Developing a monitoring program of genetic diversity: what do stakeholders say?

Rea Pärli1 · Eva Lieberherr1 · Rolf Holderegger2,3 · Felix Gugerli2 · Alex Widmer3 · Martin C. Fischer3

Received: 16 June 2020 / Accepted: 18 May 2021 © The Author(s) 2021

Abstract
Genetic diversity is a fundamental component of biological diversity, and its conservation is considered key to ensure the long-term survival of natural populations and species. National and international legislation increasingly mandates a monitoring of genetic diversity. Examples are the United Nation’s Convention on Biological Diversity (CBD) Aichi target 13 and the current post-2020 negotiations to specify a new target for maintaining genetic diversity. To date, only a few pilot projects have been launched that systematically monitor genetic diversity over time in natural populations of a broad variety of wild species. The Swiss Federal Office for the Environment mandated a feasibility study in 2019 for implementing a national monitoring of genetic diversity in natural populations. To obtain information on whether stakeholders are interested in such a systematic monitoring, what they would expect from such a monitoring and where they see respective caveats, we conducted an online survey, which 138 (42% of those surveyed) Swiss stakeholders answered. We find that Swiss stakeholders are generally aware of the lacking evidence regarding the status of genetic diversity in wild populations and species. Accordingly, most stakeholders are interested in a monitoring of genetic diversity and see opportunities for the application of its results in their work. Nevertheless, stakeholders also expressed concerns regarding financial resources and that the results of a genetic diversity monitoring program would not benefit conservation practice. Our findings highlight the importance of stakeholder engagement and demonstrate the value of a detailed stakeholder analysis prior to developing and implementing a genetic diversity monitoring program. A powerful tool for examining the constellation and interactions of the different stakeholders are social network analyses (SNAs). Finally, it is particularly important to communicate transparently about the possibilities and limitations of a genetic diversity monitoring program as well as to closely involve stakeholders from the beginning to increase the acceptance of genetic diversity monitoring and facilitate its implementation.

Keywords Conservation genetics · Genetic diversity · International obligations · Monitoring · Stakeholder analysis

Introduction
Besides the diversity of species, ecosystems and their interactions, genetic diversity is key for maintaining species diversity and essential for the long-term survival of populations and species (Hoban et al. 2013; Shafer et al. 2015; Stange et al. 2020; Hohenlohe et al. 2021). This is particularly so in view of rapidly changing environments (Sgrò et al. 2011; Norberg et al. 2012; Pauls et al. 2013; Leigh et al. 2019; De Kort et al. 2021; Des Roches et al. 2021). The United Nation’s Convention on Biological Diversity (CBD) addresses the importance of protecting genetic diversity and asks for a reduction in genetic erosion in the Aichi Biodiversity Targets (2011–2020). Aichi Target 13 specifically addresses the conservation of genetic diversity; the international communities’ first attempt to value the importance of the genetic component of biodiversity (Hoban et al. 2013). In a next step, the post-2020 target for the erosion of genetic diversity is to be elaborated in more detail (Hoban et al. 2020), and the monitoring of genetic diversity over time should be included, not only for domesticated but also for wild species (Laikre et al. 2020).
The genetic diversity of few selected, mostly emblematic or economically important species are monitored occasionally (Bruford et al. 2017). However, very few countries have established a comprehensive monitoring program on genetic diversity that would inform conservation managers about standing levels and changes in genetic diversity of a broad array of populations of wild species over time. Moreover, the monitoring of the genetic diversity of multiple species has hitherto been hindered due to high costs. However, this no longer holds true, as next-generation sequencing (NGS) costs are decreasing, making a thorough monitoring of genetic diversity realistic (Allendorf 2017; Fischer et al. 2017b; Fuentes-Pardo and Ruzzante 2017; Supple and Shapiro 2018; Meek and Larson 2019).

Switzerland is no exception: it implements the international requested Aichi Biodiversity Targets, but lacks a biodiversity monitoring program that covers genetic diversity of wild populations to date. Indeed, Switzerland’s national biodiversity strategy includes several goals that target the prevention of genetic erosion of wild species as well as the development of a program to monitor changes in genetic diversity (FOEN 2012). Switzerland currently runs a general biodiversity monitoring program focused on changes in species richness (FOEN 2012) and two monitoring programs that concentrate on changes in agricultural lands (Agroscope 2015) and nationally important habitats (FOEN 2019) such as dry meadows, mires, alluvial ecosystems and amphibian spawning sites.

The Swiss Federal Office for the Environment (FOEN) is aware of Switzerland’s lack of a genetic diversity monitoring of wild populations and has thus supported research to assess the feasibility of a genetic diversity monitoring program (Fischer et al. 2020). For such a feasibility study, a key component is the assessment of current levels of genetic diversity and the monitoring of changes in genetic diversity of species over time (Schwartz et al. 2007), covering a broad variety of wild species. As part of this feasibility study for the development of a monitoring program of genetic diversity, we conducted a stakeholder analysis, which included the identification of the relevant stakeholders as well as their viewpoints on and demands towards a potential genetic diversity monitoring program. Additionally, we used social network analysis to study the constellation and interactions of different stakeholders.

