

IUCN Species Survival Commission biobanking guidelines for conservation purposes

Hvilsom, C., Brown, A., †Bruford, M., Berner, J., Boettcher, P., Bragg, J., Calatayud, N., Costa, M., Daly, J., Dulloo, E., Fant, J., Goodale, U.M., Habul, A., Hamer, M., Heineman, K., Hoban, S., Hobbs, R., MacDonald, A., Masembe, C., Motato-Vásquez, V., Mullins, P., O´Brien, J., Russo, I-R., Ryder, O., Sole, C., Vergeer, P., Wettberg, E.B.v., Wisely, S., and Segelbacher, G.







About IUCN

IUCN is a membership Union uniquely composed of both government and civil society organisations. It provides public, private and non-governmental organisations with the knowledge and tools that enable human progress, economic development and nature conservation to take place together.

Created in 1948, IUCN is now the world's largest and most diverse environmental network, harnessing the knowledge, resources and reach of more than 1,400 Member organisations and some 15,000 experts. It is a leading provider of conservation data, assessments, and analysis. Its broad membership enables IUCN to fill the role of incubator and trusted repository of best practices, tools and international standards.

IUCN provides a neutral space in which diverse stakeholders including governments, NGOs, scientists, businesses, local communities, indigenous people's organisations and others can work together to forge and implement solutions to environmental challenges and achieve sustainable development.

Working with many partners and supporters, IUCN implements a large and diverse portfolio of conservation projects worldwide. Combining the latest science with the traditional knowledge of local communities, these projects work to reverse habitat loss, restore ecosystems and improve people's well-being.

www.iucn.org https://twitter.com/IUCN/_

About SSC

With over 10,500 members, the Species Survival Commission (SSC) is the largest of the six expert Commissions of IUCN. SSC enables IUCN to influence, encourage and assist societies to conserve biodiversity by building knowledge on the status and threats to species, providing advice, developing policies and guidelines, facilitating conservation planning, and catalysing conservation action.

Members of SSC belong to one or more of the 160 Specialist Groups, Red List Authorities, Conservation Committees and Task Forces, each focusing on a taxonomic group (plants, fungi, mammals, birds, reptiles, amphibians, fishes and invertebrates), or a disciplinary issue, such as sustainable use and livelihoods, translocation of species, wildlife health, climate change and conservation planning.

www.iucn.org/ssc

About CGSG

The IUCN SSC Conservation Genetics Specialist Group (CGSG) is one of the disciplinary Specialist Groups. The CGSG provides genetic advice on policy and management within IUCN's Species Survival Commission (SSC) and expert knowledge and assistance to SSC specialist groups. The CGSG facilitates a fuller appreciation, evaluation and conservation of genetic diversity and resources at all levels, providing a forum for all stakeholders to value and conserve this crucial element of Planet Earth's life systems.

Biobanking guidelines for conservation purposes

Hvilsom, C., Brown, A., †Bruford, M., Berner, J., Boettcher, P., Bragg, J., Calatayud, N., Costa, M., Daly, J., Dulloo, E., Fant, J., Goodale, U.M., Habul, A., Hamer, M., Heineman, K., Hoban, S., Hobbs, R., MacDonald, A., Masembe, C., Motato-Vásquez, V., Mullins, P., O´Brien, J., Russo, I-R., Ryder, O., Sole, C., Vergeer, P., Wettberg, E.B.v., Wisely, S., and Segelbacher, G.



universität freiburg

creativecommons.org/licenses/by-nc/4.0/. The user is allowed to distribute, remix, adapt, and build upon the material in any medium or format. The user must give appropriate credit to IUCN as the source of the material and indicate if changes were made to the original content. Only non-commercial uses of the work are permitted. Use of the name and logo of IUCN is not permitted in connection with adaptations, translations, or other derivative works.

Adaptations/translations/derivatives should not carry any official logo, unless they have been approved and validated by IUCN. Please contact IUCN (logo@iucn.org) to obtain permission.

When copyright of content published by IUCN, such as images, graphics or logos, is held by a third-party, the user of such content is solely responsible for clearing the rights with the right holder(s).

The user acknowledges and agrees that any transformation, adaptation, translation or alteration of the Original Content provided by IUCN "hereinafter referred to as "Original Content" is done at the user's own risk. In no event shall IUCN be liable for any damages, losses or consequences arising from the use, modification or adaptation of the Original Content. The User agrees to comply with all applicable laws and regulations when transforming, adapting or redistributing the Original Content. Furthermore, IUCN does not guarantee the quality, accuracy, integrity or legal compliance of the Original Content after its transformation or adaptation. IUCN expressly disclaims all liability for any copyright, trademark, or other legal infringement that may result from the modification or unauthorized use of the Original Content.

The designation of geographical entities in this work, and the presentation of the material, do not imply the expression of any opinion whatsoever on the part of IUCN concerning the legal status of any country, territory, or area, or of its authorities, or concerning the delimitation of its frontiers or boundaries.

The views expressed in this work do not necessarily reflect those of IUCN.

IUCN is pleased to acknowledge the support of its Framework Partners who provide core funding: Ministry of Foreign Affairs, Denmark; Ministry for Foreign Affairs, Finland; Government of France and the French Development Agency (AFD); Ministry of Environment, Republic of Korea; Ministry of the Environment, Climate and Sustainable Development, Grand Duchy of Luxembourg; the Norwegian Agency for Development Cooperation (Norad); the Swedish International Development Cooperation Agency (Sida); the Swiss Agency for Development and Cooperation (SDC) and the United States Department of State.

Published by: IUCN, Gland, Switzerland

Produced by: IUCN SSC Conservation Genetics Specialist Group (CGSG)

Copyright: © 2025 IUCN, International Union for Conservation of Nature and

Natural Resources

Recommended citation: Hvilsom, C., Brown, A., †Bruford, M., Berner, J., Boettcher, P., Bragg, J.,

Calatayud, N., Costa, M., Daly, J., Dulloo, E., Fant, J., Goodale, U.M., Habul, A., Hamer, M., Heineman, K., Hoban, S., Hobbs, R., MacDonald, A., Masembe, C., Motato-Vásquez, V., Mullins, P., O´Brien, J., Russo, I-R.,

Ryder, O., Sole, C., Vergeer, P., Wettberg, E.B.v., Wisely, S., and Segelbacher, G., (2025). Biobanking Guidelines for Conservation

Purposes. Gland, Switzerland: IUCN.

ISBN: 978-2-8317-2354-9

DOI: https://doi.org/10.2305/ECLR4913

Cover photos: Friónt fom left to right, top to bottom

Tropical forest Ecuador. Photo: © Katrin Heer

Brown bullfrog (Kaloula baleata). Photo: © Johannes Penner

Cold blood samples. Photo: © Frank Rønsholt

Giant spiny sea star (Pisaster brevispinus). Photo: © Jerry Kirkhart

Back

Photo: © Gernot Segelbacher

Layout by: Presston Brown, Ania Brown and Christina Hvilsom

Contents

Executive summary	i
Drafting process and acknowledgements	i
Scope	i
Section 1: Introduction	
1.1 What is a biobank?	
1.2 Utilising biobanks to maintain and monitor genetic diversity	
1.3 Benefits of biobanking	
1.3.1 Biobanking for domestic and wildlife fauna	-
1.3.2 Biobanking for plants	-
1.3.3 Biobanking for fungi	
1.3.4 Biobanking for microorganisms	
1.4 Biobanking and One Health	10
1.5 Biobanking Guidelines as a biodiversity resource	10
Section 2: Sample databases: Collection distribution and taxonomic representation	12
2.1 Closing the gaps	1:
Section 3: Document harmonisation	19
3.1 Vision and mission, policy, strategic action plan and internal process	20
3.2 Standard operating procedures	20
3.3 Material transfer/acquisition agreements	2
3.4 Applications and agreements for sample use and release	22
3.5 Dispute resolution	24
Section 4: Legislation and regulation	2
4.1 Levels of regulation	26
4.1.1 Sample collection regulation	28
4.2 Sample export and import	3
4.2.1 Considerations for proper sample shipping and transport	3
4.2.2 Environmental (storage) conditions	32
4.2.3 Packaging and labelling	33
Section 5: Data and databases	3.
5.1 Database systems	36
5.2 Data sharing	36
5.3 Other relevant software and programs	4(
Section 6: Creating a network	4
6.1 Connect and collaborate - the importance of networking	42
6.2 Opportunities for biobanking collaboration	43
6.3 Developing key competencies for collaboration	43
6.4 How to develop a network	44
6.5 Examples of collaborative biobanking initiatives	4.
6.6 The way forward: A global network with centralised sample data	53
References	5:
Supplementary	6.5

Executive summary

Conservation of biodiversity is challenged by the rapid advancement of global habitat loss, climate change, exploitation and more, and so, it is crucial to monitor changes at all three levels of biodiversity: genetic, species, and ecosystem diversity. Various solutions have been proposed to maintain and enhance biodiversity at all levels, but often evaluation can be problematic, as reference baselines (e.g. temporal samples) are often lacking. Biobanks, as collections of biological material from fauna, flora and fungi, offer the opportunity to provide such reference points in time and space, but also to monitor and aid conservation planning ex situ and in situ. However, many different methodological and technical challenges exist for setting up, managing and using sample collections. These Guidelines introduce different biobanking methods and highlight why and how they can support biodiversity conservation. The Guidelines call for and delineate standardised approaches, from collecting and storing samples to using and sharing data. Lastly, the Guidelines illustrate which international and national regulations have to be considered. This document aims to be a resource that guides the reader through the fundamental decision processes for establishing, managing and implementing biobanks. Only through a harmonised and standardised approach within a global network will we be able to fully utilise the potential of biobanks across the world.

