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DIANA POSLEDOVICH, ROBERT EKBLOM AND LINDA LAIKRE

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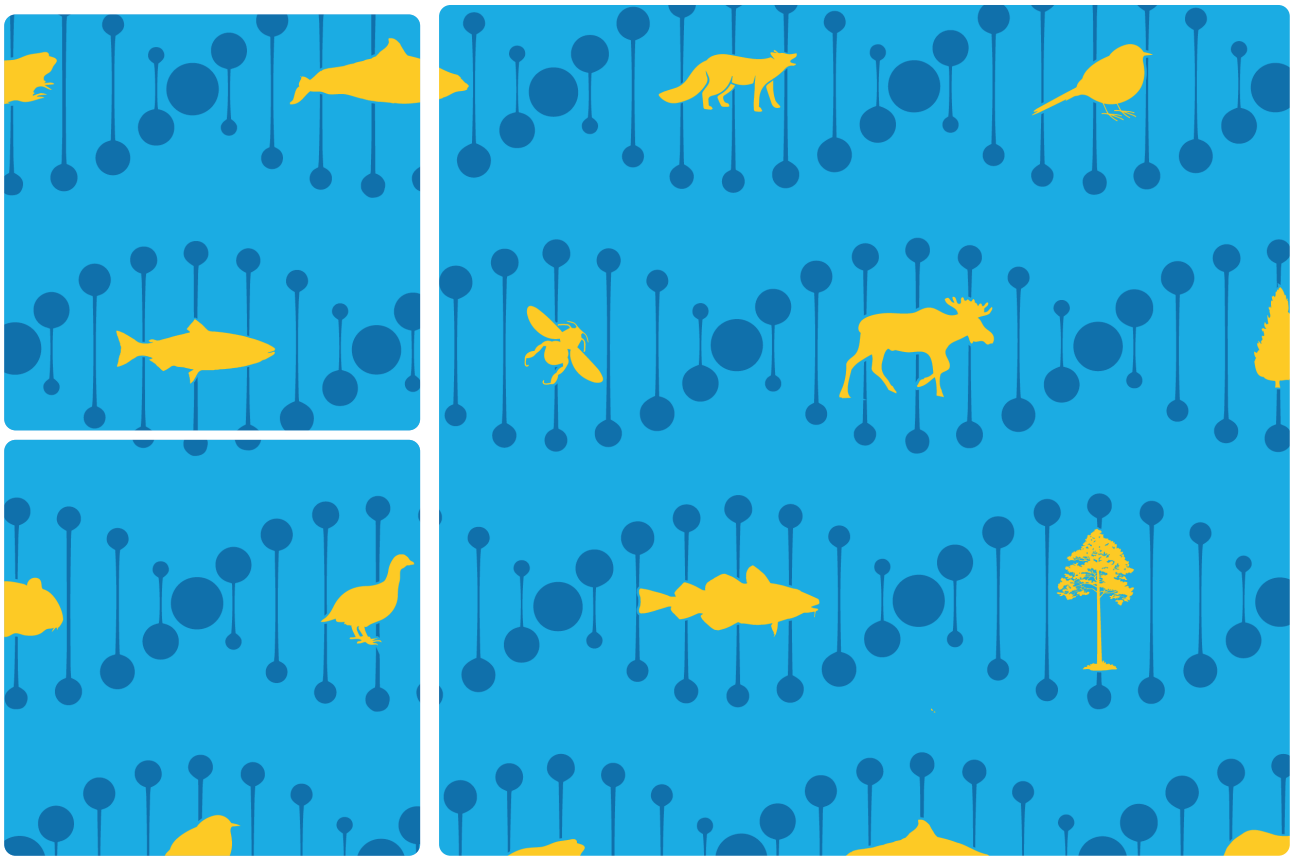

Mapping and monitoring genetic diversity in Sweden

A proposal for species, methods and costs

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Förord

Genetisk mångfald är en av tre komponenter av biologisk mångfald och en grundförutsättning för populationers och arters långsiktiga överlevnad och förmåga att anpassa sig till förändringar i miljön, till exempel genom klimatförändringar.

Miljöövervakning för genetisk mångfald är ett prioriterat utvecklingsområde och svarar på de krav som finns formulerade i etappmålet *Kunskap om genetisk mångfald* samt behov av data och kunskap för uppföljning av preciseringar om genetisk inomartsvariation inom flertalet miljökvalitetsmål. Det bidrar även till underlag för förvaltning samt internationell rapportering av status för arter och biologisk mångfald.

Som en del i arbetet med att utveckla övervakning av genetisk mångfald beställde Naturvårdsverket ett uppdrag att ta fram förslag till övervakningsprogram för genetisk mångfald hos vilda växt- och djurarter. Förslagen, vilka presenteras i denna rapport, utgör viktigt underlag inför myndighetens pågående och fortsatta arbete med att kartlägga och utveckla miljöövervakning för genetisk mångfald.

Rapporten har tagits fram genom ett samarbete mellan de populationsgenetiska forskarna Dr. Diana Posledovich och Prof. Linda Laikre vid Stockholms universitet samt Dr. Robert Ekblom vid EBC, Uppsala universitet.

Författarna är ansvariga för rapportens innehåll.

Stockholm den 25 maj 2021

Susann Östergård
Enhetschef, Naturanalysenheten
Naturvårdsverket

Preface

Genetic diversity is one of three components of biological diversity and is central for the long-term survival of populations and species, as well as their ability to adapt to environmental changes such as climate change.

Environmental monitoring of genetic diversity is a prioritized area of development and meet demands that are set by the milestone target *Knowledge about genetic diversity* within the Swedish environmental objectives system. It also contributes with knowledge and data for the assessment of specifications about genetic diversity within several environmental quality objectives, as well as for management and international reporting on species conservation status.

As part of the work on developing monitoring of genetic diversity the Swedish Environmental Protection Agency commissioned a report containing suggestions for a monitoring program of genetic diversity in wild species of plants and animals. The suggestions, which are presented in this report, are an important part of the ongoing and continued work on mapping and developing environmental monitoring of genetic diversity at the Swedish Environmental Protection Agency.

The report has been developed through a collaboration between the population genetic researchers Dr. Diana Posledovich and Prof. Linda Laikre at Stockholm University and Dr. Robert Ekblom at EBC, Uppsala University.

The authors are responsible for the content of this report.

Stockholm May 25, 2021

Susann Östergård
Head of Nature Analysis Unit
The Swedish Environmental Protection Agency

Contents

1 Sammanfattning

Biologiska övervakningsprogram är en central del för uppföljningen av konventionen för biologisk mångfald (CBD). Genetisk mångfald är identifierad av CBD som en av tre nivåer av biologisk mångfald, och den form av variation som är grunden för övriga nivåer (art- och ekosystemnivå). Målet med denna rapport är att presentera ett förslag till ett övervakningsprogram för genetisk mångfald i Sverige som kan implementeras med start 2020 och vara i bruk under många år framöver. Vi fokuserar främst på genetisk variation inom arter och inte på tekniker där genetiska analyser används för att kartlägga variation på art- och ekosystemnivå.

Genetisk variation är central för populationers överlevnad på kort sikt genom att minska risken för inavelsdepression, och på lång sikt genom att möjliggöra evolutionära anpassningar till förändrade miljöer (exempelvis som en följd av klimatförändringar). Redan 1997 uppmärksammades behovet av ett nationellt program för att övervaka genetisk mångfald. Liknande uppmaningar har sedan kommit vid flera tillfällen i forskningsartiklar, rapporter från Naturvårdsverket och genom regeringsbeslut.

Vi har utfört en omfattande litteraturgenomgång och sammanställt kunskapsläget kring genetisk mångfald i svenska naturliga populationer (delvis baserat på tidigare publicerade rapporter). I ca en tredjedel av de genomgångna studierna hade man undersökt förändringar i genetisk variation över tid.

Vi har även identifierat olika arter och populationer som anses vara lämpliga för genetisk övervakning. Bland dessa arter har vi föreslagit en inbördes prioritering baserat på flera faktorer: redan pågående insatser som möjliggör effektiv provinsamling, hotbild, representation av olika organismgrupper och genomförbarhet, samt uppskattat grova och mycket ungefärliga kostnader för övervakning av dessa. För att identifiera arter som lämpliga för genetisk övervakning och prioritera mellan dessa har vi använt oss av sju kategorier:

1) Arter som är påverkade av beskattning (jakt, fiske, etc.)
2) Arter som är listade i EU:s art-, habitat- och fågeldirektiv
3) Arter som riskerar påverkan från oönskat genflöde
4) Arter som är nationellt rödlistade enligt IUCN:s kriterier
5) Arter där den svenska populationen är genetisk särpräglad från övriga populationer
6) Populationer som förväntas vara särskilt sårbara för klimatförändringar

7) Naturliga referenspopulationer (ej hotade eller listade enligt ovanstående kriterier, men där mycket kunskap redan finns som man kan använda som utgångspunkt och referens)

Dessutom beaktades följande kriterier i bedömningen:

a) Arter som är viktiga för ekosystemets funktion
b) Pollinerande insekter (enligt särskilt direktiv från beställaren – se separat delrapport)
c) Arter med befintliga samlingar av vävnad/DNA för att kunna göra historiska jämförelser
d) Arter som redan i dagsläget är del av genetisk insamling/övervakning
e) Arter där det finns andra typer av övervakningsprogram som inkluderar manuell hantering av individer som enkelt skulle kunna utökas till att omfatta även genetisk provtagning
f) Inhemska naturliga arter som är nära besläktade med domesticerade arter

Prioriteringar gjordes så att varje art placerades i en av tre kategorier (hög, medel och låg prioritering). Vi identifierade totalt 167 arter som lämpliga för genetisk övervakning. Av dessa prioriterades 60 som ”hög”, inkluderande 15 pollinerande insekter (se separat delrapport) och 12 akvatiska arter (se separat rapport från Havs- och Vattenmyndigheten).

Eftersom den tekniska utvecklingen inom genetiska analyser just nu går väldigt fort är det svårt att uppskatta framtida kostnader för den laborativa delen av ett genetiskt övervakningsprogram. Programmet bör också vara adaptivt, så att man kan anpassa metoder allteftersom ny kunskap tillkommer och nya tekniker blir tillgängliga. Här blir det därför centralt att DNA-prover lagras på ett säkert och överskådligt sätt så att man kan gå tillbaka och analysera om äldre prover i framtiden. Upprätthållande och kurrering av biobanker med vävnadsprover bör således vara en prioriterad del av programmet.

Beroende på ambitionsnivå (med avseende på antal arter/populationer som inkluderas, vilken typ av genetiska data som samlas in och antal prov per art/population) beräknas den årliga kostnaden för övervakningsprogrammet ungefär uppgå till mellan 9 (ambitionsnivå 1), 14 (ambitionsnivå 2) och 27 (ambitionsnivå 3) miljoner kronor (inkluderande kostnaderna för de delvis separat finansierade projekten på pollinerande insekter och marina arter). För vissa enstaka arter tillkommer engångskostnader för utveckling av genetiska markörer.

För att programmet ska kunna bli framgångsrikt krävs en tydlig plan för koordinering och projektledning. För att fylla sin funktion, måste övervakningsprogrammet för genetisk mångfald pågå under lång tid framöver,

det är därför centralt att det finns en långsiktig, förutsägbar och transparent struktur för finansiering.

2 Summary

Monitoring programs are an important tool for nature conservation and maintenance of biological diversity and are essential for implementation of the UN Convention on Biological Diversity (CBD; www.cbd.int). Genetic diversity (or genetic variation) is diversity within species, and it has been identified by the CBD as one of the three levels of biological diversity to be mapped, conserved, monitored, and sustainably used. Genetic diversity provides the basis for all biological diversity and for biological evolution. Species and ecosystems depend on genetic variation for evolutionary potential, long-term survival, and resilience.

The aim of this work was to propose a monitoring program targeting genetic diversity within and between populations of species, to be implemented in Sweden in 2020, and that can be in use for many years. The main purpose of the monitoring is to quantify rates of genetic change in natural populations over contemporary time frames (from approx. 100-150 years ago until present day) and to assess any future genetic changes over the coming years and decades. The assessment will enable the detection of potential changes in genetic diversity that can affect the survival, fitness, and long-term viability of the populations and species monitored. Specifically, the mission was to i) provide suggestions for species from different taxonomic groups that are suitable for monitoring of intraspecific genetic diversity, ii) prioritize among such species, and iii) provide suggestions for sampling, methods, and approximate costs.

In order to gather the information that would serve as a basis for our evaluation, we performed a literature review of scientific studies of genetic diversity in populations of species in Sweden. The review covered the period of 2006-2019 to complement already existing reviews and knowledge compilations. We found a total of 267 studies involving 194 species of which 132 species had not been previously studied genetically in Sweden. Together with previous reviews covering the period before 2006, a total of 506 wild species (reported in 1042 publications) have been studied with respect to their within- and between population genetic diversity. A total of 70 studies include temporal genetic data and 43 of them report trends in genetic diversity over time. Genetic diversity decreased in 12 cases, 24 case studies showed stable levels of genetic diversity, and an increase of genetic diversity was reported in 9 cases. Appendix 1 provides a summary of findings from the 70 temporal studies.

In addition, we reviewed research activities, available tissue collections, and ongoing monitoring activities that involve sampling in the wild that potentially can serve as a basis for/be incorporated into monitoring of genetic

diversity (Appendix 3). Based on the collected information, we considered a total of 167 species for genetic monitoring (Figure 5).

We use the following categories to prioritize among the identified species to identify those most suitable for monitoring of genetic diversity over contemporary time frames in Sweden:

1) Species/populations subjected to substantial harvest (hunting, fishing, collecting, logging, etc.).
2) Species/populations listed in the annexes of the EU Habitats Directive and/or the EU Birds Directive.
3) Species/populations at risk of unwanted gene flow through, e.g., large-scale releases or other anthropogenic activities.
4) Red-listed species (including NT-classified species; "red-listing" refers to IUCN criteria applied at national level).
5) Swedish populations that are genetically distinct from others over the distribution range.
6) Populations likely to be strongly affected by climate change (e.g., alpine and northern boreal species, Baltic Sea species of marine origin, low elevation species likely to not tolerate increasing temperatures).
7) Natural reference populations (presumed safe and non-exploited populations where "natural" and non-human induced rates of genetic change can be monitored and knowledge on these rates obtained).

Other factors that we give attention to include:

a) species of key ecological importance, including habitat-forming species and top predators,
b) pollinators (specifically requested by SEPA for consideration),
c) species for which tissue collections are available, providing an immediate possibility for contemporary monitoring of genetic diversity,
d) species already subjected to some form of genetic monitoring,
e) species subjected to other types of monitoring where individuals are sampled or handled during which samples for genetic analysis are possible to obtain, and
f) indigenous wild relatives to domesticated species (c.f. Aichi target 13).