Experience from natural resource management shows that performing a stakeholder analysis prior to implementing such a program is crucial to get insights about potential conflicts (Prell et al. 2009; Paletto et al. 2015). Stakeholder analysis can also help with integrating genetic diversity knowledge in conservation management, hence helping to close the well-known conservation genetic gap (Hoban et al. 2013; Mimura et al. 2017; Holderegger et al. 2019; Lundmark et al. 2019; Sandström et al. 2019). Further, already involving stakeholders in the development processes can improve the acceptance of a future genetic diversity monitoring program, and enable more transparent and efficient communication (Lindgren and Persson 2010). In line with the literature, our stakeholder analysis aims to shed light onto aspects to be considered for developing and implementing a genetic diversity monitoring program, with the potential to ultimately improve its acceptance and the participation of stakeholders in any genetic diversity monitoring program.

**Materials and methods**

In line with stakeholder analysis, we first mapped the landscape of potential stakeholders (Fischer et al. 2017a). We defined stakeholders as professionals, consisting of organizations, companies or governmental authorities who have a legitimate interest in or are affected by the course or outcome of a monitoring program of genetic diversity; in short, that they will likely use the monitoring data. We categorized the stakeholders into types that represent different professional backgrounds and, thus, diverse interests (Table 1). We decided not to survey the general public as we aimed at assessing the needs and interests of those directly involved in conservation management.

Following Fischer et al. (2017a), we worked at the level of organizations and identified a total of 331 stakeholders. These included national, regional and local authorities, universities, research institutions and research networks (e.g. the Swiss Academies of Science), environmental consultancies, museums, herbaria, national data centres for species occurrence data (www.infospecies.ch.), non-governmental organizations (NGOs) and foundations. We identified stakeholders through various documents, such as the list of addresses from the political consultation process on the Swiss Biodiversity Strategy and various lists of organisations active in nature conservation and environmental protection.

Second, and after the identification of stakeholders, we conducted interviews with seven experts in spring 2019. The experts were selected from the fields of regional (n = 2) and national authorities (n = 3), environmental consultancies (n = 1), and research (n = 1). We used these expert interviews as a pre-step for developing our online questionnaire (Table 2) following established protocols and formats (Fischer et al. 2017a). We designed the interviews in a semi-structured fashion, following the same order as the questionnaire (see Appendix 1). We used the interviews to check whether our survey questions are understandable and to see whether experts have additional pivotal points to be

© Springer
addressed. We also asked the experts to verify the list of stakeholders to triangulate our identification.

In a third step, we designed the online survey for the systematic identification of the needs, interests and concerns towards a genetic diversity monitoring program of as many Swiss stakeholders as possible (see stakeholder identification above). We contacted one person per identified organization and asked this person to represent the interests of their organization when filling the online survey. We sent a reminder 14 days after the launch of the online survey and completed data collection after 24 days.

Table 1 Overview of the assignment of stakeholders to specific types, and numbers of stakeholders identified and responding to the survey

| Stakeholder type       | Description                                                                 | Stakeholders identified | Answers (in %) |
|------------------------|-----------------------------------------------------------------------------|-------------------------|----------------|
| Research               | Researchers with a focus on genetic diversity of wild species, research networks that cover genetic biodiversity | 33                       | 22 (67%)       |
| Collections/museums    | Botanical gardens and museums with samples of wild species, data centers of species occurrence data | 47                       | 27 (57%)       |
| NGOs/foundations       | Civil society organizations that include genetic diversity/biodiversity in their work | 74                       | 24 (32%)       |
| Environmental consultancies | Private sector organizations that include genetic diversity/biodiversity in their work | 72                       | 23 (32%)       |
| Regional and local authorities | Regional and local authorities responsible for nature conservation and the preservation of biodiversity | 97                       | 39 (40%)       |
| Federal authorities    | Federal authorities responsible for aspects of nature conservation and the preservation of biodiversity | 8                        | 2 (25%)        |

Table 2 List of topics that were addressed in the expert interviews and the online survey with different stakeholders

| Topics                                      | Operationalization (in stakeholder survey)                                                                 |
|---------------------------------------------|-----------------------------------------------------------------------------------------------------------|
| Importance of biodiversity loss             | Assess the urgency of different environmental problems (climate change, water pollution, loss of biodiversity etc.) on a Likert scale between not urgent at all and very urgent |
| Importance of genetic diversity             | Rank the four levels of diversity (species diversity, diversity of ecosystem, genetic diversity, diversity of interactions) from most important (rank 1) to least important (rank 4) |
| Use of data on genetic diversity            | Indicate in how many of projects/tasks of daily work data on genetic diversity would be useful (from less than 10% to 90% and more). In a second question: Indicate in how many projects/tasks genetic information is currently used (from less than 10% to 90% and more) |
| Reasons for a genetic diversity monitoring program over time | Indicate which reasons (e.g. adaptability for the future, measuring connectivity etc.) are important for the introduction of a genetic diversity monitoring program (multiple choice) |
| Fields of application and important indicators | Indicate applications for which the results of a genetic diversity monitoring program (e.g. habitat quality improvement, measuring connectivity etc.) are important (multiple choice) |
| Content of a genetic diversity monitoring program | Which taxonomic groups should be included in a genetic diversity monitoring (multiple choice). Additionally, name up to three species, that should be included in a genetic diversity monitoring program (open question) and what further considerations would be relevant for the design of a monitoring program of genetic diversity (open question) |
| Participation in the development of a genetic diversity monitoring program | Potential interest in participating in the development of a genetic diversity monitoring program (yes/no) |
| Network of important stakeholders and their interaction | From a list of all the stakeholders identified, participants had to indicate those whom they perceive as important for the development and implementation of a genetic diversity monitoring program. Second, they were asked to indicate the stakeholders with which they are already in contact regarding the topic of genetic diversity. Some stakeholders were grouped into sub-types (e.g. research institutions in general rather than specific research institution) |
The survey included single and multiple-choice questions as well as questions on relational data between different stakeholders (Creswell 2012). The survey covered several topics, ranging from the perceived urgency of environmental problems (climate change, water pollution, biodiversity loss) to the participation in the development of a monitoring program of genetic diversity and the perceived importance of actors as well as who exchanges information with whom (see exhaustive list of topics in Table 2 and the entire survey in the supporting information Appendix 1). For the latter questions on network constellation, we grouped certain stakeholders into sub-types (seven sub-types containing overall 297 stakeholders), while keeping others as distinct stakeholders (34), resulting in a selection of 41 stakeholders and sub-types.

