HISTORY QUESTIONS FOR THE CLOSE RELATIVE AND SPECIFY THIS BELOW..

LIFE HISTORY TRAIT - FECUNDITY (NUMBER OF OFFSPRING PER YEAR) *

- ◯ < 1
- ◯ 1-2
- ◯ 3-5
- ◯ 6-10
- ◯ 10s
- ◯ 100s
- ◯ 1 000s
- ◯ 10 000s
- ◯ 100 000s
- ◯ >100 000s
- ◯ Unknown
- ◯ Not applicable (e.g., semelparous)

IF SEMELPAROUS, HOW MANY OFFSPRING ARE PRODUCED IN A SINGLE EVENT?

LIFE HISTORY TRAIT - REPRODUCTIVE STRATEGY *
Please select all that apply

- ☐ Sexual
- ☐ Cross-pollination
- ☐ Asexual
- ☐ Self-pollination
- ☐ Vegetative
- ☐ Clonal
- ☐ Oviparous
- ☐ Viviparous
- ☐ Semelparous
- ☐ Iteroparous
- ☐ Other
- ☐ Unknown

IF OTHER, PLEASE LIST

LIFE HISTORY TRAIT - AGE OF ADULTS
What data exists relating to the age of adults? Please select all that apply.

- ☐ Maximum lifespan
- ☐ Median lifespan
- ☐ Age at maturity (first reproduction)
- ☐ Other
- ☐ Unknown

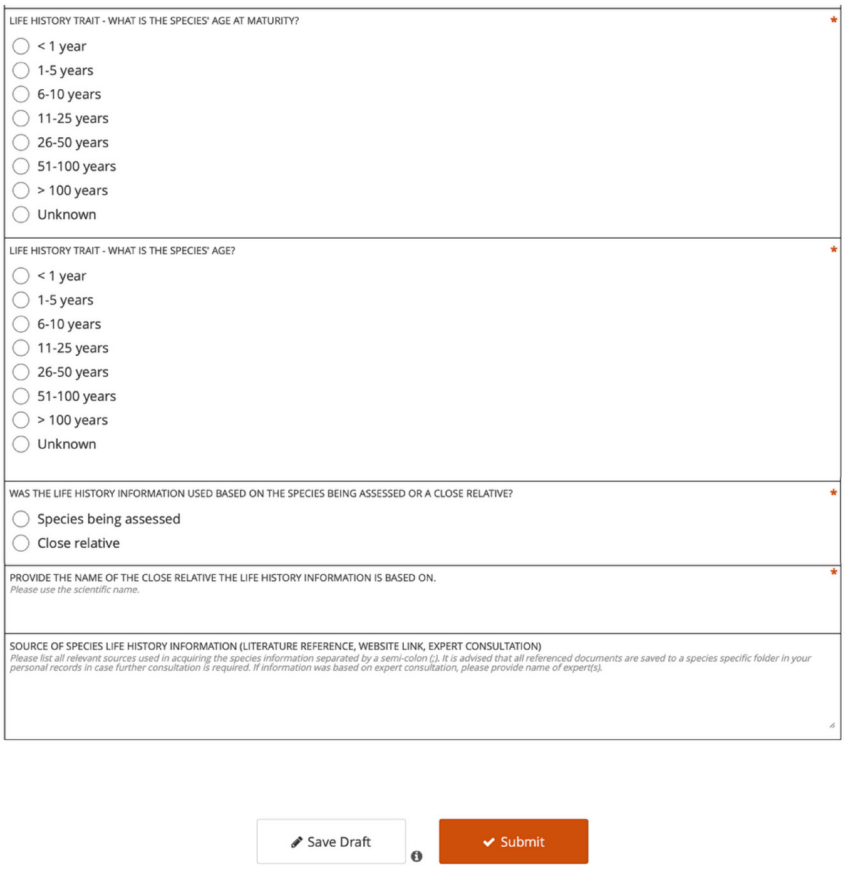
IF OTHER, PLEASE LIST

LIFE HISTORY TRAIT - WHAT IS THE SPECIES' MAXIMUM LIFESPAN? *

- ◯ < 1 year
- ◯ 1-5 years
- ◯ 6-10 years
- ◯ 11-25 years
- ◯ 26-50 years
- ◯ 51-100 years
- ◯ > 100 years
- ◯ Unknown

LIFE HISTORY TRAIT - WHAT IS THE SPECIES' MEDIAN LIFESPAN? *

- ◯ < 1 year
- ◯ 1-5 years
- ◯ 6-10 years
- ◯ 11-25 years
- ◯ 26-50 years
- ◯ 51-100 years
- ◯ > 100 years
- ◯ Unknown


LIFE HISTORY TRAIT - WHAT IS THE SPECIES' AGE AT MATURITY? *
< 1 year
1-5 years
6-10 years
11-25 years
26-50 years
51-100 years
> 100 years
Unknown
LIFE HISTORY TRAIT - WHAT IS THE SPECIES' AGE? *
< 1 year
1-5 years
6-10 years
11-25 years
26-50 years
51-100 years
> 100 years
Unknown
WAS THE LIFE HISTORY INFORMATION USED BASED ON THE SPECIES BEING ASSESSED OR A CLOSE RELATIVE? *
Species being assessed
Close relative
PROVIDE THE NAME OF THE CLOSE RELATIVE THE LIFE HISTORY INFORMATION IS BASED ON. *
Please use the scientific name.
SOURCE OF SPECIES LIFE HISTORY INFORMATION (LITERATURE REFERENCE, WEBSITE LINK, EXPERT CONSULTATION)
Please list all relevant sources used in acquiring the species information separated by a semi-colon (;). It is advised that all referenced documents are saved to a species specific folder in your personal records in case further consultation is required. If information was based on expert consultation, please provide name of expert(s).
Save Draft
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Appendix 2: Supplementary tables and figures

Table A2.1 List of reviewed National Action Plans (NAPs)

SWEDISH TITLE	REPORT NO	PERIOD	AUTHOR
Published by Naturvårdsverket (Swedish Environmental Protection Agency; SEPA)			
Åtgärdsprogram för älvängslöpare	6447	2011-2015	Wanntorp 2011
Åtgärdsprogram för alkonblåvinge och klockgentiana	5686	2007-2011	Appelqvist & Bengtsson 2007
Åtgärdsprogram för almblombock	6648	2014-2018	Malmqvist & Franc 2014
Åtgärdsprogram för ängshök	6465	2011-2015	Rodebrand 2011
Åtgärdsprogram för ängskäreplattmal	6343	2010-2014	Björklund 2010
Åtgärdsprogram för ärrlavar	5470	2005-2009	Hultengren 2005
Åtgärdsprogram för asknätsfjäril	5858	2007-2011	Eliasson 2008b
Åtgärdsprogram för barbastell	6532	2015-2019	Ahlén 2015
Åtgärdsprogram för barkkvastmossa	6431	2008-2016	Weibull 2011
Åtgärdsprogram för batavasandbi, fältsandbi och flodsandbi	6452	2014-2018	Nilsson & Wilhelm 2015
Åtgärdsprogram för björklevande vedskalbaggar i Norrland	5843	2008-2012	Wikars 2008
Åtgärdsprogram för bombmurkla	6333	2010-2014	Nitare 2009
Åtgärdsprogram för brandinsikter i boreal skog	5610	2006-2010	Wikars 2006
Åtgärdsprogram för bredbandad ekbarkbock	5469	2005-2009	Ehnström 2005
Åtgärdsprogram för brunkulla	6582	2013-2017	Länstyrelsen i Jämtlands län 2013
Åtgärdsprogram för brynia	6715	2015-2019	Weibull 2015
Åtgärdsprogram för dårgräsfjäril	5527	2005-2010	Bergman 2006
Åtgärdsprogram för dvärglåsbräken	5626	2006-2010	Svensson 2006
Åtgärdsprogram för dynglevande skalbaggar	5689	2007-2011	Ljungberg 2007
Åtgärdsprogram för elfenbenslav	6336	2010-2015	Hermansson & Jonsson 2010
Åtgärdsprogram för fågelfotsmossa	6649	2014-2019	Weibull 2014b
Åtgärdsprogram för fältgentianor i naturliga fodermarker	6681	2015-2019	Lennartsson 2015
Åtgärdsprogram för fältpiplärka	6542	2015-2019	Larsson & Fritz 2015
Åtgärdsprogram för fetörtsblåvinge	6426	2011-2015	Elmquist 2011
Åtgärdsprogram för finnögontröst	5918	2008-2012	Appelqvist et al. 2008
Åtgärdsprogram för fjällgås	6434	2011-2015	Länsstyrelsen i Norrbotten 2011
Åtgärdsprogram för fjällräv	6780	2017-2021	Elmhagen et al. 2017
Åtgärdsprogram för flikstånds	5545	2005-2010	Andersson 2006

SWEDISH TITLE	REPORT NO	PERIOD	AUTHOR
Åtgärdsprogram för fönsterspinnare (lavdagsvärmare)	5457	2005-2008	Betzholtz 2005
Åtgärdsprogram för glanstagel	6637	2014-2018	Granbo 2014
Åtgärdsprogram för gölgroda	6631	2014-2019	Lindgren et al. 2014
Åtgärdsprogram för gotlandsranunkel	5611	2006-2010	Johansson 2006
Åtgärdsprogram för gotlands-säfferotplattmal	5982	2009-2013	Björklund 2009
Åtgärdsprogram för grönfläckig padda	6406	2011-2016	Wirén 2010
Åtgärdsprogram för grynig påskrislav	5662	2006-2011	Arup 2006
Åtgärdsprogram för gulfläckig igelkottspinnare	6325	2010-2014	Elmquist 2009
Åtgärdsprogram för gullrisbock	6583	2013-2015	Nilsson 2013
Åtgärdsprogram för hällebräcka	6615	2014-2018	Svenson et al. 2014
Åtgärdsprogram för hänggräs	5421	2004-2009	Långström 2005
Åtgärdsprogram för hårig skrovellav	6364	2010-2014	Jonsson & Nordin 2010
Åtgärdsprogram för havsmurarbi	6341	2010-2014	Cederberg 2010
Åtgärdsprogram för hotade åkergräs	5659	2007-2011	Kloth 2007
Åtgärdsprogram för hotade arter på asp i Norrland	6393	2010-2014	Wikars & Hedenås 2010
Åtgärdsprogram för hotade frölöpare	6526	2012-2017	Lundkvist 2012
Åtgärdsprogram för hotade insikter på krisslor	6632	2014-2018	Björklund 2014
Åtgärdsprogram för hotade lavar på kulturved i odlingslandskap	6439	2011-2016	Hermansson & Jonsson 2011
Åtgärdsprogram för hotade vadare på strandängar	6680	2015-2019	Ottvall 2015
Åtgärdsprogram för humlepälsbi	6640	2014-2018	Cederberg 2014
Åtgärdsprogram för jättepraktbagge	6584	2013-2017	Ehnström & Bader 2013
Åtgärdsprogram för jätteköldlav	6337	2010-2015	Hermanssson 2010
Åtgärdsprogram för jordstjärnstryffel	5981	2007-2011	Jeppson 2009
Åtgärdsprogram för kalktallskogar	5967	2009-2013	Nitare 2009
Åtgärdsprogram för kärrnocka	5500	2005-2009	Wigermo & Håkansson 2005
Åtgärdsprogram för klådris	5700	2007-2010	Ljung 2007
Åtgärdsprogram för klöversobermal	5517	2005-2010	Björklund 2005
Åtgärdsprogram för kornsparv	5502	2006-2010	Ivarsson 2005
Åtgärdsprogram för korthalsad majbagge	5651	2006-2010	Sörensson & Mårtensson 2007
Åtgärdsprogram för långt broktagel	6365	2010-2015	Hermansson 2010
Åtgärdsprogram för låsbräknar i hävdade marker	6650	2014-2018	Naturvårdsverket 2014
Åtgärdsprogram för ljunghed 2022-2026	7035	2022-2026	Larsson & Hedström 2022
Åtgärdsprogram för lökgroda	5826	2008-2011	Nyström & Stenberg 2008
Åtgärdsprogram för martorn	5940	2008-2012	Bengtsson et al. 2009
Åtgärdsprogram för mnemosynefjäril	5829	2008-2012	Franzén & Imby 2008
Åtgärdsprogram för mosippa	6726	2016-2020	Stridh et al. 2016
Åtgärdsprogram för nålginst, tysk ginst och ginstlevande fjärilar	5731	2007-2011	Larsson 2007
Åtgärdsprogram för nipsippa och gotlandsippa	5672	2006-2010	Lindell 2007

SWEDISH TITLE	REPORT NO	PERIOD	AUTHOR
Åtgärdsprogram för nyckelpigespindel	6344	2010-2014	Lundberg & Gerell 2010
Åtgärdsprogram för öppna kalkrika hällmarker i Dalsland	6530	2013-2017	Hultengren 2012
Åtgärdsprogram för orangefläckig brunbagge	6554	2013-2017	Nilsson 2013
Åtgärdsprogram för ortolansparv	6781	2017-2021	Haldén 2017
Åtgärdsprogram för ostronört	5971	2009-2013	Lindholm et al. 2009
Åtgärdsprogram för rikkärr	5561	2006-2010	Sundberg 2006
Åtgärdsprogram för rödlistade fjälltaggsvampar	5609	2006-2010	Nitare 2006
Åtgärdsprogram för rökpipsvamp	5825	2007-2010	Rydberg 2008
Åtgärdsprogram för sällsynta skapanior på tidvis översvämmad ved	6655	2015-2019	Weibull 2014
Åtgärdsprogram för sandnörel	5949	2009-2014	Mattiasson 2009
Åtgärdsprogram för sandödla	6597	2014-2017	Berglind et al. 2013
Åtgärdsprogram för sandstäpp	6676	2015-2019	Rosquist 2017
Åtgärdsprogram för särskilt skyddsvärda träd	6496	2012-2016	Naturvårdsverket 2012
Åtgärdsprogram för sex hotade bokskogsarter	5553	2006-2010	Malmqvist 2006
Åtgärdsprogram för sienamusseron	6429	2011-2015	Johansson & Bohus-Jensen 2011
Åtgärdsprogram för skalbaggar i eklågor	6507	2012-2016	Nilsson 2012
Åtgärdsprogram för skalbaggar på äldre död tallved	6629	2014-2018	Wikars 2014
Åtgärdsprogram för skalbaggar på gammal asp	6573	2013-2017	Eriksson 2013
Åtgärdsprogram för skalbaggar på nyligen död tall	6599	2014-2018	Pettersson 2013
Åtgärdsprogram för skalbaggar på skogslind [på gammal lind]	5552	2006-2011	Ehnström 2006
Åtgärdsprogram för skärrande gräshoppa	6694	2015-2019	Larsson et al. 2015
Åtgärdsprogram för skirmossa	6359	2010-2014	Stenström 2010
Åtgärdsprogram för skorpdagglav	5560	2006-2011	Arup 2006b
Åtgärdsprogram för skräntärna	5702	2007-2011	Staav 2007
Åtgärdsprogram för slöjröksvamp	5544	2006-2010	Jeppson 2006
Åtgärdsprogram för smällvedel	5948	2009-2012	Grundström 2009
Åtgärdsprogram för spansk fluga	5602	2006-2008	Sörensson & Mårtensson 2006
Åtgärdsprogram för spindelört-skinnbagge	6578	2012-2016	Karlsson 2011
Åtgärdsprogram för stäppartade torrängar i Västsverige	6405	2011-2015	Sundh 2010
Åtgärdsprogram för stäppfingersvamp	6630	2014-2018	Knutsson 2014
Åtgärdsprogram för stäppspolvivel	6335	2010-2014	Lennartsson 2010
Åtgärdsprogram för steklar, myrlejon-sländor och spindlar i sanddyner	6638	2014-2018	Johansson & Jonsson 2014
Åtgärdsprogram för stinkmålla	6442	2011-2015	Olsson 2010
Åtgärdsprogram för stor ögontröst	5589	2006-2009	Bertilsson 2006
Åtgärdsprogram för större barkplattbagge	6604	2014-2018	Pettersson 2014
Åtgärdsprogram för större ekbock	6313	2010-2014	Hedin 2009b

SWEDISH TITLE	REPORT NO	PERIOD	AUTHOR
Åtgärdsprogram för stortapetserarbi, storkägelbi och Thomsonkägelbi	6332	2010-2014	Nilsson 2010
Åtgärdsprogram för storviol	6444	2011-2015	Widén 2011
Åtgärdsprogram för strandpadda	6539	2013-2017	Pröjts 2012
Åtgärdsprogram för strandsandjägare	5508	2005-2010	Berglind 2005
Åtgärdsprogram för strandskinnlav	6652	2014-2018	Hermansson 2014
Åtgärdsprogram för sumpjordtunga	5734	2007-2011	Nitare 2007
Åtgärdsprogram för svampar i ängs- och betesmarker	6423	2011-2015	Jordal 2011
Åtgärdsprogram för svampar i kalkrika ädellövbärande fodermarker	5950	2009-2013	Knutsson 2009
Åtgärdsprogram för svartfläckig blåvinge	5652	2006-2010	Elmquist & Stadel Nielsson 2007
Åtgärdsprogram för svartoxe	6334	2010-2014	Hedin 2009
Åtgärdsprogram för svartpälsbi	5743	2007-2011	Nilsson & Andersson 2007
Åtgärdsprogram för svarttåg	5632	2006-2010	Snogerup 2006
Åtgärdsprogram för svensk ögontröst	5775	2008-2012	Johansson 2007
Åtgärdsprogram för sydlig kärrsnäppa	6388	2010-2014	Flodin et al. 2010
Åtgärdsprogram för trollduvemätare	6679	2015-2019	Hydén 2015
Åtgärdsprogram för trumgräshoppa	6443	2011-2015	Kindvall 2011
Åtgärdsprogram för utter	5614	2006-2010	Bisther & Aronson 2006
Åtgärdsprogram för väddnätfjäril	5920	2008-2012	Eliasson 2008
Åtgärdsprogram för veronikanätfjäril	6371	2010-2013	Eliasson 2010
Åtgärdsprogram för vildbin och småfjärilar på torräng	6441	2011-2016	Karlsson et al. 2011
Åtgärdsprogram för vildbin på ängsmark	6425	2011-2016	Karlsson & Larsson 2011
Åtgärdsprogram för violett guldvinge	6603	2014-2018	Lindeborg 2014
Åtgärdsprogram för violgubbe	5638	2006-2011	Aronsson 2006
Åtgärdsprogram för vitryggig hackspett	6770	2017-2021	Naturvårdsverket 2017
Åtgärdsprogram för vityxne i södra Sverige	5528	2005-2008	Reinhammar 2007

Published by Havs- och Vattenmyndigheten (Swedish Agency for Marine and Water Management; SwAM)

Åtgärdsprogram för ålgräsängar	2017:24	2017-2021	Granit 2017
Åtgärdsprogram för asp	2016:27	2016-2020	Sallmén 2016
Åtgärdsprogram för bevarande av småsvalting	5499	2006-2010	Jacobson 2005
Åtgärdsprogram för bevarande av tjockskalig målarmussla	5658	2006-2009, 2016-2020	Lundberg et al. 2006
Åtgärdsprogram för flodkräfta	5955	2007-2013, 2017-2022	Edsman & Schröder 2009
Åtgärdsprogram för flodnejonöga	2022:19	2023-2027	Havs- och vattenmyndigheten 2022
Åtgärdsprogram för flodpärlmussla	2020:19	2020-2024	Havs- och vattenmyndigheten 2020
Åtgärdsprogram för flytsvalting	6387	2010-2013, 2017-2021	Gustafsson & Aremyr 2010
Åtgärdsprogram för havsnejonöga	2020:08	2020-2024	Havs- och vattenmyndigheten 2020
Åtgärdsprogram för jämtlandsmaskros	6651	2015-2019	Ljungstrand & Hedberg 2014

SWEDISH TITLE	REPORT NO	PERIOD	AUTHOR
Åtgärdsprogram för mal	2017:33	2017-2021	Havs- och vatten-myndigheten 2017
Åtgärdsprogram för murgrönsmöja	6386	2006-2012, 2017-2021	Jacobson 2011
Åtgärdsprogram för sällsynta kransalger längs kusten	2020:17	2020-2024	Zinko 2017
Åtgärdsprogram för skaftslamkrypa	2013:8	2013-2022	Ekstam 2013
Åtgärdsprogram för temporära sötvatten med fokus på organismer i naturbetesmakren, höllkar och allvarmiljöer	2019:7	2019-2023	Havs- och vatten-myndigheten 2017
Åtgärdsprogram för tumlare	2021:11	2021-2025	Havs- och vatten-myndigheten 2021
Kunskapsuppbyggande program - 15 hotade makrofytarter i permanenta vatten	2017:11	2017-2021	Zinko 2017

Table A2.2 Assessment of action plans. Table indicates the presence of intormation in the the plan about the number of populations (No. P), the number of locations or areas (No. L/A), census size on a national level (N_c Tot), census size per location/population (N_c P), locations that have been lost (Lost), performed genetic studies (Gen s) and the presence or no presence of a section of conservation genetics (Con G). N_e denotes whether there was enough information for the Ne500 indicator, for which information on locations in some form as well as census size are necessary. PM denotes whether there was enough information for the PM indicator, for which information on locations in some form and information about loss are necessary. GM denotes whether there was enough information for the the Genetic monitoring indicator, where information about whether DNA-based monitoring is ongoing for one or more population (method 1) and if there are phylogenetic or population genetic studies of the species (method 2; see section 2.3). Kobo denotes whether the NAP was used for species assessment using the KoboToolbox form.