Based on these criteria, and on reviewer comments and SEPA instructions, we ranked the 167 species into priority groups: high (60 species), medium (68 species) and low (39 species). Among the 60 high-ranked species, 15 were

pollinator species (see separate sub-report) and 12 were species that the Swedish Agency for Marine and Water Management had already prioritized as part of a separate project to develop the monitoring of genetic diversity for aquatic organisms (Johannesson & Laikre 2020).

It is not possible to suggest a single type of molecular genetic technique to be applied universally in monitoring of genetic diversity. Different molecular genetic techniques are appropriate for different populations/situations and depend on whether mapping and monitoring is already ongoing using specific markers. Furthermore, availability of genomic resources varies between species; the existence of a reference genome is noted for each species in one of the columns of Appendix 3. Finally, markers will, and should, be elaborated and evaluated over time. Even if SNP markers are used when initiating national monitoring in 2020 for a particular species, this does not imply that those markers must be used for decades to come. Rather, the monitoring program for genetic diversity must be adaptive and allow new approaches to be applied as they develop. This is also true for estimation of population genetic parameter, statistical testing, and bioinformatics approaches. As new knowledge is gained, the programs should adapt. Financial potential for such adaptive work, including evaluation between old and new markers, will continuously be needed to ensure that best practice is used in monitoring.

A very important aspect in monitoring of genetic diversity is to keep and maintain tissue samples from the collected individuals. Such collections make it possible to return to previously analysed/collected samples as new techniques develop. We have identified several important collections during this project, and we recommend an overview to be conducted of the existing tissue-bank collections. As a part of the monitoring program for genetic diversity to be initiated by SEPA in 2020, the status of these tissue-banks and associated databases should be improved to increase their visibility and ensure their long-term maintenance.

We also explore costs for a monitoring program with different levels of ambition and found that, depending on the level of ambition (with respect to the number of species/populations included, type of genetic markers employed, sample sizes, etc.), the annual costs for the program is in the range of SEK 9,000,000 (lowest ambition level), 14,000,000 (medium ambition), and 27,000,000 (highest ambition level).

For the program to be successful, a clear plan for coordination and project management is required, as well as for integration with other monitoring and management efforts. We provide several suggestions for ways forward and stress that in order to fulfil its function, the monitoring program for genetic diversity must continue for a long time. It is therefore crucial that there is a long-term, predictable, and transparent structure for its funding.

3 Introduction

Monitoring is a central aspect of conservation and maintenance of biological diversity. By systematically and continuously quantifying biodiversity over time, early detection of threats and effects of anthropogenic changes – positive or negative – are possible. The importance of biodiversity monitoring is highlighted in the UN Convention on Biological Diversity from 1992 (CBD; www.cbd.int).

The aim of this work is to present a proposal for a monitoring program targeting genetic diversity, to be implemented in Sweden from 2020, and to be used for many years to come.

Genetic techniques can be used to address a wide range of issues in species and population management, monitoring, and conservation. In a classic scientific article by Schwartz and colleagues (2007), the distinction is made between two main types of genetic monitoring, Category I and II, where the first category refers to using genetic tools for assessing species or population presence/absence (including eDNA techniques), abundance, geographic range, vital rates, etc. This type of genetic monitoring can also be used to investigate species' natural history, such as mating and dispersal (e.g. the field of molecular ecology). Category II monitoring refers to targeting genetic diversity within species and populations. This report exclusively concerns Category II monitoring, termed "conservation genetic monitoring" by Laikre et al. (2008).

The main goal of Category II genetic monitoring is to follow rates of genetic change in natural populations, which is our primary focus here. This type of monitoring allows for the detection of potential changes in such diversity that can affect the survival and fitness of the populations and species monitored. This implies monitoring genetic diversity specifically, and we try to use this terminology rather than "genetic monitoring", which is much broader and generally unspecific about whether it refers to Category I or II.

3.1 A brief background on the monitoring of genetic diversity in Sweden

Genetic diversity (synonym: genetic variation) is diversity within species and one of three aspects of biological diversity that is recognized by the UN Convention on Biological Diversity (CBD; www.cbd.int), as well as in its international and national follow-up policies (e.g., Laikre et al. 2016). Genetic diversity is expressed and quantified as genetic differences between individuals within populations (within-population genetic diversity, sometimes also referred to as "alpha-diversity") and between populations (between-population

genetic diversity, also known as "beta-diversity"). Genetic diversity provides the basis for all biological diversity and for biological evolution. Species and ecosystems depend on genetic variation for evolutionary potential, long-term survival, and resilience (Allendorf et al. 2013).

There are many examples of traits of importance for local adaptation, such as thermal tolerance, salinity tolerance, disease resistance, and phenology, that have a genetic basis (Liang et al. 2008; Dixon et al. 2015; Zhou et al. 2019; Hill et al. 2019; Tigano et al. 2020). For instance, the Atlantic herring has adapted genetically to the brackish environment of the Baltic Sea, exhibiting traits such as tolerance to lower salinity and eyesight adaptations to the light environment of the Baltic (Lamichhaney et al. 2012; Barrio et al. 2016; Hill et al. 2019).

Similarly, there are many examples of how genetic diversity can affect ecosystem function and resilience (a policy brief on this topic produced by the Cost Action G-BiKE can be found here: https://sites.google.com/fmach.it/g-bike-genetics-eu/reports-publications/policy-brief_january-2020). One such example is eelgrass – an important habitat-forming species on the Swedish west coast and in large parts of the Baltic Sea. Eelgrass meadows with high genetic diversity show higher biomass production, plant density, faunal abundance, and potential for recovery from climate extremes than eelgrass with low genetic diversity (Reusch et al. 2005). The Baltic Sea phytoplankton *Skeletonema marinoi* is another example; increased genetic variation appears coupled with increases in primary production and organic nutrients in this species (Sjöqvist & Kremp 2016).

At present (Spring 2020), genetic diversity is not included in the national or regional environmental monitoring efforts carried out by Swedish authorities. The Swedish Board of Agriculture monitors the existence and census numbers of 70 identified national breeds of domestic species (Swedish Board of Agriculture 2016) but is not measuring genetic diversity directly (but genetic diversity of pedigrees is monitored for some species).

The need to categorically measure genetic variation over time has long been recognized in Sweden (Ryman 1981; Figure 1). In 1997, the first proposal for a program for monitoring genetic diversity was presented (Laikre & Ryman 1997) following an assignment from the Swedish Environmental Protection Agency (SEPA). This proposal included an extensive review of the knowledge on genetic diversity available at that time. SEPA also requested a report on the genetic distinctiveness of populations of species in Sweden (Lönn et al. 1998). These knowledge reviews were updated ten years later in another review produced for SEPA (Lundqvist et al. 2008) and suggestions for monitoring were again put forward (Laikre et al. 2008). These updates were warranted by the Swedish 16th environmental objective that was passed by the Swedish

Parliament in 2005 (Swedish Government bill Prop. 2004/05:150). This objective was added to the already existing 15 goals from 1999 (Swedish Government bill Prop. 2000/01:130) and its focus is biological diversity (Swedish Government Report 2005/06:MJU3). The 16th environmental objective clearly states that genetic variation within and between populations of naturally occurring species shall be maintained to ensure long-term survival. Statements on what this goal should encompass include (translating from pages 206-207 of 2005/06:MJU3):
"Species are to live in long-term viable populations with sufficient genetic variation" and "species shall be distributed within their natural habitats such that the genetic variation within and between populations is sufficient." Furthermore, the government advertises that the Swedish Environmental Protection Agency will be tasked with providing an action plan for the conservation of genetic diversity (page 209 of 2005/06: MJU3).

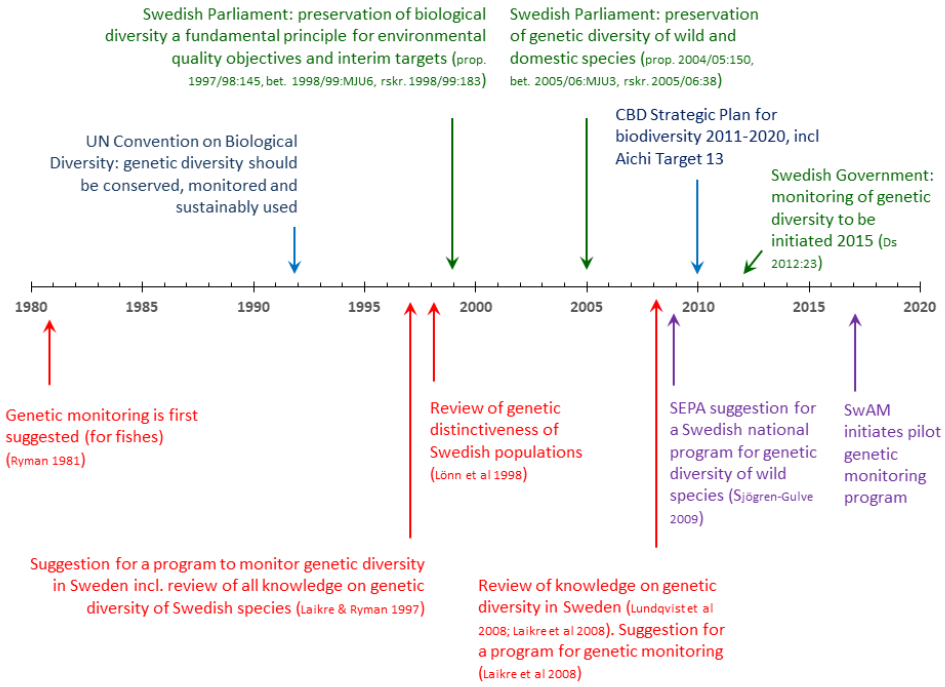

Figure 1. Timeline illustrating developments concerning monitoring of within-species genetic variation in Sweden.

Internationally, the Convention of Biological Diversity (CBD – article 2), established by the United Nations, defines biodiversity as "the variability among living organisms from all sources. This includes diversity within species, between species, and of ecosystems". In order to act against the ongoing loss of diversity, the CBD has developed the Strategic Plan for Biodiversity 2011-2020, which includes the "Aichi Biodiversity Targets". Aichi Target 13 is of special relevance for work on genetic diversity, stating that: "By 2020, the genetic

diversity […] is maintained, and strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity."

A suggestion for a Swedish national program to implement the goals for genetic diversity of the 16th environmental objective was presented to the Swedish Government by SEPA in 2009 (Sjögren-Gulve 2009 in SEPA Dnr 305-404-06 Nv). An in-depth background and review of national policy governing the conservation and monitoring of genetic variation was provided in that proposal, which has not yet been implemented.

Work on implementation of the national environmental objectives is ongoing and interim targets are identified. One such interim target concerns genetic variation and stipulates that mapping and monitoring of genetic diversity shall be initiated. The initial year for the implementation of this interim target was 2015 (Swedish Government, Department of Environment, Decision I:4 2012-04-26, M2012/1171/Ma; Ds 2012:23). The government decision states (translation from Swedish): "The interim target on the knowledge of genetic diversity implies that mapping and monitoring of genetic diversity shall be initiated by, at the latest, 2015." (Section 3.5.5 of the Appendix to the Swedish Government decision, April 26, 2012 nr I:4).

However, a new deadline for implementing this interim target was later set to 2020 (Swedish Government 2016 Ds 2017:32).

3.2 Objectives

The present project aims at suggesting a long-term program for monitoring within-species genetic diversity that can be initiated in 2020. Specifically, the mission is to: i) provide suggestions for species suitable for monitoring intraspecific genetic diversity in different taxonomic groups, ii) prioritize among such species, and iii) provide proposals for sampling, methods, and approximate costs. The focus concerns monitoring genetic diversity over contemporary time scales, which implies a historical time period of no more than approx. 100-150 years from the present day, as well as assessing any future genetic changes over the coming years and decades.

4 Methods

The time frame for this assignment has been very limited – 2.5 months – and thus we had to limit our efforts spent on reviewing the literature. Rather, we refer to already existing work in this respect (Lundqvist et al. 2008; Laikre et al. 2008; Laikre & Ryman 1997) including a relatively recent review focusing on species in the Baltic Sea (Wennerström et al. 2017), and we conducted only supplementary literature reviews to these previous reviews.

Specifically, our work comprised of a literature search to complement the literature reviews published in 2008 (Laikre et al. 2008; Lundqvist et al. 2008). This complementary literature review covered the time period of 2006-2019 and we used the same search terms as in the previous knowledge reviews (section 4.1).

4.1 Literature review for Sweden from 2006-2019

We have carried out a literature search with the aim of providing a general overview of work that has been done with respect to genetic diversity of Swedish species since the previous studies. We used the Web of Science search engine (© 2019 Clarivate Analytics) to search for published scientific papers on population genetics of wild species in Sweden.

The search was performed in October 2019 and included studies published between 2006 and December 2019. The reason for choosing 2006 as the starting year is that this was the final year included in the previous knowledge reviews (Lundqvist et al. 2008; Laikre et al. 2008). We excluded studies published in 2006 that were reported in either or both of those two previous reviews.

The search criteria included the word combinations: "genetic variation" OR "genetic variability" OR "genetic differentiation" OR "genetic divergence" OR "genetic structure" OR "genetic distance" OR "population genetics" OR "population structure" used together with (by using AND operator) ‘Swed* OR Scandinavia OR Fennoscandia’ in the topic. Web of Science categories which did not refer to wild species studies were excluded from the search results.

The final results yielded 680 studies which were manually checked for relevant material. We excluded papers that dealt exclusively with taxonomic questions and kept all the studies on species population genetics which involved sampling of at least one modern population of a wild species in Sweden and provided some form of measure of its genetic variability.

4.2 Discussions, workshops, and the review of research activities and ongoing monitoring that includes sampling in the wild

We held several discussion meetings – physical as well as video meetings – where we identified the target researchers for starting the email/direct inquires, designed the template for information on potential target species, discussed various methodological issues, agreed on species for prioritization, as well as discussed all other aspects of this work. We also participated in the workshop "Tools for monitoring genetic diversity" arranged by the Genomic BIodiveristy Knowledge for Resilient Ecosystems (G-BiKE; https://www.cost.eu/actions/CA18134/#tabs|Name:overview) Action financed by the European Cooperation in Science and Technology (COST; https://www.cost.eu/). The workshop was held in Novi Sad, Serbia, during November 21-22, 2019.

We reviewed ongoing research activities that included aspects of genetic monitoring involving temporal sample collection from individuals (i.e., not eDNA studies), followed by genetic analyses. This was done by web-based searches and email requests and/or direct communications with colleagues. The information that we asked for involved the type of genetic studies, the focal species, the publication records, whether there was a sample bank which could be made available for future temporal monitoring purposes, and what species could be of special interest for inclusion in a monitoring program. In addition, we asked for recommendations for additional contact persons. Email reminders to reply to the questions were sent twice. We also reviewed ongoing environmental monitoring efforts that included some form of sampling of species in the wild.