We used descriptive statistics to compare and analyse the answers of the different stakeholders. As only two out of eight national authorities filled out the survey, we decided to exclude them from further analysis. However, as other stakeholders identified the federal authorities as important or as information exchange partners in the survey, the federal authorities remain in the network analysis.

For questions regarding the constellation of stakeholders, we applied social network analysis (SNA), which entails the study of relationships between different stakeholders (who are represented by nodes) and the distribution of the connections between them (Wasserman and Faust 1994). In our case, this includes the identification of stakeholders who are perceived as important for developing and implementing a genetic diversity monitoring program as well as stakeholders considered as key partners for the exchange of information on genetic diversity. Based on the survey data, we designed two networks, one mapping which stakeholder perceives other stakeholders as important, and one network displaying existing information exchange on the topic of genetic diversity between the stakeholders. We used in-degree centrality, which is the number of times a survey participant mentioned a stakeholder (Borgatti et al. 2018), to identify the stakeholders perceived as most important and as the most popular partner for information exchange. To compare the two networks, we used network density, which we calculated as the number of connections between the nodes divided by the number of all possible connections (Borgatti et al. 2018).

Results and discussion

Of the 331 stakeholders that received the survey, 138 returned it. This response rate of 42% is rather high compared to other studies using online surveys in the realm of biodiversity topics (Braunisch et al. 2012). Whenever we use the term stakeholder in the presentation of the results, we refer to the sampling of 138 stakeholders who participated in the survey. As we were interested in different stakeholder types (Table 1), many of our results were aggregated at the level of these types (research, collections/museums, NGOs/foundations, environmental consultancies, authorities), with response rates ranging from 25% (federal authorities) to 67% (research; Table 1).

**Importance of the loss of biodiversity and genetic diversity**

Almost 90% of the stakeholders considered biodiversity loss to be a very important topic, while about 70% of the respondents also perceived climate change as highly relevant. Water pollution, soil degradation and air pollution were considered as less urgent. The stakeholders most often ranked genetic diversity third among the four levels of biodiversity. When comparing different stakeholder types, we observed that respondents from the types research and collections/museums ranked genetic diversity higher (>20% ranked it second or first) than other stakeholder types did. Many stakeholders commented that the task of ranking the different levels of diversity was difficult or inappropriate, because the levels of biodiversity influence each other. Others explained the lower ranking of genetic diversity by stating that investments in the diversity of ecosystems or species will also have positive effects on genetic diversity and/or that stable and large population sizes will also benefit genetic diversity.

**Use of information on genetic diversity**

The stakeholders considered the principal need for genetic data in their work as much higher than its actual use (Fig. 1). We found that for 34% of the stakeholders, genetic data would be relevant in 10–30% of their projects and tasks, and for 41% of the stakeholders such data would be relevant in 50–90% of their projects. However, more than 60% of the stakeholders stated that they actually use genetic data in less than 10% of their projects and tasks (Fig. 1b). The proportion of stakeholders who reported a use of genetic data in 50–90% of their projects was only 20%.

There is thus a clear discrepancy between desired data availability, the actual availability and the current use of genetic data by stakeholders. However, this discrepancy is not the same for all stakeholder types. It is greatest for regional and local authorities and environmental consultancies, while it is—not surprisingly—comparatively small in research (Fig. 1).

**Reasons for the introduction of a genetic diversity monitoring program**

More than 50% of the stakeholders stated that adaptability to future conditions, adaptation to climate change, connectivity...
(gene flow), and long-term survival of species are important reasons for introducing a genetic diversity monitoring program (Fig. 2). Other reasons such as measuring the fitness of a species (high genetic diversity and no inbreeding), preventing inbreeding and hybridisation or effects of translocations were mentioned by more than 20% of the stakeholders. Surprisingly, breeding and stocking were mentioned the least.

