



# GINAMO workshop on genetic diversity indicators in France

Paris, 7 February 2025

## REPORT

**This research was funded by Biodiversa+, the European Biodiversity Partnership, in the context of the GINAMO project under the 2022-2023 BiodivMon joint call. It was co-funded by the European Commission (GA No. 101052342) The Research Council of Norway, The Belgian Science Policy, L'Agence nationale de la recherche, Ministero dell'Università, Naturvårdsverket, Rymdstyrelsen, Deutsche Forschungsgemeinschaft and Innovation Fund Denmark**



SWEDISH  
ENVIRONMENTAL  
PROTECTION  
AGENCY



**The workshop was financially co-supported by:  
Office Français de la Biodiversité and Muséum National d'Histoire Naturelle**



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**Suggested citation:** Vejlggaard, C. R., Leus, K., Harribey, M-G., Heuertz, M., Garnier-Géré, P., & Hvilsom, C. (2025). *GINAMO workshop on genetic diversity indicators in France* (project report). GINAMO: Genetic Indicators for Nature Monitoring. DOI: <https://zenodo.org/records/17036942>

## GINAMO Genetic Indicators for Nature Monitoring

Genetic diversity is the foundation of biodiversity and essential for the long-term survival, adaptation, and resilience of populations, species, and entire ecosystems. While genetic diversity has long been neglected in biodiversity policy and management, the current Convention on Biological Diversity (CBD)

Kunming-Montreal Global Biodiversity Framework (GBF) includes a strong goal and target for genetic diversity conservation and also monitoring, including with indicators and for wild species. Tools and indicators to assess and monitor genetic diversity are available but are rarely applied due to the gap in knowledge transfer between conservation science and application. GINAMO is a project of Biodiversa+, The European Biodiversity Partnership, which assesses and delivers science-based and co-designed best practices and guidelines for the use of genetic diversity indicators. This will enable the routine integration of genetic criteria and indicators into biodiversity monitoring and assessments, from policy at regional, national, and EU levels, to global conventions and obligations. A key component of GINAMO is the use of facilitated group decision-making processes to partner and co-decide from the outset with the stakeholder community. This ensures that all resources produced meet their concerns, reporting duties, and monitoring needs, and that guidelines and work flows are more likely to be adopted. Easy-to-apply, standardised and automated workflows will be co-created for assessing genetic indicators to meet national reporting obligations and to incorporate genetic diversity knowledge into nature management plans.

### Main objectives

GINAMO uses existing open access genetic and non-genetic data (including Earth observation data) to best determine accurate estimates of the two genetic diversity indicators of the GBF: 1) the proportion of populations within species with an effective population size ( $N_e$ ) greater than 500 ( $N_e$  500 hereafter), and 2) the proportion of populations maintained within species. To maximise the implementation and reporting of these indicators, GINAMO designs, facilitates, and scientifically evaluates co-creation processes between scientists and country stakeholders in Belgium, Italy, Norway, Sweden and France. These processes aim to collaboratively develop workflows that are scientifically sound, appropriate, compliant with policy and easy-to-implement for nature management.

### Main activities

GINAMO focuses on generating best practices for assessing effective population size and evaluating genetic indicators from both DNA-based data and non-DNA (proxy) data from multiple sources. Additionally, GINAMO evaluates how satellite Earth observation data can be used to generate proxies to monitor genetic diversity. Workflows for existing and newly generated information will be standardised to provide easily accessible tools for researchers, nature managers and policy makers. GINAMO activities follow a co-creation approach under professional guidance by the European Regional Resource Center of the IUCN SSC [Conservation Planning Specialist Group](#) and with scientific evaluation by social scientists, so that methods and products are produced together by policy makers, nature managers, and scientists.

## Workshop process

The workshops organised by GINAMO in collaboration with local country stakeholders serve to create input to the best practice guidelines that will be produced. In order to make these as user friendly and as relevant as possible, it is important to understand the realities in which various stakeholders operate, and to understand the challenges they experience from their perspective. The challenges identified during the workshops will inform the work of the various work packages within GINAMO, when developing the science and methods behind the use of genetic indicators.

IUCN SSC CPSG Europe designed and facilitated the country workshop processes, in line with CPSG's Principles and Steps (Appendix II), and informed by preparatory meetings with a country organising group composed of GINAMO scientists from the country and selected country stakeholders with a central role in monitoring and reporting on biodiversity.