5 Results

5.1 Literature review for Sweden from 2006-2019

A total of 680 articles were retrieved in the literature search for the period 2006-2019 (section 4.1). Manual checking of these 680 studies revealed that 203 of them were of relevance to the present project. Email inquiries among researchers working in the population genetic field resulted in an additional 64 studies that had not been found in the literature search. In total, we identified 267 studies on terrestrial, freshwater, coastal, or marine species (Figure 2), reflecting the reported knowledge of genetic diversity of wild species in Sweden. Thus, 203 publications (76%), were identified via the Web of Science search engine (© 2019 Clarivate Analytics) (column "Retrieved from Web of Science search" in Appendix 2) while 64 publications (24%), were obtained via the inquiries ("Retrieved from inquiry" in Appendix 2). In total, 194 species were studied in these publications, and 132 of these species had not been studied previously with respect to genetic diversity (as reported in Laikre et al. 2008). A full reference list for the 267 papers and a list of the study species is provided in Appendix 2.

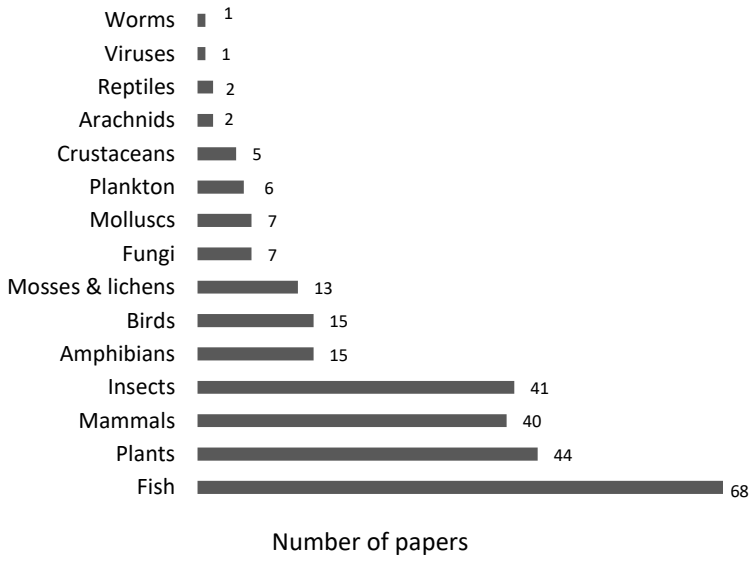

Figure 2. Number of papers (total 267) on genetic diversity of separate organism groups in Sweden identified by the present literature review that covered the period 2006-2019 that was carried out to update information from previous reviews (Lundqvist et al. 2008; Laikre et al. 2008; Laikre & Ryman 1997).

We performed a more detailed analysis of the publications reporting temporal aspects of genetic diversity. Previous work reported a total of 30 such studies (Table 1 of Laikre et al. 2008) and with our complementary search for 2006-2019 we find a total of 70 studies on temporal genetic variation of species in Sweden (summarized in Appendix 1).

The temporal studies covered the time spans of 2 to 7000 years (the latter using museum samples; Appendix 1) and investigated genetic variation in 36 species, the majority of which were fish (13) or mammals (7). The study period for 31 case studies covered less than 10 years, while for 43 cases the period spanned 10 years or more (some papers covered more than one case study and species). Contemporary time frames, defined here as all samples being from within an approx. 100-150-year period, are covered in 62 of the 70 studies.

Microsatellites (46 studies) and allozymes (14 studies) were most common among the genetic markers used to estimate genetic variability within and between populations of the species studied (Figure 3). Other markers included major histocompatibility complex MHC (2), single-nucleotide polymorphisms (SNPs) (2), mitochondrial DNA (2), amplified fragment length polymorphisms (AFLPs) (1), whole genome sequencing (1), etc. (Figure 3). Five studies used more than one technique.

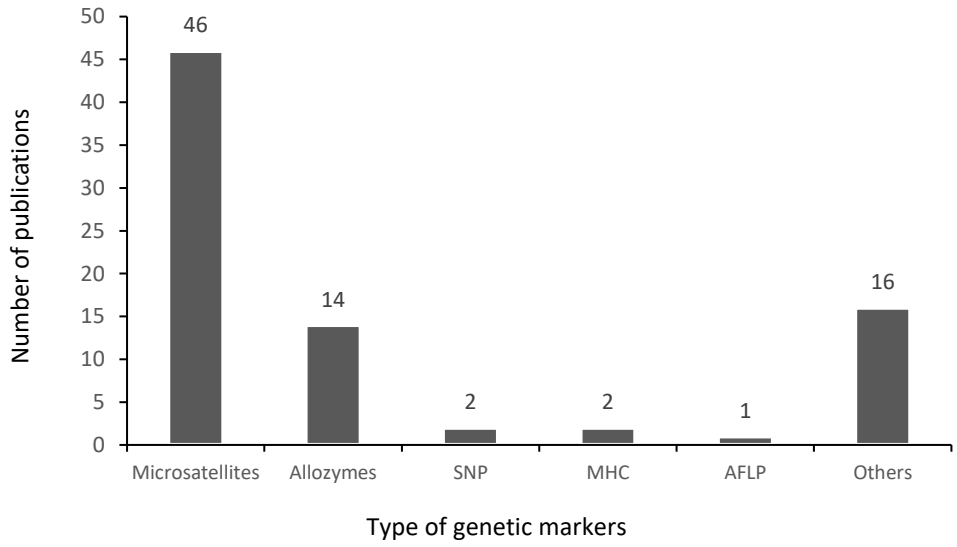

Figure 3. Types of genetic markers used in publications on temporal genetic studies of species in Sweden (Appendix 1). Note that separate papers may report results from several marker types.

Not all temporal studies interpreted the observed change in genetic diversity as increased or decreased. Among those 43 papers (out of 70) that did report such changes, 12 case studies showed a decrease, 24 case studies showed no change, and 9 case studies showed an increase of genetic diversity over time. More than one case study could be reported in the same publication.

Financial support for conducting these studies appear to largely be based on research grants awarded to certain researchers, as indicated by acknowledgements sections in the publications. However, the Swedish Environmental Protection Agency (SEPA), the Swedish Agency for Marine and Water Management (SwAM), and other authorities and organizations co-funded several studies.

5.2 Research and monitoring activities

We summarized information on efforts for separate species that, in at least some respects, related to monitoring (Appendix 3). This compilation was initiated by SEPA and we followed their instructions to continue it. We compiled information in the Excel file (Appendix 3) of species that are currently or have recently been subjected to genetic monitoring (both Category I and II of Schwartz et al. 2007 were considered), genetic mapping, or monitoring within other frameworks. Such frameworks included surveys of pollutants, presence/absence, census numbers, etc., that involve sample collection or handling of individuals where sampling for genetic analyses could be carried out. To gather this information, representatives from independent research departments and organizations were contacted for information regarding monitoring activities and/or population genetics studies in wild animals and plants in Sweden. In total, we obtained information from 62 persons (Appendix 4); a few persons not listed were contacted but we did not get a reply. The species that were eventually compiled in Appendix 3 were then prioritized according to the criteria presented below (section 6.1).

5.3 Conclusions from the literature review, discussions/workshops, and the review of research and monitoring activities

Our compilation of available information on genetic diversity of wild fauna and flora in Sweden shows that extensive information is available. For many species, there is good knowledge of the population genetic structure from mapping genetic diversity over more or less extensive parts of the species range in Sweden. There is also data on temporal genetic changes for at least 36 species (Appendix 1).

For nine species, some sort of genetic monitoring program (Category I or II; Schwartz et al. 2007, see section 1.1 above) is ongoing (brown trout, arctic fox, wolf, wolverine, brown bear), or is planned to start in 2020 (Atlantic

herring, eelgrass, Atlantic cod, Atlantic salmon). The only long-term program primarily directed towards monitoring genetic diversity (Category II) concerns brown trout and follows genetic diversity of several brown trout populations in Hotagen Nature Reserve (Natura 2000 SE0720183) in the County of Jämtland, central Sweden. Initiated in 1979, the program covers 40 years of regular sampling (Jorde and Ryman 1996; Palm et al. 2003; Charlier et al. 2011, 2012, Palmé et al. 2013; Andersson et al. 2017b, 2017a). It has no long-term secured funding and has been funded primarily via research grants.

A program that utilizes both Category I and II monitoring is currently in place for the arctic fox. Since c. 2000, a sub-population in the Helags region of Härjedalen, central Sweden, has been subjected to detailed monitoring that includes a pedigree from genetics/genomics data, as well as field observations which can be used to monitor inbreeding levels (Hasselgren et al. 2018). Such pedigree data from genetic/genomic analyses and tracking data is also available for the grey wolf, a species which has been monitored using genetic techniques since the 1990s, in addition to tracking data from the original founders of the population, since the early 1980s. The arctic fox study is supported by SEPA, but is also funded from many other sources, such as the Norwegian Environment Agency, sponsorships, and various research grants. The wolf monitoring is funded mainly by SEPA.

The wolverine and brown bear are monitored using genetic/genomic techniques primarily for individual identification (Category I; Schwartz et al. 2007; Brøseth et al., 2010; Flagstad et al., 2019). Occasionally, data is used to address questions about inbreeding levels and genetic diversity (Norman and Spong 2015, Bischof et al. 2016). These programs are funded by SEPA, but also have other funding sources.

Monitoring of genetic diversity (Category II) for Atlantic herring, Atlantic cod, eelgrass and Atlantic salmon is scheduled to start in 2020. These are the first of 12 species to be monitored through a program developed by the Swedish Agency for Marine and Water Management (SwAM; see section 6.2).

We found that extensive monitoring for non-genetic purposes is currently conducted for 37 species (Appendix 3) and previously collected samples and/or easily-added sampling could be used for monitoring genetic diversity. We compiled information on tissue bank collections that include temporal series of tissue that can be used to monitor genetic diversity over time (section 6.6).

We used all the information compiled as a basis for our suggestion for a program for monitoring genetic diversity (section 6). Species that we consider for monitoring of genetic diversity are listed in Appendix 3. These species were compiled based on the review work that we carried out. Thus, our species list is biased towards species that are already subject to some form of monitoring, research involving temporal genetic data, etc., and towards those where the

monitoring of genetic diversity might be relatively easy to link with these ongoing activities. This approach was also in line with the instructions we obtained from SEPA regarding how to pursue this task. In the sections below, we describe how we prioritized the species listed in Appendix 3, in order to provide a proposed priority list of species for recommended monitoring programs to be initiated by SEPA, or to ensure the continuation of ongoing efforts to monitor trends in genetic diversity over time.

Following the review of the first version of this report, SEPA decided that 15 of our proposed pollinator species were of particular interest and commissioned us to provide a separate proposal for the monitoring of genetic diversity of these species. We carried out this work and report the pollinators in a separate report (section 8).

6 Recommendations for monitoring genetic diversity in Sweden

6.1 Categories of species to prioritize for monitoring genetic diversity

We adopted prioritization criteria in order to prioritization the species which had relevant information on monitoring (Appendix 3), as requested by SEPA. Previous work has suggested categories of species that are particularly warranted for monitoring with respect to potential genetic changes over time (Laikre & Ryman 1997; Lundqvist et al. 2008; Laikre et al. 2008). Here, we build on those previous suggestions, and with some modifications we use the following categories for prioritizing species for monitoring genetic diversity over contemporary time frames:

1) Species/populations subjected to substantial harvest (hunting, fishing, collecting, logging, etc.).
2) Species/populations listed in the annexes of the EU Habitats Directive and/or the EU Birds Directive.
3) Species/populations at risk of unwanted gene flow through, e.g., large-scale releases or other anthropogenic activities.
4) Red-listed species (including NT-classified species; "red-listing" refers to IUCN criteria applied at national level).
5) Swedish populations that are genetically distinct from others over the distribution range.
6) Populations likely to be strongly affected by climate change (e.g., alpine and northern boreal species, Baltic Sea species with marine origin, low elevation species likely to not tolerate increasing temperatures).
7) Natural reference populations (presumed safe and non-exploited populations where "natural" and non-human induced rates of genetic change can be monitored and knowledge on such rates obtained)

Other factors that we give attention to include:

a) species of key ecological importance, including habitat forming species and top predators;
b) pollinators (specifically requested by SEPA for consideration);

c) species for which tissue collections are available providing an immediate possibility for contemporary monitoring of genetic diversity;
d) species already subjected to some form of genetic monitoring;
e) species subjected to other types of monitoring where individuals are sampled or handled during which samples for genetic analysis are possible to obtain; and
f) indigenous wild relatives to domesticated species (c.f. Aichi target 13).

In our species prioritization, we gave higher priority to species for which initiating monitoring of genetic diversity could potentially be facilitated through already ongoing sample collection/research activities, and thus more species could be involved given the same funding. An important factor for our prioritization is whether genetic and/or genomic tools are available for the species. We prioritized species for which such resources are available so that monitoring of genetic diversity can be initiated promptly. However, we also gave high priority to several species from underrepresented species groups in order to include them in a monitoring scheme, even though there was no existing sampling/research and/or genetic markers. For those species which fulfilled several of these criteria, we proposed several taxonomic groups (thus, some species with the same priority ended up being included in certain ambition levels and others not).

6.2 A program currently under development for the monitoring of genetic diversity of marine and freshwater species

The Swedish Agency for Marine and Water Management (SwAM) has already compiled a proposal including a list of species for monitoring genetic diversity to start in 2020 (Johannesson & Laikre 2020). This is the result of a three-year pilot program (2017-2019) that has proposed methods for integrating genetic biodiversity into national environmental monitoring of habitats under the responsibility of SwAM, i.e., freshwater, coastal, and marine areas. The program has been run in close collaboration with managers representing a wide range of management areas at SwAM and has included follow-ups and reporting on the framework of the EU Directives (Habitats, Marine, Water), national environmental monitoring, fisheries management, data management and hosting, and national environmental objectives, among others. The goal is to ensure that monitoring of genetic diversity will be integrated into all relevant areas of management.

After extensive discussions, twelve species have been selected based on various needs and interests from managers. The species are identified as important for socio-economic, conservation, and/or ecological reasons. There is a need to identify population genetic structure in order to assess whether exploitation or environmental change have affected population structure and within- and between-population genetic diversity. Other needs include assessing inbreeding rates in threatened species, connectivity among populations in different areas (including within and between protected areas), and the effects of conservation efforts and climate change. Some examples of hypotheses relating to these needs are that variation is declining rapidly in presumed-threatened species, that protected areas are protecting genetic diversity of key species, and that genetic distinctions can be found among spawning localities.

The program is designed to run in "cutting cycles" or "overlapping cycles", with respect to both the monitored species and the covered geographic areas. The "cutting cycles" approach is applied in other areas of SwAM's environmental monitoring work and is planned to work as follows. When the monitoring program for genetic diversity starts, four of the 12 species will be the focus of sampling during the first year. Selected areas/populations will be included to cover a restricted part of the species range. The samples will be scored, and the results reported during the second and third year of the program, respectively. During the fourth year, these species will to be sampled again, in the same or in separate areas, depending on what appears to be most relevant from results obtained during the first cycle.