Connectivity seems to be of great concern for the stakeholders. The Swiss Biodiversity Strategy (FOEN 2012) and the related Action Plan (FOEN 2017) require the implementation of an ecological infrastructure, i.e., a national network of natural and semi-natural habitats that consists of core areas for biodiversity and areas that connect them. Thus, many Swiss stakeholders are currently working on connectivity issues (e.g. setting up wildlife corridors or stepping-stone habitats), which may explain their interest in this topic. Consequently, aspects related to connectivity will have to be a prominent focus of a genetic diversity monitoring program in Switzerland. However, the effectiveness of connectivity measures is a difficult task for a monitoring
program of genetic diversity, as it needs to have specifically targeted sampling designs. When implementing such a monitoring one has to be aware of this challenging expectation and clearly report on possible limitations.

Another often named reason why a genetic diversity monitoring program should be implemented was to measure the adaptability of species to future environmental conditions and to climate change. Interestingly, climate change had very low priority for stakeholders in a study on biodiversity by Braunisch et al. (2012), which surveyed a very similar stakeholder audience in Switzerland. The stakeholders who responded to the survey of Braunisch et al. (2012) had to sort 44 research questions according to their importance. The two questions concerning climate change were ranked as 32nd and 43rd only. In contrast, our survey reflected a much higher awareness of climate change with stakeholders, which can probably be explained by the currently intensive climate change debate in society (Marris 2019).

**Areas of application and indicators**

In accordance to what has been stated above, over 70% of the stakeholders selected connectivity as an important area of application of a genetic diversity monitoring (Fig. 3). In contrast, only about 30% of the stakeholders chose urban sprawl effects, which is one of the main factors leading to fragmentation in the Swiss landscape (Schwick et al. 2018). Another area of application that was frequently selected in the survey (> 50% of the respondents) was the implementation of the Swiss Biodiversity Strategy (FOEN 2012). This shows how important these national biodiversity strategies and action plans (as required by the CBD) are for the stakeholders and hence the relevance of the current CBD post-2020 negotiations are (Hoban et al. 2020; Laikre et al. 2020).

Also with regard to the four indicators that a genetic diversity monitoring program could provide, the indicator for connectivity clearly stood out: it was chosen by more than 70% of the stakeholders (Fig. 4). In principle, however, all four proposed indicators were described as important by 50% or more of the stakeholders (Fig. 4).

The stakeholders also had the opportunity to state additional areas of application of information on genetic diversity. Corresponding topics included hybridisation (e.g. between wildcat and domestic cat), the identification of native and invasive species, and the *ex-situ* propagation and reintroduction of rare plant species. The fact that many stakeholders mentioned additional fields of application shows that there are concrete ideas about what type of data or indicators a genetic diversity monitoring should deliver.
In contrast, some of the results also indicate that the concepts underlying genetic diversity and its monitoring are not clear to all stakeholders and require careful explanation. For example, the difference between species identification with genetic tools, e.g., barcoding or eDNA metabarcoding (e.g. Bohmann et al. 2014; Deiner et al. 2017; Porter and Hajibabaei 2018), and a monitoring of genetic diversity across time were not entirely clear to all stakeholders. In consequence, some possible applications suggested by the stakeholders, such as the identification of native and non-native species, rather refer to species identification than to a monitoring of genetic diversity. Transparent communication about the possibilities and limitations of a genetic diversity monitoring program already during its developmental phase is hence important.

### Content and implementation of a potential monitoring of genetic diversity

Regarding the species selection for a genetic diversity monitoring program, stakeholders most frequently chose amphibians and insects (> 70% of respondents; Fig. 5), followed by seed plants, fishes and mammals (> 50% of respondents). Less than 40% of the respondents selected birds, and only 20% or less stated other groups of organisms like crustaceans or flatworms. In principle, the preferences of different stakeholder types were similar. Only the stakeholder type collections/museums was overrepresented among the least preferred species groups. The prominent preference for insects among stakeholders is probably due to insect decline being widely discussed in the broader society since the publication of the landmark paper of Hallmann et al. (2017) and other articles on the topic (e.g. Seibold et al. 2019). Furthermore, we assume that museums and scientific collections still have scientists with broad species knowledge and specific interest in organismic groups such as flatworms or spiders; knowledge that has otherwise vanished from many research institutions, universities or NGOs (Shaffer et al. 1998).

Moreover, stakeholders expressed their opinions regarding further elements that a genetic diversity monitoring program should consider: Both rare and common species as well as species with high or low mobility should be included. Additionally, the selection of species should be representative of certain habitat types or ecosystems, e.g., those of national importance (FOEN 2019). Many stakeholders stated that the selection of species and the design of a genetic diversity monitoring should be geared to answering questions of actual importance for conservation management. It was also stated that a genetic diversity monitoring should provide indicators for the vulnerability of populations.

The motivation of stakeholders to participate in developing a genetic diversity monitoring program was high. Overall, 67% of the stakeholders expressed interest in being involved. However, there were differences between stakeholder types. Regional and local authorities (57.9%) and NGOs/foundations (54.2%) had a below-average willingness to participate as compared to stakeholders from research (94.7%), environmental consultancies (82.6%) or collections/museums (80.8%).