Drafting process and acknowledgements

A drafting team comprised of Christina Hvilsom (Conservation Genetics Specialist Group (CGSG), Conservation Planning Specialist Group (CPSG), Animal Biobanking for Conservation Specialist Group (ABCSG)), Ania Brown (European Association of Zoos and Aquaria), Mike Bruford † (former Co-Chair CGSG), Juliana Berner, Paul Boettcher (CGSG), Jason Bragg (CGSG), Natalie Calatayud (Amphibian Specialist Group, ABCSG)), Mafalda Costa, Jonathan Daly, Ehsan Dulloo (CGSG), Jeremie Fant (CGSG), Uromi Manage Goodale (Seed Conservation Specialist Group), Adi Habul, Michelle Hamer, Katie Heineman (Center for Species Survival Biodiversity Banking), Sean Hoban (CGSG), Rebecca Hobbs, Anna MacDonald (CGSG), Charles Masembe (CGSG), Viviana Motato-Vásquez (Colombia Fungal Specialist Group), Piper Mullins, Justine O´Brien, Isa-Rita Russo (CGSG), Oliver Ryder (CGSG, Co-Chair ABCSG), Catherine Sole (CGSG), Philippine Vergeer (CGSG), Eric Bishop von Wettberg (CGSG), Samantha Wisely (CGSG), Gernot Segelbacher (Co-Chair CGSG and University of Freiburg).

We want to thank Katie Barker from GGBN, Kyle Copas and John Waller from GBIF, Rachel Thomson Species 360 and the two external reviewers Joanna Sumner and Roberta Gargiulo for providing helpful comments and input for improving the Guidelines

Scope

These Biobanking Guidelines are intended for use by researchers, conservation professionals, and policy makers to ensure that the best practices in high quality sample collection, preservation, data management and data sharing are implemented globally. Numerous biobanks exist globally and offer a wealth of genetic information. However, these collections vary in their size, function and management and most operate independently. Biobanking for humans, domesticated species and agricultural crops are essential activities that advance biobanking practice, but unless used as resources for wild species they are outside the scope of this document. These Guidelines focuses primarily on biobanking wild species as a conservation tool for safeguarding the world's biodiversity and offer;:

- 1. review of the current state of collections for three kingdoms: Fauna, Flora, and Fungi. By synthesising globally available information, our goal is to inspire collaborations toward a global biobank network to advance biodiversity conservation.
- 2. presentation of best practices for creation, implementation and use of protocols, observance of pertinent legislation and regulations, and alignment with international conventions and obligations, such as the Convention on Biological Diversity (CBD). Resources including data standards and existing data management tools specific to biobanks are referenced and described.
- 3. outline of a strategy for building a global network to facilitate knowledge and data sharing for the benefit of wild species.



Section 1: Introduction

Biodiversity, as the assemblage of living organisms including their genetic diversity and their ecosystems, is the foundation for sustaining all life on Earth. Biodiversity consists of three pillars: genetic diversity within populations and species, species diversity, and ecosystem diversity. Despite its importance, global biodiversity is declining at an alarming rate, with about 1 million species already facing extinction within the coming decades (IPBES, 2019). Human induced alterations in climate, land use and habitat fragmentation have continued to increase since the industrial revolution (CBD, 2011). We are in the midst of a sixth mass extinction; a biodiversity crisis with devastating consequences for the health and function of ecosystems, evolutionary heritage, and the adaptive potential of species, which ultimately pose a major threat to humanity (Cowie et al., 2022). Consequently, as loss of genetic variation of wild populations increases, biodiversity losses continue.

Currently, genetic variation of wild species populations is estimated to have declined six percent across 91 animal species examined (Leigh et al., 2019). Discrepancies between the Critically Endangered rankings of the IUCN Red List of Threatened SpeciesTM and contemporary genome-wide variability highlight the lack of data available for total losses of global biodiversity, and not just for species of conservation concern. To slow the rate of loss and not only preserve, but restore this diversity, there is a need to build the resources necessary to allow transformative conservation efforts. Biobanking is an effective tool to deliver these sought after results. However, scattered and biased sample diversity, data and knowledge coupled with inconsistent collection and storage methods present a major challenge to the field.

In recent years, scientific techniques and tools, such as genetic sequencing, gamete retrieval and use, and cell line propagation, have become more readily available to the conservation community (Frankham et al., 2002; Segelbacher et al., 2022). These technological advances together with decreasing costs, will create opportunities for scientific advancement. However, these opportunities can only be seized if biological samples are available for use. Adequate and appropriate sample availability can pave the way for broader use of molecular tools and techniques in helping improve biodiversity conservation in more efficient and immediate timescales (Segelbacher et al., 2022; Smith et al., 2023). For example, for many plant species that produce recalcitrant seeds (i.e., those that are cold sensitive and cannot tolerate drying inherent to orthodox seed banking) novel cryopreservation techniques may be developed and employed to overcome these challenges (Walters & Pence, 2021). But samples are needed to aid research and development of protocols to enable their long-term preservation. For endangered vertebrates, the use of preserved material (i.e., spermatozoa) combined with assisted reproductive techniques is being evaluated for uses in genetic rescue of a species as in the cases of the Przewalski's horse and the black-footed ferret, where genetically valuable clones have been produced (Sandler et al., 2021).



Propagation of plants from seed previously stored in a native plant seed bank Photo: © San Diego Zoo Wildlife Alliance

Understanding species conservation challenges and linking in situ (conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings) and ex situ (conservation of components of biological diversity outside their natural habitats) efforts is essential to save threatened species. Biobanking, as a component of ex situ conservation strategies, is critical for complementing in situ efforts, assisting, and implementing complementary long-term conservation strategies (Maxted et al., 2001). The more samples that can be preserved now, the better the unknown needs and challenges of the future can be met. Scientific techniques and tools will continue to evolve, and provided we have the materials available, these tools can be applied in new ways to answer new questions. Ensuring high quality sample material is findable and available in biobanks for these advanced technologies to make a difference in species recovery in the event of in situ population collapse is critical.

1.1 What is a biobank?

A biobank (or biorepository) is defined as a collection of biological samples and their associated information, which is systematically organised, managed according to international standards and used for research, industry, academic and conservation purposes (Hewitt & Watson, 2013; ISBER, 2023). The term 'biobank' can be used to refer to all types of biological sample collections (i.e., human, animal, plant, fungi, or microbial materials) from tissues to entire specimens, and biobanks can vary widely in their scope. Samples may be housed at different sites including genebanks, cryobanks, culture collections, botanical gardens, orchards, zoos, natural history museums and academic institutions (Thormann et al., 2006; Corrales et al., 2023; FAO 2010, 2023) and their users may include conservationists, researchers, breeders, farmers, medical doctors, veterinarians, museum curators, nature managers and database managers, among others. Many small initiatives are ad-hoc and 'project-driven' and exist as either a single or a few freezers built around specific needs (such as those in a research laboratory), while larger initiatives and networks have more resources and may operate to support overarching conservation goals. However, larger, general collections do exist, and are dedicated reference collections that are often available for a variety of research uses, usually upon request and review. Operational and organisational models of these biobank collections are dependent on the conservation and research missions, as well as their geographical range, and the size of the initiatives, (i.e., whether samples from multiple locations need to be coordinated into a centralised physical biobank, such as some national and regional biobanks).