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Åtgärdsprogram för brandinsikter i boreal skog	*Acmaeops marginata*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för skalbaggar på nyligen död tall	*Acmaeops marginatus*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för skalbaggar i eklågor	*Aesalus scarabaeoides*	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för nålginst, tysk ginst och ginstlevande fjärilar	*Agonopterix atomella*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för ängskäreplattmal	*Agonopterix bipunctosa*	Yes	Yes	Yes	No	Yes	No	No	Yes	Yes	No	Yes
Åtgärdsprogram för hotade åkergräs	*Agrostemma githago*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för bevarande av småsvalting	*Alisma wahlenbergii*	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för skalbaggar i eklågor	*Ampedus nigerrimus*	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för klöversobermal	*Anacampsis fuscella*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	Yes

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Åtgärds-program för batavasandbi, fältsandbi och flodsandbi	*Andrena batava*	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Andrena gelriae*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för vildbin på ängsmark	*Andrena humilis*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Andrena labialis*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för vildbin på ängsmark	*Andrena marginata*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärds-program för batavasandbi, fältsandbi och flodsandbi	*Andrena morawitzi*	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No
Åtgärds-program för batavasandbi, fältsandbi och flodsandbi	*Andrena nycthemera*	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No
Åtgärdsprogram för sex hotade bokskogsarter	*Anopledera scutellata*	No	Yes	No	Yes	Yes	No	No	Yes	Yes	No	No
Åtgärdsprogram för fjällgås	*Anser erythropus*	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för hotade åker-gräs	*Anthemis cotula*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för humlepälsbi	*Anthophora plagiata*	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för svartpälsbi	*Anthophora retusa*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Åtgärdsprogram för hotade åker-gräs	*Anthriscus caucalis*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för fältpiplärka	*Anthus campestris*	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	Yes
Åtgärdsprogram för dynglevande skalbaggar	*Aphodius arenarius*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för dynglevande skalbaggar	*Aphodius merdarius*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för dynglevande skalbaggar	*Aphodius quadriguttatus*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för brandinsikter i boreal skog	*Aradus angularis*	Yes	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för brandinsikter i boreal skog	*Aradus aterrimus*	No	No	No	No	No	No	No	No	No	No	No

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Åtgärdsprogram för brandinsikter i boreal skog	*Aradus laeviusculus*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för brandinsikter i boreal skog	*Aradus signaticornis*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för hänggräs	*Arctophila fulva var. pendulina*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Åtgärdsprogram för hotade åkergräs	*Arnoseris minima*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för asp	*Aspius aspius*	Yes	Yes	No	No	No	No	No	No	No	No	Yes
Åtgärdsprogram för flodkräfta	*Astacus astacus*	No	Yes	No	No	Yes	Yes	Yes	No	Yes	Yes	No
Åtgärdsprogram för smällvedel	*Astragalus penduliflorus*	No	Yes	Yes	Yes	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för hotade insikter på krisslor	*Atralata albofascialis*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för hotade åkergräs	*Avena strigosa*	Yes	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för trollduvemätare	*Baptria tibiale*	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för barbastell	*Barbastellus barbastellus*	No	Yes	Yes	No	No	No	No	Yes	No	No	Yes
Åtgärdsprogram för vildbin på ängsmark	*Biastes truncatus*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för brandinsikter i boreal skog	*Biphyllus lunatus*	No	No	Yes	Yes	Yes	No	No	No	No	No	No
Åtgärdsprogram för svampar i kalkrika ädellövbärande fodermarker	*Boletus satanas*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för skalbaggar på nyligen död tall	*Boros schneideri*	Yes	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för skalbaggar på äldre död tallved	*Bothrideres contractus*	No	No	No	No	Yes	No	No	No	No	No	No
Åtgärdsprogram för låsbräknar i hävdade marker	*Botrychium boreale*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för låsbräknar i hävdade marker	*Botrychium lanceolatum*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för låsbräknar i hävdade marker	*Botrychium matricariifolium*	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för dvärglåsbräken	*Botrychium simplex*	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	Yes

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Åtgärdsprogram för hotade åkergräs	*Bromus arvensis*	No	Yes	Yes	No	No	No	No	Yes	No	No	No
Åtgärdsprogram för hotade åkergräs	*Bromus secalinus*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för brynia	*Bryhnia scabrida*	No	Yes	Yes	No	Yes	No	No	Yes	Yes	No	Yes
Åtgärdsprogram för glanstagel	*Bryoria nitidula*	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för långt broktagel	*Bryoria tenuis*	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för strandpadda	*Bufo calamita*	Yes	Yes	Yes	No	No	Yes	Yes	Yes	No	Yes	Yes
Åtgärdsprogram för grönfläckig padda	*Bufo viridis*	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	No	Yes	Yes
Åtgärdsprogram för skalbaggar på äldre död tallved	*Buprestis novemmaculata*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för sydlig kärrsnäppa	*Calidris alpina schinzii*	No	Yes	Yes	Yes	No	Yes	Yes	Yes	No	Yes	Yes
Åtgärdsprogram för skalbaggar på äldre död tallved	*Calitys scabra*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för hotade lavar på kulturved i odlingslandskap	*Caloplaca furfuracea*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Åtgärdsprogram för hotade åkergräs	*Camelina alyssum*	Yes	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för hotade åkergräs	*Camelina microcarpa*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för hotade åkergräs	*Camelina sativa*	Yes	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för spindelörtskinnbagge	*Canthophorus impressus*	No	Yes	Yes	Yes	No	Yes	No	Yes	No	Yes	Yes
Åtgärdsprogram för skalbaggar på nyligen död tall	*Carphoborus cholodkovskyi*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för hotade insikter på krisslor	*Cassida ferruginea*	Yes	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för hotade insikter på krisslor	*Cassida murraea*	Yes	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för större ekbock	*Cerambyx cerdo*	Yes	Yes	Yes	Yes	No	Yes	No	Yes	No	Yes	Yes
Åtgärdsprogram för långhorningar i hassel och klen ek	*Cerambyx scopolii*	No	No	No	No	No	Yes	No	No	No	Yes	No

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Åtgärdsprogram för svartoxe	*Ceruchus chrysomelinus*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för skalbaggar på nyligen död tall	*Cerylon impressum*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för jätteköldlav	*Cetrelia olivetorum*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Åtgärdsprogram för jätteprakt-bagge	*Chalcophora mariana*	No	No	Yes	No	No	Yes	No	No	No	Yes	Yes
Åtgärdsprogram för sällsynta kransalger längs kusten	*Chara braunii*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Kunskaps-uppbyggande program - 15 hotade makrofyt-arter i perman-enta vatten	*Chara braunii*	No	No	No	No	No	No	No	No	No	No	No
Kunskaps-uppbyggande program - 15 hotade makrofyt-arter i perman-enta vatten	*Chara filiformis*	Yes	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för sällsynta kransalger längs kusten	*Chara horrida*	No	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
Kunskaps-uppbyggande program - 15 hotade makrofyt-arter i perman-enta vatten	*Chara rudis*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för hotade vadare på strandängar	*Charadrius alexandrinus*	Yes	No	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för steklar, myrlejonsländor och spindlar i sanddyner	*Cheiracan-thium pennyi*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för stinkmålla	*Chenopodium vulvaria*	No	Yes	No	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för nålginst, tysk ginst och ginst-levande fjärilar	*Chesias rufata*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för skalbaggar på skogslind [på gammal lind]	*Chlorophorus herbstii*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för strandsand-jägare	*Cicindela maritima*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för ängshök	*Circus pygargus*	No	Yes	Yes	No	No	No	No	Yes	No	No	Yes
Åtgärdsprogram för rikkärr	*Cochlicopa nitens*	Yes	Yes	No	No	Yes	No	Yes	No	Yes	Yes	No

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Åtgärdsprogram för stortapetserarbi, storkägelbi och Thomsonkägelbi	*Coelioxys conoidea*	Yes	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för stortapetserarbi, storkägelbi och Thomsonkägelbi	*Coelioxys obtusispina*	Yes	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för hotade insikter på krisslor	*Coleophora conyzae*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för nålginst, tysk ginst och ginstlevande fjärilar	*Coleophora genistae*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Coleophora scrabida*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för hotade arter på asp i Norrland	*Collema curtisporum*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Conisania leineri*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för dynglevande skalbaggar	*Copris lunaris*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för svampar i kalkrika ädellövbärande fodermarker	*Corinarius odoratus*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för brandinsikter i boreal skog	*Corticaria planula*	Yes	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för skalbaggar på nyligen död tall	*Corticeus fraxini*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för skalbaggar på nyligen död tall	*Corticeus longulus*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för svampar i kalkrika ädellövbärande fodermarker	*Cortinarius suaveolens*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för skalbaggar på äldre död tallved	*Cryptophagus lysholmi*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för skalbaggar på gammal asp	*Cucujus cinnaberinus*	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för hotade åkergräs	*Cuscuta epilinum*	Yes	Yes	No	No	No	No	No	No	No	No	No

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Åtgärdsprogram för hotade lavar på kulturved i odlingslandskap	*Cyphelium notarisii*	No	Yes	Yes	No	Yes	No	No	Yes	Yes	No	No
Åtgärdsprogram för hotade lavar på kulturved i odlingslandskap	*Cyphelium trachylioides*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för vitryggig hackspett	*Dendrocopos leucotos*	No	Yes	Yes	No	No	Yes	Yes	Yes	No	Yes	Yes
Åtgärdsprogram för sex hotade bokskogsarter	*Denticollis rubens*	Yes	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för gotlands-säfferotplattmal	*Depressaria nemolella*	Yes	Yes	No	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för barkkvast-mossa	*Dicranum viride*	No	Yes	No	Yes	Yes	No	No	Yes	Yes	No	Yes
Åtgärdsprogram för hotade in-sikter på krisslor	*Digitivalva valeriella*	Yes	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för skalbaggar på skogslind [på gammal lind]	*Diplocoelus fagi*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för skorpdagglav	*Diploicia canescens*	No	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för orangefläckig brunbagge	*Dircaea australis*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för stäppartade torrängar i Väst-sverige	*Draco-cephalum ruyschiana*	No	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för skalbaggar på skogslind [på gammal lind]	*Dromaeolus barnabita*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Dufourea halictula*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för vildbin på ängsmark	*Dufourea inermis*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för fönster-spinnare (lav-dagsvärmare)	*Dysauxes ancilla*	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för skaftslam-krypa	*Elatine hexandra*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Åtgärdsprogram för kornsparv	*Emberiza calandra*	Yes	No	No	Yes	No	No	No	Yes	No	No	Yes
Åtgärdsprogram för ortolansparv	*Emberiza hortulana*	Yes	No	Yes	No	No	Yes	No	Yes	No	Yes	Yes
Åtgärdsprogram för dynglevande skalbaggar	*Emus hirtus*	No	Yes	No	No	Yes	No	No	No	Yes	No	No

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Åtgärdsprogram för skalbaggar på skogslind [på gammal lind]	*Enicmus brevicornis*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för skalbaggar på skogslind [på gammal lind]	*Ennearthron pruinosulum*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för svampar i ängs-och betes-marker	*Entoloma bloxamii*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Åtgärdsprogram för nyckelpige-spindel	*Eresus sandaliatus*	Yes	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för martorn	*Eryngium maritimum*	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes	Yes
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Eublemma minutata*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för hotade åker-gräs	*Euphorbia exigua*	No	Yes	Yes	No	No	No	No	Yes	No	No	No
Åtgärdsprogram för finnögontröst	*Euphrasia rostkoviana ssp. fennica*	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No
Åtgärdsprogram för stor ögontröst	*Euphrasia rostkoviana ssp. rost-koviana*	No	Yes	No	Yes	Yes	No	No	Yes	Yes	No	Yes
Åtgärdsprogram för svensk ögon-tröst	*Euphrasia stricta var. Suecica*	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för asknätsfjäril	*Euphydras maturna*	Yes	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	Yes
Åtgärdsprogram för väddnätfjäril	*Euphydryas aurinia*	No	Yes	Yes	No	Yes	No	No	Yes	Yes	No	Yes
Åtgärdsprogram för väddnätfjäril	*Eurhodope rosella*	Yes	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Åtgärdsprogram för steklar, myrlejonsländor och spindlar i sanddyner	*Euroleon nostras*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för långhorningar i hassel och klen ek	*Exocentrus adspersus*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för hotade åker-gräs	*Galium spurium ssp. Spurium*	Yes	Yes	Yes	No	No	No	No	Yes	No	No	No
Åtgärdsprogram för nålginst, tysk ginst och ginst-levande fjärilar	*Genista anglica*	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No
Åtgärdsprogram för nålginst, tysk ginst och ginst-levande fjärilar	*Genista germanica*	Yes	No	No	No	Yes	No	No	No	Yes	No	Yes

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Åtgärdsprogram för alkonblåvinge och klock-gentiana	*Gentiana pneumonanthe*	No	No	No	No	Yes	No	No	No	No	No	Yes
Åtgärdsprogram för fältgentianor i naturliga foder-marker	*Gentianella campestris ssp. Baltica*	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
Åtgärdsprogram för fältgentianor i naturliga foder-marker	*Gentianella campestris ssp. Campest-ris*	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
Åtgärdsprogram för fältgentianor i naturliga foder-marker	*Gentianella campestris ssp. Islandica*	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No
Åtgärdsprogram för sumpjord-tunga	*Geoglossum uliginosum*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för skalbaggar i eklågor	*Gnorimus variabilis*	No	Yes	No	Yes	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för violgubbe	*Gomphus clavatus*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	Yes
Åtgärdsprogram för brunkulla	*Gymnadenia nigra*	Yes	Yes	Yes	Yes	No	No	No	Yes	No	No	Yes
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Halictus leucaheneus*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för vildbin på ängsmark	*Halictus quadricinctus*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för hotade frö-löpare	*Harpalus autumnalis*	Yes	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för hotade frö-löpare	*Harpalus flavescens*	Yes	No	Yes	No	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för hotade frö-löpare	*Harpalus hirtipes*	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för dynglevande skalbaggar	*Heptaulacus sus*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för sex hotade bokskogsarter	*Hericium erinaceus*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för elfenbenslav	*Heterodermia speciosa*	No	Yes	Yes	No	Yes	No	No	Yes	Yes	No	Yes
Åtgärdsprogram för skirmossa	*Hookeria lucens*	No	Yes	Yes	Yes	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för brandinsikter i boreal skog	*Hormopeza obliterata*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för temporära sötvatten med fokus på organismer i naturbetes-makren, höllkar och allvarmiljöer	*Hydaticus continentalis*	No	No	No	No	No	No	No	No	No	No	No

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Åtgärdsprogram för skräntärna	*Hydroprogne caspia*	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för svampar i ängs-och betes-marker	*Hygrocybe aurantio-splendens*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för svampar i ängs-och betes-marker	*Hygrocybe splendidissima*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för hotade åker-gräs	*Hypericum humifusum*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för gulfläckig igelkottspinnare	*Hyphoraia aulica*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Åtgärdsprogram för hotade åker-gräs	*Hypochoeris glabra*	No	Yes	Yes	No	No	No	No	Yes	No	No	No
Åtgärdsprogram för skalbaggar på nyligen död tall	*Ips sexdentatus*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för sex hotade bokskogsarter	*Ischnomera sanguinicollis*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för svarttåg	*Jucus anceps*	Yes	Yes	No	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för hotade åker-gräs	*Kickxia elatine*	No	Yes	Yes	No	No	No	No	Yes	No	No	No
Åtgärdsprogram för sandödla	*Lacerta agilis*	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för skalbaggar på skogslind [på gammal lind]	*Laemophloeus monilis*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för flodnejonöga	*Lampetra fluviatilis*	No	Yes	No	No	No	No	No	No	No	No	Yes
Åtgärdsprogram för sällsynta kransalger längs kusten	*Lamprot-hamnium papulosum*	Yes	Yes	No	Yes	No	Yes	No	Yes	No	Yes	Yes
Åtgärdsprogram för skalbaggar på gammal asp	*Leiopus punctulatus*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för temporära sötvatten med fokus på organismer i naturbetes-makren, höllkar och allvarmiljöer	*Lepidurus apus*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för strandskinn-lav	*Leptogium rivulare*	No	Yes	No	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för björklevande vedskalbaggar i Norrland	*Leptura nigripes*	Yes	No	No	No	No	No	No	No	No	No	No

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Åtgärdsprogram för temporära sötvatten med fokus på organismer i naturbetes-makren, höllkar och allvarmiljöer	*Limnadia lenticularis*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för hotade vadare på strandängar	*Limosa limosa*	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för rikkärr	*Liparis loeselii*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för hårig skrovel-lav	*Lobaria hallii*	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för hotade åker-gräs	*Lolium remotum*	Yes	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för hotade åker-gräs	*Lolium temulentum*	Yes	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för dårgräsfjäril	*Lopinga achine*	No	Yes	No	Yes	Yes	No	No	Yes	Yes	No	Yes
Åtgärdsprogram för flytsvalting	*Luronium natans*	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för utter	*Lutra lutra*	No	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes
Åtgärdsprogram för violett guld-vinge	*Lycaena helle*	No	Yes	Yes	Yes	No	Yes	Yes	Yes	No	Yes	Yes
Åtgärdsprogram för slöjröksvamp	*Lycoperdon mammiforme*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för spansk fluga	*Lytta vesicatoria*	No	Yes	No	No	No	Yes	No	No	No	Yes	Yes
Åtgärdsprogram för alkonblåvinge och klock-gentiana	*Maculinea alcon*	No	Yes	No	No	No	No	No	No	No	No	Yes
Åtgärdsprogram för svartfläckig blåvinge	*Maculinea arion*	No	No	No	No	No	Yes	No	No	No	Yes	Yes
Åtgärdsprogram för flodpärl-mussla	*Margaritifera margaritifera*	Yes	Yes	Yes	No	Yes	No	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för stortapets-erarbi, stor-kägelbi och Thomsonkägelbi	*Megachile lagopoda*	Yes	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för björklevande vedskalbaggar i Norrland	*Melandrya dubia*	Yes	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för veronikanät-fjäril	*Melitaea britomartis*	Yes	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för vildbin på ängsmark	*Melitta melanura*	No	Yes	No	No	No	Yes	No	No	No	Yes	No

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Åtgärdsprogram för vildbin och småfjärilar på torräng	*Melitta tricincta*	Yes	Yes	No	No	No	Yes	No	No	No	Yes	Yes
Åtgärdsprogram för korthalsad majbagge	*Meloe brevicollis*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för ostronört	*Mertensia maritima*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	Yes
Åtgärdsprogram för skalbaggar på skogslind [på gammal lind]	*Mesosa curculionoides*	Yes	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för långhorningar i hassel och klen ek	*Mesosa nebulosa*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för sandnörel	*Minuartia viscosa*	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för nålginst, tysk ginst och ginstlevande fjärilar	*Mirificarma lentiginosella*	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No
Åtgärdsprogram för hotade åkergräs	*Misopates orontium*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för klådris	*Myricaria germanica*	No	Yes	Yes	Yes	No	Yes	No	Yes	No	Yes	Yes
Åtgärdsprogram för väddnätfjäril	*Nemophora cupriacella*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för väddnätfjäril	*Nemophora minimella*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för hotade åkergräs	*Neslia paniculata*	No	Yes	Yes	No	No	No	No	Yes	No	No	No
Kunskapsuppbyggande program - 15 hotade makrofytarter i permanenta vatten	*Nitella confervacea*	No	Yes	No	No	No	No	No	No	No	No	No
Kunskapsuppbyggande program - 15 hotade makrofytarter i permanenta vatten	*Nitella gracilis*	No	Yes	No	No	No	No	No	No	No	No	No
Kunskapsuppbyggande program - 15 hotade makrofytarter i permanenta vatten	*Nitella mucronata*	No	Yes	No	No	No	No	No	No	No	No	No
Kunskapsuppbyggande program - 15 hotade makrofytarter i permanenta vatten	*Nitella syncarpa*	No	No	No	No	No	No	No	No	No	No	No

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Kunskaps-uppbyggande program - 15 hotade makrofyt-arter i perman-enta vatten	*Nitella translucens*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Kunskaps-uppbyggande program - 15 hotade makrofyt-arter i perman-enta vatten	*Nitellopsis obtusa*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för fågelfots-mossa	*Nogopterium gracile*	Yes	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för vildbin på ängsmark	*Nomada argentata*	No	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för vildbin på ängsmark	*Nomada armata*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Åtgärdsprogram för vildbin på ängsmark	*Nomada facilis*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Nomada fuscicornis*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för vildbin på ängsmark	*Nomada integra*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Nomada similis*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Nomada stigma*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för långhorningar i hassel och klen ek	*Oberea linearis*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för hotade in-sikter på krisslor	*Oidaema-tophorus vafradactylus*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för dynglevande skalbaggar	*Onthophagus illyricus*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för skalbaggar på nyligen död tall	*Orthotomicus longicollis*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för havsmurarbi	*Osmia maritima*	Yes	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för läderbagge	*Osmoderma eremita*	No	Yes	No	No	Yes	Yes	Yes	No	Yes	Yes	No
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Panurgus banksianus*	No	Yes	No	No	No	Yes	No	No	No	Yes	No

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Åtgärdsprogram för mnemosyne-fjäril	*Parnassiua mnemosyne*	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för skalbaggar på äldre död tallved	*Pedostrangalia pubescens*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för almblombock	*Pedostrangalia revestita*	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	Yes
Åtgärdsprogram för lökgroda	*Pelobates fuscus*	No	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för gölgroda	*Pelophylax lessonae*	Yes	Yes	No	No	Yes	Yes	Yes	No	Yes	Yes	Yes
Åtgärdsprogram för sex hotade bokskogsarter	*Pertusaria velata*	No	Yes	Yes	Yes	No	No	No	Yes	No	No	No
Åtgärdsprogram för havsnejonöga	*Petromyzon marinus*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	Yes
Åtgärdsprogram för hotade vadare på strandängar	*Philomachus pugnax*	No	No	Yes	No	Yes	Yes	Yes	No	No	Yes	No
Åtgärdsprogram för tumlare	*Phocoena phocoeana*	Yes	No	No	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för nålginst, tysk ginst och ginst-levande fjärilar	*Phyllonorycter staintoniella*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för långhorningar i hassel och klen ek	*Phymatodes pusillus*	Yes	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för gullrisbock	*Phytoecia nigricornis*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Åtgärdsprogram för hotade insikter på krisslor	*Pilemostoma fastuosa*	Yes	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för bredbandad ekbarkbock	*Plagionotus detritus*	No	No	No	No	Yes	No	No	No	No	No	No
Åtgärdsprogram fär Älvängs-löpare	*Platynus longiventris*	Yes	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för skalbaggar på nyligen död tall	*Platysoma lineare*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för steklar, myr-lejonsländor och spindlar i sanddyner	*Podalonia luffii*	No	No	No	No	No	Yes	No	No	No	Yes	No
Kunskaps-uppbyggande program - 15 hotade makrofyt-arter i perman-enta vatten	*Potamgeton friesii*	No	Yes	No	No	No	No	No	No	No	No	No

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Kunskaps-uppbyggande program - 15 hotade makrofyt-arter i perman-enta vatten	*Potamogeton acutifolius*	No	No	No	No	No	No	No	No	No	No	No
Kunskaps-uppbyggande program - 15 hotade makrofyt-arter i perman-enta vatten	*Potamogeton compressus*	No	No	No	No	No	No	No	No	No	No	No
Kunskaps-uppbyggande program - 15 hotade makrofyt-arter i perman-enta vatten	*Potamogeton rutilus*	No	No	No	No	No	No	No	No	No	No	No
Kunskaps-uppbyggande program - 15 hotade makrofyt-arter i perman-enta vatten	*Potamogeton trichoides*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för nålginst, tysk ginst och ginst-levande fjärilar	*Prolita solu-tella*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för skalbaggar i eklågor	*Prostomis mandibularis*	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för stäppspol-vivel	*Pseudo-cleonus grammicus*	Yes	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för skalbaggar på skogslind [på gammal lind]	*Pseudoptilinus fissicollis*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för vityxne i södra Sverige	*Pseudorchis albida ssp. albida*	No	Yes	Yes	No	No	Yes	Yes	Yes	No	Yes	Yes
Åtgärdsprogram för nålginst, tysk ginst och ginst-levande fjärilar	*Pseudoterpna pruinata*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för trumgräs-hoppa	*Psophus stridulus*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	Yes
Åtgärdsprogram för stäppartade torrängar i Väst-sverige	*Pulmonaria angustifolia*	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för nipsippa och gotlandsippa	*Pulsatilla patens*	Yes	No	Yes	No	No	Yes	No	Yes	No	Yes	Yes
Åtgärdsprogram för mosippa	*Pulsatilla vernalis*	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för nipsippa och gotlandsippa	*Pulsatilla vulgaris gotlandica*	Yes	No	No	Yes	No	Yes	No	Yes	No	Yes	Yes
Åtgärdsprogram för större bark-plattbagge	*Pytho kolwensis*	No	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes

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Åtgärdsprogram för jordstjärns-tryffel	*Radiigera flexuosa*	Yes	Yes	No	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för stäppfinger-svamp	*Ramaria roellinii*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för långbens-groda	*Rana dalmatina*	Yes	Yes	Yes	No	No	Yes	Yes	Yes	No	Yes	Yes
Åtgärdsprogram för hotade åker-gräs	*Ranunculus arvensis*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för murgröns-möja	*Ranunculus hederaceus*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	Yes
Åtgärdsprogram för gotlands-ranunkel	*Ranunculus ophioglossi-folius*	No	Yes	No	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för hotade åker-gräs	*Rhinanthus serotinus ssp apterus*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för långhorningar i hassel och klen ek	*Ropalopus femoratus*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för rödlistade fjälltaggsvampar	*Sárcodon fénnicus*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för rödlistade fjälltaggsvampar	*Sárcodon fuligíneoviolá-ceus*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för rödlistade fjälltaggsvampar	*Sárcodon gláucopus*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för rödlistade fjälltaggsvampar	*Sárcodon joiídes*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för rödlistade fjälltaggsvampar	*Sárcodon lépidus*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för rödlistade fjälltaggsvampar	*Sárcodon léucopus*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för rödlistade fjälltaggsvampar	*Sárcodon lundéllii*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för rödlistade fjälltaggsvampar	*Sárcodon martioflávus*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för rödlistade fjälltaggsvampar	*Sárcodon scabrósus*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för rödlistade fjälltaggsvampar	*Sárcodon versipéllis*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för bombmurkla	*Sarcosoma globosum*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för hällebräcka	*Saxifraga osloënsis*	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för hotade åker-gräs	*Scandix pecten-veneris*	No	No	No	No	No	No	No	No	No	No	No

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Åtgärdsprogram för sällsynta skapanior på tidvis översvämmad ved	*Scapania apiculata*	No	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för sällsynta skapanior på tidvis översvämmad ved	*Scapania carinthiaca*	No	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för sällsynta skapanior på tidvis översvämmad ved	*Scapania glaucocephala*	No	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	No
Åtgärdsprogram för fetörtsblåvinge	*Scolitantides orion*	No	Yes	Yes	No	No	No	No	Yes	No	No	Yes
Åtgärdsprogram för hotade insikter på krisslor	*Scopula virgulata*	Yes	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för nålginst, tysk ginst och ginstlevande fjärilar	*Scotopteryx luridata*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för nålginst, tysk ginst och ginstlevande fjärilar	*Scotopteryx mucronata*	No	Yes	No	No	Yes	No	No	No	Yes	No	No
Åtgärdsprogram för nålginst, tysk ginst och ginstlevande fjärilar	*Scythris crypta*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för flikstånds	*Senecio erucifolius*	Yes	Yes	No	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Åtgärdsprogram för hotade åkergräs	*Sherardia arvensis*	No	Yes	Yes	No	No	No	No	Yes	No	No	No
Åtgärdsprogram för mal	*Siluris glanis*	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Åtgärdsprogram för hotade åkergräs	*Spergula arvensis var. Maxima*	Yes	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för vildbin och småfjärilar på torräng	*Sphecodes cristatus*	No	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för steklar, myrlejonsländor och spindlar i sanddyner	*Sphex funerarius*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för hotade lavar på kulturved i odlingslandskap	*Sphinctrina anglica*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för hotade åkergräs	*Stachys arvensis*	No	Yes	Yes	No	No	No	No	Yes	No	No	No
Åtgärdsprogram för skärrande gräshoppa	*Stauroderus scalaris*	Yes	Yes	No	No	No	Yes	No	No	No	Yes	Yes

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Åtgärdsprogram för sex hotade bokskogsarter	*Stenagostus rhombeus*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för brandinsikter i boreal skog	*Stephanopachys linearis*	Yes	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för brandinsikter i boreal skog	*Stephanopachys substriatus*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för grynig påskrislav	*Stereocaulon incrustatum*	Yes	Yes	No	No	Yes	Yes	No	No	Yes	Yes	No
Åtgärdsprogram för ärrlavar	*Sticta fuligonosa*	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No
Åtgärdsprogram för ärrlavar	*Sticta limbata*	Yes	Yes	Yes	No	Yes	No	No	Yes	Yes	No	No
Åtgärdsprogram för ärrlavar	*Sticta sylvatica*	No	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No
Åtgärdsprogram för stäppartade torrängar i Västsverige	*Stipa pennata*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för skalbaggar på skogslind [på gammal lind]	*Synchita separanda*	No	No	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för nålginst, tysk ginst och ginstlevande fjärilar	*Synvopacma suecicella*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för jämtlandsmaskros	*Taraxacum crocodes*	No	Yes	Yes	Yes	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för hotade insikter på krisslor	*Tebenna bjerkandrella*	Yes	Yes	No	No	No	Yes	No	No	No	Yes	No
Åtgärdsprogram för kärrnocka	*Tephroseris palustris*	Yes	Yes	No	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes
Kunskapsuppbyggande program - 15 hotade makrofytarter i permanenta vatten	*Tolypella canadensis*	No	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för skalbaggar på äldre död tallved	*Tragosoma depsarium*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för sienamusseron	*Tricholoma joachimii*	No	Yes	Yes	No	No	Yes	No	Yes	No	Yes	No
Åtgärdsprogram för temporära sötvatten med fokus på organismer i naturbetesmakren, höllkar och allvarmiljöer	*Triops cancriformis*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för bevarande av tjockskalig målarmussla	*Unio crassus*	No	Yes	No	No	Yes	Yes	No	No	Yes	Yes	Yes

Swedish title	Species	No. P	No. L/A	N_c Tot	N_c P	Lost	Con G	Gen S	N_e	PM	GM	Kobo
Åtgärdsprogram för björklevande vedskalbaggar i Norrland	*Upis ceramboides*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för rökpipsvamp	*Urnula craterium*	No	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	No
Åtgärdsprogram för hotade åkergräs	*Valerianella dentata*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för hotade åkergräs	*Veronica triphyllos*	No	No	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för rikkärr	*Vertigo geyeri*	No	Yes	Yes	No	No	No	No	Yes	No	No	No
Åtgärdsprogram för storviol	*Viola elatior*	No	Yes	Yes	Yes	No	No	No	Yes	No	No	No
Åtgärdsprogram för fjällräv	*Vulpes lagopus*	Yes	No	Yes	No	No	No	Yes	Yes	No	Yes	Yes
Åtgärdsprogram för hotade arter på asp i Norrland	*Xyletinus tremulicola*	No	Yes	Yes	No	No	No	No	Yes	No	No	No
Åtgärdsprogram för hotade arter på asp i Norrland	*Xylomya czekanovskii*	Yes	Yes	No	No	No	No	No	No	No	No	No
Åtgärdsprogram för ålgräsängar	*Zostera spp.*	No	No	No	No	No	Yes	Yes	No	No	Yes	No

Table A2.3 Additional information per species assessment about assessed number of (No.) populations and estimated number of populations with N_e above 500, the number of extinct populations and the global threat status (LC = Least Concern, VU = Vulnerable, NT = Near Threatened, EN = Endangered, DD = Data Deficient).

Species	Taxonomic group	No. extant pop.	No. pop. > 500	No. extinct pop.	Global Red List
Bombina bombina	amphibian	4	1	0	LC
Bufo bufo	amphibian	12	12	0	LC
Bufotes viridis	amphibian	13	0	2	LC
Epidalea calamita	amphibian	69	0	6	LC
Hyla arborea	amphibian	2	1	1	LC
Lissotriton vulgaris	amphibian	57	57	1	LC
Pelobates fuscus	amphibian	15	0	5	LC
Pelophylax esculentus	amphibian	2	1	3	not assessed
Pelophylax lessonae	amphibian	4	0	0	LC
Rana arvalis	amphibian	11	11	0	LC
Rana dalmatina	amphibian	8	3	0	LC
alternative assessment	amphibian	4	3	0	LC
Rana temporaria	amphibian	11	11	0	LC
Triturus cristatus	amphibian	150	15	1	LC
Alisma wahlenbergii	angiosperm	5	2	2	VU
Chenopodium vulvaria	angiosperm	3	0	2	not assessed
Eryngium maritimum	angiosperm	4	0	1	LC
Euphrasia officinalis officinalis	angiosperm	34	5	20	not assessed

Species	Taxonomic group	No. extant pop.	No. pop. > 500	No. extinct pop.	Global Red List
Euphrasia stricta suecica	angiosperm	10	3	20	not assessed
Genista germanica	angiosperm	1	0	12	LC
Gentiana pneumonanthe	angiosperm	200	20	0	LC
alternative assessment	angiosperm	200	0	0	LC
Gymnadenia nigra	angiosperm	75	0	25	EN
Jacobaea erucifolia	angiosperm	2	0	1	not assessed
Juncus anceps	angiosperm	3	0	1	not assessed
Luronium natans	angiosperm	4	1	2	LC
Mertensia maritima	angiosperm	6	0	2	not assessed
Myricaria germanica	angiosperm	13	1	7	not assessed
Pseudorchis albida	angiosperm	60	0	35	LC
Pulsatilla patens	angiosperm	5	5	1	DD
Pulsatilla vernalis	angiosperm	840	0	285	LC
Pulsatilla vulgaris gotlandica	angiosperm	4	1	0	VU
Ranunculus hederaceus	angiosperm	4	0	1	LC
Ranunculus ophioglossifolius	angiosperm	2	0	3	LC
Sabulina viscosa	angiosperm	1	0	49	not assessed
Saxifraga osloënsis	angiosperm	7	3	4	VU
Tephroseris palustris	angiosperm	1	0	3	not assessed
Anser erythropus	bird	1	0	1	VU
Anthus campestris	bird	1	0	4	LC
Calidris alpina schinzii	bird	8	0	0	LC
Charadrius alexandrinus	bird	0	NA	3	LC
Circus pygargus	bird	1	0	0	LC
Dendrocopos leucotos	bird	5	0	12	LC
Emberiza calandra	bird	2	0	0	LC
Emberiza hortulana	bird	2	0	1	LC
Ficedula albicollis	bird	1	1	0	LC
Hydroprogne caspia	bird	1	0	0	LC
alternative assessment	bird	7	0	6	LC
Limosa limosa	bird	7	0	0	NT
Brachythecium novae-angliae	bryophyte	20	0	3	LC
Dicranum viride	bryophyte	30	0	2	not assessed
Coregonus albula morphotype trybomi	fish	1	0	3	DD
Gadus morhua	fish	3	3	0	VU
Lampetra fluviatilis	fish	127	127	0	LC
Leuciscus aspius	fish	15	0	0	LC
Petromyzon marinus	fish	14	0	5	LC

Species	Taxonomic group	No. extant pop.	No. pop. > 500	No. extinct pop.	Global Red List
Salmo salar	fish	36	7	17	LC
Silurus glanis	fish	6	0	6	LC
Geastrum flexuosum	fungus	1	0	0	not assessed
Gomphus clavatus	fungus	284	0	116	not assessed
Agonopterix bipunctosa	invertebrate	6	0	3	not assessed
Anacampsis fuscella	invertebrate	13	NA	0	not assessed
Anthophora plagiata	invertebrate	2	0	5	LC
Baptria tibiale	invertebrate	3	0	2	not assessed
Canthophorus impressus	invertebrate	100	0	0	not assessed
Cerambyx cerdo	invertebrate	1	0	2	VU
Chalcophora mariana	invertebrate	2	0	6	not assessed
Depressaria nemolella	invertebrate	2	0	0	not assessed
Dysauxes ancilla	invertebrate	1	0	0	not assessed
Eresus sandaliatus	invertebrate	2	0	0	not assessed
Euphydryas aurinia	invertebrate	45	0	11	LC
Euphydryas maturna	invertebrate	2	0	4	DD
Harpalus autumnalis	invertebrate	1	0	0	not assessed
Harpalus flavescens	invertebrate	2	0	1	not assessed
Lopinga achine	invertebrate	2	2	0	not assessed
Lycaena helle	invertebrate	5	0	9	EN
Lytta vesicatoria	invertebrate	4	NA	2	not assessed
Margaritifera margaritifera	invertebrate	286	286	421	EN
Melitaea britomartis	invertebrate	2	0	8	NT
Melitta tricincta	invertebrate	7	1	2	NT
Parnassius mnemosyne	invertebrate	4	0	10	LC
Pedostrangalia revestita	invertebrate	25	0	16	VU
Phengaris alcon	invertebrate	50	0	0	not assessed
Phengaris arion	invertebrate	8	1	0	NT
Psophus stridulus	invertebrate	80	0	0	LC
Pytho kolwensis	invertebrate	14	0	4	DD
Scolitantides orion	invertebrate	5	0	3	LC
Stauroderus scalaris	invertebrate	10	2	6	LC
Unio crassus	invertebrate	20	2	55	EN
Alces alces	mammal	3	2	0	LC
Barbastella barbastellus	mammal	6	1	0	NT
alternative assessment	mammal	1	1	0	NT

Species	Taxonomic group	No. extant pop.	No. pop. > 500	No. extinct pop.	Global Red List
alternative assessment	mammal	6	0	0	NT
Canis lupus	mammal	1	0	0	LC
Capreolus capreolus	mammal	3	3	0	LC
Castor fiber	mammal	1	1	0	LC
Cervus elaphus elaphus	mammal	2	0	0	not assessed
Erinaceus europaeus	mammal	18	2	0	LC
alternative assessment	mammal	18	0	0	LC
Gulo gulo	mammal	1	0	0	LC
Halichoerus grypus	mammal	5	1	0	LC
alternative assessment	mammal	2	1	0	LC
Lepus timidus	mammal	6	3	0	LC
Lutra lutra	mammal	4	0	1	NT
Muscardinus avellanarius	mammal	12	12	1	LC
Myotis bechsteinii	mammal	2	0	0	NT
Phoca vitulina	mammal	5	1	0	LC
Phocoena phocoena	mammal	3	0	0	LC
Sicista betulina	mammal	3	3	0	LC
Sorex isodon	mammal	2	0	0	LC
Ursus arctos	mammal	3	0	0	LC
Vulpes lagopus	mammal	3	0	0	LC
Vulpes vulpes	mammal	2	2	0	LC
Botrychium simplex	pteridophyte	8	0	4	EN
Anguis fragilis	reptile	10	10	0	LC
Coronella austriaca	reptile	11	0	0	LC
alternative assessment	reptile	7	2	0	LC
Lacerta agilis	reptile	22	0	3	LC
Natrix natrix gotlandica	reptile	2	0	0	not assessed
Natrix natrix natrix	reptile	8	8	0	LC
Vipera berus	reptile	14	12	0	LC
Zootoca vivipara	reptile	13	13	0	LC
Bryoria nitidula	other	6	0	4	not assessed
Bryoria tenuis	other	38	0	5	not assessed
Heterodermia speciosa	other	10	0	5	not assessed
Lamprothamnium papulosum	other	2	0	0	not assessed
Leptogium rivulare	other	18	0	6	NT
Lobaria hallii	other	9	0	1	not assessed

Table A2.4 Average indicator value (± standard deviation) for range categories based on the species assessments of Table 5. The categories are defined in accordance with IUCN guidelines. Number of species in each category is given in parenthesis. Results for Kruskal-Wallis rank sum test; Ne500 indicator: chi-square = 35.8, df = 1, p-value < 0.005, PM indicator: chi-square = 10.9, df = 1, p-value < 0.005.

Species range	Ne500 indicator	PM indicator
Restricted range	0.06 ± 0.19	0.71 ± 0.29
	(68)	(71)
Wide ranging	0.45 ± 0.44	0.87 ± 0.20
	(47)	(47)

Table A2.5 Average indicator values (± standard deviation) for the different Red List categories (LC = Least Concern, VU = Vulnerable, NT = Near Threatened, EN = Endangered, DD = Data Deficient, RE = Regionally Extinct). Number of species in each category inparenthesis. Results for Kruskal-Wallis rank sum test; Ne500 indicator: chi-square = 55.1, df = 5, p-value < 0.005, PM indicator: chi-square = 31.1, df = 6, p-value < 0.005.

National Red List Category	PM indicator	Ne500 indicator
CR	0.61 ± 0.35	0.00 ± 0.00
	(17)	(16)
EN	0.68 ± 0.26	0.05 ± 0.17
	(40)	(39)
VU	0.85 ± 0.14	0.12 ± 0.27
	(15)	(15)
NT	0.89 ± 0.15	0.21 ± 0.33
	(20)	(20)
LC	0.94 ± 0.14	0.68 ± 0.40
	(26)	(26)
DD	0.25 ± *NA*	0.00 ± *NA*
	(1)	(1)
RE	0.00 ± *NA*	NaN ± *NA*
	(1)	(1)

Table A2.6 Pairwise comparisons of Ne500 indicator results from Table A2.5. Table shows p-values from Wilcoxon rank sum test with continuity correction (Bonferroni).

	CR	DD	EN	LC	NT
DD	-	-	-	-	-
EN	1.000	1.000	-	-	-
LC	< 0.005	1.000	< 0.005	-	-
NT	0.019	1.000	0.111	0.004	-
VU	0.456	1.000	1.000	0.001	1.000

Table A2.7 Pairwise comparisons of PM indicator results from Table A2.5. Table shows p-values from Wilcoxon rank sum test with continuity correction (Bonferroni).

	CR	DD	EN	LC	NT	RE
DD	1.000	-	-	-	-	-
EN	1.000	1.00	-	-	-	-
LC	0.015	0.984	< 0.005	-	-	-
NT	0.264	1.000	0.046	1.00	-	-
RE	1.00	1.000	1.000	0.984	1.000	-
VU	1.00	1.000	0.457	0.538	1.000	1.000

Table A2.8 Pairwise comparisons of Ne500 indicator results for different taxonomic groups. Table shows p-values from Wilcoxon rank sum test with continuity correction (Bonferroni). Kruskal-Wallis chi-square = 26.1, df = 10, p-value = 0.004. Amp = Amphibian, Ang = Angiosperm, Bryo = Bryophyte, Fun = Fungus, Inv = Invertebrate, Mam = Mammal, Oth = Other, Pte = Pteridophyte, Rep = Reptiles.

	Amp	Ang	Bird	Bryo	Fish	Fun	Inv	Mam	Oth	Pte
Ang	1.000									
Bird	0.71	1.000								
Bryo	1.000	1.000	1.000							
Fish	1.000	1.000	1.000	1.000						
Fun	1.000	1.000	1.000	1.000	1.000					
Inv	0.11	1.000	1.000	1.000	1.000	1.000				
Mam	1.000	1.000	1.000	1.000	1.000	1.000	0.62			
Oth	0.56	1.000	1.000	1.000	1.000	1.000	1.000	1.000		
Pte	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Rep	1.000	1.000	1.000	1.000	1.000	1.000	0.34	1.000	0.85	1.000

Table A2.9 Pairwise comparisons of PM indicator results for different taxonomic groups. Table shows p-values from Wilcoxon rank sum test with continuity correction (Bonferroni). Kruskal-Wallis chi-square = 37.98, df = 10, p-value < 0.005. Amp = Amphibian, Ang = Angiosperm, Bryo = Bryophyte, Fun = Fungus, Inv = Invertebrate, Mam = Mammal, Oth = Other, Pte = Pteridophyte, Rep = Reptiles.

	Amp	Ang	Bird	Bryo	Fish	Fun	Inv	Mam.	Oth	Pte
Ang	0.072									
Bird	1.000	1.000								
Bryo	1.000	1.000	1.000							
Fish	1.000	1.000	1.000	1.000						
Fun	1.000	1.000	1.000	1.000	1.000					
Inv	1.000	1.000	1.000	1.000	1.000	1.000				
Mam	0.381	1e-05	0.190	0.281	0.304	1.000	0.003			
Oth	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.016		
Pte	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.549	1.000	
Rep	1.000	0.022	1.000	1.000	1.000	1.000	0.586	1.000	1.000	1.000

Table A2.10 Results from Wilcoxon paired signed rank test for comparison of indicator values between Thurfjell et.al (2022) and this study (see section 4.5). V = sum of postive ranks.

	Ne500 indicator	PM indicator
Mammals	V = 3, p-value = 0.014	V = 31, p-value = 0.078
Amphibians	V = 3, p-value = 0.014	V = 10, p-value = 0.583
Reptiles	V = 0, p-value = 0.125	V = 1, p-value = 1.000
Total	V = 56.5, p-value = 0.014	V = 82, p-value = 0.065

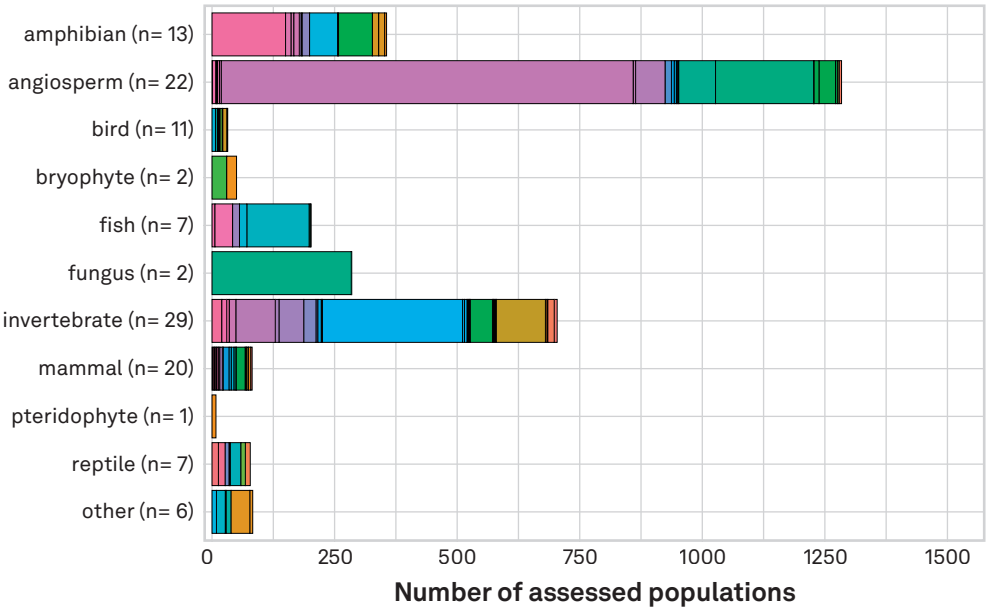


Figure A2.1 Number of populations assessed in total per taxonomic group, with each colour representing a separate species.

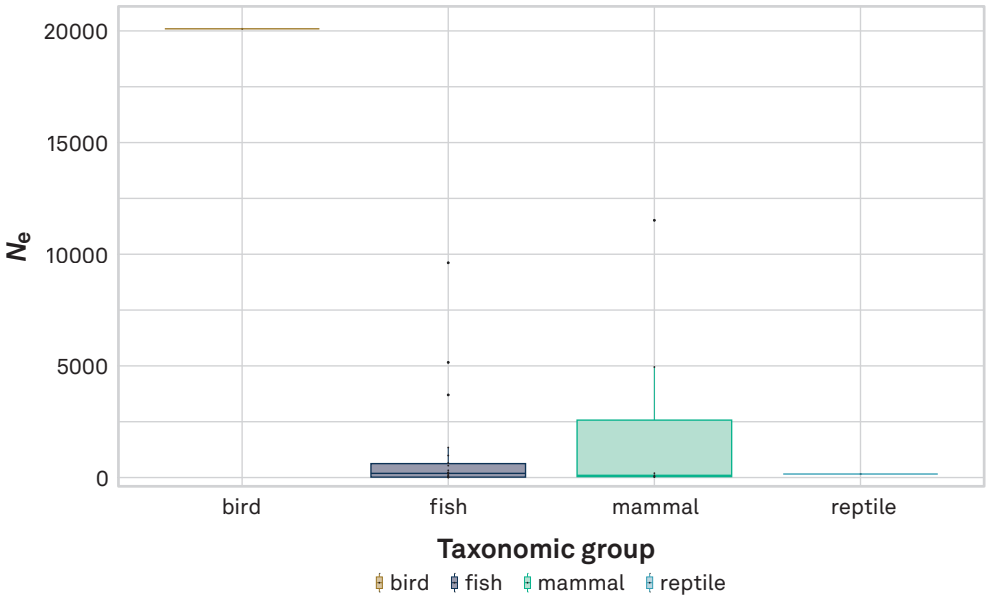


Figure A2.2 N_e estimates from DNA-based studies, presented for populations, per taxonomic group. Black lines indicate the median, and the boxes show first and third quartiles.