The stakeholders most frequently specified the expected costs as the obstacle for developing and implementing a genetic diversity monitoring program. Stakeholders were concerned that administrations will not have the time and financial resources to be involved in and contribute to a genetic diversity monitoring program. Furthermore, some stakeholders were concerned that an additional monitoring program might generate large amounts of data that would not be used in practice, because tools and detailed knowledge to translate the results of a genetic diversity monitoring into concrete recommendations for conservation activities are (currently) missing. Hence, there is a need for more applied research to fill this gap. Specifically, research would need to consult and work with the stakeholders to elaborate how to make the data and derived indicators from such a monitoring directly applicable for practitioners. In addition, the monitoring program itself could interface more directly with stakeholders and work on making the data accessible, easy interpretable and directly usable.

### Network of stakeholders

Our social network analysis identified stakeholders who were perceived as important for developing and implementing a
national genetic diversity monitoring program as well as those who were considered as key partners for the exchange of information on genetic diversity. The social network graph in Fig. 6A displays who perceives whom as important for the implementation of a genetic diversity monitoring program. Each node in the figure represents a stakeholder or a subtype of stakeholders, colored by stakeholder type (according to Table 1). The size of the node indicates the centrality of the stakeholder. Arrows indicate who named whom as being important. We only specified the names of those stakeholders that were most central in Fig. 6. The stakeholder most often named was the federal authority, that is, the Swiss Federal Office for the Environment (FOEN). This indicates the central role of the federal authority for developing a monitoring program. However, also stakeholders from research, collections/museums and regional authorities were amongst the top five central stakeholders indicated as being important.

When comparing the network of the importance of stakeholders (Fig. 6A) to that displaying current information exchange between stakeholders (Fig. 6B), one observes several differences. The density of the network of important stakeholders (0.6; Fig. 6A) was 3-times higher than that of the information exchange network (0.2; Fig. 6B). This means that many more stakeholders were named as being important than actually being involved in information sharing. This is not surprising, as it takes more resources to exchange information than to be perceived as important. Interestingly, research institutions rather than the federal authority are the most frequently named stakeholders for current exchange on genetic diversity issues. This shows the pivotal role of research institutions for sharing information in the context of a genetic diversity monitoring program. Moreover, regional authorities for nature and landscape conservation were more prominent than federal authorities or collections/museums. It is interesting to note that the stakeholders perceived as important (Fig. 6A) did not fully match those that were partners for information exchange (Fig. 6B). The different roles of stakeholders could be important here: the perceived high importance of, but lack of information exchange with federal authorities could originate from them being mainly responsible for legal framing and distribution of funds, while they are not primarily involved in the specific implementation of results of a genetic diversity in conservation management. Nevertheless, federal authorities play a crucial role in establishing guidelines for conservation management for regional authorities, which applies to many countries outside Switzerland. Furthermore, certain stakeholder types such as environmental consultancies were neither prominent in the network of important stakeholders nor in the information exchange network and, thus, were placed in rather peripheral positions in the networks (Fig. 6). However, 82.6% of the stakeholder type environmental consultancies expressed their interest in participating in the further development of
a genetic diversity monitoring program and especially so in the implementation of the monitoring (e.g. collection of samples; see above), among other reasons driven by economic interests.

**Conclusions**

Our stakeholder analysis aimed at inferring the interests and needs of stakeholders regarding a potential genetic diversity monitoring program in Switzerland. Our findings show that
stakeholders have a clear interest in a monitoring of genetic diversity. Although they ranked the importance of genetic diversity below species or ecosystem diversity, stakeholders emphasized the lack of knowledge about the extent and loss of genetic diversity and the associated urgency to act. In the absence of specific information, enhancing species and ecosystem diversity were considered beneficial for genetic diversity. Furthermore, we identified a clear discrepancy between the need for and the current availability or use of genetic data, which may impede conservation management for sustaining genetic diversity of populations and species. Consequently, many stakeholders see a genetic diversity monitoring as a potential benefit for their work and formulated specific expectations.

Although many of the stakeholders are in favour of genetic diversity monitoring, authorities see many obstacles and uncertainties for the implementation of the results of a genetic diversity monitoring. They fear high costs in terms of time and money, but limited results that are useful for conservation action. This is especially problematic, as regional authorities were named as important stakeholders as well as important information exchange partners in the social network analysis. For implementing a genetic diversity monitoring transparent communication about the potential, but also the limitations of a genetic diversity monitoring is needed (Walsh et al. 2015; Enquist et al. 2017; Gosselin et al. 2018; Holderegger et al. 2019).

While we studied Swiss stakeholders, our results are likely relevant for developing a genetic diversity monitoring in other contexts for several reasons. First, despite the importance of genetic diversity for the long-term persistence of species and ecosystems (Reusch et al. 2005; Breed et al. 2019; Stange et al. 2020), very few countries are systematically monitoring the levels of genetic diversity in natural populations of a wide variety of wild species to date (Mimura et al. 2017). However, the mandate for genetic diversity monitoring will probably be further accentuated in the post-2020 process (Laikre et al. 2020), as new CBD genetic indicators are currently under discussion: These may have far-reaching consequences, as they will guide conservation actions and reporting for member countries until 2050 (Hoban et al. 2020). To set up a genetic diversity monitoring program, stakeholder and social network analyses are powerful tools to derive the most relevant stakeholders as well as tailor communication channels and outreach strategies (Bodin and Crona 2009). While our results are Swiss specific, our approach is applicable for developing monitoring programs in other contexts. Social network analysis sheds light on how key stakeholders could be used as knowledge brokers, distributing information to their larger networks, while peripheral stakeholders could, if needed, be targeted specifically (Bodin and Crona 2009). For example, our network analysis indicated that environmental consultancies are currently in peripheral positions in the networks, but that a large percentage of this stakeholder type wants to participate in the development of a genetic diversity monitoring program and especially in the implementation. This hence provides insight to the federal authority that they need to specifically target this actor type during the development and implementation process.