## Process

In preparation of the workshops, a generic workflow was developed (Fig 1), that outlines the main steps that need to be taken within a country in order to be able to report genetic indicators to the CBD. This workflow was used as the basis for the discussions during the workshop.

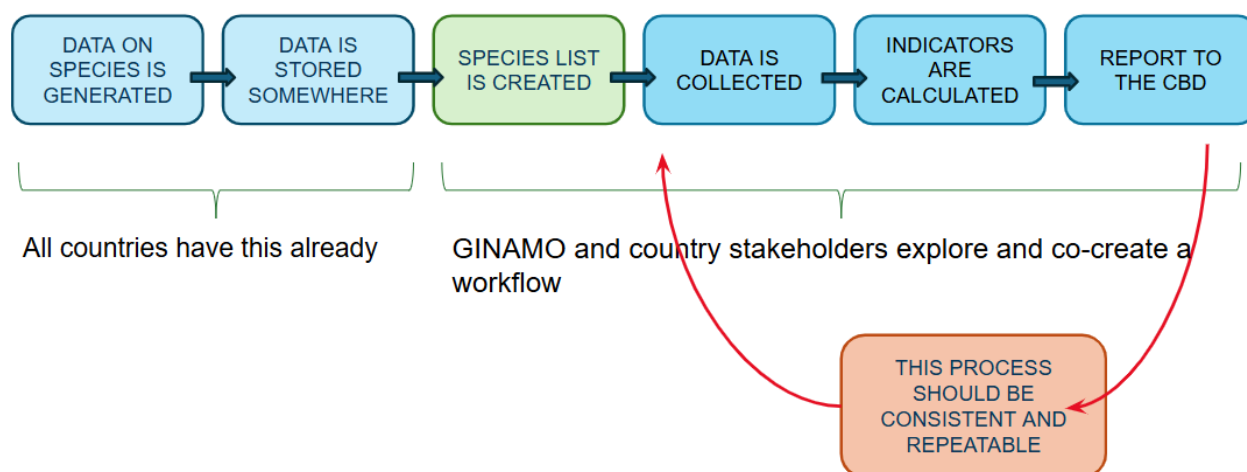


Fig 1. The generic workflow used as a base for the workshop.

The agenda for the workshop can be found in Appendix I. Following an introduction to the GINAMO project and the genetic indicators, as well as to the workshop process and generic workflow, the active part of the workshop started. Participants first identified where in the workflow they felt their institution could have a role to play. Next, the generic workflow was divided into three parts:

1. Selection of the species to monitor and report on.
2. Data collection, indicator calculation, and storing and structuring of metadata for future reporting cycles.
3. Preparing the relevant parts of the CBD report.

For each of these three parts, the participants:

- A. Discussed their knowledge of the current situation in France.
- B. Identified the challenges facing them as stakeholders, or the country as a whole, in order to end up with a fully functional, and repeatable workflow that can routinely and consistently produce genetic indicators for consecutive reporting cycles to CBD.

At the end of the workshop, the participants reviewed all the challenges and selected those for which they felt that developing solutions may benefit from collaboration with GINAMO (in other words, from co-creating solutions); versus those challenges that clearly need to be solved in-country.

## Participants

The country organising group identified the stakeholders that would be invited to the workshop. A matrix was developed to help identify stakeholders that represented a wide variety of workflow steps, skills, roles and responsibilities, as well as geographical placement, when relevant. Not all the identified stakeholders were able to participate in the workshop, but they will all receive this report.

21 stakeholders from various French institutions participated in the in-person workshop at the Muséum National d'Histoire Naturelle (National Natural History Museum) in Paris. .

## Workshop evaluation

GINAMO's social scientists will evaluate the entire co-creation process. In order to evaluate the country workshops, a survey was prepared and completed by all participants before and after the workshop. The only parts from that survey included in this report are any answers to the question: "List any stakeholders who could have made a valuable contribution but were not present at this workshop". The overall results from this evaluation will be shared at a later stage.

## Workshop results

### Workshop outcomes

1. An overview of the current situation in France with regards to: genetic monitoring and reporting, genetic and proxy data gathering and databases, already existing workflows, important stakeholder groups, scientific views regarding the use of the *Ne 500* headline indicator, etc.
2. A list of challenges facing the stakeholders and the country to have a fully functional workflow that is repeatable for consecutive reporting cycles for the CBD.
3. A selection of those challenges for which developing solutions may benefit from collaboration with GINAMO (in other words, from co-creating solutions); versus those challenges that clearly need to be solved in-country.