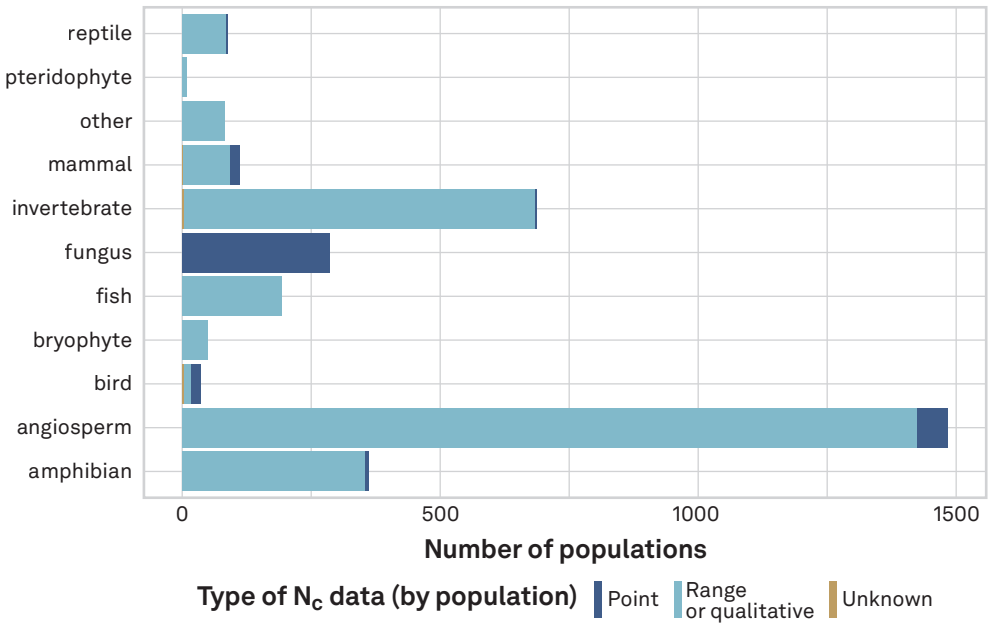


Figure A2.3 The type of N_c data available presented per population, in each taxonomic group.

Appendix 3: Detailed assessments for amphibian and reptile species in Sweden

The potential use of Red List data, the Swedish national biogeographic survey, citizen science data (primarily Artportalen), scientific articles and reports, and expert consultations for assessing genetic diversity indicators is illustrated here through detailed assessments of amphibian and reptile species in Sweden. The indicator assessments, for three indicators: the PM indicator, the Ne500 indicator, and the DNA-based monitoring, are presented below in alphabetical order by organism group and scientific name.

Amphibians

Bombina bombina, Fire-bellied toad (Klockgroda)

PM INDICATOR

Estimated number of current populations: 4
Estimated number of past populations (year 1978): 4
Proportion of populations maintained: 4/4 = 1

The fire-bellied toad had completely disappeared from Sweden by the 1960s but was later reintroduced in three areas in south Sweden (Scania/Skåne) using individuals from Denmark (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Stenberg and Nyström, 2010). There have also been illegal introductions around Mölle on the northwestern coast of Scania.

The extent of occurrence (EOO) is estimated at 3,900 km² (3,500 – 4,500 km²) and the area of occurrence (AOO) at 380 km² (350 – 400 km²; Thurfjell et al., 2020). The biogeographic survey identified 53 localities (Nyström et al., 2020).

For the assessment a dispersal radius of one km was used to estimate the connection between occurrences. The resulting clusters correspond to the four areas of re-introduction, from which the populations have grown (Figure A3.1). The largest cluster of occurrences is found around Baldringe in the central part of Scania (Skåne), which likely correspond to a single large metapopulation. Based on this we assess that there are four populations currently.

The Action Plan mentions an occurrence in Vårdgårda, east of Gothenburg (Stenberg and Nyström, 2010; not featured on the map), which is likely a result of

frogs that have been moved illegally, and this location is no longer occupied (Ekoll AB, pers.comm.). We have disregarded this occurrence in our assessment.

Ne500 INDICATOR

Populations with N_e above 500: 1
Proportion of populations with N_e above 500: 1/4 = 0.25

The Action Plan estimates the census at 10,000 individuals (Stenberg and Nyström, 2010). Most are found in Baldringe. Mölle probably has around 200 individuals and Stendala 100. Only three males were found in Bäckhalladalen 2009 (Stenberg and Nyström, 2010). The survey between 2013 – 2018 found 1,779 males, estimating the population at 2,600 (Nyström et al., 2020). In 2018 – 2021 they surveyed 20 localities and found 459 males (Ekdahl et al., unpublished). The Red List assessment estimates the population to 7,600 (2,400 – 10,000) (Thurfjell et al., 2020). The population has grown from 200 individuals, to 3,500, and to 7,500 since 1997 (Thurfjell et al., 2020). Based on this, we estimate that the population in central Scania (Baldringe) is above 5,000 reproductive individuals and the other three populations have less than 5,000 reproductive individuals.

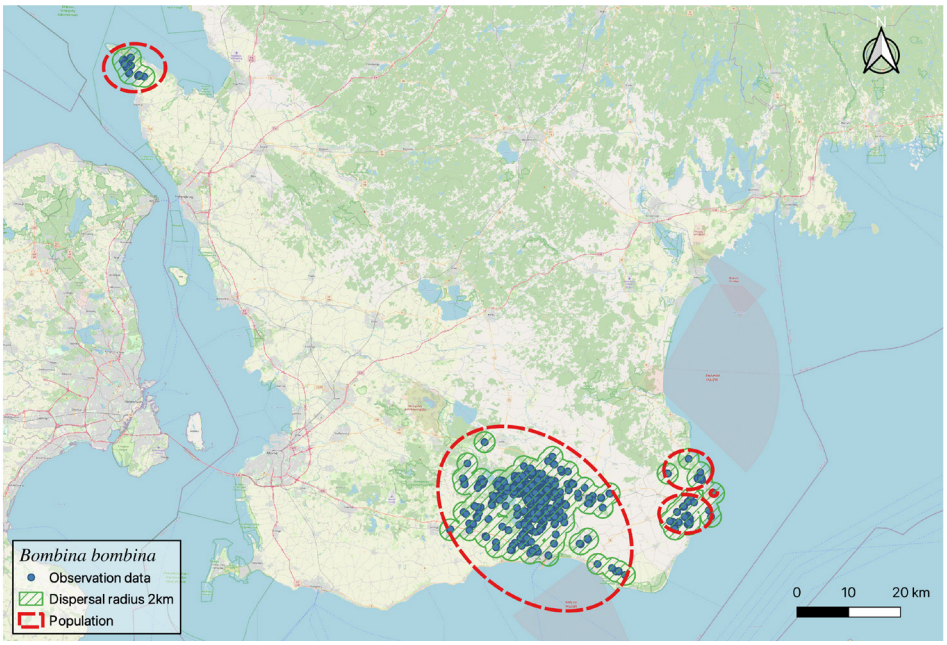


Figure A3.1 Assessment of fire-bellied toad (*Bombina bombina*) based on observation data from Artportalen 2000 – 2023.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: No

The reintroduction was made using individuals from four populations in Denmark. The population in Mölle is an illegal introduction with central European origin. Genetic studies show that the localities around Stendala and Bäckhalladalen

show a genetic profile consistent with the reintroductions, whilst the population around Baldringe is admixed with genes of Central European origin (Stenberg and Nyström, 2010). To our knowledge, there are no ongoing genetic monitoring efforts and we have not found any temporal studies on genetic diversity.

Bufo bufo, Common toad (Vanlig padda)

PM INDICATOR

Estimated number of current populations: 12
Estimated number of past populations (year 1978): 12
Proportion of populations maintained: 12/12 = 1

The common toad has a continuous distribution throughout all of Sweden (Cedhagen and Nilsson, 1978; Ahlén et al., 1995). The extent of occurrence is estimated at 545,000 km² (Thurfjell et al., 2020). Based on genetic clustering with at least four clusters (Thörn et al., 2021), we divided the distribution into several areas (Figure A3.2) as a proxy for populations, and counted the islands of Öland and Gotland as separate populations.

Ne500 INDICATOR

Populations with N_e above 500: 12
Proportion of populations with N_e above 500: 12/12 = 1

The common toad is widespread in Sweden, and we find it unlikely that population numbers are lower than 5,000 reproductive individuals in any of our defined clusters.

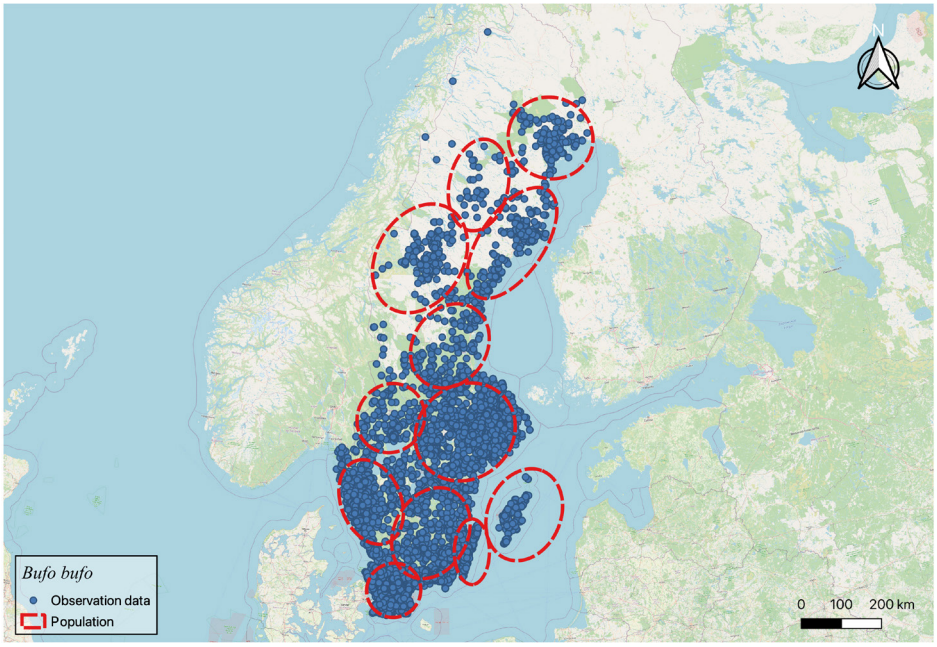


Figure A3.2 Estimated populations of common toad (*Bufo bufo*) based distribution and genetic studies (see text). Occurrence is based on observation data from Artportalen 2000 – 2023.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: Yes

Genetic studies show decreased variation toward northern latitudes. There is genetic structure with 4 – 5 clusters along a latitudinal gradient (Thörn et al., 2021; Cortázar-Chinarro, 2019; Cortázar-Chinarro et al., 2022). Monitoring of genetic diversity has been initiated by SEPA (Höglund, pers. comm.).

Bufo viridis, European green toad (Grönfläckig padda)

PM INDICATOR

Estimated number of current populations: 13
Estimated number of past populations (year 2000): 15
Proportion of populations maintained: 13/15 = 0.87

The Red List assessment estimates the number of areas to four, the extent of occurrence to 26,000 km² (20,000 – 28,000 km²) and the area of occurrence to 250 km² (230 – 280 km²; Thurfjell et al., 2020). The Action Plan lists six populations, larger ones at Limhamn, Eskilstorp and Utklippan, and smaller at Högaborg, Lernacken and Flommen (Wirén, 2010).

The biogeographic surveys between 2013 – 2018 identified 16 active localities in Scania (Skåne), Blekinge and on the island of Öland (Nyström et al., 2020). The survey between 2019 – 2021 identified five active localities in Scania and on Öland (Ekdahl et al., unpublished).

In addition to the six populations mentioned in the Action Plan we have counted localities with confirmed reproduction as established populations on Öland, in Norra hamnen (Malmö) and northwest Scania; we excluded localities that are considered extirpated based on expert opinion (Ekoll AB; Figures A3.3, A3.4). Based on older distribution maps, there is a loss of distribution (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995), but it is difficult to attribute losses to defined populations.

Ne500 INDICATOR

Populations with N_e above 500: 0
Proportion of populations with N_e above 500: 0/13 = 0

The national census is estimated to 3,000 (Thurfjell et al., 2020). The Action Plan estimates the total census to 1,200, with approximately 600 adults at Utklippan, 440 at Limhamn, 80 in Eskilstorp, 40 in Lernacken and less than 10 at Flommen and Högaborg (Wirén, 2010). The biogeographic survey between 2013 – 2018 estimated 630 adults based on their findings (Nyström et al., 2020), and between 2019 – 2021 399 adults were found during the surveys in Scania (Skåne), which included 16 adults at Eskilstorp, 19 at Flommen, 339 at Norra hamnen, nine at Klaghamnsudden, and one more unspecified locality (Ekdahl et al., unpublished). Based on this we have assessed all current populations as below 5,000 individuals.

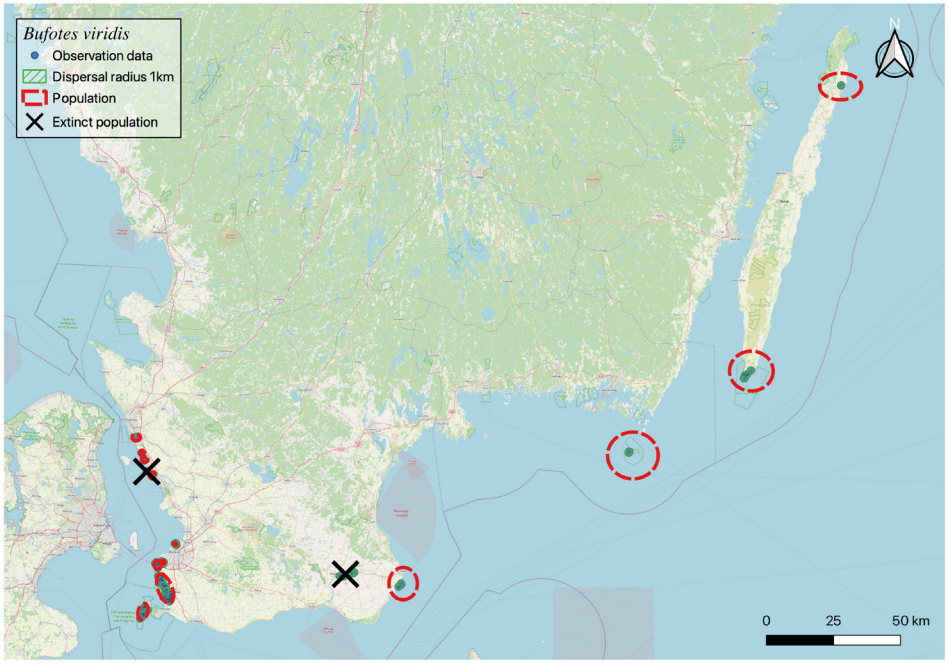


Figure A3.3 Distribution of green toad (*Bufo viridis*) based on observation data from Artportalen 2000 – 2023 and expert consultation. Red circles indicate current populations (13 in total).

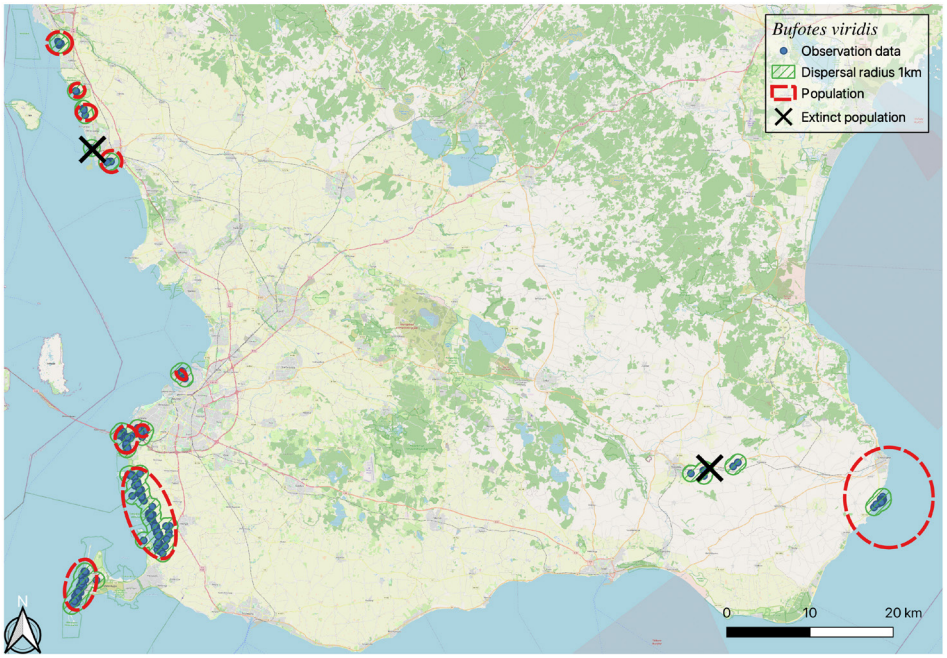


Figure A3.4 Distribution of green toad (*Bufo viridis*) in Scania (Skåne) based on observation data from Artportalen 2000 – 2023 and expert consultation. Red circles indicate the identified populations (9 featured in this figure).

DNA-BASED MONITORING INDICATOR
Genetic monitoring: Yes

Phylogeographic studies show that populations in Sweden share mitochondrial DNA with the closely related *B. sitibundus* in eastern Europe (Stöck et al., 2006). MHC variation and variation in microsatellite markers is lower in Swedish populations compared to continental Europe (Höglund et al., 2022). Monitoring of genetic diversity has been initiated by SEPA (Höglund, pers. comm.).

Epidalea calamita, Natterjack toad (Strandpadda)

PM INDICATOR
Estimated number of current populations: 69
Estimated number of past populations (year 2000): 75
Proportion of populations maintained: 69/75 = 0.92

The natterjack toad's distribution is divided in two areas, along the west coast and in the south of Sweden (Nyström et al., 2020), which is also indicated in older maps (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995). The extent of occurrence is estimated at 53,900 km² and the area of occurrence at 600 km² (500 – 650 km²; Thurfjell et al., 2020).

The biogeographic survey identifies 15 islands with reproducing populations in Västra Götaland and 62 localities in the southern distribution (Nyström et al., 2020).

The survey in 2019 – 2021 identified locations on seven islands in Västra Götaland, and 11 localities in Scania (Skåne), Blekinge, and Halland (Ekdahl et al., unpublished). The Action Plan identifies 60 populations in Västra Götaland, four in Halland, 40 in Scania and 16 in Blekinge (Pröjts, 2012).

Genetic studies indicate limited gene flow between the islands in Västra Götaland (Rogell et al., 2010). We have therefore counted islands as separate populations (Figure A3.5), which amounts to 53 populations in this area. The population boundaries in the southern distribution were estimated based on a potential dispersal of four km, and expert consultations (Ekoll AB; Jacob Höglund; Figures A3.5, A3.6). We estimated 69 populations in total.

Ne500 INDICATOR
Populations with N_e above 500: 0
Proportion of populations with N_e above 500: 0/69 = 0

The Red List assessment estimates the population to 2,550 (990 – 3,350) reproductive individuals (Thurfjell et al., 2020). Based on the findings from the biogeographic survey the populations in Västra Götaland is estimated at 1,700 reproductive individuals and the population in south of Sweden 160 reproductive individuals (Nyström et al., 2020). The Action Plan estimates the population sizes to 32,700 in Västra Götaland, 300 in Halland, 1,000 in Scania and 900 in Blekinge (Pröjts, 2012).

The entire census for Västra Götaland is large, at least in terms of the Action Plan, however, this is spread over several small metapopulations (islands). Therefore, we estimate that all current populations have census sizes below 5,000.

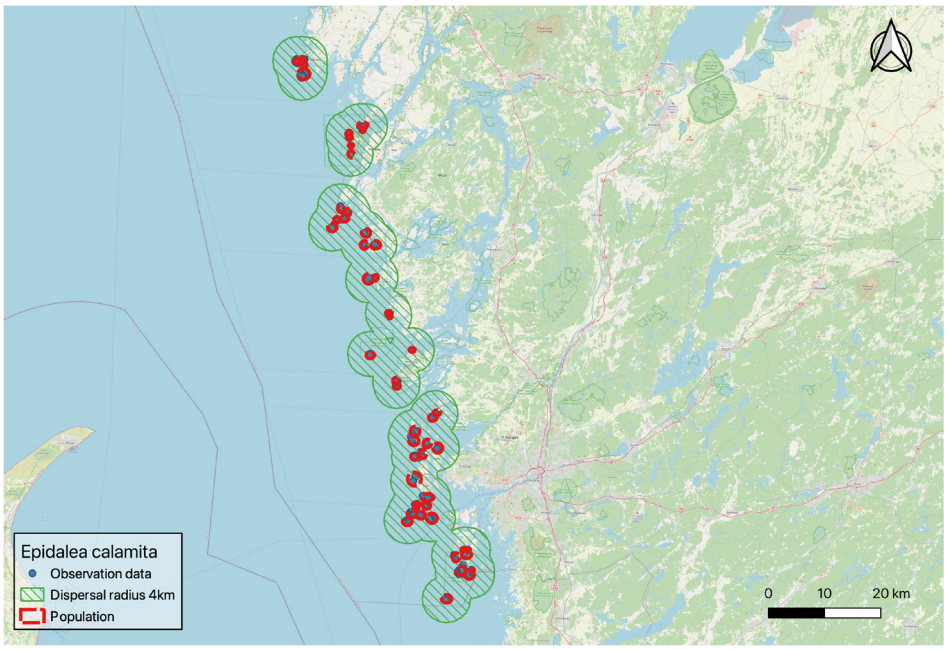


Figure A3.5 Distribution of natterjack toad (*Epidalea calamita*) in Västra Götaland, based on observation data from Artportalen 2000 – 2023. Populations are based on information from action plan, expert opinion, and genetic studies.