Second, our analysis shows that regional and local authorities are important to include in a potential genetic diversity monitoring program. Our stakeholder analysis shows where action is required to engage these actors, as the regional and local authorities had a below-average willingness to participate as compared to other stakeholders. At the same time, the regional authorities were amongst the top five central stakeholders indicated as being important in the network analysis. Again, this indicates where the federal authority should focus its energy when mobilizing the stakeholders to participate.

Finally, our stakeholder analysis shows the importance of connecting national authorities, who have the political mandate to coordinate national conservation programs with research institutions that have the knowledge and technology to develop and perform a genetic diversity monitoring program. Our results show that links to data centers and scientific collections are viewed as important for species selection and sampling. Our social network analysis showed that the wide collaboration and information exchange between research institutions, federal and regional authorities as well as collections and museums is critical for the implementation of a national monitoring of genetic diversity. Using stakeholder analysis results for targeting actors or learning about the critical links between actors is a valuable insight for other national authorities when developing and implementing a genetic diversity monitoring program.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s10592-021-01379-6.

Acknowledgements This research was supported by the Swiss Federal Office for the Environment (FOEN), and we thank G. Litsios and six anonymous reviewers for helpful inputs.

Author contributions All authors conceived the study. RP, EL and MCF designed the questionnaire, with contribution of RH. RP performed the stakeholder analyses and compiled the data, with the help of EL. RP, EL and MCF wrote the manuscript with contributions of RH, FG and AW.

Funding Open Access funding provided by ETH Zurich. This research was funded by the Swiss Federal Office for the Environment (FOEN).

Data availability Not applicable.

Code availability Not applicable.
Declarations

Conflict of interest The authors declare no competing interests.

Ethical approval Not applicable.

Consent to participate Not applicable.

Consent for publication Not applicable.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article’s Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article’s Creative Commons licence and your intended use is not otherwise in a credit line to the material, this article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made.

References

Agroscope (2015) Agrarumweltindikatoren, Arten und Lebensräume - Landwirtschaft – Espèces et milieux agricoles’, ALL-EMA. Agroscope, Zürich

Allendorf FW (2017) Genetics and the conservation of natural populations: allozymes to genomes. Mol Ecol 26:420–430

Bodin Ö, Crona BI (2009) The role of social networks in natural resource governance: what relational patterns make a difference? Glob Environ Chang 19:366–374

Bohm K, Evans A, Gilbert MTP, Carvalho GR, Creer S, Knapp M, Yu DW, de Bruyn M (2014) Environmental DNA for wildlife biology and biodiversity monitoring. Trends Ecol Evol 29:358–367

Borgatti SP, Everett MG, Johnson JC (2018) Analyzing social networks. SAGE Publications, London

Braunisch V, Home R, Pellet J, Arlettaz R (2012) Conservation science relevant to action: a research agenda identified and prioritized by practitioners. Biol Conserv 153:201–210

Breed MF, Harrison PA, Blyth C, Byrne M, Gaget V, Gellie NJC, Groom SVC, Hodgson R, Mills JG, Prowse TAA, Steane DA, Mohr JJ (2019) The potential of genomics for restoring ecosystems and biodiversity. Nat Rev Genet 20:615–628

Bryja J, Frith K, Gaggiotti OE, Galbusera P, Godoy JA, Hoe-zel AR, Nichols RA, Primmer CR, Russo I-R, Segelbacher G, Siegismund HR, Silvoni M, Vernesi C, Vilà C, Bradford MW (2013) Bringing genetic diversity to the forefront of conservation policy and management. Conserv Genet Resour 5:593–598

Creswell JW (2012) Educational research: Planning, conducting, and evaluating quantitative and qualitative research. Pearson Education, Boston, MA

De Kort H, Prunier JG, Ducatez S, Hannon O, Baguette M, Stevens VM, Blanchet S (2021) Life history, climate and biogeography interactively affect worldwide genetic diversity of plant and animal populations. Nat Commun 12:516

Deiner K, Bik HM, Mächler E, Seymour M, Lacoursière-Roussel A, Altermatt F, Creer S, Bista I, Lodge DM, de Vere N, Pfender ME, Bernatchez L (2017) Environmental DNA metabarcoding: transforming how we survey animal and plant communities. Mol Ecol 26:5872–5895

Des Roches S, Pendleton LH, Shapiro B, Palkovacs EP (2021) Conserving intraspecific variation for nature’s contributions to people. Nature Ecol Evol 5:574–582

Enquist CAF, Jackson ST, Garfin GM, Davis FW, Gerber LR, Littell JA, Tank JL, Terando AJ, Wall TU, Halpern B, Hiers JK, Morelli TL, McNie E, Stephenson NL, Williamson MA, Woodhouse CA, Yung L, Brunswk MW, Hall KR, Hallett LM, Lawson DM, Moritz MA, Nydick K, Pairis A, Ray AJ, Regan C, Safford HD, Schwartz MW, Shaw MR (2017) Foundations of translational ecology. Front Ecol Environ 15:541–550