During the third year of the program, the sampling of two additional species will be initiated, and these will be scored and reported during the fourth and fifth year. Subsequently, new sampling of these species will occur in the sixth year, etc. Thus, the program is designed to expand over a three- to four-year period into its full expansion in the fifth year, when all 12 species will be involved in some form of annual monitoring (sampling, screening, reporting, or planning for future sampling). This approach will allow an adaptive program where increasing knowledge can be used to modify and improve monitoring efforts. By testing hypotheses, the program will evolve, and the questions and hypotheses that arise from the results of the program will aid in its further development (cf. Flanagan et al. 2018; Mimura et al; 2017). This will also allow for a restricted budget, which was a specific request from SwAM.

The program is planned to start in 2020, and the suggested focal species for this year are Atlantic cod, Atlantic herring, Atlantic salmon, and eelgrass. The budget requirements from SwAM allows approximately 400 individuals per species to be sampled and screened for genetic variation. For three of these species, previous samples are available in tissue banks, which can provide

measures of temporal genetic change already within the first cycle for these species. In the present report, we include and prioritize the species already identified by SwAM and we recommend SwAM to start the monitoring program for genetic diversity in 2020, as previously planned (Johannesson & Laikre 2020).

6.3 Proposal for a program for monitoring contemporary genetic changes starting 2020

Our proposal for the program is based on the information gathered on a total of 167 species considered for monitoring of genetic diversity (Appendix 3). We have proposed a relative ranking of the listed species based on the prioritization criteria above (section 6.1), using the ranks high (high priority), medium (medium priority), and low (low priority). The ranking takes the following into account:

- all prioritization categories,
- all additional factors, and
- the availability of established genetic research/network/genetic resources, which allows monitoring to begin immediately.

With this foundation, we then aimed to select species for broad taxonomic representation. Furthermore, we included considerations from SEPA, and comments provided by reviewers of the first version of this report. Several managers reviewed the report and commented on the species list. In particular, SLU Swedish Species Information Centre provided a careful review of our ranking (Figure 4).

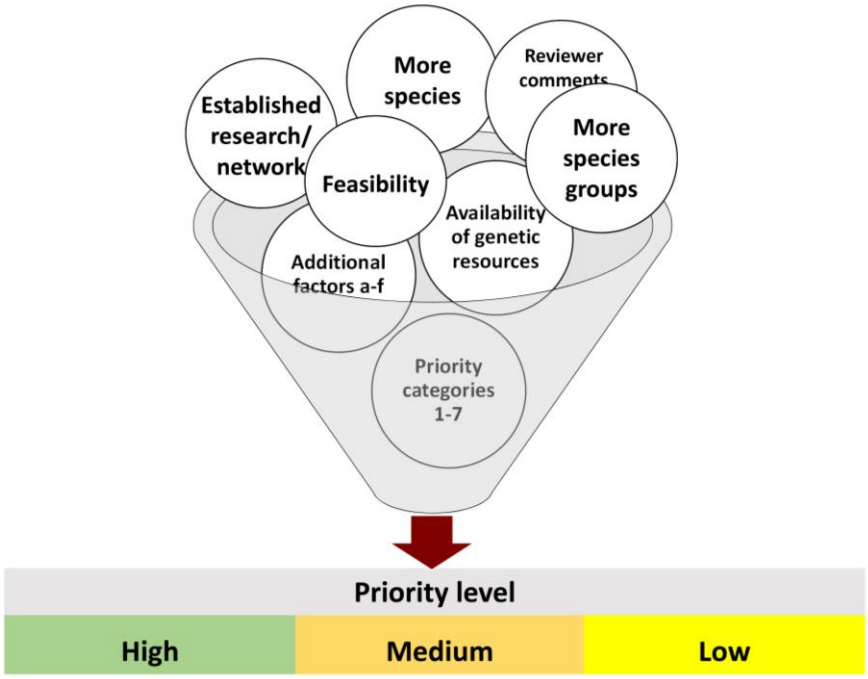

Figure 4. Factors considered for prioritizing 167 species identified for potential monitoring of genetic diversity (Appendix 3).

Of the 167 species considered (Appendix 3), 60 species are ranked as high priority. These include 9 terrestrial mammals, 2 marine mammals, 9 birds, 2 amphibians, 8 fishes, 1 marine and 1 freshwater invertebrate, 16 insects, 5 forest trees, 2 wild relatives to crops, 2 mosses, 2 algal, and 1 grass species (Figure 5; Appendix 3). The 16 insects are all pollinating species: 3 solitary bee species, 11 bumble bees, and 2 butterfly species. Fifteen of these pollinators were selected by SEPA after the first review of this report for a special sub-report and proposal on pollinators (section 6.4).

The 60 species include three large carnivores (wolf, brown bear, and wolverine) for which genetic programs are already in place, but for which genetic diversity is not routinely followed (genetics are used for other purposes; Table 1). These also include the 12 species identified by SwAM, and 15 species of pollinators described in a separate sub-report (Sub-report on pollinator species; section 6.4).

No. of species

Species group	Subgroup	High	Medium	Low	Species group
Mammals	Carnivores	5			Mammals
	Rodents & shrews	2	3	6	
	Marine mammals	2	2		
	Bats			3	
	other non-carnivores	2	1	1	
Birds	Birds of prey		2		Birds
	Water birds		1	2	
	Passerines	5	9	5	
	Gamebirds	3	1		
	Waders	1		1	
Amphibians	Frogs	1	1	1	Amphibians
	Toads	1	2		
	Newts		2		
Reptiles	Snakes		1		Reptiles
Fish		8	9	6	Fish
Invertebrates	Mussels	2			Invertebrates
	Amphipods		1		
	Arachnids			1	
	Insects	16	21	6	
	Snails			1	
Vascular plants	Woody plants	6	9		Vascular plants
	Grasses	1	1	2	
	Herbs	1	2	1	
Mosses		2		1	Mosses
Lichens				1	Lichens
Algae		2		1	Algae
		60	68	39	

Figure 5. Ranking among 167 species identified as potentially suitable for monitoring of genetic diversity (Appendix 3).

Clearly, these are only a few species, and several groups of organisms are missing. We stress, however, that these species are proposed due in large part to the presence of already ongoing efforts that would be relatively easy and cost-effective to maintain or modify in order to include the monitoring of genetic diversity.

We stress that temporal genetic aspects are the focus of the monitoring, and it is important that predictable and stable long-term funding for these efforts will become available. Similarly, the full geographic range of the species cannot be covered at once. Rather, in an initial step, monitoring of genetic diversity will focus on separate populations/population segments/regions for most species (exceptions include large carnivores already subjected to genetic monitoring where large parts of the distribution range are already covered). For each species monitored, we suggest that the process for prioritizing areas/populations includes open and transparent science-management discussions and workshops led by SEPA, similar to the process carried out in the work for SwAM (Johannesson & Laikre 2020).

An initial study over parts of the distribution range will provide information on whether genetic changes do occur, how large they are, what they might be caused by, etc. This information will aid in determining the monitoring frequency for this particular population/metapopulation, and it will aid in determining the populations, population systems, regions, and/or

parts of the distribution range that could be covered in future monitoring. Time frames between sampling occasions relate to generation time, and it is important to keep track of the number of generations between sampling occasions, as this time will affect conclusions from effective population size assessments, among other factors (c.f., Ryman et al. 2014, 2019, forthcoming work). Typically, sampling from one generation apart up to a few generations apart appears reasonable, but for species with already available tissue bank collections, monitoring over longer periods will also be of interest and will need to be evaluated for each particular species.

6.4 A separate sub-report for pollinator species

With respect to pollinating insects, we received further instructions from SEPA following our first submission of this report. After taking our initial ranking of pollinators into account (which included 16 high-ranked species: 3 solitary bee, 11 bumblebee, and 2 butterfly species), SEPA specified 15 of these species as of interest for further investigation (2 butterfly, 10 bumblebee, and 3 bee species). We were asked to propose a program for monitoring genetic diversity for each of these species. We were also informed that a relatively extensive budget was available for pollinating insects in general, and thus we did not have to limit the proposal to low budget suggestions (as for other species). A separate sub-report was prepared on the pollinators as requested by SEPA (see Section 8 for full reference to the sub-report on pollinator species).

Table 1. Ranking of the species considered for monitoring of genetic diversity in Sweden. The colour indicates the ranked priority; green=high priority, orange=medium priority, yellow=lowest priority. Ambition levels indicate what efforts are possible for separate species (ambition level 1 is the lowest ambition and 3 the highest). For species with no ongoing sampling effort only ambition level 2 or 3 might be possible (see section 6.10.1 for more details). P = Pollinators; species selected by SEPA for separate effort (see section 6.4 and sub-report 1 reference in section 8), S = SwAM; species selected by the Swedish Agency for Marine and Water Management for monitoring of genetic diversity (section 6.2; Johannesson & Laikre 2020). See Appendix 3 for more details on each species and on cost calculations.

Species group	Subgroup	Species	Ambition level		
			1	2	3
Mammals	Carnivores	Wolf (*Canis lupus*)	*	*	*
		Brown bear (*Ursus arctos*)	*	*	*
		Wolverine (*Gulo gulo*)	*	*	*
		Eurasian lynx (*Lynx lynx*)			*
		Arctic fox (*Vulpes lagopus*)	*	*	*
	Rodents & shrews	Field vole (*Microtus agrestis*)	*	*	*
		Red-backed vole (*Myodes glareolus*)	*	*	*
		European beaver (*Castor fiber*)		*	*
		Grey-sided vole (*Myodes rufocanus*)		*	*
		Shrew (*Sorex araneus*)		*	*
		Eurasian pygmy shrew (*Sorex minutus*)			*
		Norway lemming (*Lemmus lemmus*)			*
		Wood lemming (Myopus schisticolor)			*
		Northern red-backed vole (*Myodes rutilus*)			
		Root vole (*Microtus oeconomus*)			
		Masked shrew (*Sores caecutiens*)			
	Marine mammals	Harbor porpoise (*Phocoena phocoena*)		*	*
		Ringed seal (*Pusa hispida*)	S	S	S
		Grey seal (Halichoerus grypus)			*
		Harbor seal (*Phoca vitulina*)			*
	Bats	Brandt's bat (*Myotis brandtii*)			
		Greater mouse-eared bat (*Myotis myotis*)			
		Common pipistrelle (*Pipistrellus pipistrellus*)			
	Other non-carnivores	Moose (*Alces alces*)	*	*	*
		Red deer (Cervus elaphus)		*	*
		Mountain hare (*Lepus timidus*)		*	*
		Wild boar (*Sus scrofa*)			
Birds	Birds of prey	Golden eagle (*Aquila chrysaetos*)	*	*	*
		White-tailed eagle (*Haliaeetus albicilla*)		*	*
	Water birds	Common murre (*Uria aalge*)			*
		Common eider (*Somateria mollissima*)			*

		Long-tailed duck (*Clangula hyemalis*)			*
	Passerines	Wheatear (Oenanthe oenanthe)		*	*
		Great reed warbler (*Acrocephalus arundinaceus*)	*	*	*
		Collared flycatcher (*Ficedula albicollis*)	*	*	*
		Bluethroat (Luscinia svecica)		*	*
		Willow warbler (*Phylloscopus trochilus*)		*	*
		Eurasian skylark (*Alauda arvensis*)		*	*
		Ortolan bunting (*Emberiza hortulana*)		*	*
		Weed warbler (*Acrocephalus scirpaceus*)			*
		Yellowhammer (*Emberiza citrinella*)		*	*
		European greenfinch (*Carduelis chloris*)			*
		Common house martin (*Delichon urbica*)			*
		Common starling (*Sturnus vulgaris*)			*
		European pied flycatcher (*Ficedula hypoleuca*)		*	*
		Red-backed shrike (*Lanius collurio*)			*
		Eurasian tree sparrow (*Passer montanus*)			*
		European robin (*Erithacus rubecula*)			
		White wagtail (*Motacilla alba*)			
		Common whitethroat (*Sylvia communis*)			*
		Lesser whitethroat (*Sylvia curruca*)			
	Gamebirds	Black grouse (*Lyrurus tetrix*)		*	*
		Rock ptarmigan (*Lagopus muta*)	*	*	*
		Willow ptarmigan (*Lagopus lagopus*)	*	*	*
		Hazel grouse (*Tetrastes bonasia*)			*
	Waders	Great snipe (*Gallinago media*)		*	*
		Southern dunlin (*Calidris alpina schinzii*)			
Amphibians	Frogs	Moor frog (*Rana arvalis*)	*	*	*
		Common frog (*Rana temporaria*)			
		Pool frog (*Pelophylax lessonae*)			
	Toads	Natterjack toad (*Epidalea calamita*)	*	*	*
		Common toad (*Bufo bufo*)		*	*
		European green toad (*Bufo viridis*)		*	*
	Newts	Smooth newt (*Lissotriton vulgaris*)			*
		Northern crested newt (*Triturus cristatus*)		*	*
Fish		European perch (*Perca fluviatilis*)	*	*	*
		Arctic char (*Salvelinus alpinus*)	S	S	S
		European catfish (*Silurus glanis*)	*	*	*
		Brown trout (*Salmo trutta*)	* S	* S	* S
		Viviparous eelpout (*Zoarces viviparus*)	S	S	S
		Atlantic herring (*Clupea harengus*)	S	S	S

		Atlantic cod (*Gadus morhua*)	S	S	S
		Atlantic salmon (*Salmo salar*)	S	S	S
		Northern pike (*Esox lucius*)		*	*
		Common roach (*Rutilus rutilus*)			*
		Burbot (*Lota lota*)		*	*
		European eel (Anguilla anguilla)		*	*
		Pikeperch (Sander lucioperca)		*	*
		European sprat (*Sprattus sprattus*)		*	*
		Vendace (*Coregonus albula*)		*	*
		European flounder (*Platichthys flesus*)			*
		Common dab (Limanda limanda)			*
		3-spined stickleback (*Gasterosteus aculeatus*)			
		Whitefish (*Coregonus lavaretus complex*)			
		Common bream (*Abramis brama*)			*
		Plaice (*Pleuronectes platessa*)			*
		Turbot (*Scophthalmus maximus*)			*
		Corkwing wrasse (*Symphodus melops*)			*
Invertebrates	Mussels	Freshwater pearl mussel (*Margaritifera margaritifera*)	S	S	S
		Blue mussel (*Mytilus edulis*)	S	S	S
	Amphipods	Benthic amphipod (*Monoporeia affinis*)			*
	Insects	Green-veined white (*Pieris napi*)	P	P	P
		Parnassius apollo (*Parnassius apollo*)	P	P	P
		Grey-backed mining bee (*Andrena vaga*)	P	P	P
		Grey-banded mining bee (*Andrena denticulata*)	P	P	P
		Orange-legged furrow-bee (*Halictus rubicundus*)	P	P	P
		Garden bumblebee (*Bombus hortorum*)	P	P	P
		Short-haired bumblebee (*Bombus subterraneus*)	P	P	P
		Broken-belted bumblebee (*Bombus soroeensis*)	P	P	P
		Bombus pascuroum	P	P	P
		Bombus terrestris			*
		Bombus lapidarius	P	P	P
		Arctic bumblebee (*Bombus polaris*)	P	P	P
		Golden-belted bumble bee (*Bombus balteatus*)	P	P	P
		Bombus hyperboreus	P	P	P
		Bombus lapponicus	P	P	P
		Mountain bumblebee (*Bombus monticola*)	P	P	P
		Speckled wood (*Pararge aegeria*)			*
		Anthocharis cardamines			
		Aglais urticae		*	*