This report collects the results from the workshop in France, and reflects the thoughts, assumptions and knowledge of the participants at the time of the workshop, but does not claim to give the full picture of the status and challenges with regards to the reporting of genetic indicators to the CBD in France. The aim of this report is to inform further work by GINAMO and hopefully it will also prove to be a useful first step towards further work and collaboration within France, to develop and implement a national workflow.

### Where in the workflow stakeholders' institutions might contribute

The workshop participants identified where in the workflow they felt their institution might have a role to play. The results are in the table below. Please note that this does not constitute an exhaustive list of stakeholders required for each workflow step.

<b>Data on species is generated and data about species is stored</b>	<b>Species list to monitor and report on</b>	<b>Data is collected, structured and stored</b>	<b>Indicators are calculated and stored</b>	<b>The report to the CBD is written and submitted</b>
OFB - Office Français de la biodiversité	PatriNat - centre d'expertise et de données sur le patrimoine naturel	ORGP - Organisations régionales de gestion de la pêche	ONF - Office National des forêts	

INRAE	CEN (expertise dans =/ régions pour aider à choisir)	ISYEB -The Institut de Systématique, Evolution, Biodiversité	GINAMO	
GINAMO	IGN - Inventaire Forestier	PNDB - Pôle national de données de biodiversité	IGN - Inventaire Forestier	
SIB - le système d'information de la biodiversité	ISYEB -The Institut de Systématique, Evolution, Biodiversité	PatriNat - centre d'expertise et de données sur le patrimoine naturel	PNDB - Pôle national de données de biodiversité	
PNDB - Pôle national de données de biodiversité	INRAE	INREA	ISYEB -The Institut de Systématique, Evolution, Biodiversité	
PatriNat - centre d'expertise et de données sur le patrimoine naturel	GINAMO	GINAMO	MTE - This is Ministère de la transition écologique, de la biodiversité, de la forêt, de la mer et de la pêche	
MNHN - Muséum national d'histoire naturelle	ONF - Office National des forêts	ONF - Office National des forêts	PatriNat - centre d'expertise et de données sur le patrimoine naturel(storage)	
ISYEB -The Institut de Systématique, Evolution, Biodiversité		MTE - This is Ministère de la transition écologique, de la biodiversité, de la forêt, de la mer et de la pêche	Univ Lyon 1 - LEHNA	



ONF - Office National des forêts				
IGN - Inventaire Forestier				
IFREMER				
ARCHiMER / HAL				
INPN - Inventaire national du patrimoine naturel				
UMR Biogeco - Biodiversité Gènes et Communautés				
Univ Lyon 1 - LEHNA				
les CEB en général				

The following organisations were identified as missing from the workshop:

- Nature conservation associations
- Managers and coordinators of the NAP for threatened species (NAP= National Action Plans)
- Biodiversity Policy Office of the Water and Biodiversity Department (DEB) representing the National Biodiversity Strategy
- Ministry of ecological transition: DAEI (Direction de l'action européenne et internationale)
- People working specifically in the overseas territories
- People from institutions that do actual monitoring work
- People in charge of data ("geomateams" =implying an expertise in data spatial distribution) in nature protection associations
- Naturalists collecting data
- Field managers.

- General management of the Ministry of ecological transition (MTE) directly in charge of reporting
- NGOs
- Citizen stakeholders in general
- GBIF
- CBD

## Challenges

The workflow for reporting to CBD was divided into three parts, and for each part, the workshop participants identified a list of challenges facing the stakeholders and the country to have a fully functional workflow that is repeatable for consecutive reporting cycles for the CBD.

After identifying the challenges, the participants reviewed them all and selected those for which they felt that developing solutions may benefit from collaboration with GINAMO (in other words, from co-creating solutions); versus those challenges that clearly need to be solved in-country. It was possible to mark a challenge as both a co-creation candidate and as a challenge that needs national work to be solved - but that is not indicated in this report. The challenges marked with (G) are the ones that were suggested for co-creation.

## Species list to monitor and report on (and associated data generation challenges)

**Discussion (mostly consensus)** on what should be achieved for the genetic indicators reporting to the CBD

- A pragmatic approach could be used to start with. Indicators have been calculated for France, based on proxy data, for approx. 80 species in the 9 countries paper. These could be used for the upcoming report in February 2026 and applied to more species. For the following reports the species list should be increased to 1500 species if possible. See guidelines from the CBD. (<https://www.cbd.int/doc/c/92cf/b458/18519b4c0b487bf9bfc23988/sbstta-26-inf-14-en.pdf>).
- The selection process should prioritize species based on their representativity in terms of taxa, ecosystem, species life history traits (LHTs) (see references above, and in the [Presentation](#), this is also part of GINAMO's workplan).
- For the first report, mostly use existing data and later identify gaps where generating new data is needed.