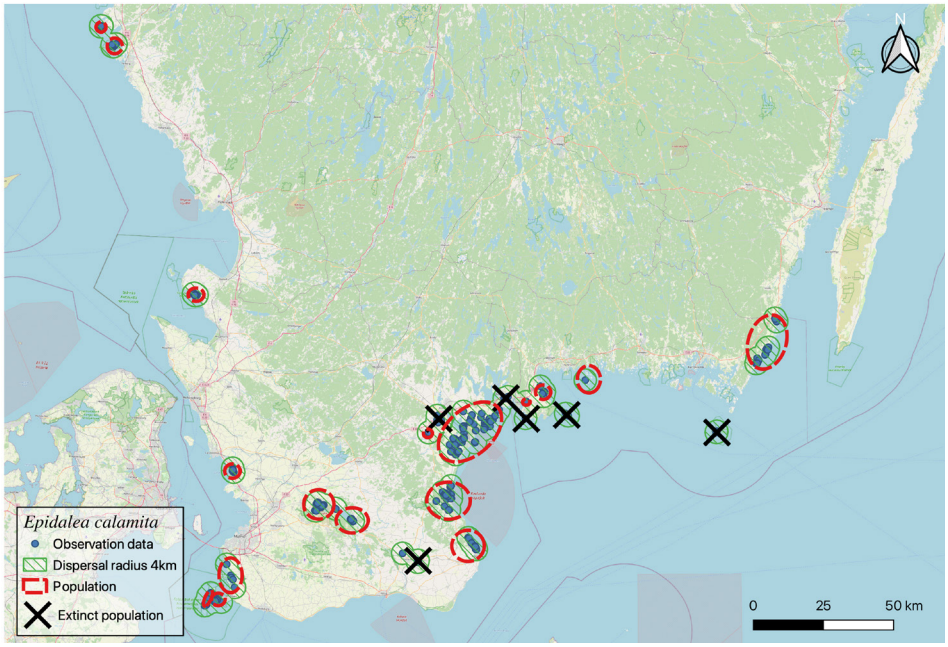


Figure A3.6 Distribution of natterjack toad (*Epidalea calamita*) in southern Sweden from observation data from Artportalen 2000 – 2023. Population structure is based on expert opinion and information from the biogeographic survey and action plan.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: Yes

The islands on the west coast do not show any isolation by distance (Höglund, pers. comm.), genetic variation is low, and there is genetic structure among islands (Rogell et al., 2010). Monitoring of genetic diversity has been initiated by SEPA (Höglund, pers. comm.).

Hyla arborea, European tree frog (Lövgroda)

PM INDICATOR

Estimated number of current populations: 2
Estimated number of past populations (year 1978): 3
Proportion of populations maintained: 2/3 = 0.67
Species decline: 30 %

The natural distribution is in Scania (Skåne; Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995), however there are illegal introductions in Halland and Blekinge (Nyström et al., 2020; Figure A3.7). The extent of occurrence is estimated at 2,900 km² (2,100 – 5,000 km²) and the area of occurrence as 1,100 km² (1,000 – 1,200 km²; Thurfjell et al., 2020). The Action Plan divides the distribution in Scania in two areas (Edenhamn and Sjögren-Gulve, 2001). The biogeographic survey between 2013 – 2018 identifies 52 main localities in the area with 88 supporting smaller localities (Nyström et al., 2020). The survey in 2019 – 2021 identified current occurrences in Halland but not in Blekinge (Ekdahl et al., unpublished). Seven new localities were identified in Scania (Ekdahl et al., unpublished). The earlier distribution includes Blekinge, however these findings are older and is therefore not included in this assessment.

Dispersal distance is 4 – 6 km, however it can extend up to 12 km. There is a more or less continuous distribution in east-central Scania with no apparent clustering. Based on a dispersal radius of four km, this area constitutes a single metapopulation. This is also indicated by demographic studies in the area (Edehamn et al., 2000) and confirmed by expert consultation (Ekoll AB). Occurrences in western Scania that could be considered as separate have disappeared, however, illegal introductions in Halland have resulted in a reproducing population (Ekoll AB, pers. comm.). We therefore estimate that there currently are two populations (Figure A3.7) and that one population has disappeared.

Ne500 INDICATOR

Populations with N_e above 500: 1
Proportion of populations with N_e above 500: 1/2 = 0.5

The Red List assessment estimates the number of reproductive individuals as 18,000 (16,000 – 25,000; Thurfjell et al., 2020). The estimated number of individuals in the Action Plan is 20,000 (Edenhamn and Sjögren-Gulve, 2001). Based on the geographic survey, the population is Scania is 18,000 (Nyström et al., 2020). The

population declined from 1,900 – 2,000 by approximately 30 %, but has since recovered and grown by approximately 70 % (Thurfjell et al., 2020). We assess that the census refers to the metapopulation in Scania, and that the population in Halland (illegally introduced) is smaller than 5,000 reproductive individuals.

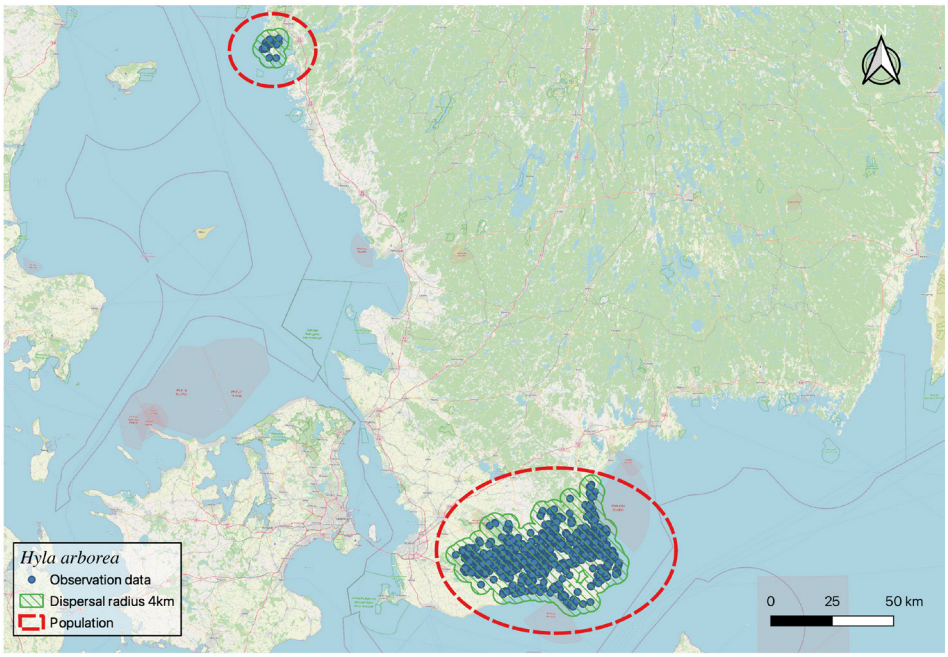


Figure A3.7 Distribution of tree frog (*Hyla arborea*), based on observation data from Artportalen 2000 – 2023, Red circles represent populations.

DNA-BASED MONITORING INDICATOR
Genetic monitoring: No

To our knowledge there are no ongoing monitoring efforts and no temporal studies on genetic diversity. We did not find any genetic studies that show population substructure, however allozyme variation among local populations across the distribution indicate isolation by distance (Edenhamn et al., 2000).

Lissotriton vulgaris, Smooth newt (Mindre vattensalamander)

PM INDICATOR
Estimated number of current populations: 57
Estimated number of past populations (year 1960): 58
Proportion of populations maintained: 57/58 = 0.98

The species is widely distributed in Sweden (Figure A3.8). The extent of occurrence is estimated to 460,000 km² (Thurfjell et al., 2020). There are no signs of decline. Older maps (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al.,

1995) split the distribution into two separate areas, indicating at least two populations. The smooth newt in northern Sweden was previously considered a separate sub-species, but this is no longer the case. Comparisons with the older distribution do not indicate any loss in range. There is one known location (Stensele, Lappland) that has disappeared.

When mapping the observation data along with a dispersal radius of one km the resulting clusters indicate more than 100 populations in Scania alone (Figure A3.9). However, this is likely due to lack of data rather than lack of occurrence. The number of locations is probably higher than indicated from the map, which would have resulted in fewer clusters. Since the dispersal between locations is estimated to be limited, we have subdivided the distribution into units using major roads as a guide and limiting the width of the area to 150 km. This yield 57 populations including Öland and Gotland (Figure A3.10).

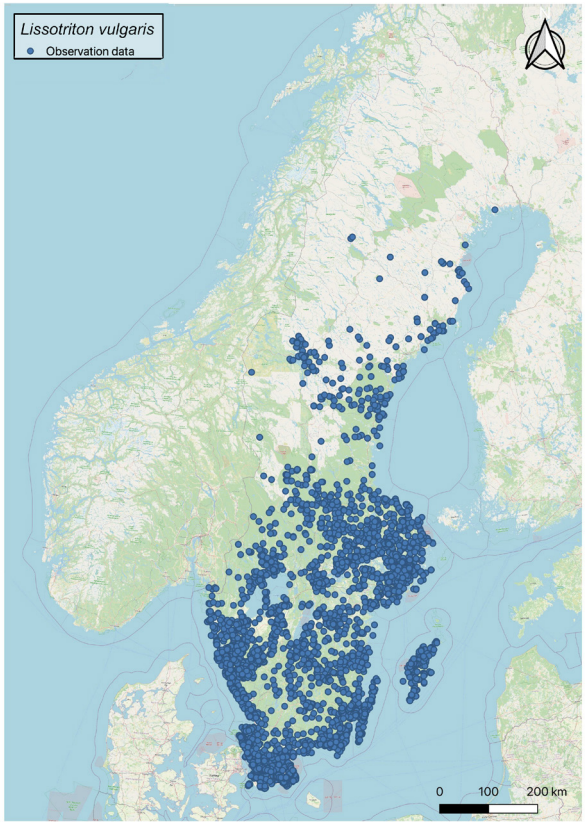


Figure A3.8 Distribution of smooth newt (*Lissotriton vulgaris*) based on observation data from Artportalen between 2000 – 2023.

Ne500 INDICATOR

Populations with N_e above 500: 57
Proportion of populations with N_e above 500: 57/57 = 1

There is no census available. However, we find it unlikely that population sizes are below 5,000.

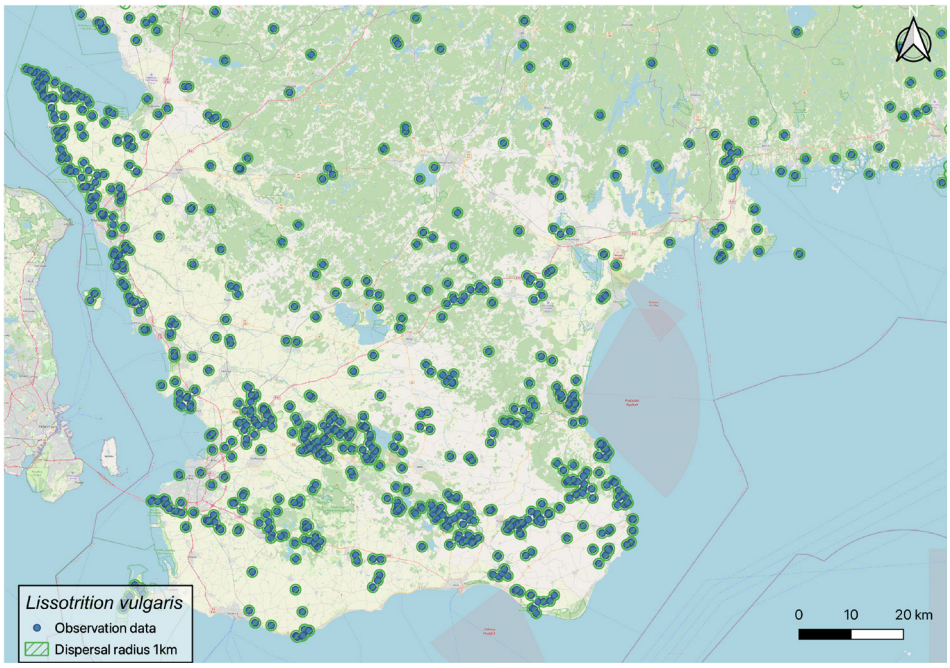


Figure A3.9 Observation data of smooth newt (*Lissotriton vulgaris*) from Artportalen 2000 – 2023 together with a one km dispersal radius yields over 100 clusters in Scania (Skåne).

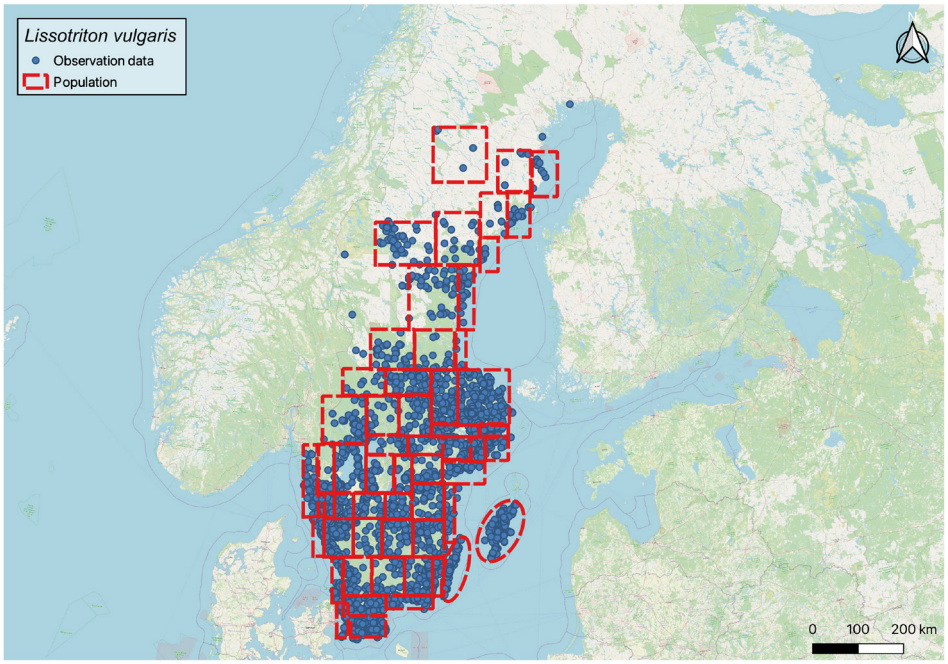


Figure A3.10 Suggested subdivision of the distribution of smooth newt (*Lissotriton vulgaris*). The boarders of the units (populations) are approximate.

DNA-BASED MONITORING INDICATOR
Genetic monitoring: No

To our knowledge there are no ongoing monitoring efforts and no temporal studies on genetic diversity. However, genetic studies show differences in effective migration in urban and rural areas (Stensjö, 1998; Davis, 2020) and allozyme differences indicate isolation by distance across the country (Stensjö, 1998).

Pelobates fuscus, Spadefoot toad (Lökgroda)

PM INDICATOR
Estimated number of current populations: 15
Estimated number of past populations (year 1996): 20
Proportion of populations maintained: 15/20 = 0.75
Species decline: 99 %

The entire Swedish distribution of spadefoot toad is found in Scania (Skåne) (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Nyström and Stenberg, 2008a; Nyström et al., 2020). The number of areas is estimated at eight, the extent of occurrence is estimated at 3,600 km² (3,000 – 3,800 km²) and the area of occurrence at 300 km² (250 – 320 km²; Thurfjell et al., 2020).

The biogeographic survey contained 117 localities. In 2013 – 2018 individuals were found in 71 out of these (Nyström et al., 2020). During the survey in 2020 individuals were found in 20 of 47 surveyed waters. The distribution has declined, and previous localities are now vacant (Nyström et al., 2020). The Action Plan divides the distribution into six areas (Nyström and Stenberg, 2008a). These areas can further be subdivided into potential populations based on a 500 m dispersal radius (Nyström et al., 2011).

Based on earlier surveys the species has declined from 400 known localities in 1959 to 65 localities in 1993 – 1997. Since then, the occurrences of the species have increased due to restoration of waters to approximately 126 localities in 2010. The estimated number of populations was then 17, however, only nine were considered viable (more than 100 males; Thurfjell et al., 2020).

The species is still distributed in the areas described in the Action Plan (Nyström and Stenberg, 2008a; Figure A3.11) as well as a rediscovered area around Revinge in south-central Scania. However, several waters have disappeared and five of the known metapopulations, can be considered extinct (Ekoll AB, pers. comm.). The metapopulation boundaries have been determined based on a 500 m dispersal radius and potential dispersal barriers in the habitat in combination with expert consultation (Ekoll AB). Based on this we identified 15 current populations (Figure A3.11)

Ne500 INDICATOR

Populations with N_e above 500: 0
Proportion of populations with N_e above 500: 0/15 = 0

The national census is estimated at 1,530 (1,000 – 3,000) reproductive individuals (Thurfjell et al., 2020). This means that no single population can be above 5,000. In the biogeographic survey between 2013 – 2018, a total of 1,150 males were identified in 71 waters (Nyström et al., 2020). However, only 7 % of the waters had 50 or more males and the average number of males per locality was 9.4 (Nyström et al., 2020). Similarly, in surveys for the Action Plan, 85 % of all males were found in only two waters (Nyström and Stenberg, 2008a). This means that most of the populations have a critically low number of individuals. The 1,530 census is a decline from the previous estimate of 1,942 individuals in 2010, yet an increase compared to the census in 1993 – 1997 of approximately 610 adults (460 males; Nyström et al., 2020).

DNA-BASED MONITORING INDICATOR

Genetic monitoring: No

To our knowledge there are no ongoing monitoring efforts and no temporal studies on genetic diversity. We found one phylogeographic study utilizing mitochondrial DNA that includes one individual from Sweden (Eggert et al., 2006).

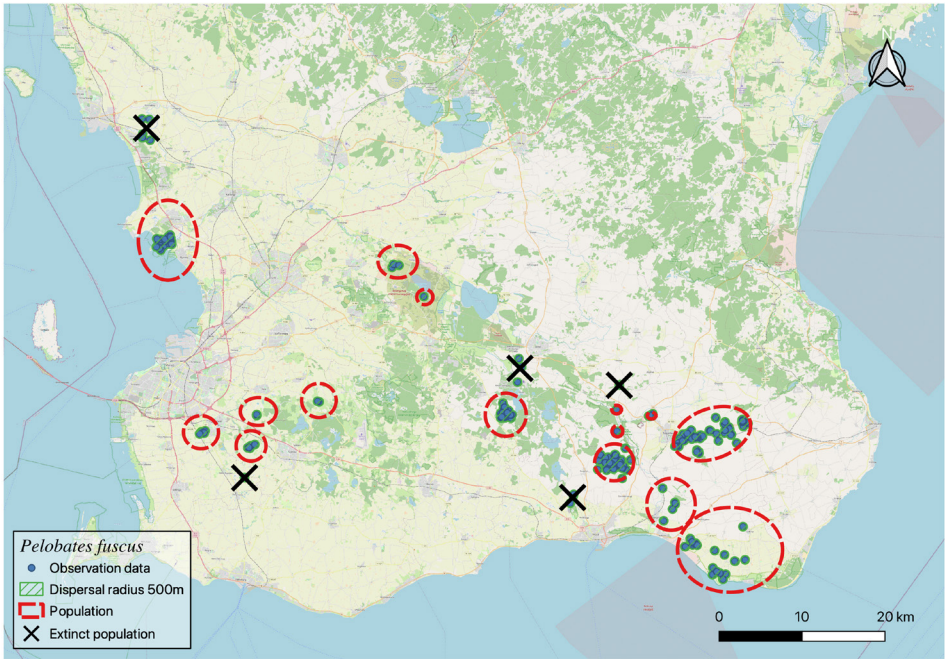


Figure A3.11 Current distribution of spadefoot toad (*Pelobates fuscus*) based on observation data from Artportalen 2000 – 2023, modified. Red circles represent suggested populations based on expert consultations.

Pelophylax esculentus, Edible frog (Ätlig groda)

PM INDICATOR

Estimated number of current populations: 2
Estimated number of past populations (year 1990): 5
Proportion of populations maintained: 2/5 = 0.4

The edible frog is mainly found in southwest Scania (Skåne; Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995). Additional occurrences have been identified in Småland (now extinct), Uppland (now extinct), southeast Scania (now extinct), and in Östergötland (Thurfjell et al., 2020). The Östergötland population is in a complex with pool frog (*P. lessonae*; Arioli and Jakob, 2007).

Extent of occurrence is estimated to 30,000 km² (20,000 – 35,000 km²); there is no estimated area of occurrence (Thurfjell et al., 2020). The species is assessed as increasing (Thurfjell et al., 2020). The EU habitat directive report estimated the continental distribution to 3,200 km² (Aronsson et al., 2020). We estimate that the distribution in Scania constitutes one metapopulation, and that there is one population in Östergötland with active hybridization (Figure A3.12).



Figure A3.12 Estimated current populations of edible frog (*Pelophylax esculentus*). Occurrence is based on observation data from Artportalen 2000 – 2023.

Ne500 INDICATOR

Populations with N_e above 500: 1
Proportion of populations with N_e above 500: 1/2 = 0.5

The EU habitat directive report estimated the continental population to 20,000 individuals (Aronsson et al., 2020). The same population size is indicated for the national census in the Red List assessment (Thurfjell et al., 2020). This number likely represents the population in Scania. The number of individuals in the Östergötland population is described as low, which we interpret as below 5,000 (Thurfjell et al., 2020). In 2004, a survey for the Östergötland country board identified 40 individuals (Arioli and Jakob, 2007).

DNA-BASED MONITORING INDICATOR

Genetic monitoring: No

To our knowledge, there are no ongoing monitoring efforts and no temporal studies on genetic diversity. The edible frog is a hybrid species, originating from hybridization between pool frog (*P. lessonae*) and the lake frog (*P. ridibundus*). It can be found in three types of systems, all-hybrid populations, or in complex with either parental species (LE system or RE system, Pruvost et al., 2013; Jakob, 2007; Arioli, 2007). In Sweden, except for the population in Östergötland, it is found in all-hybrid populations. Furthermore, individuals can be either triploid or diploid. The composition of genotypes (triploid or diploid) over time have been studied in Sweden (Jakob, 2007; Arioli, 2007), but the genetic diversity has not been monitored.

Pelophylax lessonae, Pool frog (Gölgroda)

PM INDICATOR

Estimated number of current populations: 4
Estimated number of past populations (year 1975): 4
Proportion of populations maintained: 4/4 = 1

The Swedish distribution of pool frog is limited to a stretch on the coast of Uppland, a location in Östergötland, and a few recently discovered localities in Blekinge that are most likely the result of an accidental introduction (Ahlén et al., 1995; Nyström et al., 2020; Lindgren et al., 2014, Figure A3.13).

The extent of occurrence is estimated to 10,190 km² (1,050 – 11,000 km²), and the area of occurrence to 260 km² (240 – 300 km²). The number of areas is estimated to six (2 – 10; Thurfjell et al., 2020).

The biogeographic survey identifies 30 localities and 256 supporting waters in Uppland, divided into three metapopulations, and two localities and ten supporting waters in Blekinge (Nyström et al., 2020). The survey in 2013 – 2018 found occurrences in 158 waters with active reproduction in 130 waters. The survey between 2019 – 2021 had positive results in 38 out of 67 surveyed waters in Uppland, seven out of eight waters in Blekinge and two out of 27 waters in Östergötland (Ekdahl et al., unpublished).

The distribution in Uppland is considered three metapopulations (Lindgren et al., 2014; Tegelström and Sjögren-Gulve, 2004; Nyström et al., 2020) and there is one population in Östergötland (complex with edible frog; Arioli and Jakob, 2007), and one population in Blekinge (Figures A4.13, A4.14). The occurrence in Blekinge is not included in the Red List and Article 17 assessments, therefore we have excluded it in our assessment as well.