The term 'biobanking' is a general one that commonly involves sample preservation through freezing (i.e., -20 oC or -80 oC), dry storage, or cryopreservation (i.e., -196 oC). As such, different terms surrounding the preservation and use of biological materials carry different meanings and should be used accordingly. Cryopreservation specifically describes a process of preservation of living cells (i.e., organelles, cells, tissues) where when cooled to very low temperatures, their biological and chemical reactions are dramatically reduced, a phenomenon that can lead to the possible long-term preservation of cells and tissues (Jang et al., 2017) as well as seeds (Thormann et al., 2006; Dulloo et al., 2010) with the potential to revive them in the future. In plants, for example, cryopreservation protocols have been developed for more than 200 species (Panis, 2009), while the seeds of most seed plants can be dried and stored at -20 oC for later regeneration, following general guidelines for orthodox seed banking (MSB, 2015; CPC, 2019).

The preservation of bacteria and fungi was already established by pioneers from the 19th and early 20th centuries (Day & Stacey, 2008). This pioneering work has been improved and refined with new approaches and fundamental research into cryobiology, which has enabled the preservation of diverse and complex cell cultures and tissues. However, it should be noted that many challenges remain. For instance, many protocols have been suggested to be suitable for preservation of fungi, although no individual preservation technique has been successfully applied to all fungi (Crespo et al., 2000; Smith & Ryan, 2003; Espinel-Ingroff et al., 2004). Cryopreservation in liquid nitrogen and freeze-drying (lyophilization) are the methods recommended by the American Type Culture Collection (Lee, 1991) for

fungal repositories, however, many taxa, cell lines, and multicellular structures remain as "recalcitrant" to current preservation methodologies. These fungi often include those that do not sporulate in culture such as Basidiomycota, and others which are difficult to maintain in culture or are facultative pathogens (Smith & Ryan, 2003; Paoli, 2005; Day & Stacey, 2007).

Globally, there is a wide array of sample types that are stored in biobanks (see e.g. Corrales & Astrin, 2023 for an overview of sample and preservation types). Such existing biobank sample types include various bodily fluids and tissues (i.e., blood, serum, plasma, milk, organ tissue, faeces, "live cell" gametes or cell lines) (see Section 2) from various fauna, as well as seeds, plant tissues, whole or partial specimens, live cell tissues and cell lines from flora and funga (Figure 1). Each of these sample types, representing either single individuals or entire species, may serve as a puzzle piece, potentially filling in key knowledge gaps, or contributing to a wider body of knowledge regarding biodiversity health and conservation. In addition to species-related biological information (i.e., omics [genomics, transcriptomics, proteomics, metabolomics], biomarkers for diseases or pathological conditions), biobanks also provide crucial information on the genetic composition at the individual, population and/or species level and thus can help in maintaining or restoring genetic diversity.



Photo: © Frank Rønsholt

1.2 Utilising biobanks to maintain and monitor genetic diversity

Genetic diversity (genetic variation within populations and species) is a fundamental component of biodiversity. It contributes to function and structure in all ecosystems and to resilience and/or productivity in agriculture, aquaculture, and forestry systems. Currently, genetic diversity has relevance to global policy targets including CBD Kunming Montreal Global Biodiversity Framework (Goal A) and Target 4 "Threatened species are recovering, genetic diversity is being maintained..."; Sustainable Development Goal (SDG) 2.5, 'maintain genetic diversity', and Global Strategy for Plant Conservation Complementary Actions 2, 4c, 4d, 4e, 8b, and 11 (regarding respectively, genetically appropriate material for restoration, conservation of genetic diversity, use of genetic diversity in climate mitigation and adaptation, and genetic diversity for ecosystem function). Genetic diversity can be used as a metric of species health, and in some cases, genetic data are cheaper and easier to gather than other methods of biodiversity monitoring (Carroll et al., 2018; Hoban et al., 2022). Further, historical or even ancient samples allow insight into past ecology, diversity, evolutionary events and processes, and their relevance for the extant populations. Such samples can allow assessment of genetic diversity of a species prior to anthropogenic impact (Roycroft et al., 2021; Jensen et al., 2022; Burbano & Gutaker, 2023).

There are many instances where genetic information can inform conservation efforts and management strategies, and the application of genetic data and tools to aid conservation policy and practice (Brandies et al., 2019; Bertola et al., 2023, Holderegger et al. 2019). These tools can also help guide breeding management to ensure optimal genetic diversity is represented and preserved, supporting the integrated conservation practices of wild and captive populations under the One Plan Approach (Byers et al., 2013). The goal of the One Plan framework is to foster interactive cooperation between ex-situ and in-situ efforts in order to identify strategies or actions necessary for in-situ species conservation. Included in this work toward more comprehensive species conservation planning is the consideration of if and how ex-situ species management may align with goals identified as important for survival of the species. In-situ conservation protects species in their native habitat, while ex situ conservation ensures specimens are available for research, breeding, and education activities that ultimately support reintroduction efforts, to prevent species from going extinct (Guerrant et. al., 2004). Additionally, implementing genetic monitoring programs in wild populations may help provide early warning signals of population decline and genetic erosion (Hvilsom et al., 2022).

Many biobank sample collections aiming to serve as genetic resources fall short of capturing true genetic diversity of species and their populations within their collections. Because they are often not collected based on specific sampling criteria, these collections may overlook significant diversity within and between populations, potentially limiting the scope and utility of research conducted on these samples. To address this gap, more work is needed to establish metrics or indicators that can reliably assess the genetic diversity within sample collections and enable a more comprehensive sampling strategy. This approach is especially critical when biobanking resources are limited, as it allows for strategic prioritisation in sample collection to more accurately capture and preserve diversity, thereby maximising the utility and inclusiveness of biobank resources.

1.3 Benefits of biobanking

Proper sample collection and management is not only key for contemporary health and population management research, but can aid future biodiversity research. Conservation strategies cannot mitigate the biodiversity losses currently faced through habitat preservation alone and economic constraints make the logistics of in situ ecological management impractical (Upton, 2020; Hu et al., 2021). The role of ex situ conservation breeding programmes in the preservation, reintroduction, and translocation of species has alleviated the immediate pressure of extinction for several species (IUCN SSC, 2014; Abeli et al., 2020; Bragg et al., 2021; Hilderbrandt et al., 2021; Turghan, Jiang and Niu, 2022).

Inherently challenged by financial and spatial limitations, ex situ programmes face other obstacles such as the small number of founding individuals used to start a breeding programme, infertility due to lack of natural environmental cues or extended lifespan in captivity and the effects of captivity itself on genetic diversity and breeding success (Robert, 2009; Witzenberger and Hochkirch, 2011; Wade et al., 2016; Farquharson et al., 2018; Bragg et al., 2019; Upton, 2020). In conservation of plant genetic resources, some of the key challenges are the loss of seed viability and the need for regeneration which, if not carried out properly, can be a source of genetic erosion in genebanks and lead to genetic drift and viability selection in accessions (Fu, 2017; Hoban, 2019). A comprehensive understanding of the rate of change and differing effects of these conservation programmes across taxonomic groups is critical to successfully combat loss of genetic diversity. Biobanks can alleviate spatial and logistical limitations providing long-term, indefinite storage of genetic diversity that can be incorporated at a later date (Kier et al., 2009). For fauna, cryopreserved samples offer an additional strategy with which to bolster genetic diversity with assisted and advanced assisted reproductive technology (ART and aART, respectively), which encompass a wide array of different techniques with the ultimate purpose of creating offspring with varying degrees of assistance (Bolton et al., 2022). For example, semen from genetically valuable black-footed ferret males is regularly banked for use in subsequent generations of captively bred animals to slow down genetic drift (Santymire et al., 2016).