		Polygonia c-album			
		Carterocephalus palaemon			
		Callophrys rubi			
		Lasiommata megera			
		Coenonympha arcania			
		Maniola jurtina			
		Polyommatus icarus			
		Ochlodes sylvanus			
		Polyommatus amandus			
		Boloria selene			
		Brenthis ino			
		Melitaea athalia			
		Cryptic wood white (*Leptidea juvernica*)			*
		Wood white (*Leptidea sinapis*)			*
		Real's wood white (*Leptidea realii*)			*
		Norfolk damselfly (*Coenagrion armatum*)			*
		Arctic bluet (*Coenagrion johanssoni*)			*
		Emerald damselfly (*Lestes sponsa*)			*
		Macroplea mutica			
		Hermit beetle or Russian leather beetle (*Osmoderma eremita*)			
		Common bluetail damselfly *(Ischnura elegans*)			*
		Banded demoiselle (*Calopteryx splendens*)			*
		Slender ground-hopper (*Tetrix subulata*)			*
		Common ground-hopper (*Tetrix undulata*)			*
	Arachnids	*Anthrenochernes stellae*			
	Snails	Grove snail (*Cepaea nemoralis*)			
Vascular plants	Woody plants	Norway spruce (*Picea abies*)	*	*	*
		Scots pine (*Pinus sylvestris*)	*	*	*
		European beech (*Fagus sylvatica*)		*	*
		Field elm (*Ulmus minor*)		*	*
		Wych elm (*Ulmus glabra*)		*	*
		European crab apple (*Malus sylvestris*)		*	*
		European hornbeam (*Carpinus betulus*)			
		Sessile oak (*Quercus petraea*)			
		English yew (*Taxus baccata*)			
		Swedish whitebeam (*Sorbus intermedia*)			
		European white elm (*Ulmus laevis*)			
		European ash (*Fraxinus excelsior*)			*
		Field maple (*Acer campestre*)			*

		Large-leaved lime (*Tilia platyphyllos*)			
		Wild cherry (*Prunus avium*)			*
	Grasses	Eelgrass (*Zostera marina*)	S	S	S
		European feather grass (*Stipa pennata*)			*
		Fennel pondweed (*Potamogeton pectinatus*)			
		Common wild oat (*Avena fatua*)			
	Herbs	Field mustard (*Brassica rapa*)		*	*
		Gymnadenia nigra			*
		Wild carrot (*Daucus carota*)			*
		Onerow yellowcress (*Nasturtium microphyllum*)			
Algae		*Fucus radicans*	S	S	S
		Fucus vesiculosus	S	S	S
		Black carageen (*Furcellaria lumbricalis*)			
Mosses		Red-stemmed feathermoss, or Schreber's big red stem moss (*Pleurozium schreberi*)		*	*
		Splendid feather moss (*Hylocomium splendens*)		*	*
		Scapania apiculat			
Lichens		Lamb snow lichen (*Stereocaulon coniophyllum*)			*

6.5 Molecular genetic methods for monitoring genetic diversity of proposed species

Molecular genetic tools for mapping and monitoring genetic diversity have been evolving rapidly ever since the allozyme technique was introduced for large-scale screening of natural animal and plant populations in the 1970s (Allendorf et al. 1977; Allendorf & Utter 1978). Presently, genomic tools are becoming available for an increasing number of wild animals and plants and therefore have a growing potential to be used in genetic monitoring (Shafer et al. 2015; Montero et al. 2018). A wide variety of genetic markers are already in use in ongoing genetic monitoring programs (Appendix 2, 3), including allozymes, RFLP, candidate gene sequencing, mtDNA, microsatellites, more or less extensive SNP arrays, ddRAD-sequencing, genotyping by sequencing, Pool-sequencing, whole genome de novo sequencing, and individual resequencing (for some of these terms see: https://www.fws.gov/r7/gem/glossary). In connection with ongoing monitoring, new genetic markers and techniques have continuously been introduced, validated for consistency, and applied as they have become available, as in the studies of e.g., arctic fox (Hasselgren et al. 2018), wolverine (Ekblom et al. 2018), and brown trout (Andersson et al. 2017; Kurland et al. 2019).

While we advocate that individual whole-genome resequencing is ultimately the most informative approach for monitoring genetic biodiversity, there are currently several drawbacks to this approach, primarily with respect to the resources needed, e.g., costs for resequencing and bioinformatics analyses. Furthermore, means of assessing contemporary genetically effective population size (Ne; Allendorf & Ryman 2002) are currently not available and validated for sub-structured populations using genomic data. Thus, other approaches such as microsatellites, SNPs, etc., are still also valid options for monitoring genetic diversity. In addition, markers such as MHC, allozymes, or other coding loci may be applicable for addressing particular issues. In several cases, it might be important to monitor adaptive genetic variation – i.e., genetic markers reflecting variation at genes under selection in local environments resulting in genetic adaptations to local environmental conditions. In a few cases, such variation might have already been identified and of immediate use to the proposed program described here. An example is the Atlantic herring, which has been selected for monitoring by SwAM. In the Atlantic herring population, genetic structure is difficult to identify without the use of selected markers (Lamichany et al. 2012; Barrio et al. 2016; Hill et al. 2019). A Fluidigm SNP assay has been developed based on such markers for population genetic monitoring in the Atlantic-Baltic area (Prof. Leif Andersson, pers. comm.). In other species, information on potential adaptive genetic variation is not yet available but might be identified in the initial steps of monitoring genetic variation, particularly if whole-genome resequencing techniques are applied.

For the proposed prioritized species, the suitability of different genetic techniques will depend on whether specific markers are currently in use in ongoing mapping and monitoring projects. Additionally, genomic resources vary between species; the existence of a reference genome is marked for each species in one of the columns (Appendix 3). Finally, markers will, and should be, elaborated and evaluated over time. If, for example, SNP markers are used for a particular species at the start of national monitoring in 2020, this does not imply that those markers must be used for decades to come. Rather, the monitoring program for genetic diversity must be adaptive and allow for the development of new approaches. This is also true for population genetic parameter estimation, statistical testing, and bioinformatics approaches. As new knowledge is gained, the programs should adapt. Financial potential for such adaptive work, including the evaluation of old vs. new markers, will continuously be needed to assure that best practice is used in monitoring.

6.6 Prioritize tissue banks

A critical aspect of monitoring genetic diversity is to keep and maintain tissue samples from the collected individuals (cf. Jackson et al. 2012) because it allows previously analysed/collected samples to be re-analysed as new techniques emerge. The samples need to be stored safely and data on the samples must be computerized in databases that are available to researchers and managers. During this work, we became aware of several shortcomings with respect to tissue banks and associated databases. These include a general lack of information on which tissue banks and databases are available, what the tissue banks contain (databases not always available, or not complete), if samples can be easily searched, the quantity of available tissue/DNA, and the rules of use for this material. Such information is vital for planning monitoring activities. Thus, we recommend making an overview of the existing tissue-bank collections and improving their status with respect to databases and visibility as a part of the monitoring program for genetic diversity to be initiated by SEPA in 2020.

There are several collections of tissue which can provide excellent contributions to the monitoring of genetic diversity. Some of these collections include detailed information on where each specimen was collected (detailed geographic location or coordinates). However, this information is not easily accessible. Thus, we further underline the importance of conducting work to more thoroughly compile the availability of archives that can be used in monitoring genetic diversity.

We identified three large tissue banks, the largest being the Environmental Specimen Bank at the Natural History Museum ("Miljöprovbanken") in Stockholm, which carries over 300,000 individual samples representing 190 species. For a majority of these species, less than 100 individual samples are available, but for approx. 30 species relatively extensive time series are available. The SLU Aqua freshwater lab carries approx. 20,000 individual samples from 18 fish species. This material is primarily otoliths, but tissue is also available for several fish species. The Department of Zoology at Stockholm University holds a frozen tissue bank with over 160,000 individual samples from 35 species, including fish, mammals, birds, and a forest tree (Norway spruce), with many time series.

Other tissue banks include those for green-veined white butterfly and speckled wood butterfly at Stockholm University. SLU Umeå holds collections of grey red-backed vole, field vole, and Norway lemming. The National Veterinary Institute (SVA) has a biobank with samples from harbour porpoise, wild boar, and bats, while Lund and Uppsala Universities have collections of several small bird species and amphibians. Samples collected within the

framework of National Environmental Monitoring Programs are also stored at the National Veterinary Institute (SVA) and the Swedish University of Agricultural Sciences (SLU). A large collection of pinned insects (>10,000) that was started in 2005-2006 can be made available for genetic analysis from the nature consulting company Calluna AB (Magnus Stenmark, head of Ecocom Nord sector and environmental consultant, pers. communication). Many researchers hold additional sample banks.
Our conclusion is that these tissue collections are highly valuable resources for monitoring genetic diversity and it is vital that these collections are maintained. Therefore, we propose that an extensive overview of tissue banks be carried out, focusing on the improvement of detailed digital information on samples and their availability.

6.7 Literature revision and guidelines for use of knowledge

Considerable knowledge is available and is continuously generated on the genetic diversity of species in Sweden. Several previous reviews have summarized existing knowledge and we provide a brief update here. We propose that methods for the continuous review and synthesis of knowledge on genetic diversity are created within the framework of a genetic diversity monitoring program. Such continuous reviews should be funded by SEPA and/or SwAM and the reviews should be made accessible to managers and others who may benefit from this information. Furthermore, guidelines on how to consider and use genetic information in various management efforts should be communicated by SEPA and SwAM to national, regional, and local managers (cf. Sandström et al. 2016, 2019; previous research programs have provided example guidelines here: bambi.gu.se/baltgene; http://www.congressgenetics.eu/; https://www.fws.gov/r7/gem).

6.8 Research project evaluating potential problems with temporal ascertainment bias

During this work, we have identified a potential problem with ascertainment bias when using restricted SNP markers for the monitoring of isolated vs. non-isolated populations (discussions including Prof. Nils Ryman, Stockholm University). We envision that this might be a problem when an SNP panel is developed using samples from the population that is to be monitored. To clarify, the SNPs chosen for studying a population are developed by selecting

markers based on their variability at the time of development. When variability patterns of samples from the same population are compared between different points in time, we would expect less genetic variation (provided that the population is isolated). We suggest that this issue of potential ascertainment bias be evaluated within a brief research assignment funded by SEPA, within the framework of the program for genetic diversity monitoring.

6.9 Project coordination and management

Several aspects must be considered to ensure the long-term success of a national program to monitor genetic diversity. The motives behind the program need to be understood and agreed upon by the managers who are directly involved in its realization across sectors (such as those coordinating sampling with other efforts or distributing results), and in order to ensure that the results are effectively used in all relevant sectors. For instance, the results from monitoring genetic diversity will be relevant for managers working with national environmental objectives, the EU Habitats Directive, the EU Birds Directive, the EU Marine Strategy Framework, EU water directives, EU Action Plans for threatened species, red-listing, protected areas, and many more. Currently, genetic diversity is lacking from several of these areas, and thus, efforts should be made to integrate genetics into management and implementation within those frameworks. Such efforts could include workshops, discussion hubs, seminars, etc.

Previous work has shown that time and platforms are needed for continuous knowledge exchange between managers and conservation genetic scientists. This has been demonstrated by the experiences of a multidisciplinary research effort (BONUS BAMBI; www.bambi.gu.se) that focuses on the integration of genetic knowledge in biodiversity management in Sweden and neighbouring countries (Laikre et al., 2016; Sandström et al., 2016; Lundmark et al. 2017, 2019; Sandström et al. 2019), as well as from a three-year program within SwAM to elaborate and integrate a monitoring program for genetic diversity (Johannesson & Laikre 2020). Such platforms need to include physical meetings, workshops, and projects where managers and scientists exchange information, discuss management issues, and work together while monitoring genetic diversity. We propose that knowledge platforms that facilitate exchange between management and scientists are formed and funded (see further Klütsch & Laikre, 2020).

The main agencies in Sweden that are responsible for monitoring genetic diversity in wild populations are the Swedish Environmental Protection Agency (SEPA), the Swedish Agency for Marine and Water Management (SwAM), and

the Swedish Forest Agency (SFA). However, results from monitoring will be relevant to a wide range of players outside these agencies, including regional and local agencies, various organizations and researchers, as well as the general public. Thus, efforts are needed to ensure transparency, and the availability of data, databases, and results. Funding for efforts ensuring coordination and accessibility, as well as outreach and science communication to policy makers and the public, is therefore proposed. Similarly, we propose the funding of one part-time coordinator at each of the fore mentioned organizations (SEPA, SwAM, and SFA), where one of them would be responsible for leading and coordinating these efforts (through, e.g., organizing joint meetings, workshops, communication, outreach activities, planning, etc.). Furthermore, we propose that a group of external conservation genetic experts are linked with these coordinators to form a leading team (c.f. "Populationsgenetiska Kansliet" at CBM in Sjögren-Gulve et al. 2009). Costs for these efforts are estimated to be SEK 1,500,000 annually.

6.10 Costs for the proposed monitoring of genetic diversity

To estimate the approximate yearly cost of monitoring genetic diversity, we associated four groups of cost categories for each species based on existing preconditions, such as ongoing DNA- and non-DNA-based monitoring schemes, genetic research, and genetic resources.

Cost category 1 - additional costs for the ongoing DNA-based monitoring schemes

For a few of the proposed populations/species (e.g., the large carnivores, including wolf, wolverine, and brown bear), there are already ongoing surveys of genetic variation that are financed by SEPA, as part of population management. For such cases, we expect that funding for these projects will continue independently of the new effort to monitor genetic diversity outlined here. We suggest additional limited funding of approx. SEK 100,000 per species per year, to secure long-term availability and ease of access to samples and data analyses/management, in relation to the monitoring of genetic diversity (assessing measures of genetic diversity over time; cf. Johannesson & Laikre 2020). These additional population genetic and/or bioinformatics analyses can be carried out by a scientist who can analyse data from several species at a time. Since long-term data is already available, this work can start immediately.