- When selecting representative lists of species, build on work that has already been done, for example, with the **IUCN Red List assessments** (MNHN and OFB)
- **The choice of the species list also depends on the objectives behind the reporting.** Keep in mind that this reporting should serve France's conservation policies and not only the reporting to the CBD. → Maybe it would be useful to have several lists according to specific conservation objectives?
- Selected species for reporting should be followed in the long-term to catch the temporal evolution of genetic diversity in France.
- To make the list of species useful for management, nature managers should be involved when choosing the species.
- For terrestrial species, prioritisation exercises have already been carried out by the [Terrestrial Biodiversity Monitoring Framework](#) that is managed by [PATRINAT \(see here\)](#) and that can be used to avoid repeating similar work and further respond to challenges of where to start when choosing species.

**Challenges** to integrate in the longer term (following reports):

- Data availability. **Taxa that are usually poorly represented must be taken into account** to ensure the indicator reflects biodiversity across different ecosystems: **in particular marine species but also invertebrates, etc.** (G)
- Data gaps remain, particularly for Data Deficient (DD) species of the IUCN. → report on this lack of data? (G)
- **Overseas territories (e.g., French Guiana, Polynesia and Caribbean islands) must be included**, as they host a significant portion of France's biodiversity, but data availability and representativity remain a challenge. (G)
- How do we ensure long term commitment and monitoring?
- Should we include domesticated species as well? (G)
- How can we take into account species that cross borders? (G)
- How to align with other European countries? (G)

*Data is collected, structured and stored and the indicators are calculated*

### **Discussion**

- Methods: microsatellites (30 individuals/population) or SNPs. Effective population size,  $N_e$ , was traditionally estimated with temporal methods but the Linkage Disequilibrium method is now mainly used.
- Mainly, DNA data sources are from research publications archived in databases like NCBI, DRYAD; Zenodo, etc.. A publication upcoming to map global population-level nuclear genetic data availability that can be used to extract data for France (Paz-Vinas et al. 2023, <https://ecoevorxiv.org/repository/view/6162/>)

- In France actions exist at the national level with nature managers ([e.g. PNA](#)) and research, which produce DNA data.

### ***Challenges***

- Various methods of Ne estimation are available, and applying them to conservation practice might be complex (see [Fedorca et al. 2024](#); [Waples 2024](#)). For that reason it would be relevant to rely on a community of population geneticists.
- A difficulty may be to identify DNA data sampled in France but from foreign researchers (see Paz-Vinas et al 2023, <https://ecoevorxiv.org/repository/view/6162/>)
- A challenge is the availability and standardization of metadata for genetic data, although genetic data are quite well standardized already. FAIR data are needed (see Leigh et al. 2024, <https://www.nature.com/articles/s41559-024-02423-7>). (G)

### **b. Non-DNA Data (proxies)**

### ***Discussion***

- Many databases with useful proxies can be used : GBIF, INPN, IGN.... However, many different types of data are available and need to be prioritized and standardized (as proposed in [Mastretta-Yanes et al. 2024](#)).  
FAIR data is needed in general. These methods require expert validation who have knowledge about the different species.
- It is not enough to only study species already on the IUCN red list because there is little correlation overall between IUCN conservation status and the Ne500 headline indicator (see [Mastretta-Yanes et al. 2024](#)). But reinjecting these indicators into the IUCN red list in the future would be interesting.