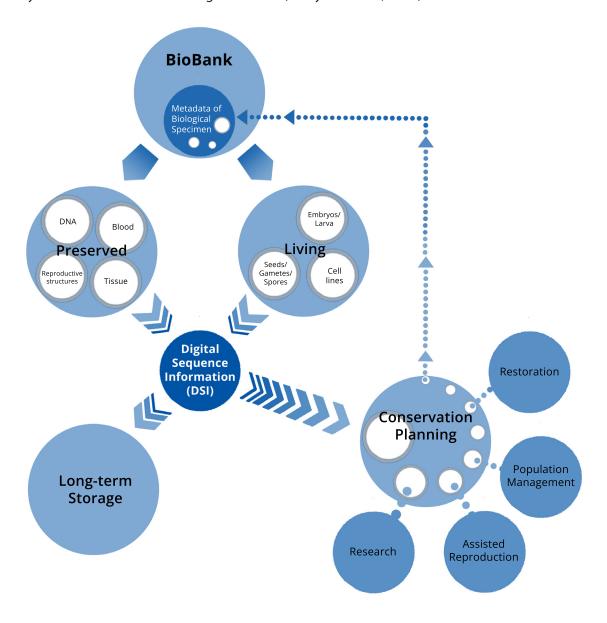


Figure 1. Overview on different sample types and materials for different taxa and their potential use in a typical biobank. Created by report authors.

1.3.1 Biobanking for domestic and wildlife fauna

ARTs and biobanks, as cost-effective strategies to reproduce, preserve, and manage genetic diversity, are more established for humans (Sherman, 1980) and commercially important species (Tiersch, et al., 2007; Walters et al., 2009) including agricultural crops (Curry et al., 1995; Ruta et al., 2020), livestock (Verma et al., 2012; Moore and Hasler, 2017;), birds (Blesbois, 2007), and biomedical animal models (Li et al. 2006). Historically, commercial needs have driven significant investment into development of protocols and infrastructure to build frozen repositories, whereas recognition of their utility has been slow or largely ignored for wildlife conservation (Della Togna et al., 2020). In light of a worsening biodiversity crisis, views towards the value of biorepositories as well as the relevance of ARTs are fortunately changing and the use of biobanks as conservation tools for the rescue of plants, animals, funga and microbial communities are increasingly valued (Herrick, 2019; Clulow et al., 2022; Kulak et al., 2022).

Domestic species, especially those used in agriculture or biomedicine, are often extensively studied and possess advanced genomic and reproductive science resources. When these domesticated model species are congeners and closely related to species of interest, they can serve as valuable tools for understanding the target species. Genomes from domestic species have been used as references for unannotated wildlife genomes (Hohenlohe et al., 2021), and reproductive techniques developed for domestic species have been applied to wildlife (Comizzoli and Wildt 2017). Although each species is ecologically, physiologically, and behaviorally unique, domestic species can provide critical insights into evolutionarily similar species. For instance, domestic ferrets have been used to enhance the reproductive capabilities of both European mink (Mustela lutreola) and black-footed ferrets (Amstislavsky et al., 2008). Similarly, the domestic dog has served as a reference genome for various canid species, including the highly inbred Channel Island Fox (Urocyon littoralis; Robinson et al., 2016).

1.3.2 Biobanking for plants

Biobanking for plants has had a strong agricultural focus over the last century, given the threats posed to the genetic diversity of local crops by improved high-yielding varieties during the agricultural revolution (Scarascia-Mugnozza and Perrino, 2002; Peres 2016). Historically, Indigenous knowledge led to local stewardship of many wild species, with about 100,000 species used by mankind, of which 30,000 species are edible, 7,000 crop species are used as food at local levels, 120 crop species are important at the national scale, 30 crop species provide 90% of the world's calories and only four crops provide 60% of the calories and proteins consumed globally (Prescott-Allen and Prescott-Allen, 1990; Wilson, 1992; Palacios, 1998). However, colonising powers such as Great Britain, France, Belgium, Spain and the Netherlands made collections across empires, often finding crops or potential crops in one area, studying them in a botanic garden, and then expanding production in other areas. Notable examples, with legacies of biopiracy, include the development of the coffee and rubber trades (e.g., Jackson 2008). Both of these now global commodities grew out of Indigenous knowledge of unique plants, but grew into global value chains in the past few centuries.

In the 20th century, efforts to find and harness useful crop germplasm became more formal and systematic, with the development of national germplasm genebanks, such as the USDA National Plant Germplasm System, the Nordic Seed Vault (and later, the Svalbard Global Seed Vault) and the Soviet seed bank, the first of its kind (now the Vavilov Institute in the Russian Federation) (Scarascia-Mugnozza and Perrino, 2002). In addition to the large international collections built and hosted by the Consultative Group on International Agricultural Research (CGIAR) research centres, more than 1500 national crop germplasm collections have been established by most nations (FAO, 1996, 2010). Among these collections there is a considerable history of exchange of material, even among geopolitical adversaries. It is estimated that there are currently 7.4 million accessions of crop germplasm globally, of

which only 2 million may be representing unique accessions, and fewer still are utilised as plant genetic resources (Mondal, Kumar & Gnanesh, 2023). These collections include approximately 2% or less of non-cultivated species (although there are notable outliers like the USDA NPGS that is ~15% wild material) and poorly represent the diversity of wild crop relatives, let alone the broader diversity within floras (Castaneda-Alvarez et al., 2016).

In the past few decades, efforts to biobank non-cultivated plants have expanded, with efforts led by botanic gardens being particularly critical. The Global Strategy for Plant Conservation has identified an aim of 75% of threatened plant species to be held in ex-situ collections, including seedbanks. In addition to the conservation of wild species, there is a clear need for these efforts to conserve and respect traditional Indigenous ecological knowledge of these species.



1.3.3 Biobanking for fungi

Conserving biodiversity in fungal and microbial communities faces immense challenges given the sheer number of distinct organisms. Currently, over 155,000 fungal species have been described (Kew Royal Botanic Gardens, 2023). However, estimates based on high-throughput sequencing methods suggest that as many as 2.2–3.8 million fungal species are estimated to exist (Hawksworth & Lücking, 2017; Niskanen et al., 2023), most of which are yet to be described and cultured. Ritter et al. (2020) demonstrated that a single teaspoon of Amazonian soil may contain as many as 400 Operational Taxonomic Units (OTU) of fungi, roughly equivalent to as many genetically separate species (Paton et al., 2020). At the current rate of discovery, it will take more than 700 years to describe them all. Biobanks may therefore become an invaluable tool for accelerated discovery and characterization of microorganisms and their potential beneficial uses for humans (Paoli, 2005). Existing collections represent the existing fungal diversity rather poorly (Overmann and Smith, 2017), as aspects of their biology make preserving their diversity more difficult than for many other organisms. Culture collections use different methods to maintain original characters, including the viability and purity of the preserved species. However, the main limitation is that only 40% of fungal species can be easily cultivated in artificial media, but not some parasitic or biotrophic species (Wu et al., 2019; Antonelli et al., 2023). For this reason, not all can be preserved ex situ in biobanks using traditional methods and more studies are necessary to find alternatives to preserve tissues or structures in the long term. To this end, innovations in advanced cooling technology are facilitating method development to preserve non-culturable fungi. The infrastructure needed to maintain the collections and the most commonly used methods such as cryopreservation and freeze-drying are expensive. As only 25 of the globally threatened or near threatened species of fungi are held in culture collections, there is a need to unite conservation aims with collecting ambitions in the future and secure long term funding to maintain collection globally (Antonelli et al., 2023).

1.3.4 Biobanking for microorganisms

Similarly, there is still a need to develop infrastructure to support the microbiome research community (Ryan et al., 2019). It is essential that microorganisms are deposited in collections to ensure that they are available for study. However, just over 17% of those described, are cultured and publicly available. The World Data Centre for Microorganisms provides a global view of microorganisms that are held and available from the microbial resource centres registered with them. They make almost 3.2 million strains of microbes available for reference and research; of these, 849,724 are fungal strains from 793 culture collections in 77 countries and regions. These collections and strains are disproportionately geographically distributed, with most existing in Europe (250 collections), and North America (197 collections).



Micropropagation of the Endangered coastal sage scrub oak (Quercus dumosa) [right] and San Diego mountain mahogany (Cercocarpus minutiflorus) [left]. Photo: © San Diego Zoo Wildlife Alliance

1.4 Biobanking and One Health

Complex problems require cross-disciplinary knowledge and expertise to appropriately define and combat, especially on an international scale. 'One Health' is the interdisciplinary integration of human, non-human animal, and environmental health, as the three fields are inextricably linked (Bertram et al., 2024). Meant to promote collaborative efforts across multiple disciplines on local, national, and global scales, a One Health framework should be applied to increase cooperative research and to incorporate animal and human health data to bridge knowledge gaps regarding environmental health risks (Cunningham, Daszak and Wood, 2017), which present complex and ever-evolving threats to these already complex systems.