Ne500 INDICATOR

Populations with N_e above 500: 0
Proportion of populations with N_e above 500: 0/4 = 0

The local populations are described as small, with 50 – 200 adults. The number of reproductive individuals is estimated at 5,000 (3,000 – 9,000; Thurfjell et al., 2020). This is consistent with the biogeographic survey in 2013 – 2018 that estimated the population to 4,800 (Nyström et al., 2020). The survey between 2019 – 2021 found a total of 545 adult frogs in Uppland, 123 adults in Blekinge, and 21 adults in Östergötland (Ekdahl et al., unpublished).

We therefore estimate that all current population consist of less than 5,000 reproductive individuals. There is an older estimation of effective population size from one of the populations, based on allozymes (Sjögren-Gulve and Berg, 1999).

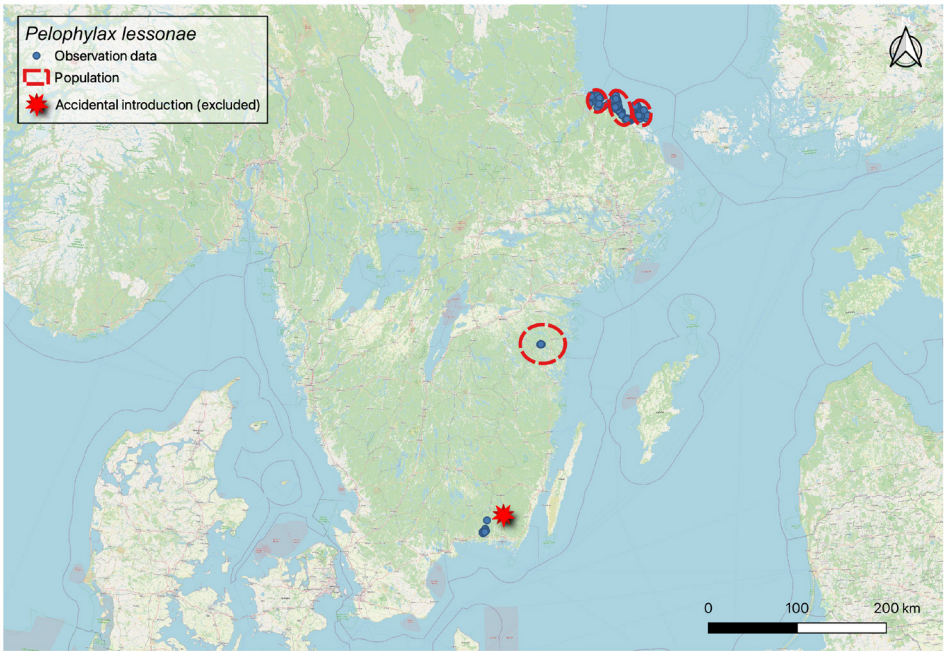


Figure A3.13 Distribution of pool frog (*Pelophylax lessonae*) based on observation data from Artportalen 2000 – 2023, modified. Assessed populations are marked with red circles. The red star denotes an accidentally established population of continental origin that has been excluded from the assessment.

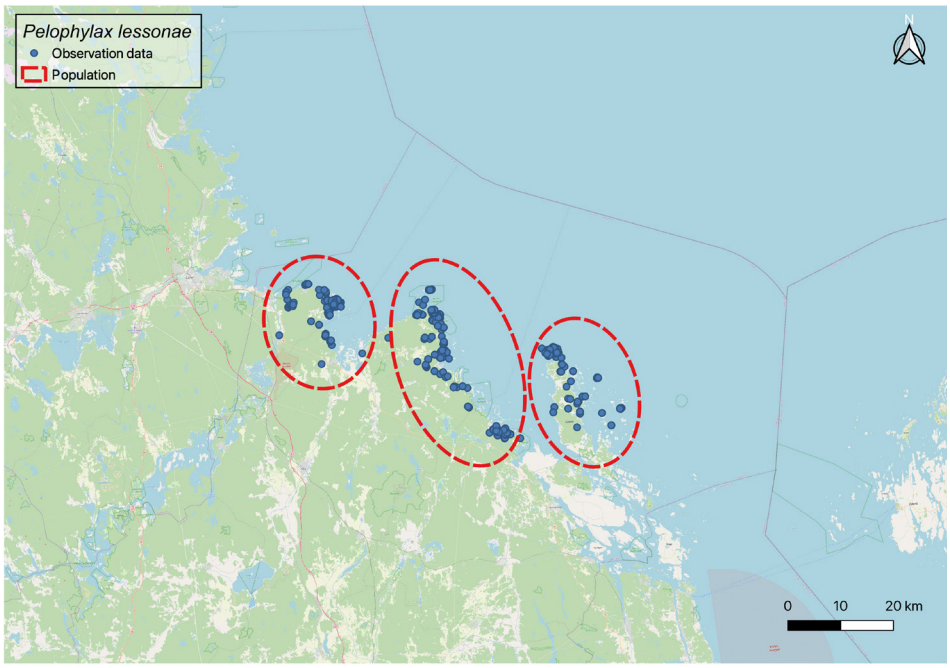


Figure A3.14 Pool frog (*Pelophylax lessonae*) in Uppland. Red circles show the three meta-populations found in the area.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: No

To our knowledge there are no ongoing monitoring efforts and no temporal studies on genetic diversity. However, the metapopulations in Uppland have been studied for genetic diversity and to determine the origin of the populations (Sjögren-Gulve and Berg, 1999; Zeisset and Beebee, 2001; Tegelström and Sjögren-Gulve, 2004; Sjögren, 1991). The results indicate that the populations in Uppland are natural to the region. The population in Östergötland is of unknown origin but suspected to be natural to the area as well. In contrast, the population in Blekinge is of continental origin and believed to have been introduced by accident (Lindgren et al., 2014; Nyström et al., 2020).

Rana arvalis, Moor frog (Åkergroda)

PM INDICATOR

Estimated number of current populations: 11
Estimated number of past populations (year 1978): 11
Proportion of populations maintained: 11/11 = 1

The moor frog is common in Sweden and the distribution is continuous from north to south (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995). The extent of occurrence is estimated at 500,000 km^2 (Thurfjell et al., 2020). In the report for the EU habitat directive, the distribution of the moor frog

is divided into 42,800 km² in the alpine zone, 378,500 km² in the boreal zone, and 24,900 km² in the continental zone (Aronsson et al., 2020).

Considering that there are likely gaps in the observation data and a dispersal radius of two km, the entire distribution is linked together, apart from the islands of Öland and Gotland. However, genetic studies show genetic structure, with at least four clusters (Rödin-Mörch et al., 2019.). We have therefore divided the country into sections and arrived at an estimation of nine clusters on the mainland and separate populations on the islands (Figure A3.15).

Ne500 INDICATOR

Populations with N_e above 500: 11
Proportion of populations with N_e above 500: 11/11 = 1

The Red List assessment estimates the national census at 300,0000,000 individuals (Thurfjell et al., 2020). This is divided by 25,000,000 in the alpine zone, 250,000,000 in the boreal zone, and 17,500,000 in the continental zone in the report for the EU habitat directive (Aronsson et al., 2020).

The moor frog is very common, and it is unlikely that any of the suggested areas (Figure A3.15) include less than 5,000 mature individuals. Estimated effective sizes of clusters all exceed 500 (Rödin-Mörch et al., 2019).

DNA-BASED MONITORING INDICATOR

Genetic monitoring: Yes

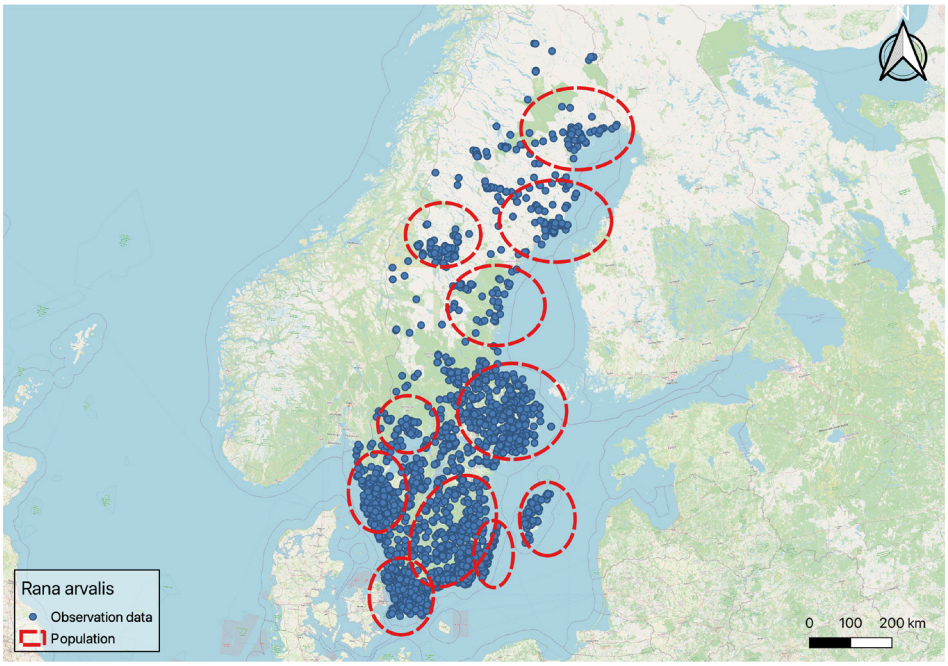


Figure A3.15 Distribution of moor frog (*Rana arvalis*) based on observation data 2000 – 2023 from Artportalen. Red circles represent suggested population subdivision based on partial genetic information (see text for details).

Monitoring of genetic diversity has been initiated by SEPA (Höglund, pers. comm.). Genetic studies show patterns of isolation by distance and low but significant differentiation among populations even at small distances which are likely impacted by selective forces (Rödin-Mörch et al., 2021; Richter-Boix et al., 2013; Hangartner et al., 2011; Knopp and Merilä, 2009; Knopp et al., 2007). There is a pattern of lower within-population variation toward the north of Sweden (Sjögren-Gulve and Berg, 1999).

Both mtDNA and microsatellites show two postglacial recolonizations routes (Knopp and Merilä, 2009). Patterns on neutral genetic diversity show at least four clusters that correspond to the sampling regions across a latitudinal gradient (Rödin-Mörch et al., 2019). MHC II variation along latitudinal gradient along with microsatellites, shows two clear clusters with substructure within with no evidence of gene flow between populations along the gradient (Cortázar-Chinarro et al., 2017). Variation in antimicrobial peptide (AMP) does not show any structure along a latitudinal gradient (Cortázar-Chinarro et al., 2020).

Rana dalmatina, Agile frog (Långbensgroda)

PM INDICATOR

Estimated number of current populations: 8
Estimated number of past populations (year 1978): 8
Proportion of populations maintained: 8/8 = 1

The number of areas is estimated to eight (7 – 9). The extent of occurrence is estimated to 13,000 km² (11,000 – 15,000 km²), and the area of occurrence to 1,300 km² (1,000 – 1,500 km²; Thurfjell et al., 2020). Reported distribution estimates for the EU habitat directive are 5,900 km² in the boreal zone, and 4,700 km² in the continental zone (Aronsson et al., 2020).

The distribution is divided into an area in southeastern Scania (Skåne), a larger area stretching from Blekinge to southeast Småland and on Öland (Figure A3.16). The agile frog is found in approximately 720 waters, 139 in Scania, 212 in Blekinge, 51 in Småland, and 316 on Öland (Thurfjell et al., 2020; Ahlén, 2013). The biogeographic survey between 2013 – 2018 included a total of 193 localities, and agile frog was found in 78 % of the surveyed waters (Nyström et al., 2020). The Action Plan indicates a loss of 25 % of occurrences (Ahlén, 2013), however it is difficult to attribute this to loss of populations, and there is no clear loss of range based on earlier occurrence maps (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995).

The Action Plan clearly states that the 8 – 9 populations are isolated from one another (Ahlén, 2013). Hower, the distribution from occurrence data (Figure A3.16) does not suggest eight populations. Since the dispersal capacity of the agile frog is good, we have used a potential dispersal distance of four km to assess population boundaries. The resulting map suggests four rather than eight clusters (Figure A3.17). One possible explanation is that populations numbers have increased and that the populations are now in contact with another. Another explanation is that the distribution appears larger due to erroneous observation data. We have therefore assessed the species in two different ways. One with four populations

(Figure A3.17) and one with eight populations instead (Figure A3.18). The estimation of number of populations do not affect the assessment of the PM Indicator at this point, since loss of populations in this case is based on loss of range.

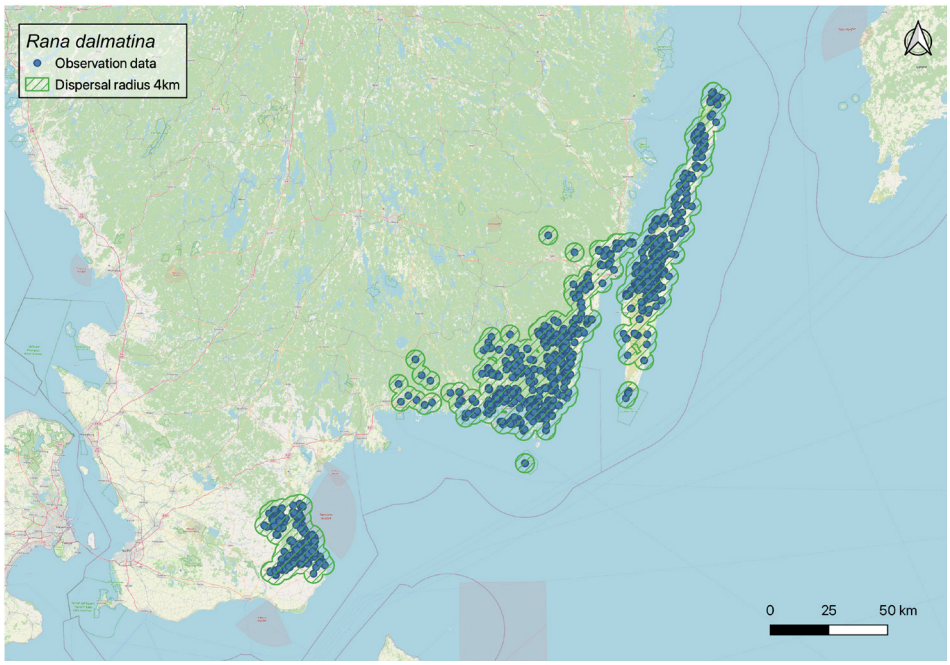


Figure A3.16 Distribution of agile frog (*Rana dalmatina*) based on observation data from Artportalen 2000 – 2023. Green areas represent a potential dispersal distance of four km.

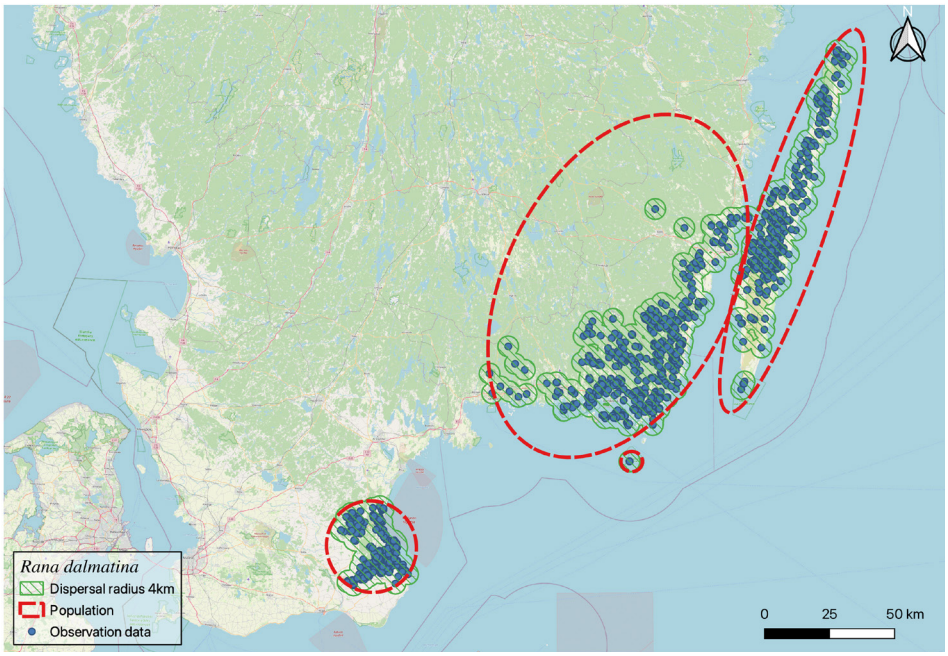


Figure A3.17 Alternative population structure for agile frog (*Rana dalmatina*) based on observation data from Artportalen 2000 – 2023 in combination with potential dispersal radius.

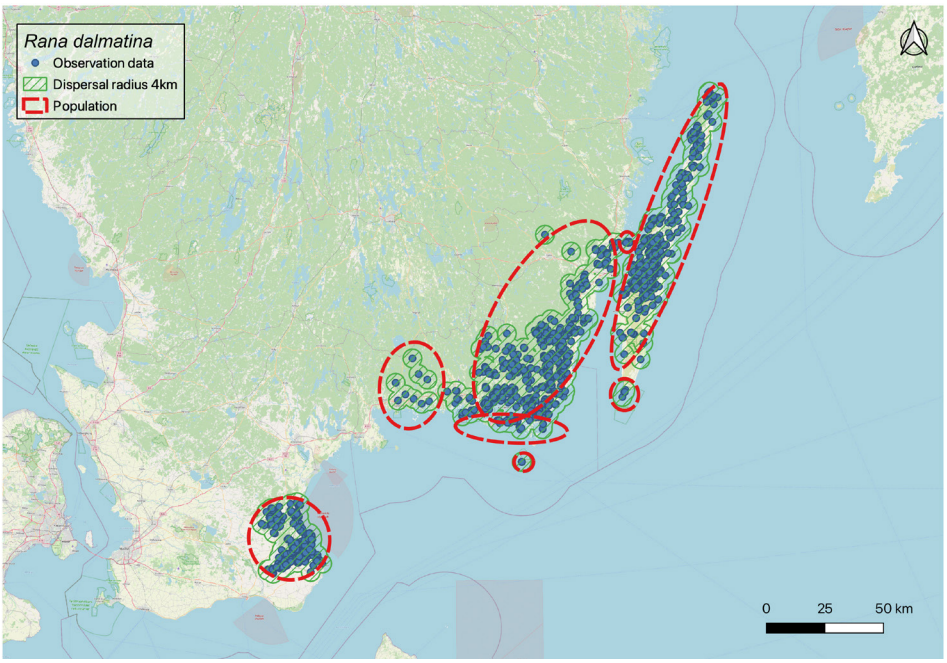


Figure A3.18 Observation data 2000 – 2023 from Artportalen (modified) for agile frog (*Rana dalmatina*). Red circles represent population subdivision based on occurrence data and information from the Action Plan (see text for more details).

Ne500 INDICATOR

Populations with N_e above 500: 3
Proportion of populations with N_e above 500: 3/8 = 0.38
Proportion of populations with N_e above 500 for alternative assessment: 3/4 = 0.75

The total census is estimated to 46,600 reproductive individuals (Thurfjell et al., 2020). The 2019 report for the EU habitat directive estimated the population to 31,500 individuals in the boreal zone and 15,100 in the continental zone (Aronsson et al., 2020). The biogeographic survey between 2013 – 2018 estimated the population in Blekinge to 14,600, the population in Scania to 10,500, 3,500 in Småland, and 54,500 on Öland (Nyström et al., 2020). Based on this we estimate that the larger population on Öland, the population in Scania, and the larger population in Blekinge have population sizes above 5,000 reproductive individuals and that the remaining populations are smaller than this.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: No

To our knowledge, there are no ongoing monitoring efforts and no temporal studies on genetic diversity. We found one phylogeographic study that includes one sampled population from Sweden. The study includes microsatellite variation (Vences et al., 2013). There is a reference in the Action Plan to unpublished studies

on genetic variation in the Swedish agile frog, which show higher variation on Öland compared to mainland populations (Ahlén, 2013).

Rana temporaria, Common frog (Vanlig groda)

PM INDICATOR

Estimated number of current populations: 11
Estimated number of past populations (year 1978): 11
Proportion of populations maintained: 11/11 = 1

The common frog is widespread in Sweden and can be found across the entire country except for the islands of Öland and Gotland (Thurfjell et al., 2020). Extent of occurrence is estimated at 575,000 km^2 (Thurfjell et al., 2020). The 2019 report for the EU habitat directive divides the distribution 103,800 km^2 in the alpine zone, 375,500 km^2, boreal zone and 23,300 km^2 in the continental zone (Aronsson et al., 2020).

We have divided the country into subregions (Figure A3.19) on the basis of a minimum of five genetic clusters across the gradient (Jansen van Rensburg et al., 2018). This yielded 11 potential populations. Based on older distribution maps, there has been no loss of range in the past 50 years (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995).

Ne500 INDICATOR

Populations with N_e above 500: 11
Proportion of populations with N_e above 500: 11/11 = 1

The entire census is estimated at 300,000,000 individuals (Thurfjell et al., 2020). The 2019 report habitat directive divides the population into 55,000,000 in the alpine zone, 250,000,000 in the boreal zone, and 11,000,000 in the continental zone (Aronsson et al., 2020). Based on this information, we find it unlikely that any subpopulation is below 5,000 individuals.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: Yes

Genetic studies indicate isolation by distance and genetic structuring even at small spatial scales (Johansson et al., 2007). Landscape structure and differentiation in life history traits are important factors that influence spatial structure and gene flow (Richter-Boix et al., 2010). Within-population variation decreases toward the north and population differentiation increases (Jansen van Rensburg et al., 2018). Monitoring of genetic diversity has been initiated by SEPA (Höglund, pers. comm.).

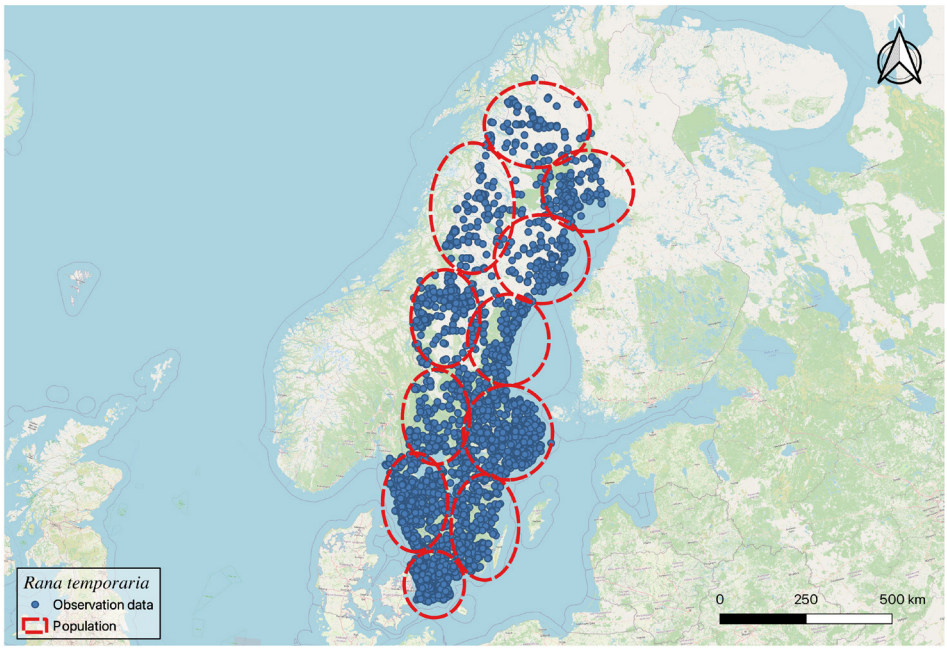


Figure A3.19 Estimation of populations of common frog (*Rana temporaria*) based on distribution and population genetic structure (see text). Occurrence is based on observation data from Artportalen 2000 – 2023.