Fischer M, Ingold K, Ivanova S (2017a) Information exchange under uncertainty: the case of unconventional gas development in the United Kingdom. Land Use Policy 67:200–211

Fischer MC, Pärli R, Gugerli F, Holderegger R, Lieberherr E, Widmer A (2020) Machbarkeitsstudie zur Untersuchung des Zustands und der Veränderung der genetischen Vielfalt: Verzettelung, Inzucht und Anpassungsfähigkeit. ETH Zurich, under mandate from the FOEN, Zürich

Fischer MC, Rollsteb C, Leuzinger M, Roumet M, Gugerli F, Shimizu KK, Holderegger R, Widmer A (2017b) Estimating genomic diversity and population differentiation – an empirical comparison of microsatellite and SNP variation in Arabidopsis halleri. BMC Genomics 18:69

FOEN (2012) Swiss Biodiversity Strategy. FOEN, Bern

FOEN (2017) Action Plan for the Swiss Biodiversity Strategy. FOEN, Bern

FOEN (2019) Liste der National Prioritären Arten und Lebensräume [List of National Priority Species and Habitats]. FOEN, Bern

Fuentes-Pardo AP, Razzante DE (2017) Whole-genome sequencing approaches for conservation biology: advantages, limitations and practical recommendations. Mol Ecol 26:5369–5406

Gosselin F, Cordonnier T, Bilger I, Jappiot M, Chauvin C, Gosselin M (2018) Ecological research and environmental management: we need different interfaces based on different knowledge types. J Environ Manage 218:388–401

Hallmann CA, Sorg M, Jongejans E, Siepel H, Hofland N, Schwan H, Stenmans W, Müller A, Sumser H, Hörrt T, Goulson D, Kroon H (2017) More than 75 percent decline over 27 years in total flying insect biomass in protected areas. PloS One 12:e0185809

Hoban S, Bruford M, D’Urban J, Lopes-Fernandes M, Heuertz M, Hohenlohe PA, Paz-Vivas I, Sjögren-Gulve P, Segelbacher G, Vernesi C, Aitken S, Bertola LD, Bloomer P, Breed M, Rodríguez-Correa H, Funk WC, Grueber CE, Hunter ME, Jaffe R, Liggins L, Merchaj J, Moharrek F, O’Brien D, Ogden R, Palma-Silva C, Pierson J, Ramakrishnan U, Simo-Driossart M, Tani N, Waits L, Laikre L (2020) Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. Biological Conservation 248:108654

Hoban SM, Hauffe HC, Pérez-Espiona S, Arntzen JW, Bertorelle G, Bryja J, Frith K, Gaggiotti OE, Galbusera P, Godoy JA, Hoezl AR, Nichols RA, Primmer CR, Russo I-R, Segelbacher G, Siegismund HR, Silvoni M, Vernesi C, Vilà C, Bradford MW (2013) Bringing genetic diversity to the forefront of conservation policy and management. Conserv Genet Resour 5:593–598

Hohenlohe PA, Funk WC, Rajora OP (2021) Population genomics for wildlife conservation and management. Mol Ecol 30:62–82

Holderegger R, Balkenhol N, Bolliger J, Engler JO, Gugerli F, Hochkirch A, Nowak C, Segelbacher G, Widmer A, Zachos FE (2011) Information exchange under uncertainty: the case of unconventional gas development in the United Kingdom. Land Use Policy 67:200–211

Hohenlohe PA, Ruffnel HD, Schwartz MW, Shaw MR (2017) Foundations of translational ecology. Front Ecol Environ 15:541–550

Laikre L, Hoban S, Bruford MW, Segelbacher G, Allendorf FW, Gajardo G, Rodriguez AG, Heurertz M, Hohenlohe PA, Jaffé R, Johannesson K, Liggins L, MacDonald AJ, Orozco-Correa H, Pálmer SA, Palma-Silva C, Pierson J, Ramakrishnan U, Simo-Driossart M, Tani N, Waits L, Laikre L (2020) Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. Biological Conservation 248:108654

Hoban SM, Hauffe HC, Pérez-Espiona S, Arntzen JW, Bertorelle G, Bryja J, Frith K, Gaggiotti OE, Galbusera P, Godoy JA, Hoezl AR, Nichols RA, Primmer CR, Russo I-R, Segelbacher G, Siegismund HR, Silvoni M, Vernesi C, Vilà C, Bradford MW (2013) Bringing genetic diversity to the forefront of conservation policy and management. Conserv Genet Resour 5:593–598

Hohenlohe PA, Funk WC, Rajora OP (2021) Population genomics for wildlife conservation and management. Mol Ecol 30:62–82

Holdereger R, Balkenhol N, Bolliger J, Engler JO, Gugerli F, Hochkirch A, Nowak C, Segelbacher G, Widmer A, Zachos FE (2019) Conservation genetics: linking science with practice. Mol Ecol 28:3848–3856