One Health recognizes that the health of human populations, and global ecosystems is intimately linked to the understanding and preservation of genetic diversity in plant and animal species. By safeguarding the genetic richness of these organisms, we can better address pressing challenges such as emerging diseases, climate change adaptation, and food security. Biobanking and biorepositories serve as valuable resources for research, conservation, and the development of novel technologies, in line with a One Health approach. It is crucial for more biodiversity research to be conducted within a One Health framework, including sample and metadata storage, to effectively define, communicate and mitigate risks. Without it, public perception of wildlife and plant conservation may ultimately be irreversibly harmed, leading to less tolerance and value of wildlife and conservation (Buttke et al., 2015).



Tissue biopsy from a southern white rhino (Ceratotherium simum simum). Photo: © San Diego Zoo Wildlife Alliance

1.5 Biobanking guidelines as a biodiversity resource

Biobanking faces many challenges, including a lack of standardisation of the methods and quality of sample collection and storage, data capture and management, and formal documentation and traceability. Furthermore, a lack of more globalised and accessible database and management systems presents additional obstacles, impeding sample visibility and sharing. If samples are not being properly

processed with relevant data recorded into a reliable, easy to use and shared registration system, then standards of curation will suffer, and samples will not be as readily accessible for use in research. Guidelines towards standardising how samples and their metadata are processed, stored, and managed, as well as examples of existing database platforms that offer solutions to these challenges will be addressed in this document. New networks can serve to connect sample repositories for the advancement of robust and timely use of this important conservation resource. Currently, the field of biobanking for conservation and population management contains many silos that hinder a global overview of existing sample collections and our understanding of how individual efforts complement each other or overlap. Understanding the landscape of in situ and ex situ biobanking can provide a roadmap for the sensible use of samples for filling identified biodiversity research gaps. It is imperative that these samples are managed and utilised in a responsible way across all initiatives. Therefore, it is pivotal to establish common standards of good practice and information sharing regarding these invaluable resources for the conservation and research communities and ultimately work towards the creation of a global biobanking network that operates within these standards. Similar approaches for best practices in genetic data management and accessibility have been proposed by Leigh et al., 2024.

The biodiversity crisis is a global one, not unique to any particular region, nation, or taxa, but a widespread and shared issue. As such, any hope of a solution needs to arise from global collaboration. Understanding how biobanking helps to combat loss of biodiversity is the first step to aligning interests and understanding. These guidelines will illuminate the current state of sampling and sample availability in the largest international sample databases, devise recommendations for implementation of more unified standards and methods for sample collection, storage, data management and resource sharing to unite efforts, and streamline research, thereby helping get the global conservation community closer to producing robust conservation management policies in meaningful time frames.





Section 2: Sample databases: Collection distribution and taxonomic representation

The incorporation of genetic resources with accompanying data is slowly gaining traction by the scientific community, government agencies and other stakeholder groups involved in biodiversity conservation and management. Increasingly, there are national and institutional conservation plans that acknowledge, or actively incorporate, the need for biobanking into their conservation priorities, as well as coordinating efforts among international groups which work to combine in-situ, ex-situ and biobanking efforts for some critical taxa (See: Supplementary for examples)

The two globally largest open sample databases are the Global Genome Banking

Network (GGBN), created to be an open source platform from which any interested party can access information and engage in the legal exchange of samples held by member institutions, and the Global Biodiversity Information Facility (GBIF) (See Resources). Both databases hold data on biomaterial samples from wild species throughout the globe, illustrated and counted per continent (Figure 2 and 3, Supplementary table 1 and 3) and for the 17 megadiverse countries (Supplementary table 2 and 4).



Figure 2: Summarising GGBN sample data across geographical continents. Each ring represents a kingdom. Outer ring: Fauna, central ring: Funga, inner ring: Flora. Each ring is further divided into GGBN sample type categories: culture, DNA, tissue and unknown. Unknown category is miscellaneous physical samples, not identified by the contributor. Created by report authors.



Figure 3: Preserved: Preserved Specimen; Material: Material Sample; Living: Living specimen. The figure summarises GBIF sample data across continents. Each ring represents a kingdom. Outer ring: Fauna, central ring: Funga, inner ring: Flora. Each ring is further divided into GBIF sample type categories; Preserved Specimen, Material Sample and Living Specimen. Material Sample covers miscellaneous samples that are deemed different from the two other categories by the contributor. Living Specimen is a sample that is living i.e., a plant in a botanical garden or a living animal in a zoo. Preserved Specimens are samples stored in a preserving agent, dried, or on an herbarium sheet. Created by report authors.

For the purpose of these IUCN Guidelines, a thorough analysis was performed on both databases, to identify biological samples that can be used for genetic conservation. Both databases were analysed for sample types and categories, including physical samples useful for extracting DNA or proliferation. For GGBN, sample types are distinguished in the 'KindOfUnit' field, and include tissue", "culture", "DNA", "unknown" and "specimen category". The "specimen category" included: some tissue, culture, DNA and unknown samples, which were extracted and re-classified into the correct category (i.e. "tissue", "culture", "DNA" or "unknown") using the PreparationType field. The GBIF categorises specimens as follows: "Living Specimen," referring to living organisms such as plants in botanical gardens or animals in zoos, and "Preserved Specimen," which includes preserved items like plants on herbarium sheets or preserved fish in jars (source: GBIF Basis of Record https:// docs.gbif.org/course-data-use/en/basis-of-record.html). The "Material Sample" category does not have a formal determination on the Basis-of-Record page, but GBIF describes this as miscellaneous samples distinct from the other two categories. However, not all samples in these categories are physical specimens. To obtain an accurate count of physical samples in the GBIF database, a filtering by catalogue number was performed, as per GBIF recommendations. Based on the data extracted from the databases, the kingdom fauna is the most prominently represented in both databases (Supplementary Figure 4 and 10), with 6,150,555 samples registered in GGBN and 107,510,792 in GBIF. Flora is represented with 712,467 in GGBN and 109,321,650 in GBIF, and funga with 18,148 in GGBN and 15,860,028 in GBIF. For GGBN fauna, Arthropoda and Chordata are most represented across the DNA, tissue and culture categories. For funga, Ascomycota and Basidiomycota are most represented across DNA, tissue, culture and unknown categories. For flora, Tracheophyta (vascular plants) is most represented across DNA, tissue and unknown categories. Both tissue and DNA are most frequently recorded, whereas culture is less well represented.

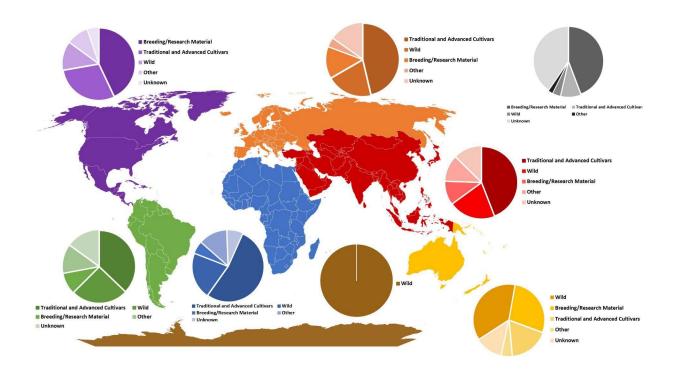


Figure 4: Summarising Genesys sample data across continents. Samples are grouped by 'Biological Status of Accession'. Categories including subcategories; Breeding/Research Material: Breeders's line, Synthetic population, Hybrid, Founder stock/base population, Inbred line, Segregating population, Clonal selection, Genetic stock, Mutant, Cytogenetic stock, Other genetic stock; Traditional and Advanced Cultivar: Traditional cultivar/landrace, Advanced or improved cultivar; Wild: Natural, Seminatural/wild, Semi-natural/sown; Other: Weedy, Other, GMO. The grey pie chart illustrates samples with Not Specified origin constituting 1.073.596 samples in total. Created by report authors.

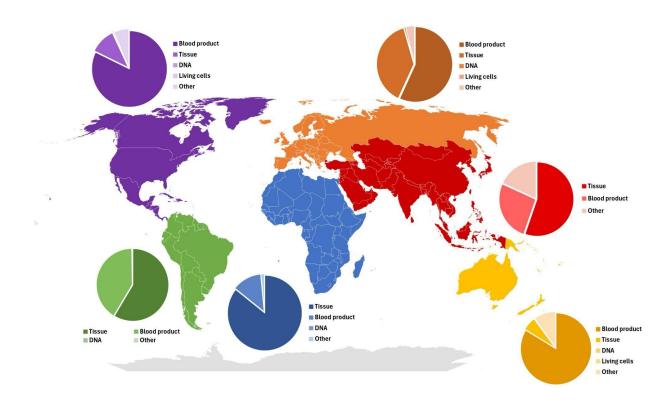


Figure 5: Summarising ZIMS sample data across continents. Samples are grouped by 'Sample Type'. Categories including subcategories; Tissue: Tissue, Carcass; Living Cells: Embryo, Semen/sperm, Ovum, Cell Culture; Blood Product: Plasma, Whole blood, Packed RBC's, Other blood product; DNA; Other: Feces, Mucus, Saliva, Other sample. Created by report authors.