Cost category 2 - additional costs for the ongoing monitoring of genetic diversity in research

For a number of populations/species, there are ongoing long-term research projects generating useful sample collections and data on genetic variation which are valuable to monitoring genetic diversity. As these are typically coordinated by individual research groups at universities and are funded by research grants, their inclusion relies on the willingness of individual researchers to participate in the project. We propose that some funding (approx. SEK 150,000 annually) be allocated to such research projects, in order to secure the continuation of field work and to aid in tissue collection/storage and project management. In addition, some funding should be given to such research projects for maintaining already-generated genetic/genomic data (SEK 50,000 per time point) and to conduct new genetic/genomic analyses, where needed (see below). In cases where new field work needs to be initiated, the costs will depend heavily on the specific situation but should be estimated to extend to at least SEK 150,000 per time point and species/population.

Cost category 3 - additional costs for ongoing non-DNA-based monitoring schemes

A number of monitoring schemes issued by agencies, such as SEPA, SwAM, and the Swedish Forest Agency, have already established networks for consistent collection of sample material within the frameworks of population surveys, bird-ringing, analyses for heavy metal and organic substance content, etc. These current and ongoing sampling plans have the potential to be included in the monitoring program for genetic diversity, with the addition of costs for genetic and data analysis of the collected samples. We suggest funding of approx. SEK 300,000 per 100 samples per year to be allocated for this category.

Cost category 4 - additional costs for species not included into any pre-existing monitoring schemes

For the species that are not currently a part of any ongoing genetic research, sampling, or monitoring, project management will need to be established. This would include fieldwork for tissue collection, sample storage, genetic analyses, data storage, and data presentation. The proposed costs for this are estimated at approx. SEK 400,000 per 100 samples per year.

Cost category 5 – one-time costs for developing of genetic markers

The costs for conducting new genetic/genomic analyses in the future are difficult to evaluate since the technology is constantly improving. These costs are also highly dependent on the number of individuals sampled per time point

and at what interval each species/population should be sampled. The following are some approximate suggestions.

- Genotyping of microsatellite/SNP markers: we propose that reasonable sample sizes include 50-100 samples per population and time point, at a cost of approx. SEK 100,000 per 100 samples.
- Genotyping by sequencing/ddRAD-sequencing: we propose sample sizes of approx. 50 individuals per population and time point, at a cost of SEK 100,000 for 500 samples.
- Resequencing (only where reference genome is available): 20 samples per population and time point, at an estimated cost of SEK 100,000 per 20 samples.

As a general estimate to cover the different ambition levels of monitoring, we propose a sum of SEK 200,000 for the development of genetic markers.
In addition, there will be costs for bioinformatics, data analyses, and reporting. These tasks can be included for each species and assigned to separate research groups to perform (as in other environmental monitoring efforts), or they can be assigned to a few persons who carry out analyses for several species. Regardless, we expect these tasks to be carried out by highly qualified population geneticists and bioinformaticists. Therefore, we expect these responsibilities to include salary costs of approx. SEK 2,000,000 annually.

6.10.1 Estimated costs for monitoring genetic diversity based on ambition level

It is difficult to precisely estimate the cost of genetic analysis for monitoring, as this depends on many factors, such as the type of markers used, the number of samples analysed, and the time interval between sampling. Furthermore, as outlined above, genetic methodologies are constantly being developed and improved. In line with the instructions from SEPA, we propose three different levels of ambition, from low to high, in order to exemplify what kind of data can be generated under different budget regimes.

In Appendix 3, under columns “Ambition level 1-3 of monitoring” in sheet “Species overview”, we specify the cost category and the proposed sampling interval/size for each of the included species. A lack of information in these columns means that a species is not suggested for monitoring. Sheet “Cost estimations” provides approximate annual cost calculations (column “Annual cost per 100 samples, SEK”) for each species and ambition level. Note that these are speculative estimations; more precise calculations and setups for monitoring

programs will be possible in collaboration with the appointed implementor groups.

In Appendix 3, when suggesting a sampling interval, we were guided by the following ideas:

- For most of the species, the sampling interval was approximately equal to the generation time for that species (to our best guess).
- To reduce costs, the sampling interval for short-lived species, such as passerine birds, rodents, and shrews, corresponded to every second generation, and every third generation for invertebrates (except for the pollinator species included in the sub-report on pollinators).
- If an ongoing sampling scheme had the potential to be included in the proposed monitoring program, the sampling interval was chosen to match that scheme (e.g. every fifth year for mosses).

Ambition Level 1

This is the lowest level of ambition and is primarily based on existing summary data from other projects (together with some limited additional genetic analyses).

- Pollinators: 15 pollinator species are proposed in a separate program for monitoring genetic diversity, starting in 2020 (see the Sub-report on pollinators). This program has its own funding, so it entails no additional costs. These 15 species are marked as “pollinators” in Appendix 3.
- SwAM species: 12 marine and freshwater species are currently included in a SwAM genetic diversity monitoring program with its own funding proposal (cf. section 4.2.; Johannesson & Laikre 2020). We have included proposed costs for that program here, but without details per species. The 12 species are marked as “SwAM” in Appendix 3.
- Maintenance of ongoing long-term monitoring efforts, including genetic diversity, for five species. Several programs are already running which include genetic data (see section 5.3 above). These include brown trout in Hotagen Nature Reserve, arctic fox in the Helags area, as well as wolf, brown bear, and wolverine, which are currently in Category I monitoring. It is vital that these programs continue, and we propose support to ensure their maintenance. For the programs with a Category I monitoring focus, we propose funds to ensure that the data generated by the programs can be analysed to address questions concerning the maintenance of genetic diversity, which is not currently carried out regularly.

- Another 11 high priority-level species that are already included in various monitoring projects with established networks for tissue collection and storage.
- One medium priority-level species which is already being monitored.

The expected cost for Ambition Level 1 is as follows:

- the pollinator program: 2,432,000 SEK annually, plus a one-time cost for the development of genetic markers, ranging from 1,183,000 to 1,759,000 SEK, depending on the chosen setup (Sub-report on pollinators, Appendix sIII);
- the SwAM program: 1,500,000 SEK annually;
- all other species: 943,500 SEK annually (see Appendix 3, sheet "Cost estimations"); and
- additional annual costs of 1,500,000 SEK for personnel at SEPA/SwAM and external expertise support, as well as 2,000,000 SEK for management and salaries.

Ambition Level 2

The middle level of ambition includes:

- all 44 species from Ambition Level 1 with increased sampling effort (potentially more populations) and data production. Shorter sampling intervals and higher sample size numbers are suggested at this level.
- Additionally, 14 species with high-priority and 20 with medium-priority levels.

The expected cost for Ambition Level 2 is as follows:

- the pollinator program: 3,223,000 SEK annually plus a one-time cost for the development of genetic markers, ranging from 1,391,000 to 2,258,000 SEK, depending on the chosen setup (see Appendix sIII);
- the SwAM program: 2,000,000 SEK annually;
- all other species: 4,470,000 SEK annually plus a one-time cost of 200,000 SEK for the development of genetic markers (see Appendix 3); and
- additional annual costs of 1,500,000 SEK for external expertise support, as well as 2,000,000 SEK for management and salaries.

Ambition Level 3

This is the highest ambition level. It expands the sampling effort and increases the level of detail of information on genetic diversity generated for each species. This level includes:

- all 78 species from Ambition Level 1 and 2 with increased sampling effort (potentially more populations) and data production. Shorter sampling intervals and higher sample sizes are suggested at this level.
- Additionally, it includes three high-priority species, 27 medium-priority species, and 16 low-priority species, including those without previously generated genetic markers.

The cost for Ambition Level 3 is as follows:

- the pollinator program: 4,147,000 SEK annually, plus a one-time cost for the development of genetic markers, ranging from 1,892,000 to 3,470,000 SEK, depending on the chosen setup (see Appendix sIII);
- the SwAM program: 3,000,000 SEK annually;
- all other species: 12,203,500 SEK annually plus a one-time cost of 800,000 SEK for the development of genetic markers (see Appendix 3, sheet “Cost estimations”); and
- additional annual costs of 1,500,000 SEK for external expertise support, as well as 2,000,000 SEK for management and salaries.

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9 Appendices and sub-report on pollinators

Appendix 1

Summary of 70 temporal genetic studies for species occurring naturally in Sweden that were identified in the literature search from Laikre et al. 2008 (30 studies) and updated for the period 2006-2019 within the present study (40 studies). Papers marked with an asterisk * were added within the framework of the present report.

Appendix 2

Results from a complementary literature review to identify publications from 2006-2019 on genetic diversity of natural animal and plant populations in Sweden. A total of 267 publications were identified. This literature complements those found and reported in reviews by Laikre et al. 2008 and Lundqvist et al. 2008. *Separate excel file available at* https://www.naturvardsverket.se/978-91-620-6959-9

Appendix 3

Species considered for the genetic diversity monitoring program with ranking for their prioritization regarding monitoring of genetic diversity. *Separate excel file available at* https://www.naturvardsverket.se/978-91-620-6959-9

Appendix 4

Persons that we have contacted via email, phone, or video/physical meeting, from whom we have obtained information used in the present report.

Reference for sub-report on pollinators

Posledovich D., R. Ekblom, and L. Laikre. 2021. Mapping and monitoring genetic diversity in Sweden: Suggestions for pollinating species. Swedish Environmental Protection Agency Report 6958, 2021, ISBN 978-91-620-6958-2, available at https://www.naturvardsverket.se/978-91-620-6958-2

9.1 Appendix 1

The following is a summary of 70 temporal genetic studies for species occurring naturally in Sweden that were identified in the literature search from Laikre et al. 2008 (30 studies) and updated for the period 2006–2019 within the present study (40 studies). Papers marked with an asterisk * were added within the framework of the present report.

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
Fish ▼							
Arctic char (*Salvelinus alpinus*)	Hatchery and wild populations were compared for differences in allele frequency change. **No differences** could be detected. But see comments by Ryman et al. (1993).	869 (45-180 per sampling site/occasion)	Hornavan, Rensjön, Ottsjön, Torrön, northern Sweden	4 consecutive years (1983-1986)	Allozymes (3)	Nyman and Ring 1989	--------
Atlantic cod (*Gadus morhua*)	Temporally **stable** genetic differentiation among spawning populations of Atlantic cod	636	11 locations at the Western coast of Sweden, Skagerrak	12 years (2000-2011)	Microsatellites (8)	André et al. 2016*	Formas; GU Centre for marine evolutionary biology (Cemeb); Swedish Agency for Marine and Water Management (SwAM); European Fisheries Fund; Norwegian Research Council; EU Interreg funds
Atlantic herring (*Clupea harengus*)	Significant **temporal differentiation** over two years at two locations. Interpreted as genetically divergent spawning waves.	2440 (34-100 per sampling site/occasion)	11 locations, Baltic Sea	2 years (four occasions)	Microsatellites (9)	Jørgensen et al. 2005	Danish Ministry for Food, Agriculture and Fisheries; Danish Agricultural and Veterinary Research Council; Danish Natural Science Research Council (21-04-0045)
	No temporal divergence over two years in 18 spawning aggregations.	5841 (400-1332 per sampling region/ occasion)	North Sea, Skagerrak	2 years	Microsatellites (9)	Ruzzante et al. 2006	Funded by the European Union within the fifth framework program
	No change in the amount of genetic variation or spatial structure, temporal differentiation is weak over time	546 historical and 1237 modern samples	5 locations, the Baltic Sea and Skagerrak	~ 20 years (1979-80 vs. 2002-03)	Microsatellites (9), allozymes (11)	Larsson et al. 2010*	European Union within the Framework Programme 5; Formas; Swedish Research Council VR; Sven and Lilly Lawski's Fund; Carl Tryggers Stiftelse; Stockholm Marine Research Centre; BONUS Baltic Organisations' Network for Funding Science EEIG

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
Atlantic salmon (*Salmo salar*)	The **hybrid frequency increased** over the 7-years	685 (302 and 686 per sampling year)	1 location, Dalaälven at Älvkarleby	7 years (1989-95)	Allozymes (2)	Jansson and Öst 1997*	National Board of Fisheries; Vattenfall AB; Swedish Council for Forestry and Agricultural Research
	Stocking of Sävarå with non-indigenous *S. salar* over a 17-year period has not resulted in replacement or any extensive introgression (**stable GD**)	98 modern samples vs. 116 donor strain samples	Multiple locations, N Sweden, Sävarå	~ 17 years (1989–2005)	Microsatellites (8)	Nilsson et al. 2008*	National Board of Fisheries; FoMa (Fortlöpande Miljöanalys SLU via Swedish Council for Forestry and Agricultural Research)
	Temporal genetic changes have occurred due to a combination of genetic admixture and random allele frequency fluctuations in small populations (genetic drift).	546 (4-82 per sampling site/year)	>10 locations, Gullspångsälven, Vänern, Klarälven	49 years	Microsatellites (9)	Palm et al. 2012*	Fiskeriverket, County Administrative Board of Västra Götaland; Formas
	Salmon-trout hybrids represented 6% of the sampled salmon (1961-2012); the proportion of the hybrids among ascending salmon, trout and hybrids increased to >10 % by 2012; the proportion of salmon strays was 2-3% (2004-2012) (**hybridisation increased**)	946 (13-181 per sampling year/age group)	1 location, Mörrumsån	52 years	Microsatellites (18)	Palm et al. 2013*	Fiskeriverket; WWF; Sveaskog AB; Göte Borgströms Foundation; Formas
	Stable stock composition between the years, regional differences in the proportion of farmed salmon in the catch	2850 (33-293 per sampling site/year)	18 locations, Baltic Sea along the eastern coast of Sweden	2 years	Microsatellites (17)	Östergren *et al.* 2015*	Swedish Agency for marine and water management (HaV); EU data collection program DCF; FORMAS
	Decrease in genetic divergence and diminished isolation by distance patterns meaning that today's populations are more genetically similar than a century ago. **Increase in genetic diversity** and a clear change in genetic composition within populations	893 historical & 787 contemporary samples	13 locations, along the Eastern coast of Sweden	~100 years (1920-30 vs. 1961-63 vs. 2010-15)	SNP (82)	Östergren et al. Manuscript*	Formas