Triturus cristatus, Great crested newt (Större vattensalamander)

PM INDICATOR

Estimated number of current populations: 150
Estimated number of past populations (year 1960): 151
Proportion of populations maintained: 150/151 = 0.99

The habitat directive estimates the distribution to 169,500 km² in the boreal zone and 22,500 km² in the continental zone (Aronsson et al., 2020). Meanwhile the Red List assessment estimates the EOO to 29,000 km² (25,000 – 35,000 km²). The species has declined by approximately 34 % (Thurfjell et al., 2020; Malmgren, 2007).

The distribution of the great crested newt includes the southern and central parts of Sweden and the northern coast (Figure A3.20). The great crested newt lives in metapopulations. However, many locations are likely isolated since it is a poor disperser and shows low effective migration among locations (Stensjö, 1998). The major occurrences are clustered along the coasts, inland in south/central Sweden, and on Öland (Thurfjell et al., 2020; Malmgren, 2007). Estimated number of locations differ between sources, from 500 – 600, 900, to 2,000 (Nyström and Stenberg, 2008b; Malmgren, 2007; Thurfjell et al., 2020).

Mapping the distribution along with a dispersal radius of one km yields over 500 clusters. To account for missing data (lack of observations) we used a radius of four km instead. We used major roads and rivers as a guide (Figure A3.21), joined

together clusters located close to one another, and arrived at 150 clusters (Figures A3.22 – A3.24). This approximates potential populations.

Judging from older maps, there is no loss of distribution range (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995). However, the Red List assessment indicates an ongoing decline (Thurfjell et al., 2020). But it is difficult to attribute this to defined populations. The Action Plan identifies a population in Stensele, Lappland that is now extinct (Malmgren, 2007).

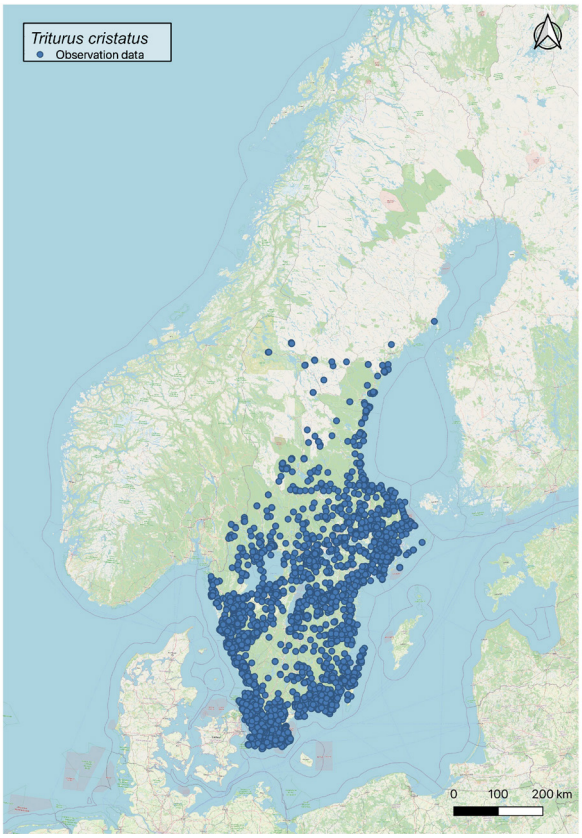


Figure A3.20 Current distribution of great crested newt (*Triturus cristatus*) based on observation data 2000 – 2023 from Artportalen.

Ne500 INDICATOR

Populations with N_e above 500: 15
Proportion of populations with N_e above 500: 15/150 = 0.1

The total census is estimated to 200,000 reproductive individuals (Thurfjell et al., 2020). A Habitats Directive report estimate the population to be 165,000 in the boreal zone and 55,000 in the continental zone (Aronsson et al., 2020).

With a total number of 200,000 reproductive individuals nationally, the average number of individuals in our estimated 150 populations is approximately 1,300 individuals. According to the Action Plan, many of the locations are small and isolated. There are approximately 900 known waters, with around

100 – 1,000 individuals per location (Malmgren, 2007). Assuming our estimated 150 populations, each population would represent six of the 900 known locations. This would mean between 600 – 6,000 individuals per population.
The largest numbers are found along the coast, in the south, and on Öland according to the Action Plan and Artfakta.se (Malmgren, 2007; Thurfjell et al., 2020). This represents roughly 30 of our proposed populations. A few of these may represent populations larger than 5,000, whilst many of the 150 estimated populations are likely less than 500 individuals. We estimate that the populations along the coasts and southern Sweden may be larger, corresponding to 15 populations (10 %).

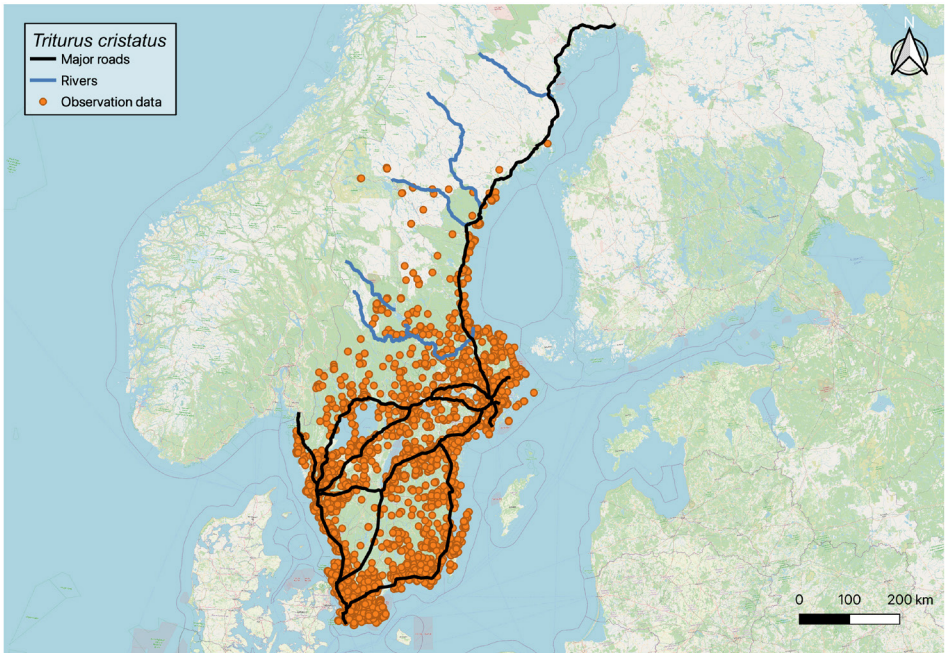


Figure A3.21 Distribution of great crested newt (*Triturus cristratus*) based on observation data from Artportalen 2000 – 2023 together with approximate placement of major roads and river systems in Sweden.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: No

To our knowledge there are no ongoing monitoring efforts and no temporal studies on genetic diversity. Genetic studies show isolation by distance and differentiation over a small distance (Stensjö, 1998). Studies also indicate that the great crested newt is more sensitive to fragmentation and shows less effective migration compared to the smooth newt (Stensjö, 1998).

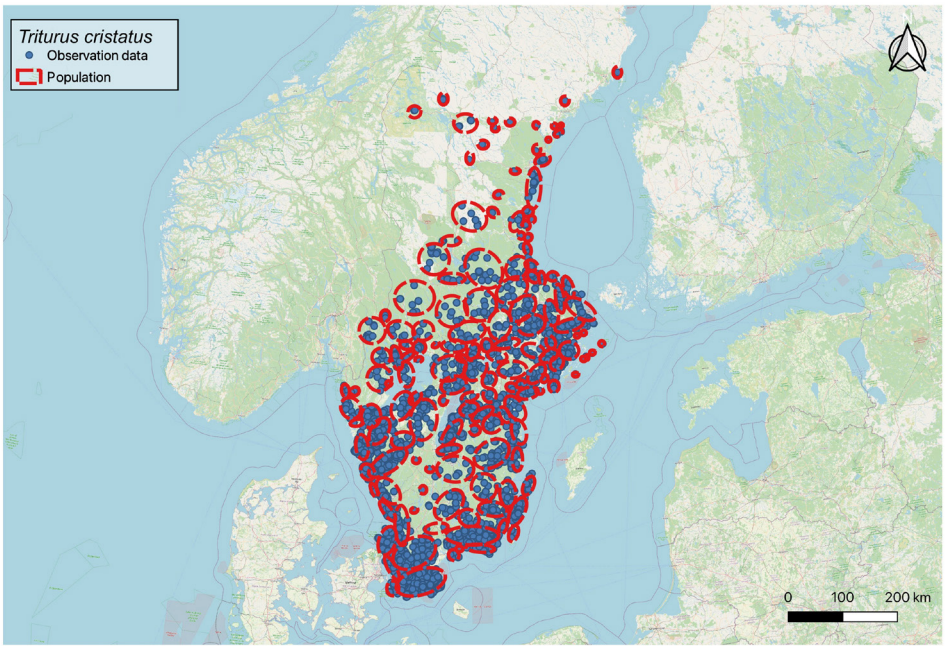


Figure A3.22 Estimated populations of great crested newt (*Triturus cristatus*). Occurrences are based on observation data from Artportalen 2000 – 2023.

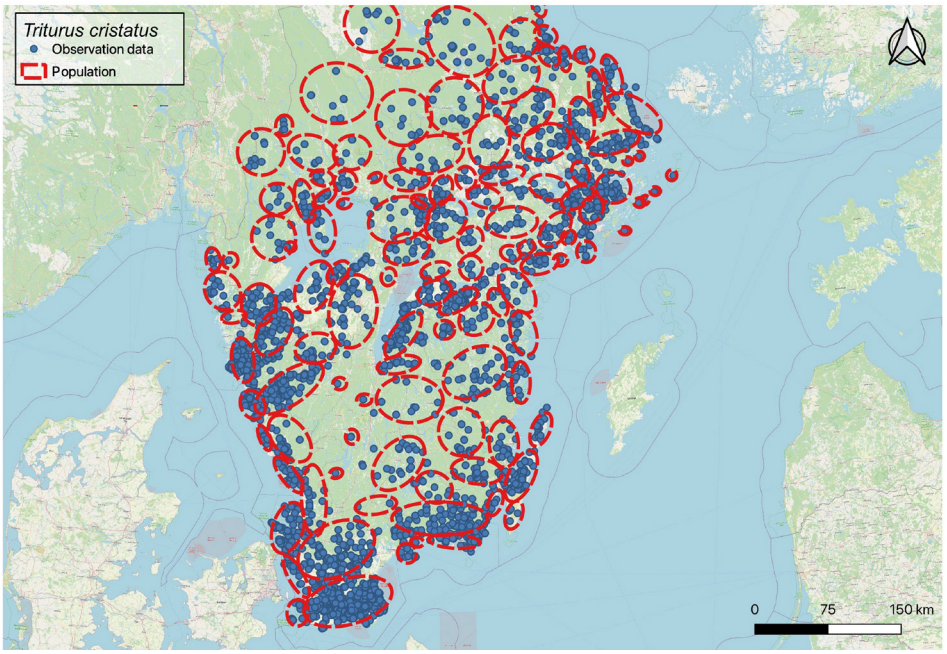


Figure A3.23 Estimated southern populations of great crested newt (*Triturus cristatus*). Occurrences are based on observation data from Artportalen 2000 – 2023.

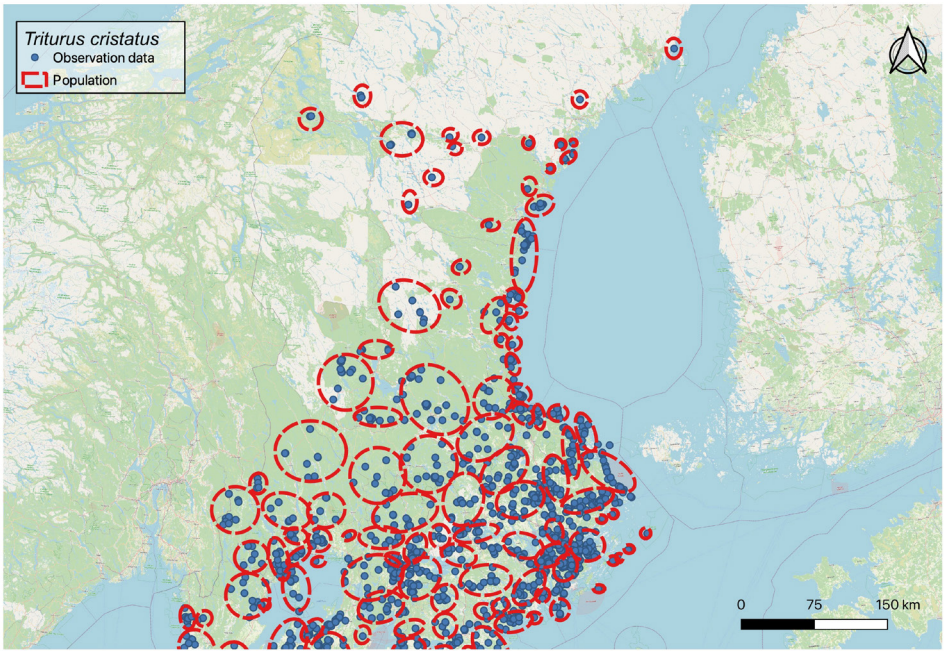


Figure A3.24 Estimated northern populations of great crested newt (*Triturus cristatus*). Occurrences are based on observation data from Artportalen 2000 – 2023.

Reptiles

Anguis fragilis, Slow worm (Kopparödla)

PM INDICATOR

Estimated number of current populations: 10
Estimated number of past populations (year 1978): 10
Proportion of populations maintained: 10/10 = 1

The distribution covers Götaland, Svealand and extends north to Skellefteå (Figure A3.25). Extent of occurrence is estimated to 360,000 km^2, and there is no available estimation of area of occurrence (Thurfjell et al., 2020). The Red List assessment indicates no evidence of decline (Thurfjell et al., 2020). We compared the current distribution to older maps (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995) and found no evidence of a loss of range. The species is therefore assessed as having maintained its populations in the last 50 years.

Since we do not know anything about the population substructure, we divided the distribution into sections of roughly 200 km radius, plus the island of Öland (Figure A3.26). This method yields ten populations.

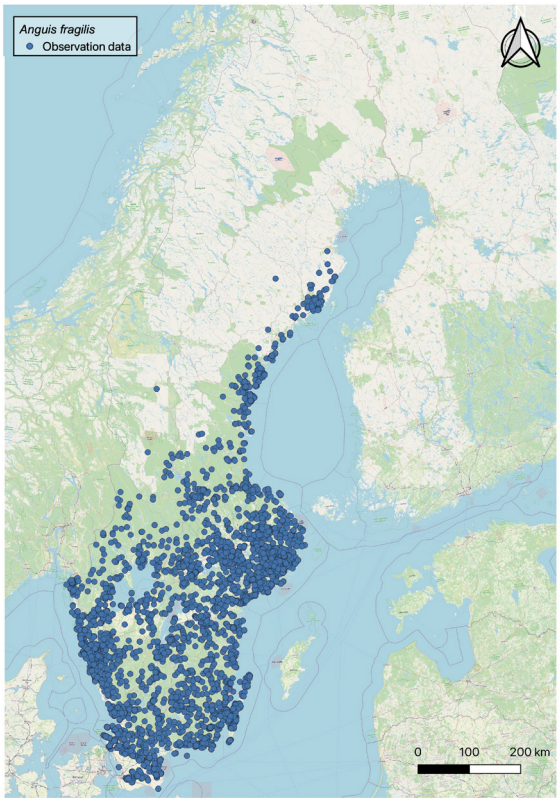


Figure A3.25 Current distribution of slow worm (*Anguis fragilis*) based on observation data 2000 – 2023.

Ne500 INDICATOR

Populations with N_e above 500: 10
Proportion of populations with N_e above 500: 10/10 = 1

There is no census size available, beyond that it is estimated to be above 10,000 reproductive individuals (Thurfjell et al., 2020). The species is described as common; therefore, the populations most likely have population numbers above 5,000.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: No

To our knowledge there are no ongoing monitoring efforts and no temporal studies on genetic diversity. We found one phylogenetic study that includes one sample from Sweden, which indicates a southern post-glacial colonization route (Jablonski et al., 2017).

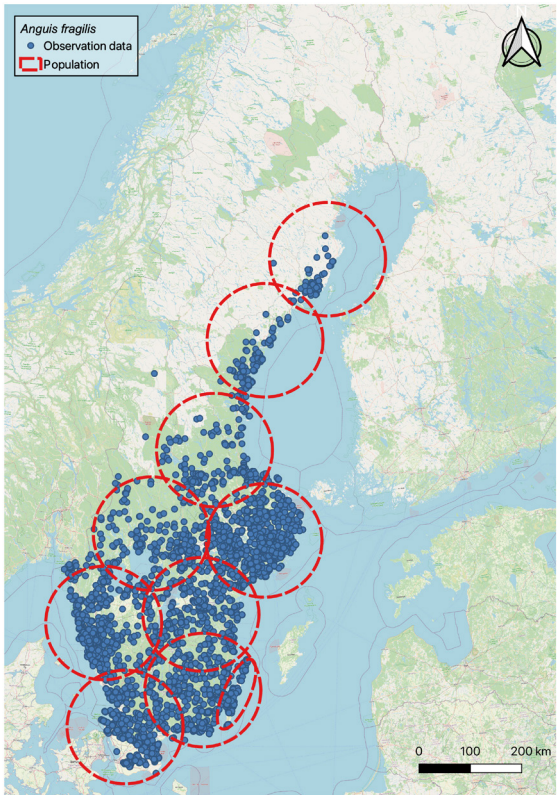


Figure A3.26 Suggested population subdivision for slow worm (*Anguis fragilis*) based on observation data (2000 – 2023) from Artportalen.

Coronella austrica, Smooth snake (Hasselsnok)

PM INDICATOR

Estimated number of current populations: 11
Estimated number of past populations (year 1978): 11
Proportion of populations maintained: 11/11 = 1
Alternative proportion of populations: 7/7 = 1

The species and habitat directive report estimate the extent of occurrence to 62,000 km² in the boreal region and 7,900 km² in the continental region (Aronsson et al., 2020). The extent of occurrence for the Red List is 175,000 km² and the area of occurrence 3,600 km² (Thurfjell et al., 2020).

The distribution includes the east coast from Scania (Skåne) to Uppland, the west coast north of Bjärehalvön, around Vänern, Vättern, Närke, Mälardalen, and the islands of Öland and Gotland. The species has declined by 30 % since year 2000 (Thurfjell et al., 2020), although it is difficult to attribute this to populations based on older distribution maps (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995).

We counted the islands of Öland and Gotland as separate populations and divided the rest of the distribution into potential clusters arriving at 11 potential

populations (Figure A3.27). Another possibility is that there are fewer larger clusters where the distribution along the coasts is connected (Figure A3.28).

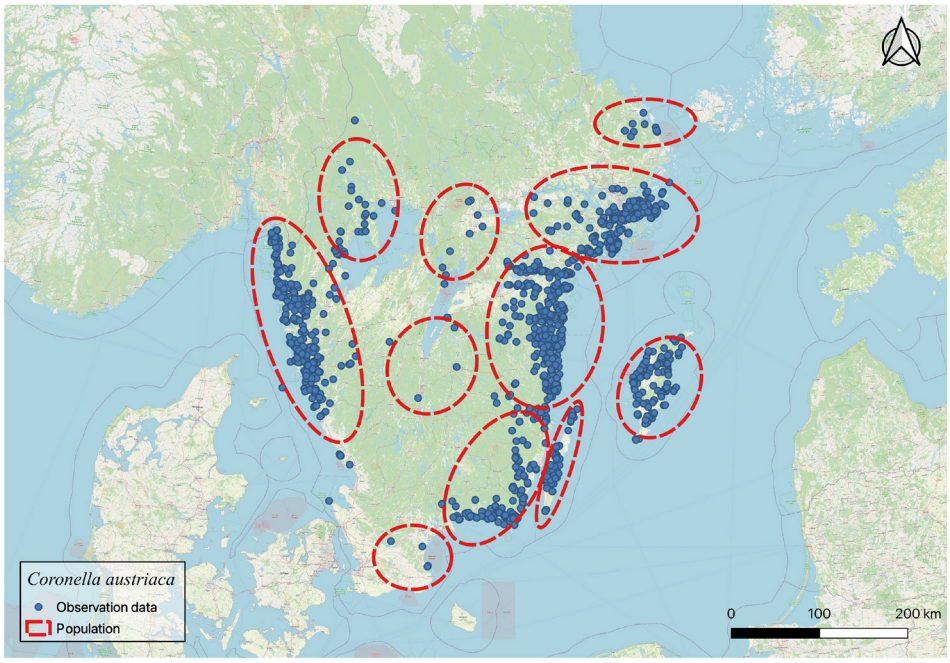


Figure A3.27 Estimated populations of smooth snake (*Coronella austrica*) with eleven populations. Occurrence is based on observations from Artportalen 2000 – 2023.

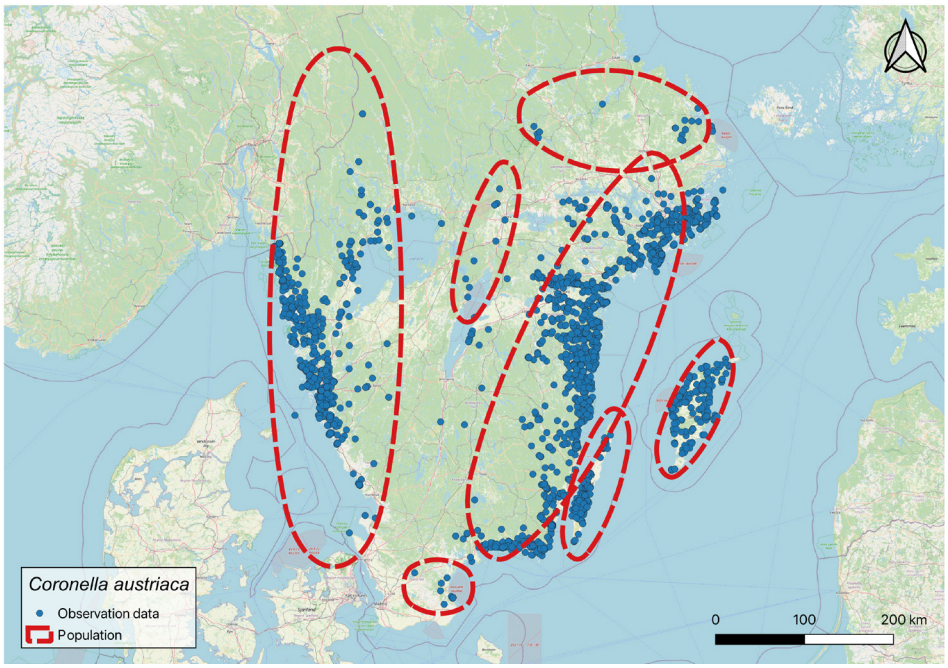


Figure A3.28 Estimated populations of smooth snake (*Coronella austrica*) with seven populations. Occurrence is based on observations from Artportalen 2000 – 2023..