Several other databases exist, both open access and closed, which may hold important information on samples of relevance to biodiversity conservation. GENESYS is one such open access database where genebanks, institutes, and research centres upload and share collection data on crops, which can be used as a resource for wild plants. This database contains nearly 4.4 million records, serving two main end users: breeders and researchers aiming to enhance crop productivity and develop resilient cultivars using the genetic diversity stored in genebanks. Many of the seeds and plant materials listed on GENESYS can be requested from their respective genebanks, subject to specific conditions. Closed databases are normally only available through subscription as in the Zoological Information Management System (ZIMS). This database is a key resource for collecting and sharing animal data, aiding institutions in managing collections and supporting global conservation efforts. ZIMS integrates animal husbandry and veterinary modules into a master database, housing millions of records on over 22,000 species and ten million animals, making it the largest data set for ex situ wildlife populations. An overview of global representation of sample types in GENESYS and ZIMS can be seen in Figure 4 and Figure 5, respectively.

2.1 Closing the gaps

Better curation:

Globally, the largest open-access databases, GGBN and GBIF, hold information on millions of samples, though there is uneven representation on both taxonomical and geographical scales. Each database presents unique challenges but shares a common feature: a helpdesk to assist with any queries. GGBN is an open-source database containing samples from the three kingdoms (Animalia, Plantae, and Fungi). The data catalogue is fully up to date with multiple searchable functions, including sample

types such as blood, tissue, culture, DNA, and unknown. However, the statistics and graph functions are not currently usable due to outdated sample count information, an issue GGBN is aware of and working to resolve. GENESYS is another open-source database focused solely on physical flora samples and their long-term storage locations. Although easy to use, nearly one-third of the samples lack gathering site information, with locations noted instead of being entered into the designated information slot. Improved curation of these databases, including accurate and comprehensive data entry, would significantly enhance their usability and reliability.

Streamlining search processes:

GBIF is a comprehensive open-source database that includes both machine and human observations, occurrences, and physical samples. However, discerning physical samples is challenging as categories like "Living specimen," "Preserved specimen," and "Material sample" may also include electronic results classified by the contributing databases. Using catalogue numbers can help address this issue. Nevertheless, GBIF does not subdivide physical samples into specific types, requiring researchers to refer to the individual contributing databases for this information. GBIF is working on implementing this division. To facilitate use, it would be beneficial to create an overview of samples in different categories and enable searches by sample type. Offering a more diverse range of graphical representations, including adjustable maps that can zoom in continent-level views, would be a useful feature for these large databases.



Pressing herbarium vouchers associated with conservation seed collections. Photo: © San Diego Zoo Wildlife Alliance



Blood samples of endangered species held in the EAZA Biobank. Photo: © Jonas Verhuist

The role of centralised and global repositories as resources:

All three databases—GGBN, GBIF, and GENESYS—aggregate individual collections where contributors may make their stored samples available for researchers to request for projects. Researchers are required to cite the original collection from which samples are obtained. Given the existence of multiple large open-source databases, an option to cross-check sample availability across databases would be beneficial to avoid requesting the same sample multiple times and potentially duplicating research. ZIMS, a closed database, provides insight into collections not accessible to the broad public. Even though some databases are closed, they should be encouraged to share at least a minimum amount of information on publicly available, open-source databases to more accurately map biodiversity representation in biorepositories and identify gaps to be filled. Before making any sample available for research, sample holders should ascertain proper rights and permissions established for sharing and use.

Encourage making samples publicly searchable in an open access database:

To facilitate more effective use of these databases, it is crucial that all samples be made searchable in a curated database that is publicly accessible. This would ensure transparency, reproducibility, and broader access to valuable data. For instance, when examining the representation of the 17 megadiverse countries in GGBN and GBIF, the United States stands out with 46,092,922 samples across all kingdoms (44,709,847 GBIF-listed samples and 1,383,075 GGBN-listed samples), making it the most sampled country compared to countries with lower representation, such as Malaysia (876,356 GBIF-listed samples) and the Democratic Republic of the Congo (4,244 GGBN-listed samples). Despite the differences between databases, there is a noticeable skew in sample availability among the 17 megadiverse countries. Notably, samples from the Fungi kingdom are the least represented throughout all countries. Addressing these disparities through a coordinated, global effort to curate and share data will enhance the scientific community's ability to map biodiversity accurately and identify areas needing more attention.



Section 3: Document harmonization

Biobanks can generally be imagined as service providers, providing materials to a client (i.e., a researcher) for use. The services provided form the basis for organising the biobank and its management, as well as establishing collection goals and a strategy and plan of action to achieve those goals. Once the implementation of the strategy and action plan begins, a complementary requirement for the successful operation of the biorepository is a system of documentation that will both guide consistency in the various actions and processes involved in biobank management, aid uniform implementation of established processes and help to identify shortcomings and measure how well services are being provided. Documentation is also critical in outlining the relationship between the biobank and its user, and among biobanks working with the same or similar organisms and genetic resources. For example, documents and protocols detailing how material is handled and stored can not only be used to ensure standardised training across biobank staff within an institution, but also be shared across biobanks to help achieve a higher level of standardisation.

Documents may also be shared with users to offer operational transparency and help them make informed decisions about samples they wish to acquire (i.e., cold chain information, QA/QC). Legal documentation pertaining to ownership and use are also critical. This includes documents associated with the establishment and operation of the biobank itself, as well as agreements between the biobank and sample providers and/or users of the material and any other necessary documents pertaining to regulations and permitting (see Section 4: Legislation and Regulations). For example, it should be clear who maintains ownership of the material after it is transferred and/or used, and whether or not material may be used for commercial purposes, as well as make arrangements for sample derivatives and disposal.

The extent of this documentation may range from a set of standard operating procedures (SOPs) and an internal management system for material acquired, assessed, and distributed by the biobank, to a full-scale formal Quality Management System (QMS). In the latter case, the biobank may undertake self-directed or third-party auditing and evaluation. The International Organization for Standardization (ISO) has recently developed the standards ISO 20387:2018, General requirements for biobanking (ISO, 2018), which can provide a basis for either self-assessment or for full-scale quality certification. Figure 6 illustrates a general summary of the minimum set of documentation recommended to guide and ensure proper operation of a biobank (Yuille, 2013). The layered triangle form of this figure reflects both the importance of individual documents within each stratum, and the relative bulk of each document group. For example, the vision and mission document should be relatively brief, but it is of fundamental importance for establishing the basis for the existence of the biobank and directing all underlying processes, while 'forms and documents' establish the foundation on which the whole framework of the biobank operates.

In these guidelines we will address all levels in the hierarchy (Figure 6) but will emphasise two subtypes of documentation, namely (i) standard operating procedures (SOPs) and (ii) forms, documents, records and agreements, specifically material transfer agreements (MTA), and applications and agreements for sample use.

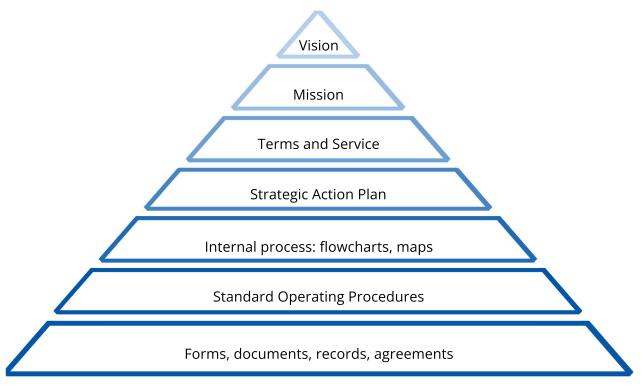


Figure 6. Hierarchy of operational documents for biobank operations (Adapted from Yuille, 2013)

3.1 Vision and mission, policy, strategic action plan and internal process

The vision and mission statements outline the overall purpose of the biobank and reason(s) for its existence, in terms of both the present and future. The mission statement outlines the "today", specifying the biobank's activities in context of its primary goals and objectives. The vision statement addresses the "tomorrow", capturing the longer-term aspirations of the biobank and the outcomes the initiative hopes to eventually achieve. The policy documentation, or Terms of Service, will cover the terms under which the biobank will operate, including how it will relate with, and obligations to, key stakeholders. The policy documents will also address governance of the biobank and its organisational structure. The biobank personnel should be listed and duties and roles of each should be clearly outlined. Memberships of internal and external committees and other groups that play a role in governance should be indicated and the purposes of such groups should be defined. In their 2012 Best Practices for Repositories, the International Society for Biological Environmental Repositories (ISBER) addresses this point by calling for the establishment of biobank-specific access policies, describing them as a key mechanism for access governance (Langhof et al., 2017). The strategic action plan will stipulate, in detail, goals of the biobank and steps to accomplish its mission and eventually achieve its vision. This document may include priorities for day-to-day biobank operation and the associated actions to be undertaken to address those priorities.