### ***Challenges***

- There are significant biases in observational data due to uneven taxonomic or geographic coverage. There is an interest in identifying and reporting species for which there is a lack of data. (G)
- There is a concern about the uncertainty around Ne estimates that use proxy data → A solution might be to also implement the reporting on the range of uncertainty of proxy-based Ne estimates. (G)
- What is the robustness of the proxy data in relation to DNA based data? France could decide not to use some proxies that do not give accurate estimates. In the case of some coarse proxies, the variability of the type of data might be very wide, with a challenge on standardization. (G)

- $N_e/N_c$  ratio is used a lot, but it is not yet known for all species groups (this is part of the work of GINAMO). One ratio per taxonomic group can be used. If the ratio is not known, a ratio of 0.1 can be used as by a rule-of-thumb recommendation that is generally conservative ([Hoban et al. 2024](#)); more specific collaborative work could be conducted to determine appropriate  $N_e/N_c$  ratios for country-relevant taxa. (G)
- Why is regeneration not taken into account in these indicators (would indicate the impact of the contemporary environment directly). In tree species in particular, not accounting for regeneration might lead to genetic indicators not being as informative as expected. Ongoing work is underway with forestry stakeholders to address this issue. (G)
- Some IFREMER data has not been authorised for use in the Red list. So beware of cases where you think the data is accessible and public when in fact it is not.

### ***Population delimitation challenges***

- Defining populations is critical for estimating genetic indicators but may be a major challenge in various species. (G)
- Different ways to delimit populations:
  - With genetic approaches:
    - Genetic data for population structure might be used if available
    - Evolutionary Significant Units (ESUs) can help identify populations.
  - With ecological & geographic approaches
    - Defined based on habitat continuity, expert knowledge, and species traits.
- Species spatial distribution may change due to fragmentation, shift, expansion or decline over time, making temporal comparisons difficult across reports → make sure to have overlapping methodologies and species across reports in time. (G)
- Delimitation of populations requires expert validation to ensure consistency → this raises the question on how to ensure neutrality of experts? And how to deal with different opinions? Develop a peer-review-like system to validate population delineation?
- Involving local experts in that step might be time consuming but seems a good way to involve citizens in the indicators' reporting process.
- Question of transboundary populations. How to deal with that? There might be a need to develop common actions with other European countries. (G)

## **The report to the CBD is written and submitted**

### ***Discussion***

- France is 100% sure to report the genetic indicators to the CBD.
- The “Ministères de l'Aménagement du territoire et de la transition écologique” has a working group preparing the report to the CBD for all indicators. It is currently looking for workflows that

already exist, for example workflows that for reporting to international organizations (like the IUCN for example)

- Ongoing discussion about deciding if it is more appropriate to provide one report only for all territories, or one for metropolitan areas and others for overseas territories. What are the other countries doing (e.g. Denmark with Greenland)?
- IUCN Red List Status reporting is a good opportunity for comparison of how the reporting might be done.
- A working group for reporting exists. Waiting for validation at COP16. Probably there will be a seminar organised with all the actors who produce data to report all the indicators.
- Is it appropriate and how can France involve the civil society and NGOs in this work, while keeping it scientifically sound at the same time?
- If the number of identified populations of a given species is large, recommendations can be made on how to consider a representative subset of them; maybe not estimate the indicators for all the populations?

### *Challenges*

- Looking for joint actions with other European countries?
- The skills and data exist but we need to decide who is responsible for managing the process of collecting the data, compiling them and organizing them into a workable report. Need to design an organisation that will be in charge to prepare the reporting for these indicators? Set up a working group of experts for the different taxa?
- In all cases, people who are going to write the report need information on how to calculate the indicators (GINAMO France, MNHN could support these steps)
- For the reporting process to benefit conservation strategies in France, there is a need to look at its development across time, with a long-term approach

### *Miscellaneous challenges that GINAMO could potentially support*

- Feedback on data used for genetic indicators in other European countries (GINAMO countries) (G)
- The EU signed the GBF as a separate party: there will be a Europe-level reporting - it might be interesting to access the initiative (data used and persons responsible)
- Reporting on migratory species (G)
- Reporting on transboundary species; it requires coordination between countries (G)
- If species lists are evolving/increasing between successive reports: assurance of consistency in indicator values

- Assessing the representativeness of poorly monitored species (G)
- Inclusion of microorganisms into the reporting (G)
- Inclusion of marine species into the reporting (G)
- Connection of steps in the reporting workflow, representativeness, geographical scale of reporting

## Conclusions by the stakeholders and Next steps for France - with support from MNHN, OFB and GINAMO

- Formalise who collects the data and prepares it for reporting
- Formalise whether the report should be declined in one part for metropolitan France and one part for the five DROM
- Measures along these lines are currently being prepared by OFB-MNHN with support of GINAMO members from France.
- In practice, to enhance France's 2026 CBD report on genetic indicators beyond the set of ca. 80 species included in a proof of concept, the workshop organisers have expressed to the "Ministères de l'Aménagement du territoire et de la transition écologique" the need to hire two staff members for a year ("Ingénieur d'étude" level, cost ca. 100,000 EUR) to help assemble the data for the February 2026 reporting. The reporting could be declined into a part for metropolitan France, and a part for the five main overseas territories. The recruited staff members would benefit from GINAMO, MNHN and OFB's expertise via an "advisory board" (or similar) to be created.