Ne500 INDICATOR

Populations with N_e above 500: 0
Proportion of populations with N_e above 500: 0/11 = 0
Alternative assessment of N_e above 500: 2/7 = 0.28

The census is estimated at 9,000 (6,000 – 12,000) reproductive individuals (Thurfjell et al., 2020). The 2019 report to the habitat directive estimates the population to be 7,500 individuals in the boreal zone and 1,500 in the continental zone (Aronsson et al., 2020). Based on this, we estimate that all the current populations have less than 5,000 reproductive individuals. Another possible scenario is that there are fewer larger clusters and that two of these clusters are large enough to hold 5,000 individuals, however this implies that the total census is at the larger end of the estimate (12,000).

DNA-BASED MONITORING INDICATOR

Genetic monitoring: No

To our knowledge, there are no ongoing monitoring efforts and no temporal studies on genetic diversity

Lacerta agilis, Sand lizard (Sandödla)

PM INDICATOR

Estimated number of current populations: 22
Estimated number of past populations (year 2000): 25
Proportion of populations maintained: 22/25 = 0.88

The main distribution of sand lizard is in Scania (Skåne), Blekinge, Kalmar and south Östergötland, while more fragmented in Halland, Jönköping, Västra Götaland, Södermanland, Värmland and Dalarna, with possibly earlier distribution in Stockholm, Uppsala, and Gävleborg (Thurfjell et al., 2020; Berglind et al., 2013).

The extent of occurrence is estimated at 150,000 km² and the area of occurrence is estimated to be 1,256 km² (1,000 – 1,500 km²; Thurfjell et al., 2020). The habitat directive report estimates (EOO) to be 275,000 km² in the boral zone and 16,200 km² in the continental zone (Aronsson et al., 2020). The species declined by 30 % (20 – 40 %) since year 2000 (Thurfjell et al., 2020; Berglind et al., 2013).

The Red List assessment estimates that the largest subpopulation is 500 individuals, and that the total population is 11,000 (Thurfjell et al., 2020). Based on this information, there should be at least 22 populations (subpopulations). Therefore, we divided the distribution into 22 potential clusters (Figure A3.29). Thirty-seven local populations were identified as gone (Berglind et al., 2013). If the current 290 localities correspond to 22 populations, then 37 localities correspond to approximately three lost populations.

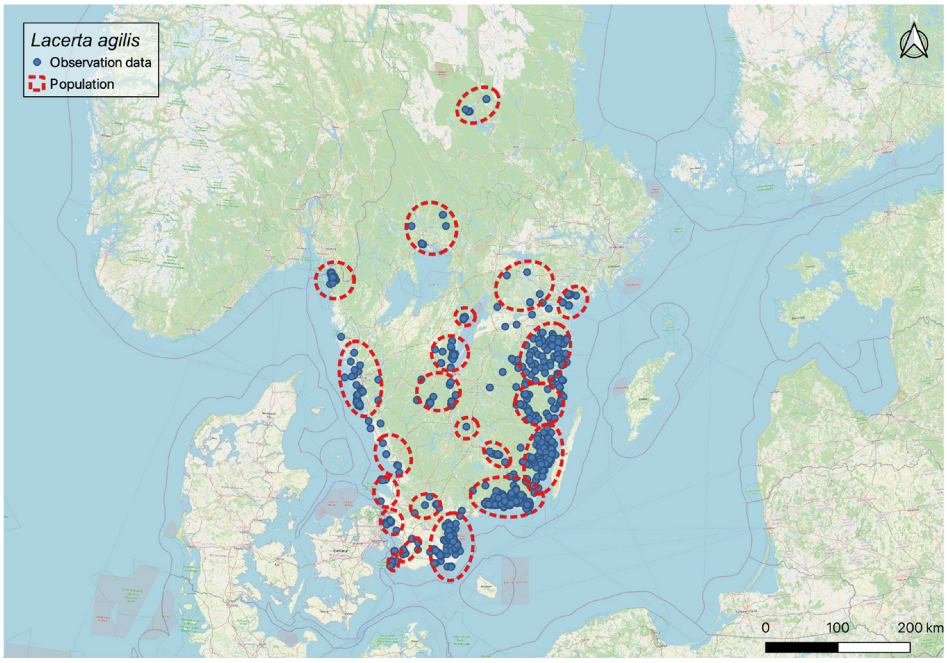


Figure A3.29 Estimated populations of sand lizard (*Lacerta agilis*). Occurrence is based on observation data from Artportalen between 2000 – 2023.

Ne500 INDICATOR

Populations with N_e above 500: 0
Proportion of populations with N_e above 500: 0/22 = 0

The census is estimated at 11,000 (7,700 – 14,700), with the largest subpopulation of 500 (Thurfjell et al., 2020). The species and habitat directive report 2019 estimates the population to be 6,200 in the boreal zone and 5,000 in the continental zone (Aronsson et al., 2020).

The Action Plan estimates population sizes to be 20 – 40 individuals per location (290 locations; Berglind et al., 2013). The total census is estimated at 11,000 (7,700 – 14,700) reproductive individuals. Loss in the last twenty years is 20 – 40 % (Thurfjell et al., 2020). Based on the total census, and the estimation of the size of sub-populations, we assess that all current populations have less than 5,000 reproductive individuals.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: No

Genetic studies show low genetic variation within populations, a high degree of population differentiation, and low gene flow (Gullberg et al., 1998, 1999; Madsen et al., 2000), especially in the northern distribution (Gullberg et al., 1997). Genetic variation is low in Swedish populations compared to central Europe. There is genetic structuring across and within regions (Gullberg et al., 1998, 1999; Madsen et al., 2000). To our knowledge, there are no ongoing monitoring efforts and no temporal studies on genetic diversity.

Natrix natrix natrix, Grass snake (Snok)

PM INDICATOR

Estimated number of current populations: 8
Estimated number of past populations (year 1978): 8
Proportion of populations maintained: 8/8 = 1

The distribution is continuous across Sweden, including Götaland, Svealand, and the southern coast of Norrland. The species has declined during the 1900s (Thurfjell et al., 2020), but there is no available estimation of how much. The extent of occurrence excluding Gotland is estimated to be 330,000 km² (Thurfjell et al., 2020). The grass snake on Gotland is considered a subspecies. It is assessed separately in the Red List (Thurfjell et al., 2020); we therefore evaluated it separately (see below). We divided the county into subunits, arriving at eight potential clusters (Figure A3.30). Based on older distribution maps, there is no loss of range (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995).

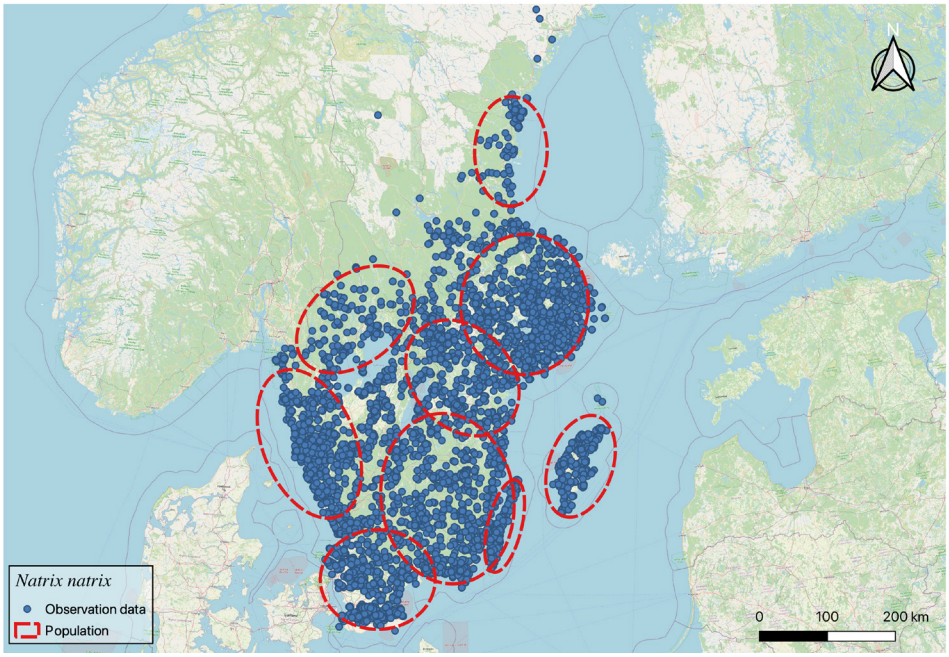


Figure A3.30 Estimated population clusters of grass snake (*Natrix natrix natrix*) and Gotland grass snake (*Natrix natrix gotlandica*). Occurrence is based on observation data from Artportalen 2000 – 2023.

Ne500 INDICATOR

Populations with N_e above 500: 8
Proportion of populations with N_e above 500: 8/8 = 1

There is no information on the estimated census, beyond that it is larger than the limit for the Red List criteria (Thurfjell et al., 2020). We estimate that all current populations have a census size above 5,000 reproductive individuals.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: No

To our knowledge there are no ongoing monitoring efforts and no temporal studies on genetic diversity.

Natrix natrix gotlandica, Gotland grass snake (Gotlandssnok)

PM INDICATOR

Estimated number of current populations: 2
Estimated number of past populations (year 1978): 2
Proportion of populations maintained: 2/2 = 1

This is a variety of the mainland grass snake (*Natrix natrix natrix*) that is only found on Gotland and close islands (Figure A3.30). The status as subspecies is debated, however there is a separate evaluation available in the Red List (Thurfjell et al., 2020). The extent of occurrence is estimated to be 5,840 km² (5,800 – 5,900 km²) and the area of occurrence at 500 km² (250 – 700 km²). The species is declining and was previously more common. The distribution includes the islands of Lilla Karlsö, Stora Karlsö, Fårö, and Gotska Sandön (Thurfjell et al., 2020). We have considered two populations based on the distance between the main island and Gotska Sandön (Figure A3.31).

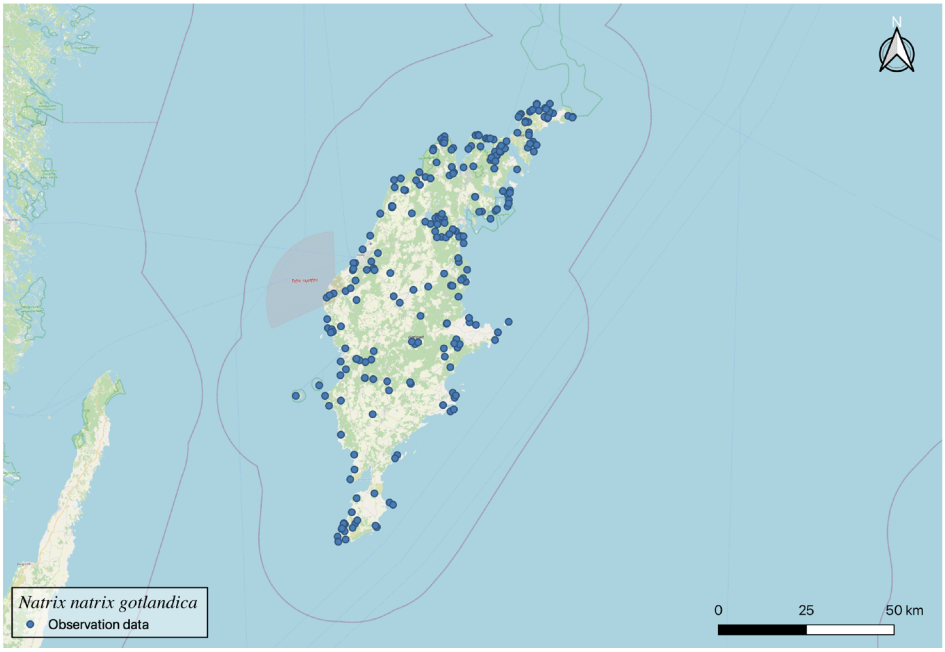


Figure A3.31 Observation data of *Natrix natrix gotlandica*, the grass snake subspecies found on the island of Gotland, 2000 – 2023 from Artportalen.

Ne500 INDICATOR

Populations with N_e above 500: 0
Proportion of populations with N_e above 500: 0/2 = 0

Reproductive individuals are estimated to 1,800 (1,500 – 2,100; Thurfjell et al., 2020). Based on this information, we assess that all current populations have population sizes below 5,000.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: No

To our knowledge there are no ongoing monitoring efforts and no temporal studies on genetic diversity in *Natrix natrix gotlandica*.

Vipera berus, European viper (Huggorm)

PM INDICATOR

Estimated number of current populations: 14
Estimated number of past populations (year 1978): 14
Proportion of populations maintained: 14/14 = 1

The European viper is widespread and common across the entire country. The extent of occurrence is estimated to 534,000 km^2 (Thurfjell et al., 2020). There is knowledge of two isolated populations (Madsen et al., 2023) that we have included in our assessment. The remaining range has been divided into subunits (Figure A3.32). We estimated the distribution to consist of 14 clusters, including the isolated populations from literature. Comparisons with older distribution maps (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995) does not show any evidence of decline.

Ne500 INDICATOR

Populations with N_e above 500: 12
Proportion of populations with N_e above 500: 12/14 = 0.86

There is no census estimate available in the Red List, only that it is above the threshold for the Red List criteria (Thurfjell et al., 2020). Published articles refer to at least two isolated population with critically low number of individuals (Madsen et al., 2023).

Based on this information, we estimate that two populations have an N_e below 500, and the remaining populations have an N_e above 500.

DNA-BASED MONITORING INDICATOR

Genetic monitoring: Yes

There is no genetic monitoring for the species as whole, but there is a population in Smygehuk, where genetic diversity has been studied for several years (Madsen et

al., 2004; Madsen et al., 1996). There have also been temporal comparisons of genetic variation for a population at Hallands Väderö (Madsen et al., 2023).

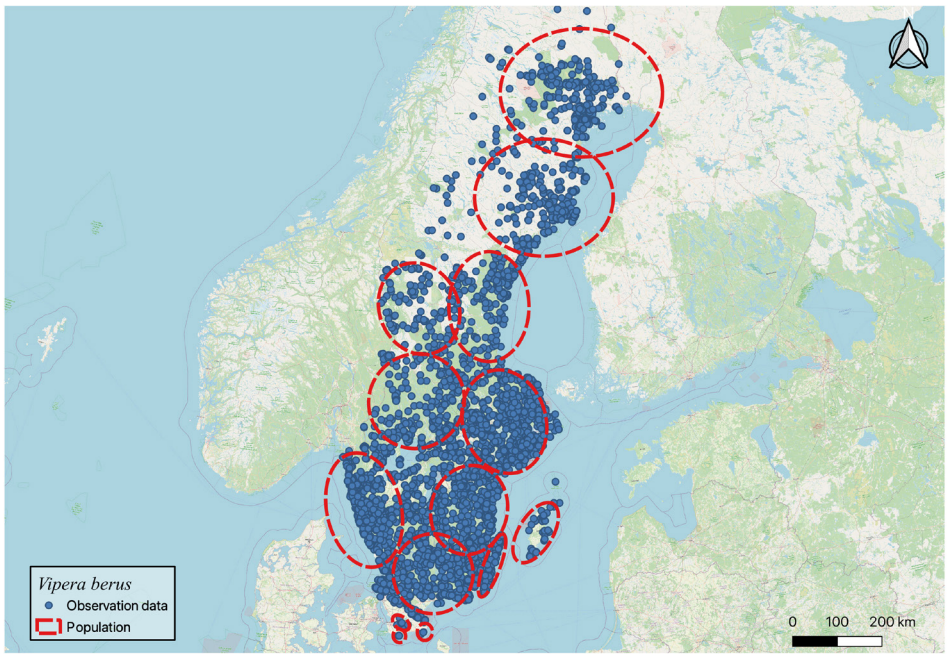


Figure A3.32 Estimated population clusters of European viper (*Vipera berus*). Occurrence is based on observation data from Artportalen 2000 – 2023.

Zootoca vivipara, Viviparous lizard (Skogsödla)

PM INDICATOR

Estimated number of current populations: 13
Estimated number of past populations (year 1978): 13
Proportion of populations maintained: 13/13 = 1

The viviparous lizard is common and distributed across the entire country. The extent of occurrence is estimated to be 583,100 km^2 (Thurfjell et al., 2020). Comparisons with older distribution maps (Cedhagen and Nilsson, 1978; Cedhagen and Nilsson, 1991; Ahlén et al., 1995) does not show any indication of decline. We divided the country into subunits of approximately 200 km (Figure A3.33). This yields 13 clusters.

Ne500 INDICATOR

Populations with N_e above 500: 13
Proportion of populations with N_e above 500: 13/13 = 1

There is no available estimate of census in the Red List assessment (Thurfjell et al., 2020). The viviparous lizard is common and widespread; we therefore find it likely that the population clusters have more than 5,000 reproductive individuals.

DNA-BASED MONITORING INDICATOR
Genetic monitoring: No

There are no ongoing monitoring efforts and no temporal studies on genetic diversity, to our knowledge.

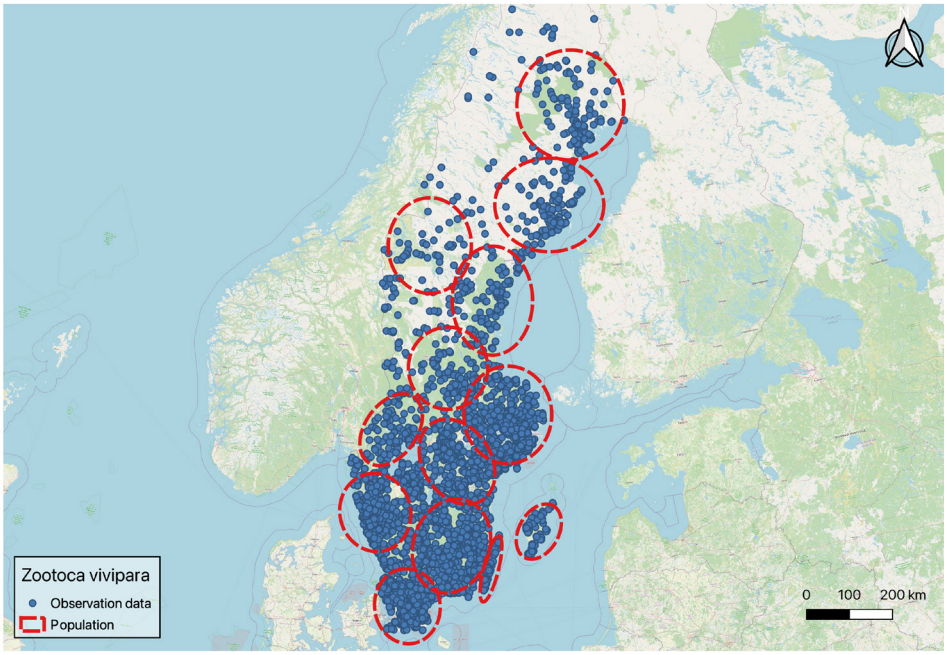


Figure A3.33 Estimated population clusters of viviparous lizard (*Zootoca vivipara*). Occurrence is based on observation data from Artportalen 2000 – 2023.

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Appendix 4: Interview questions for the Red List committee coordinators

Questions for the Red List committee coordinators (here translated to English, the original version in Swedish is found below).

Background on the Committee

1. How many members are in the group?
2. How are members elected? What is required to be selected?
3. How long does the assignment last?

The Committee's current work

1. What does the Red List assessment process look like for the committee's species groups? (e.g. estimating distributions and censuses)
2. Describe the process for an individual species, going from the current classification to an updated one.
3. Which sources of information are used for the assessments?
4. Is genetic variation taken into account in any way in the current process?

Prerequisites for including the indicators

1. In which way do you assess that the work flow for the committee would need to be modified to make assessments for the genetic diversity indicators (number of populations, population sizes, loss over time)?
2. How much time do you estimate this would correspond to?
3. How much work would be required in addition to what is done today to assess the number of subpopulations?
4. How much work would be required beyond what is done today to assess the size of individual subpopulations? (incl. over or under 5,000)
5. How much work would be required beyond what is done today to assess loss (5 – 120 years) of subpopulations or distribution?
6. What proportion of the species within the committee's responsibility do you think it would be possible to produce assessments for?
7. Are there any particular challenges with regard to the Committee's species groups, both within the framework of the Red List and in relevance to the indicator assessments?

Original questions (in Swedish)

Frågor – Rödlistan kommittéer.

Bakgrund om kommittén

1. Hur många medlemmar ingår i gruppen?
2. Hur väljs medlemmarna? Vad krävs för att bli utvald?
3. Hur länge pågår medlemmarnas uppdrag?

Kommitténs nuvarande arbete

1. Hur ser processen ut inför Rödlistan för kommitténs artgrupper? (exempelvis uppskatta utbredning och census)
2. Beskriv arbetet med en enskild art från nuvarande klassificering till en uppdaterad.
3. Vilka kunskapskällor används i arbetet?
4. Beaktas genetisk variation på något sätt i nuvarande arbete?

Förutsättningar för att inkludera indikatorerna

1. Hur bedömer du att arbetet i gruppen skulle behöva modifieras för att göra dessa bedömningar (antalet populationer, populationernas storlekar, förlust över tid)?
2. Vilken tidsåtgång bedömer du att detta skulle motsvara?
3. Hur mycket arbete skulle krävas utöver det som görs idag för att bedöma antalet subpopulationer?
4. Hur mycket arbete skulle krävas utöver det som görs idag för att bedöma storleken på enskilda subpopulationer? (inkl. över eller under 5 000)
5. Hur mycket arbete skulle krävas utöver det som görs idag för att bedöma förlust (5 – 120 år) av subpopulationer eller utbredning?
6. Hur stor andel av arterna inom kommitténs ansvar bedömer du att det skulle vara möjligt att ta fram bedömningar för?
7. Finns det några speciella utmaningar när det gäller kommitténs artgrupper, både inom ramen för rödlistan och i relevans till indikatorbedömningarna?

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MONITORING OF GENETIC DIVERSITY



Monitoring genetic diversity in Sweden with new indicators for the CBD Kunming-Montreal Global Biodiversity Framework

In December 2022, the Fifteenth Conference of the Parties (COP 15) to the Convention on Biological Diversity (CBD) agreed on a new global framework for biological diversity – the Kunming-Montreal Global Biodiversity Framework (GBF). The GBF is associated with a monitoring framework that includes the monitoring of genetic diversity through a headline indicator (A.4): the proportion of populations within species with an effective population size, N_e > 500 and a complementary indicator (A.CY.22): the proportion of populations maintained within species. As these indicators can be assessed without the use of genetic data, they are often referred to as proxy indicators. A third indicator for genetic diversity has also been proposed: the number of species and populations for which genetic diversity is monitored using DNA-based methods. International efforts are ongoing to provide guidelines for assessing these indicators at national levels. In this report, methods are developed and applied to calculate genetic diversity indicators for over 100 species in Sweden, using already existing data from the red-listing process, species' National Action Plans, the Swedish national biogeographic survey, citizen science data, scientific articles, reports, and taxonomic expert consultations.

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