3.2 Standard operating procedures

Usually, SOPs, as a collection of multiple documents, deal with internal processes. These processes may include not only technical aspects, but also steering and support issues. Such documents may, for example, describe the flow of material from its acquisition and data entry (See Supplementary for an example of a metadata SOP) to its entry into the physical infrastructure of the biobank, followed by its preparation, accession and storage and eventual distribution. A similar document should describe the flow of information associated with each sample. In most instances, each process will be associated with its own specific operating protocol, as will be described in Section 3.2. The more detailed these documents are, the more standardisation and control can be implemented for quality assurance and longevity of the sample and its associated data.

One primary goal of a biobank is to provide consistently high-quality samples and data to facilitate scientific research, discovery, and conservation efforts. This goal is facilitated by the establishment of best-practice guidelines unifying either evidence-based or consensus-based practices, protocols, and policies. The ISO 20387:2018 - General requirements for biobanking - international standard was developed to promote confidence in biobanking institutions and procedures. Internationally, a number of institutions and networks, predominantly for human medicine, and to a lesser extent agriculture, have taken the initiative to develop and distribute their own comprehensive best-practice guidelines, which are valuable resources for any biobank seeking to establish their own institutional procedures. We will not duplicate these here, but instead provide a framework and link to a number of comprehensive, readily available resources that can be extrapolated and applied to wildlife, botanical and fungal biobanking, if not address them specifically.

We encourage any parties interested in building or maintaining a biospecimen or genetic repository to also contact regional resources such as museums, botanical gardens, herbariums, zoos, aquariums, culture collections and universities, which should be aware of, and follow, relevant local legislative requirements (see Section 4: Legislation and Regulations). Biobanking practitioners are further encouraged to stay abreast of current literature characterising best-practice sampling and handling protocols specific to species/taxa of interest, sample type and field conditions. When compiling an operations manual and standard operating procedures for a collection or facility, clearly documented operating procedures and policies should be developed and maintained for:

Biospecimen handling.

- biospecimen collection, preparation, and storage protocols/requirements
- biosafety/ disease risk
- specimen labelling and identification
- shipping and receiving protocols (see Section 3).

Data and database management (see Section 5).

- a formal record management process and system (i.e., LIMS)
- data management and storage plan
- data security and sharing
- minimum data requirements
- biospecimen tracking (barcoding system).

Legislation and regulation (see Section 4).

- material transfer agreements: ownership and use
- guardianship and custodianship agreements (Traditional owner groups)
- sample transport and shipping
- sample discard/return/reuse protocols
- ethical and permitting requirements
- IP/privacy policies.

Infrastructure management.

- · building, personnel and biospecimen security
- · biosecurity considerations
- equipment monitoring, maintenance, repair, and calibration records
- occupational Health and Safety
- safety and waste disposal
- procedures to investigate, document and report staff injuries and exposures
- emergency response plan
- discontinuation plan

As with many long-term, multifaceted investments, it is important to periodically review and revise protocols and standard operating procedures to comply with changing regulations and stay up to date on the latest legal, ethical, and scientific practices.

3.3 Material Transfer/Acquisition Agreements

The Material Transfer Agreement (MTA), or Material Acquisition Agreement (MAA), is a document critical in establishing ownership chain of custodianship and expectations of material quality, transfer and use (including use of any sample derivatives), and establishing and protecting any agreements on financial or other compensation, intellectual property rights and personal data (See Section 4: Legislation and Regulation).

MTAs vary widely from institution to institution, and while templates and recommendations exist (See Supplementary), no formal standard practices have been put in place. Table 1 lists the recommended minimum standard information for an MTA. This document specified the parties involved, the objectives of the exchange of material and rights and responsibilities of the parties. Regarding the description of the material, this information should include for each sample being transferred: the species name from which the sample was collected (both common and scientific), any relevant identification information (i.e., transponder, band, tags), local institutional ID or reference number, any related and existing database reference (i.e., ZIMS ID/ GAN), sample type and amount, date of collection, collector, and storage or preservation information, if applicable (i.e., stored in ethanol). Exchange of material involving multiple samples may be managed with a single MTA, repeating only the description of the material for each distinct sample or group of similar samples.

Who?	Identification of parties and contact information
	• sender
	• receiver
What?	Description of the material
	 sample type, amount
	 date of sample collection
	 species (common, scientific name)
	 unique identifier (local/ global, e.g., ZIMS GAN)
	 media/ storage, preservation information
When?	Effective date and validity
Where?	Institutions involved
	storage facility
	research facility
Why?	Specific objectives of the MTA
	material uses
	arrangements for data/publishing
How?	Rights and duties of the provider
	Rights and duties of recipient
	Financial arrangements and ownership
Additional information	Warranty / liability dispute settlement
	Arrangements about general data protection
	Project-specific amendments

Table 1. Minimum standard information to be included in a material transfer agreement (MTA). Adapted from Animal Genetic Resources Guidelines.

3.4 Applications and agreements for sample use and release

The ultimate goal for establishing a biobank is to create a collection of material which is actively used for improving the knowledge of, and status of a given organism of interest, by serving as a resource for research or as a source of material that can be used to propagate the organism and manage its genetic diversity in situ. Therefore, biobank material is initially collected with the expectation that it will be eventually distributed internally or to a third party for use in research or conservation (Figure 7). However, specimens held in biobanks are often costly and/or difficult to collect, process and store and exist in a finite quantity. Biobank material may also involve intellectual property or other stipulations made by the original provider, and/or established by national legislation or formal international agreements, such as the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilisation of the Convention on Biological Diversity (CBD, 2011) (See Section 4: Legislation and Regulation). Therefore, the distribution of material from a biobank collection requires the establishment of review processes to evaluate legitimate requests for material use and documentation addressing both the associated policy and procedures, including application review policies, as well as written agreements/contracts between the biobank management and the user of the material.

Access policies of biobanks specify the governance of sample and data sharing. The distribution policy will be the key document, as it will guide the content of the application for access to material and the review process to be undertaken when deciding upon material release. The policy must define the variables that may influence the decision on distribution of material and establish rules for guiding the decision to grant or deny access to the material. Among the important variables that are usually

considered are the following: (i) type of individual/organisation making the request, (ii) proposed use of the requested material, (iii) capacity/experience of the requestor as it relates to use of the material as proposed, (iv) types and quantities of material requested, and (v) timing of the release and use of the material whether for research, commercial application or other (Verlinden et al., 2014).

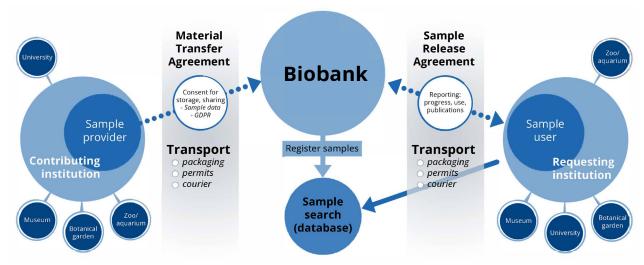


Figure 7. Example workflow/ process for contributors and biobanks for submitting, searching for and requesting samples across different institutions. Created by the report authors.

The application procedure must ensure that the information provided by the requestor includes all the variables considered to be important in the decision on material distribution. The biobank manager (or other person/body) must then review the application in light of the distribution policy. The biobank manager's final decision for distribution of material will then include the following considerations (among others): (i) allowed uses of the material and types of users, (ii) capacity of users to successfully exploit the material, (iii) existence of other potential sources of the material, (iv) minimum amounts of a given material that must remain in the biobank and any obligations of the user to return unused sample, (v) sharing of information and other benefits arising from material utilisation by the user, and (vi) adherence to relevant laws and regulations. Procedures for distribution will address issues such as how the material is to be packaged and shipped, how any compensation will be provided, and the process and timeline for which the user can confirm or deny that the material acquired meets their expectations (Table 2).