## Next steps

The GINAMO work packages will assess all challenges selected by the five countries as potentially benefiting from collaboration between GINAMO and the country stakeholders. The GINAMO work package members will assess if and how these can be incorporated into their work, and how the country stakeholders might be able to contribute. The result of this will then be reported back to the country workshop participants, together with potential next steps.

## Reference materials

Introductory [Presentation](#) of the workshop, on genetic diversity conservation within the Convention on Biological Diversity's Kunming-Montreal Global Biodiversity Framework, genetic indicators and GINAMO work plan.

France has committed to the Kunming-Montreal Global Biodiversity Framework and must report to the CBD using novel genetic indicators for the first time, among a large range of indicators, first in February 2026, and then periodically, typically every three to four years. Critical steps are the selection of species to report on, collecting and interpreting available data on them for the calculation of indicators, and using a reproducible approach to building successive reports. Guidelines for these steps are available:

- CBD guidelines:  
<https://www.cbd.int/doc/c/92cf/b458/18519b4c0b487bf9bfc23988/sbstta-26-inf-14-en.pdf>
- Guidelines from the Coalition of Conservation Genetics:  
<https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/>
- <https://doi.org/10.17161/bi.v18i.22332>
- Genetic diversity must be protected because it allows for the long-term persistence, resilience and adaptive potential of species.
  - policy brief: <https://g-bikegenetics.eu/en/multimedia-policy-briefs-pubs/policy-briefs>
- The genetic indicators are pragmatic and can be computed using DNA data or non-DNA proxy data.
  - <https://doi.org/10.1093/biosci/biae006>
  - <https://doi.org/10.1007/s10592-024-01632-8>
- These indicators have been tested and validated for use in 9 countries, including Belgium.
  - <https://doi.org/10.32942/X2WK6T>
- National Biodiversity Strategies and Action Plans (NBSAPs) can be improved to include the protection of genetic diversity.
  - <https://doi.org/10.1093/biosci/biae106>



## APPENDIX I: Workshop Agenda

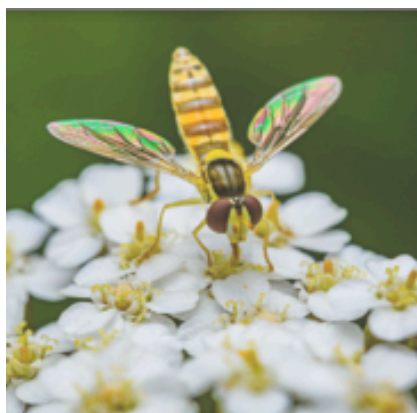
### ORDRE DU JOUR

- |   |   |
|---|---|
| <b>09.30</b> Bienvenue / Introduction / Enquête                               | <b>13.00</b> Situation actuelle et défis (SAD):<br>liste des espèces                  |
| <b>10.10</b> Présentation GINAMO et<br>indicateurs génétiques                 | <b>14.00</b> SAD: Collecte de données et<br>calcul des indicateurs                    |
| <b>10.40</b> <b>PAUSE</b>   | <b>14.45</b> <b>PAUSE</b>   |
| <b>10.50</b> Processus de l'atelier / flux de<br>travail pour le rapportage   | <b>15.00</b> SAD: rapportage à la Convention<br>sur la Diversité Biologique<br>(CDB)) |
| <b>11.05</b> Présentation des participants /<br>implication organisationnelle | <b>15.30</b> Classer les défis  |
| <b>12.00</b> <b>DÉJEUNER</b>  | <b>16.15</b> Prochaines étapes / Enquête  |
|   | <b>17.00</b> <b>FIN</b>   |



Photo: Julia Geue, GINAMO

## APPENDIX II: IUCN SSC CPSG



Our **mission**: to save threatened species by increasing the effectiveness of conservation efforts worldwide

Our **mantra**: every species that needs a plan is covered by an effective and implemented plan



### For over 40 years we've accomplished this by:

- Providing culturally sensitive and respectful facilitation for stakeholder-inclusive conservation action planning.
- Developing and sharing innovative, interdisciplinary science-based tools and methods.
- Building capacity for species conservation planning worldwide.