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
Baltic cisco (*Coregonus albula*)	Long-term effective population size in spring-spawners was about 20 times lower than autumn-spawners, with signs of long-term gene flow in both directions and a **recent genetic bottleneck** in spring-spawners (**decreased GD**)	376	Southern Sweden, Lake Fegen	~ 40 years (1960s vs 1990-2000)	Microsatellites (9)	Delling and Palm 2019*	Swedish Research Council for Environment, Agricultural Sciences and Spatial Planning
Brown trout (*Salmo trutta*)	Large **allele frequency change** in hatchery stocks compared with corresponding natural populations.	455 (12-103 per sampling site/occasion)	3 locations, Rivers Indalsälven, Umeälven	11 years	Allozymes (2)	Ryman and Ståhl 1980	Gote Borgstroms stiftelse for fiske- och vattenviird; Swedish Natural Science Research Council (EI 3746-002, -004, and -007)
	0.03% of genetic variation explained by variation between years (**stable GD**)	612 (100-106 per sampling site/occasion)	3 lakes, Jämtland, central Sweden	2 years	Allozymes (35)	Ryman 1983	National Swedish Environment Protection Board; Swedish Natural Science Research Council
	Significant allele frequency change over 15 consecutive cohorts in four mountain lakes. Estimated effective population sizes were 52 - 480.	5899 (~100 per sampling site/occasion)	4 populations, Jämtland, central Sweden	15 years	Allozymes (14)	Jorde and Ryman 1996	Swedish Natural Science Research Council; Swedish Environmental Protection Agency
	The **hybrid frequency increased** over the 7-years period	1231 (781 and 450 per sampling year)	1 location, Dalaälven at Älvkarleby	7 years (1989-95)	Allozymes (2)	Jansson and Öst 1997*	National Board of Fisheries; Vattenfall AB; Swedish Council for Forestry and Agricultural Research
	Haplotype frequency shifts among 14 consecutive cohorts in a mountain lake population. Estimated female effective population size was 58.	704 (40-66 per sampling occasion)	1 population, Jämtland, central Sweden	14 years	mtDNA	Laikre et al. 1998	Swedish Natural Science Research Council; Swedish Environmental Protection Agency; Research Council of Norway (no.109332/410)
	Temporal **stability** was estimated in seven sections of a small forest stream - temporal change was found within one section.	661 (27-78 per section/ occasion)	7 sections of Färsån, central Sweden	2 years	Microsatellites (5)	Carlsson and Nilsson 2000	European Community Structural Funds
	Significant genetic divergence among cohorts within streams. Average female effective size just below 30. Migration between populations maintains variability.	879 (1-44 per sampling site/cohort)	13 streams, Island of Gotland	6 cohorts	mtDNA	Laikre et al. 2002	EU/EC Structural Fund 5b, Swedish National Board of Fisheries; Foundation for Strategic Environmental Research MISTRA; Swedish Natural Science Research Council (NFR); Erik Philip-Sörensen Foundation

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
	Temporal **stability** of the observed structure over four years. Considerable temporal shifts within two populations. The estimated effective population sizes were 19 and 48.	2028 (2 populations, ~100 per sampling site/occasion)	2 stream populations, Jämtland, central Sweden	20 years	Allozymes (17)	Palm et al. 2003a	Swedish Natural Science Research Council; Foundation for Strategic Environmental Research MISTRA; Swedish Research Council for Environment, Agricultural Science and Spatial Planning (FORMAS); Erik Philip-Sörensen Foundation; Research Council of Norway
	Allele frequencies differed significantly between wild and sea-ranched populations but were due to **temporal genetic changes** within populations.	273 (20-40 per sampling site/occasion)	1 location, River Dalälven, central Sweden	4 years	Allozymes (17), Microsatellites (8)	Palm et al. 2003b	Formas; Foundation for Strategic Environmental Research MISTRA; Commission of the European Communities, Agricultural and Fisheries (FAIR) specific RTD programme, CT-97-3498
	Sävaå population is unique, but likely some introgression has occurred with non-indigenous *S. trutta* (**no introgression increase**)	49 modern samples vs. 76 donor strain samples	Multiple locations, N Sweden, Sävaå	~ 12 years (1995–2006)	Microsatellites (8)	Nilsson et al. 2008*	National Board of Fisheries; FoMa (Fortlöpande Miljöanalys SLU via Swedish Council for Forestry and Agricultural Research)
	No genetic variation between the locations.	285 (2-51 per sampling site/year)	10 locations, Gullspångsälven, Klarälven	72 years	Microsatellites (10)	Palm et al. 2012*	Fiskeriverket; County Administrative Board of Västra Götaland; Formas
	Temporal genetic **stability** over 30 years	3225	1 location, Jämtland, Blanktjärnen	31 years (1980-2010)	Allozymes (14)	Charlier et al. 2012*	Swedish Research Council; Formas; BONUS Baltic Organizations' Network; Carl Trygger Foundation
	Cryptic structure remains **stable** over the two decades monitored	4140 (72–150 per sampling site/year)	2 locations, Trollsvattnen lakes	19 years (1987–2005)	Allozymes (14), Microsatellites (7)	Palmé et al. 2013*	Formas; Swedish Research Council; Carl Tryggers Stiftelse; BONUS Baltic Organisations' Network for Funding Science EEIG; National Evolutionary Synthesis Center; National Center for Ecological Analysis and Synthesis
	Substantial population structure formed by 3 genetically distinct groups, **increase** in proportion of the Siljan trout strain	558 (1-60 per sampling site/year)	16 locations, upper Österdalälven and Storån + hatchery stock in Särna	10 years	Microsatellites (10)	Dannewitz et al. 2014*	County Administrative Board of Dalarna
	The allozyme divergence remains **stable** over the sampling years and cohorts, with a slight significant	7107 (3-431 per sampling site/year)	11 locations, Östra and Västra	28 years (1987-2014)	Allozymes (14)	Andersson et al. 2017a*	Formas; Swedish Research Council; Swedish Agency for Marine and Water Management

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
	decreasing trend for sampling years but not for cohorts		Trollsvattnet lake system, Jämtland				
	The genetic variation (heterozygosity) tends to **increase** over time in several of the lakes and populations (Trollsvattnen, Flyn, Haravattnet and Haravattsån Fallet)	22859 (22-387 per sampling year/lake)	9 lakes, Jämtland, Hotagen Natural Reserve	32 years (1987-2015)	Allozymes (14)	Andersson et al. 2017b*	--------
	Substantial **annual variation** in the proportions of different stock groups in the Gulf of Finland catches, which much varied depending on the sampling site on the gulf and time of the fishing season	840	The Gulf of Finland	9 years	Microsatellites (17)	ICES 2018*	--------
European catfish (*Silurus glanis*)	The difference between the populations existed both in the past and exists in the future	320 modern samples	3 locations, Båven, Emån, Möckeln	≈ 65 years (1940 vs. 1982-2007)	Microsatellites (10)	Palm et al. 2008*	Formas; National Board of Fisheries in Sweden (Fiskeriverket); Swedish Research Council
European eel (*Anguilla anguilla*)	**Genetic variation among temporal samples** within sites clearly exceeded the spatial component. The results support the panmixia hypothesis for this species.	2626 (22-60 per sampling site/occasion for the temporal samples)	41 locations, temp. samples from 12 locations	9 years	Microsatellites (6)	Dannewitz et al. 2005	Formas; National Board of Fisheries in Sweden (Fiskeriverket); Financial Instrument for Fisheries Guidance (FIFG); Institute for the Promotion of Innovation by Science and Technology (IWT) in Flanders, EU contract EELREP (Q5RS-2001-01836)
European flounder (*Platichthys flesus*)	Temporal **stability** over the 2 years period	94	1 location in Sweden, Gotland	2 years (2003-04)	Microsatellites (9)	Hemmer-Hansen et al. 2007*	--------
Northern pike (*Esox lucius*)	**Stable** genetic structure over a decade	791 (129 earlier vs 662 later)	major part of the Baltic Sea	10 years (2001-2010)	Microsatellites (17)	Wennerstrom et al. 2017*	Formas; BONUS project BAMBI; European Union's Seventh program for research, technological development and demonstration; Swedish Research Council

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
Perch (*Perca fluviatilis*) & roach (*Rutilus rutilus*)	**Stable** levels of gene diversity over time for both species	688 (perch), 687 (roach)	1 location, the Biotest basin, Forsmark	24 years (1977- 2000)	Microsatellites (5)	Demandt 2010*	--------
Plaice (*Pleuronectes platessa*)	Temporal **stability** over the 2 years period	101 (50 per sampling year)	1 location, Pomeranian Bay (the Baltic Sea)	2 years (2006-2007)	Microsatellites (8)	Was et al. 2010*	Technological Sector Research Programme: Strand III Core Research Strengths Enhancement (2004–2007)
Three-spined stickleback (*Gasterosteus aculeatus*)	**Negligible temporal differences** in allele frequencies, genetic diversity and differentiation (**stable GD**)	150 (32-48 per sampling year/location)	2 locations, Fiskebäckskil and Sikeå (the Baltic Sea)	6 years (2003-2009)	Microsatellites (15)	DeFaveri and Merilä 2015*	--------
Turbot (*Scophthalmus maximus*)	A significant part of the genetic variance could be explained by **variation** among years within locality.	706 (16-50 per sampling site/occasion)	8 locations, Atlantic, North, and Baltic Seas	7 years	Microsatellites (8)	Nielsen et al. 2004	Danish Ministry of Food, Agriculture and Fisheries
	Strong temporal change exceeding the spatial divergence among sampling localities.	136 (30-56 per sampling occasion for the temporal part of the study)	1 location, Island of Gotland, southern east coast of Sweden	3 years (2002-2004)	Microsatellites (8)	Florin and Höglund 2007	--------
Mammals ▼							
Arctic fox (*Vulpes lagopus*)	**Lower levels of genetic variation** after a bottleneck in the early 20th century. Approx. 25% of microsatellite alleles and 50% of haplotypes were lost (decreased GD).	82 (51 and 31 per period)	Scandinavia	173 years (1831-1924 vs. 1995-2004)	Microsatellites (5), mtDNA	Nyström et al. 2006	EU-Life Nature to the SEFALO+ project
	The population exhibited a tenfold increase in average inbreeding coefficient with a final level corresponding to half-sib mating (**decreased GD**).	205	1 location, southernmost subpopulation in Sweden (Helagsfjällen, Jämtland County)	9 years (2000-2009)	Microsatellites	Norén et al. 2016*	EU LIFE; Swedish Nature Protection Agency; WWF; Fjällräven AB; Cronstedt Foundation; Formas, EkoKlim
	Genetic rescue due to natural immigration and gene flow: reduction in population average	543	1 location, southernmost subpopulation	5 years (2010-2015)	Microsatellites	Hasselgren et al. 2018*	EU LIFE; WWF; Fjällräven AB; Royal Physiographic Society of Lund; Swedish Research Council (Formas), ECOFUNC;

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
	inbreeding coefficient and **increase** in allelic richness (by 41%) within 5 years.		in Sweden (Helagsfjällen, Jämtland County)				EU/Interreg Sweden Norway to Felles Fjellrev I and II; Norwegian Environment Agency
	High connectivity and asymmetric migration rates across the region; more recently colonized sampling regions received immigrants from multiple sources; **no clear clines in allele frequency** or genetic diversity (**stable GD**)	44 historical and 417 modern samples (235 from Sweden)	throughout Fennoscandia	~100 (1835-1941)	Microsatellites (21)	Norén et al. 2015*	Formas; Önnesjö foundation, Göoran Gustafsson foundation for Nature and Environment in Lappland; foundation in memory of Oscar och Lili Lamm; Tullberg foundation for biological research; Norwegian Environment Agency and ECOFUNC
Red fox (*Vulpes vulpes*)	Eradication program of the American mink on the Koster Islands **decreased** its allelic richness; increased its genetic structuring while the effective population size did not change. In comparison, the population from the Swedish coast showed no changes in genetic diversity	205	Skagerrak, Koster Islands archipelago and the mainland	6 years (2006-2011)	Microsatellites (21)	Zalewski et al. 2016*	--------
American mink** (*Neovison vison*)	**Decline** in haplotype numbers across the bottleneck; small but significant decline in autosomal allelic richness in the southern subpopulation	121 (73 historical and 48 modern samples)	Throughout the distribution range	110 years (1830-1940)	Hypervariable mtDNA alleles, Microsatellites (19)	Xenikoudakis et al. 2015*	Swedish Research Council, Formas
Brown bear (*Ursus arctos*)	The estimated effective population size was 45 in southern Scandinavian, and the migration rate between this and adjacent populations 0.01.	240 (22-127 per sampling and time interval)	4 regions in Scandinavia	18 years	Microsatellites (18)	Tallmon et al. 2004	Swedish Environmental Protection Agency; Norwegian Directorate for Nature Management; Norwegian Institute for Nature Research; Swedish Association for Hunting and Wildlife Management; WWF-Sweden, Orsa Besparingsskog, private foundations: Université Joseph Fourier; Centre National de la Researche Scientifique
Eurasian otter (*Lutra lutra*)	Gene diversity decreased slightly but not significantly from 2002 to 2003 but increased significantly between	139 (23-65 per sampling year)	Central Sweden, Uppland	3 years (2002-04)	Microsatellites (8)	Björklund and Arrendal 2008*	Formas; Marie-Claire Cronstedts Stiftelse; Sophia von Anderssons Stiftelse; Helge Ax:son Johnsons Stiftelse; Lennanders Stiftelse

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
	2003 and 2004. The difference between 2002 and 2004 was not significant (**stable GD**)						
	Otters in the south were affected by the bottleneck, demonstrated by a decline in genetic diversity and a shift in genetic composition. Population structure and diversity of otters in the north remained mostly unchanged (**both decreased and stable GD**)	81 historic and 51 modern samples from museum collections	6 locations, Gothenburg & Scania, Småland, Stockholm, Dalarna, Västernorrland, Norrbotten	~ 180 years (1833-2013)	Microsatellites (12)	Tison et al. 2015*	Swedish Research Council
Grey wolf (*Canis lupus*)	Significant negative relationship between birth year and proportion of polymorphic microsatellite loci (**decreased GD**).	15	Sweden	18 years (1977-1994)	Microsatellites (12), mtDNA	Ellegren et al. 1996	Swedish Environmental Protection Agency
	Loss of one Y chromosome haplotype over the period (**decreased GD**)	14	Scandinavia	23 years (1977-2000)	Y chromosome markers	Sundqvist et al. 2001	Direktoratet for Naturforvaltning (Norway); Swedish Environmental Protection Agency; Swedish Research Council for Agriculture and Forestry; Swedish Hunting Association; Nordic Arctic Research Program; Olle Engkvist, Carl Trygger, Oscar and Lili Lamms, and Sven and Lilly Lawskis foundations; Knut and Alice Wallenberg foundation
	About 40% of allelic diversity and 30% heterozygosity lost over the study period (**decreased GD**).	57	Museum samples, Scandinavia	~150 years (1829-1979)	Microsatellites (19), mtDNA	Flagstad et al. 2003	Norwegian and Swedish Environmental Protection Agencies; Trygger and Engqvist foundations, Swedish Hunting Association; Bergvall foundation; Nordic Ministry of Councils; Swedish Research Council for Agricultural and Forestry; Knut and Alice Wallenberg foundation
	Evidence of **increased** heterozygosity, allelic diversity, population growth and outbreeding after the arrival of one immigrant.	124	Scandinavia	~170 years (1829-2001)	Microsatellites (12-19)	Vilà et al. 2003	Environmental Protection Agencies in Norway and Sweden; Olle Engkvist and Carl Trygger foundations; Swedish Hunting Association; Nordic Council of Ministers; Knut and Alice Wallenberg foundation