Laikre L, Hoban S, Bruford MW, Segelbacher G, Allendorf FW, Gajardo G, Rodriguez AG, Hedrick PW, Heurertz M, Hohenlohe PA, Jaffé R, Johannesson K, Liggins L, MacDonald AJ, Orozco-Correa H, PeulsTF, Squiach TH, Rodriguez-Correa H, Russo I-RM, Ryman N, Vernesi C (2020) Post-2020 goals overlook genetic diversity. Science 367:1083
Leigh DM, Hendry AP, Vázquez-Domínguez E, Friesen VL (2019) Estimated six percent loss of genetic variation in wild populations since the industrial revolution. Evol Appl 12:1505–1512

Lindgren K-O, Persson T (2010) Input and output legitimacy: synergy or trade-off? empirical evidence from an EU survey. J Eur Publ Policy 17:449–467

Lundmark C, Sandström A, Andersson K, Laikre L (2019) Monitoring the effects of knowledge communication on conservation managers’ perception of genetic biodiversity – a case study from the Baltic Sea. Mar Policy 99:223–229

Marris E (2019) Why young climate activists have captured the world’s attention. Nature 573:471–472

Meek MH, Larson WA (2019) The future is now: amplicon sequencing and sequence capture usher in the conservation genomics era. Mol Ecol Resour 19:795–803

Mimura M, Yahara T, Faith DP, Vázquez-Domínguez E, Colautti RI, Araki H, Javadi F, Núñez-Farfán J, Mori AS, Zhou S, Hollingsworth PM, Neaves LE, Fukano Y, Smith GF, Sato Y-I, Tachida H, Hendry AP (2017) Understanding and monitoring the consequences of human impacts on intraspecific variation. Evol Appl 10:121–139

Norberg J, Urban MC, Vellend M, Klausmeier CA, Loeuille N (2012) Eco-evolutionary responses of biodiversity to climate change. Nat Clim Chang 2:747–751

Paletto A, Hamunen K, Meo ID (2015) Social network analysis to support stakeholder analysis in participatory forest planning. Soc Nat Resour 28:1108–1125

Pauls SU, Nowak C, Bălînt M, Pfenninger M (2013) The impact of global climate change on genetic diversity within populations and species. Mol Ecol 22:925–946

Porter TM, Hajibabaei M (2018) Scaling up: a guide to high-throughput genomic approaches for biodiversity analysis. Mol Ecol 27:313–338

Prell C, Hubacek K, Reed M (2009) Stakeholder analysis and social network analysis in natural resource management. Soc Nat Resour 22:501–518

Reusch TBH, Ehlers A, Hämmerli A, Worm B (2005) Ecosystem recovery after climatic extremes enhanced by genotypic diversity. Proc Natl Acad Sci USA 102:2826–2831

Sandström A, Lundmark C, Andersson K, Johannesson K, Laikre L (2019) Understanding and bridging the conservation-genetics gap in marine conservation. Conserv Biol 33:725–728

Schwartz MK, Luikart G, Waples RS (2007) Genetic monitoring as a promising tool for conservation and management. Trends Ecol Evol 22:25–33

Schwick C, Jaeger J, Hersperger A, Cathomas G, Muggli R (2018) Zersiedelung messen und begrenzen. Massnahmen und Zielvorgaben für die Schweiz, ihre Kantone und Gemeinden. [Measuring and Limiting Urban Sprawl. Measures and Targets for Switzerland, its Cantons and Municipalities]. Haupt, Bern

Seibold S, Gossner MM, Simons NK, Blüthgen N, Müller J, Ambarli D, Ammer C, Baudhuin J, Fischer M, Habel JC, Linsenmair KE, Nauss T, Penone C, Prati D, Schall P, Schulze E-D, Vogt J, Wölflauer S, Weisser WW (2019) Arthropod decline in grasslands and forests is associated with landscape-level drivers. Nature 574:671–674

Sgro CM, Lowe AJ, Hoffmann AA (2011) Building evolutionary resilience for conserving biodiversity under climate change. Evol Appl 4:326–337

Shafer ABA, Wolf JBW, Alves PC, Bergström L, Bruford MW, Brännström I, Colling G, Dalén L, De Meester L, Ekbлом R, Fawcett KD, Fior S, Hajibabaei M, Hill JA, Hoezel AR, Höglund J, Jensen EL, Krause J, Kristensen TN, Kruitjen M, McKay JK, Norman AJ, Ogden R, Österling EM, Ouborg NJ, Piccolo J, Popović D, Primmer CR, Reed FA, Roumet M, Salmina J, Schenkar T, Schwartz MK, Segelbacher G, Senn H, Thalouw J, Valtosen M, Veale A, Vergeer P, Vijay N, Vilà C, Weissensteiner M, Wenerström L, Wheat CW, Zielinski P (2015) Genomics and the challenging translation into conservation practice. Trends Ecol Evol 30:70–87

Shafer HB, Fisher RN, Davidson C (1998) The role of natural history collections in documenting species declines. Trends Ecol Evol 13:27–30

Stange M, Barrett RDH, Hendry AP (2020) The importance of genomic variation for biodiversity, ecosystems and people. Nat Rev Genet 22:89–105

Supple MA, Shapiro B (2018) Conservation of biodiversity in the genomics era. Genome Biol 19:131

Walsh JC, Dicks LV, Sutherland WJ (2015) The effect of scientific evidence on conservation practitioners’ management decisions. Conserv Biol 29:88–98

Wasserman S, Faust K (1994) Social network analysis: Methods and applications. Cambridge University Press, New York, NY, US

Publisher’s Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.