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
	Increased heterozygosity following the arrival of one immigrant wolf.	90	Scandinavia	23 years (1978-2001)	MHC class II (3)	Seddon and Ellegren 2004	Norwegian and Swedish Environmental Protection Agencies; Nordic Council of Ministers; Knut and Alice Wallenberg foundation
	A pedigree for a population founded in 1983 was constructed. Inbreeding coefficients ranged from 0 to 0.41. Litter size was reduced with increased inbreeding (**decreased GD**).	163	Scandinavia	19 years (1983-2002)	Microsatellites (32) and pedigree data	Liberg et al. 2005	Swedish Environmental Protection Agency; Worldwide Fund for Nature (Sweden); Swedish Association for Hunting and Wildlife Management; private foundation 'Olle och Signhild Engkvists Stiftelser'; Norwegian Directorate for Nature Management; Norwegian Institute for Nature Research; Norwegian Ministry of Environment; Formas
	Individual heterozygosity **decreased** during the 1980s followed by an **increase** in 1990-1991 after arrival of one migrant.	180 (108 Scandinavian, 72 Finnish)	Scandinavia	23 years (1977-2000)	SNP (24)	Seddon et al. 2005	Norwegian and Swedish Environmental Protection Agencies; American Kennel Club Canine Health Foundation; US Army Grant DAAD19-01-1-0658; training grant T32 HG00035 (HGP); Knut and Alice Wallenberg Foundation
	Immigrant wolves during the period 2002-2005 were monitored. Four out of 14 wolves were immigrants.	14	Scandinavia	5 years (2002-2005)	Microsatellites (20), mtDNA	Seddon et al. 2006	Norwegian and Swedish Environmental Protection Agencies; Knut and Alice Wallenberg Foundation
Mountain hare (*Lepus timidus*)	Significant level of genetic differentiation all the population pairs; the mountain hare on Gotland became extinct at one point, with subsequent re-colonization events	40 ancient and 90 modern samples	16 locations in Sweden: Gotland, Åland, mainland Southern Sweden	~6000-7000 years	Mitochondrial D-loop	Ahlgren et al. 2016*	Berit Wallenberg Foundation; Palmska Foundation; Albert & Maria Bergström's Foundation; Greta Arwidsson's Foundation; Swedish Research Council
Reptiles ▼							
Common European viper (*Vipera berus*)	**Increase** in the number of MHC alleles after genetic rescue intervention	14 (7 per year)	Skåne, Smygehuk	9 years (1996-99)	MHC class I loci	Madsen et al. 1999*	--------
Birds ▼							

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
Collared flycatcher (*Ficedula albicollis*)	Levels of genetic diversity highly similar between the two time points. No genetic differentiation between time points (**stable GD**)	85 (45+40)	Gotland	(1993-2015)	Whole genome sequences	Dutoit 2017*	--------
Great reed warbler (Acrocephalus arundinaceus)	Genetic similarity between individuals decreased over time in a population founded by a few individuals in 1978. Individual homozygosity in males declined (**increased GD**).	242 (collected between 1987-1993)	1 population, Kvissmaren, central Sweden	7 years	Microsatellites (10), DNA-fingerprinting	Hansson et al. 2000	Swedish Natural Science Research Council (NFR); Swedish Forest and Agricultural Research Council (SJFR); National Swedish Environment Protection Board (SNV); Royal Swedish Academy of Science (Ahlstrand and Hierta-Retzius Foundations); Lunds Djurskyddsfond; Olle Engkvist Byggmästare Foundation
Lesser white-fronted goose (*Anser erythropus*)	Genetic variability in mtDNA has **increased** six-fold during the past 140 years despite the precipitously declining population	29 historical samples from Sweden and 33 modern samples from Fennoscandia and West Russia	7 areas in Lappmark, Lapland, Norrbotten, Scania	~ 140 years (1860-1946 vs 1988–2000)	Microsatellites (7), mtDNA haplotypes	Ruokonen et al. 2010*	Swedish Research Council; Academy of Finland
Willow grouse (*Lagopus lagopus*)	Spatial and temporal allele frequency variation each represented 3% of the gene diversity.	640 (10-88 per sampling site/occasion)	5 localities, central and northern Scandinavia	3 years (1978-1980)	Allozymes (6)	Gyllensten 1985	Swedish Natural Science Research Council; C. F. Liljevalch Jr. Foundation; Nordic Council for Wildlife Research
Blue-tailed damselfly (*Ischnura elegans*)	Population differentiation in 2002 was significantly smaller than in 2004 in the neutral loci. The type and/or strength of selection on morph frequencies in this system can change substantially between years	8-34 per sampling site/location	12 locations, Southern Sweden, Lund	2 years (2002-04)	Amplified fragment length polymorphism (AFLP) (3)	Abbott et al. 2008*	Swedish Research Council VR, Oscar & Lilli Lamms Stiftelse; Formas
	Negative frequency-dependent selection maintaining the phenotypic stasis and genetic diversity in the populations (**stable GD**)	6413	12 locations, Southern Sweden, Lund	12 years (2000-11)	Color polymorphism alleles	Le Rouzic et al. 2015*	European Commission; European Union Seventh Programme; Swedish Research Council; Erik Philip Sörenssons Stiftelse

Insects ▼

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
Fruit fly (*Drosophila subobscura*)	Reduced frequencies of the o_5 chromosome inversion in the two populations (3.7 and 1.8%) when compared with previous studies (14.3%) (**decreased GD**).	--------	2 populations, Gävle and Lilla Edet, central Sweden	--------	Chromosomal inversions	Mestres et al. 1994	Dirección General para la Investigación Cientifica y Técnica (Spain); Comissió Interdepartamental de Recerca i Tecnologia, Generalitat de Catalunya
Spear-winged fly (*Dipsa bifurcata*)	Approx. 20% higher within population genetic variation in autumn compared to spring samples. C. 82% of the variance due to differences between seasons, 15% due to differences among localities.	2915 (30-278 per sampling site/occasion)	4 populations, Skåne, southern Sweden	8 years	Allozymes (2)	Niklasson et al. 2004	Nordic Foundation (NorFA). JT was supported by travel grants from the European Science Foundation to visit the Department of Ecology and Genetics, University of Aarhus, Denmark.
Worms ▼							
Pygospio elegans, marine polychaete	Variation in genetic structure indicating drift in temporal samples of the populations from the Baltic Sea	271 (39-53 per sampling year/location)	2 locations in Sweden, Ängsö, Fårö	3 years (2008-10)	Microsatellites (8)	Kesäniemi et al. 2014*	Biological Interactions Graduate School (University of Jyväskylä); Jenny and Antti Wihuri Foundation; Danish Research Council; EU Marie Curie ITN Speciation.
Plants ▼							
Crow garlic (wild onion, wild garlic; *Allium vineale*)	Considerable genetic heterogeneity among sites and within sites among sampling years.	389 (12-23 per sampling site/occasion)	5 locations, Skåne, Island of Öland, southern Sweden	4 years (1995-1998)	RAPD	Ceplitis 2001	Jörgen Lindström fund; Swedish Natural Science Research Council
Scots pine (*Pinus sylvestris*)	One common haplotype present in modern, 100- and 10,000-year-old pollen samples indicate a persistent population through the postglacial period (**stable GD**).	50 (9-30 per time period)	1 population, Holtjärnen, Dalarna, central Sweden	~9 900 years	Plastid DNA	Parducci et al. 2005	Formas, Swedish Foundation for International Cooperation in Research and Higher Education (STINT); Carl Trygger Foundation (LP); Ministry of Education, Culture, Sports, Science and Technology of Japan (YS)
Algae ▼							
Narrow wrack (*Fucus radicans*)	Dominance of a few very large old clones over extensive spatial and temporal scales	198	16 locations, coastal areas of the Baltic Sea	10 years (2003-2012)	Microsatellites (9)	Ardehed et al. 2015*	Swedish Research Councils (Formas and VR); EU BONUS program
Plankton ▼							

Species group/ species	Observations/change in genetic diversity (GD)	Sample size (no ind.)	Sampling area	Time span	Type and no. of loci	Reference	Funding
Bacterio-plankton community	Strong temporal shifts in bacterioplankton assemblages with repeatable seasonal succession	8 (1 water sample per time point)	1 location, the Baltic Sea (Landsort Deep station)	2 years (2003-04)	Hypervariable region V6 of the 16S rRNA gene	Andersson et al. 2010*	Swedish Research Council; Carl Trygger Foundation; WM Keck foundation award
Pentapharsodinium dalei, dinoflagellate	High genetic diversity and subpopulation shifts coinciding with changes in hydrographic conditions	5 sediment layers (several subsamples in each)	1 location, Western coast, Koljö Fjord	~ 85 (1922-2006)	Microsatellites (6)	Lundholm et al. 2017*	Danish Research Council; Gothenburg Marine Research Centre; VILLUM Foundation, Denmark; Danish DFF
Skeletonema marinoi, bloom-forming diatom	Shifts in genetic diversity between years (changes in the dominant population)	480 (29-95 per sampling year/location)	4 locations, Gullmar Fjord on the Swedish west coast	2 years (2007–2009)	Microsatellites (8)	Godhe and Harnstrom 2010*	Formas; Sida; University of Gothenburg Marine Research Centre (GMF); C.F. Lundströms Stiftelse; Stiftelsen Oscar och Lilli Lamms Minne; Magnus Bergvalls Stiftelse; Lars Hiertas Minnesfond; Birger och Birgit Wåhlströms Minnesfond; Kapten Carl Stenholms Donationsfond
Viruses ▼							
Varroa destructor, ectoparasitic mite of honeybees	Significant changes in the genetic structure of the mite populations with the time, more pronounced changes in population infesting the mite-resistant honeybee colonies than in the mite-susceptible colonies	432 (41-146 per sampling year/hive)	30 hives, Gotland	10 years (2009-18)	Microsatellites (9)	Beaurepaire et al. 2019*	Formas; Ricola Foundation Nature and Culture; Vinetum Foundation; Persephone Charitable and Environmental Trust; EC funded National Program through the Swedish Board of Agriculture

** *American mink is an introduced non-native species in Sweden*

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9.2 Appendix 4

The following is a list of those contacted via email, phone, or video/physical meeting, who provided information used in the present report. Those who did not reply are not included here.

- Karolina Aloisi, Nordic Genetic Resource Centre (Nordgen)
- Anna Palmé, Nordic Genetic Resource Centre (Nordgen)
- David Diez, The Swedish Museum of Natural History, Stockholm
- Johan Kroon, Forestry Research Institute of Sweden, Skogforsk
- Sanna Black-Samuelsson, Swedish Forest Agency
- Tanja Slotte, Stockholm University
- Anna Westerbergh, Swedish University of Agricultural Sciences, SLU
- Martin Lascoux, Uppsala University
- Erik Svensson, Lund University
- Frank Johansson, Uppsala University
- Magne Friberg, Lund University
- Matthew Webster, Uppsala University
- Nils Ryman, Stockholm University
- Christopher Wheat, Stockholm University
- Karl Gotthard, Stockholm University
- Tom Oliver, University of Reading
- Matthew Greenwell, University of Reading
- Frauke Ecke, Swedish University of Agricultural Sciences, SLU Umeå
- Magnus Stenmark, regional manager / biologist at Ecocom, Gävle
- Anders Forsman, Linnaeus University
- Mikael Hedrén, Lund University
- Markus Franzén, Linnaeus University
- Niclas Backström, Uppsala University
- Jacob Höglund, Uppsala University
- Emily Baird, Stockholm University

- Stefan Palm, Swedish University of Agricultural Sciences, SLU Aqua
- Johan Charlier, Swedish County Administrative Board
- Per Ericson, Swedish Museum of Natural History (personal meeting)
- Olle Karlsson, Swedish Museum of Natural History
- Fredrik Ronquist, Swedish Museum of Natural History
- Kerstin Johannesson, University of Gothenburg
- Carl André, University of Gothenburg
- Elisabeth Nyberg, Swedish Environment Protection Agency
- Joakim Hjelm, Swedish University of Agricultural Sciences, SLU Aqua
- Jens Olsson, Swedish University of Agricultural Sciences, SLU Aqua
- Michele Casini, Swedish University of Agricultural Sciences, SLU
- Jan Sondell, Kvismaren Bird Observatory
- Lars Gustafsson, Uppsala University
- Anna Qvarnström, Uppsala University
- Tomas Pärt, Swedish University of Agricultural Sciences, SLU
- Debora Arlt, Swedish University of Agricultural Sciences, SLU
- Jonas Waldenström, Ottenby Bird Observatory
- Magnus Hellström, Ottenby Bird Observatory
- Dennis Hasselquist, Lund University
- Staffan Bensch, Lund University
- Bengt Hansson, Lund University
- Peter Bahlenberg, Ånnsjöns Bird Observatory
- Ingela Källén, Ånnsjöns Bird Observatory
- Anna Maria Johansson, Swedish University of Agricultural Sciences, SLU
- Karin Norén, Stockholm University
- Peter Hellström, The Swedish Museum of Natural History, Stockholm
- Michael Schneider, Länsstyrelsen Västerbotten
- Anna Hellström, Swedish Environment Protection Agency
- Erica Stigblom, Swedish Environment Protection Agency
- Klas Allander, Swedish Environment Protection Agency
- Jens Andersson, Swedish Environment Protection Agency
- Maria Jansson, Swedish Agency for Marine and Water Management

- Anna Hasslow, Swedish Agency for Marine and Water Management

Mapping and monitoring genetic diversity in Sweden

a proposal for species, methods and costs

DIANA POSLEDOVICH, ROBERT EKBLOM AND LINDA LAIKRE

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Biologiska övervakningsprogram är en central del för uppföljningen av de nationella miljömålen och konventionen för biologisk mångfald (CBD). Genetisk mångfald har identifierats av CBD som en av tre nivåer av biologisk mångfald, och den form av variation som är grunden för övriga nivåer (art- och ekosystemnivå).

Målet med denna rapport är att presentera ett förslag till ett övervakningsprogram för genetisk mångfald i Sverige.

Vi fokuserar främst på genetisk variation inom arter och inte på tekniker där genetiska analyser används för att kartlägga variation på art- och ekosystemnivå. Vi har identifierat arter som anses vara lämpliga för genetisk övervakning, och föreslagit en inbördes prioritering baserat på flera faktorer: redan pågående insatser som möjliggör effektiv provinsamling, hotbild, representation av olika organismgrupper och genomförbarhet.

Monitoring programs are an important tool for nature conservation and maintenance of biological diversity and are essential for implementation of the UN Convention on Biological Diversity (CBD). Genetic diversity (or genetic variation) is diversity within species, and it has been identified by the CBD as one of the three levels of biological diversity to be mapped, conserved, monitored, and sustainably used.

Genetic diversity provides the basis for all biological diversity and for biological evolution. Species and ecosystems depend on genetic variation for evolutionary potential, long-term survival, and resilience. We propose a monitoring program targeting genetic diversity within and between populations of species. We identify species suitable for genetic monitoring and suggest a prioritisation of these based on existing activities, threat levels, taxonomical representation and feasibility.

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