Use of samples	How a sample can or cannot be used (including other	
	distribution and adherence to laws/ regulations).	
Ownership	Clearly define ownership of material after transfer and ownership of any products of the sample.	
Confidentiality	Any details/ information regarding staff or institutions involve that wish to retain privacy.	
Research data/ publications	Providing project updates, status/ completion, products produced and any rights to obtain raw or analysed data, being alerted to publications, questions of authorship/ credit, etc.	
Release/ liability	Diseases/ hazards associated with the sample, liability for loss of sample permits/transfer, who is responsible for due diligence on permits required, costs associated with sample return or disposal, define what happens to a sample at the conclusion of its use/ the project.	
Any other clauses or stipulations	i.e., governing law, dispute resolution, conditions/amendments.	
Signing	Acknowledgement of approval of contract/ agreement to terms.	

Table 2. Considerations for a request for sample use agreement form.

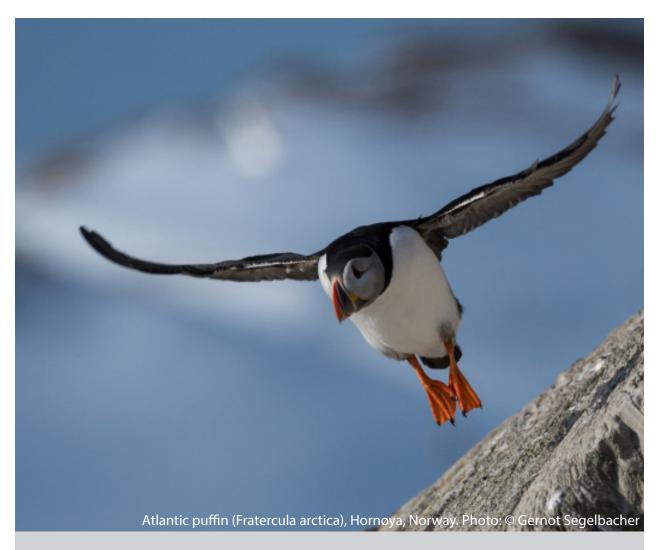
The application must also address the requirements for the requestor to report about the material use back to the biobank (i.e., publications), acknowledgement of the biobank and other forms of recognition, and any actions to be undertaken for linking samples to results (i.e., sample identifier, test results or sequence data). The contract/agreement will formally outline and document that the biobank and user have agreed on the major issues stipulated by the biobank's material utilisation policy and procedures. Because the policies and procedures, as well as uses and circumstantial considerations, will differ from one biobank to another, the development of a simple, standard agreement is not straight-forward, but various resources providing frameworks of models for material distribution agreement are available for consultation.

3.5 Dispute resolution

Dispute resolution in contractual arrangements such as material transfer or sample use agreements typically involves a structured process to address conflicts and disagreements between the parties. These agreements often govern the exchange and use of valuable biological materials, data, or other resources, making dispute resolution a critical component. The specific mechanism for resolving disputes can vary, but it commonly includes negotiation and communication between the involved parties to find an amicable solution. If disputes cannot be resolved through negotiation, the agreement may stipulate mediation or arbitration by a neutral third party to find a mutually acceptable resolution. Arbitration involves a more formal process where an arbitrator reviews the dispute and makes a binding decision. Dispute resolution may need to adhere to the laws of either party's home nation. These processes provide a structured and legal framework for resolving conflicts while avoiding costly and time-consuming litigation. Ultimately, the goal is to protect the interests of both parties in a timely manner while preserving their collaborative relationships, which are often critical in scientific research. Non-compliance with contractual agreements may have significant consequences, both legal and reputational. Non-compliance may lead to termination of an agreement, and therefore loss of access to materials and data, and potential financial penalties. Similarly, non-compliance or breach of trust may damage the reputation of the non-compliant party and impact potential future collaborations and opportunities.



Clear outline of structure, setup and expectations facilitates smooth sample backup exchange for the EAZA Biobank . Photo: © report authors.



Section 4: Legislation and regulation

Biological specimens from animals, plants and fungi present a challenge to biobank facilities due to the array of regulatory agents involved, with each specimen having unique regulatory and permitting requirements. Despite the complexity of acquiring samples for biobanking, curators, researchers and institutions can work to navigate the global regulatory system and maintain regulatory compliance. Failure to comply with permitting can lead to severe penalties and consequences. Research institutions can revoke research privileges, regional and national agencies can levy large fines and criminal charges, and international authorities can even imprison researchers for violations. Complying with regulations is one step in ensuring that wild populations of animals, plants and fungi as well as Indigenous people's autonomies are protected from exploitation or abuse. It is with this regulatory compliance mindset that a curator or collector should navigate the process of permitting, a process that may often be arduous, confusing, and seemingly disorganised. The permits necessary to be compliant with regulatory agencies may vary based on the species of material origin, the type of sample collected, the purpose of the study, where the samples are/will be collected, and where the samples will ultimately be processed, analysed and stored. The key to successfully meet regulatory standards is to break down the process of acquiring samples into constituent components: collection, exportation, transportation, importation, and storage (Figure 8).



Figure 8. Summary of the five regulatory steps (collection, export, transport, import and storage) to consider when collecting specimens for biobanking. At each step, multiple agencies and authorities must be considered for regulatory compliance. Created by the report authors.

While some research organisations and universities have personnel to assist with the permitting of sample handling and collection, others do not. A registrar or dedicated curator can aid in permitting, but it may also fall to the individual researcher to navigate the maze of agencies that regulate research on biospecimens and issue permits (Sikes & Paul, 2013). Biobank personnel and users should keep in mind that regulatory responsibilities may change over time. Requirements can be reassigned among agencies, new species can become regulated, and for every governing body the process or timeline for permitting samples may vary. This overview of the permitting and compliance process provides a brief, rudimentary roadmap so that responsible parties can begin to consider how to navigate their relevant regulatory bodies and utilise resources that can assist in the process. Note that this is not an exhaustive roadmap and that factors may vary across individual cases.

4.1 Levels of regulation

International:

International law and treaties govern aspects of compliance that are ubiquitous to all biobank curators, with most concern placed on regulations on import and export of endangered species. Transferring biological material between labs and countries requires permitting at the stages of sample collection, transport, and storage, at both national and international levels. Examples of such international legislation include The International Treaty on Plant Genetic Resources for Food and Agriculture, the Convention on Biological Diversity and the Cartagena Protocol on Biosafety, the Convention on International Trade in Endangered Species of Wild Fauna and Flora, and the Agreement under the United Nations Convention on the Law of the Sea on the Conservation and Sustainable Use of Marine

Biological Diversity of Areas beyond National Jurisdiction (See Supplementary). Laws vary widely and are subject to change, as such, an exhaustive list of resources is not included in these Guidelines. We encourage consulting governmental agencies or organisational points of contact who are experts in export/import (Figure 8).

The Convention on Biological Diversity (CBD) is a multilateral treaty with three main goals that include the conservation of biological diversity, the sustainable use of its components and the fair and equitable sharing of benefits that arise from genetic resources. It is an international piece of legislation that has been ratified by 196 nations (Convention on Biological Diversity, 2022). Within each country, federal and state legislation work to address and mitigate biodiversity losses, with the most common approaches to slowing or halting this loss performed through biodiversity offsets. Biodiversity offsets are "measurable conservation outcomes that result from actions designed to compensate for significant, residual biodiversity loss from development projects" and have relied on on-the-ground managerial actions that manage habitat and species loss (Burgin, 2008; McKenney and Kiesecker, 2009; OECD, 2016).

The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity (known as the Nagoya Protocol on Access and Benefit Sharing [ABS]), was introduced in 2010 and is a supplementary agreement to the 1992 Convention on Biological Diversity. This agreement addresses the regulation of "genetic resources" such as tissues, seeds, plants, fungi and microorganisms. In many countries, Nagoya regulations for exporting and importing material exist, but it is often still unclear what documentation must be completed and who the responsible authorities are. Strong differences among countries exist and while not every country is a party to Nagoya, many are nevertheless affected. For example, the USDA National Genetic Resources Program follows Nagoya rules for material subject to it, even though the U.S. is not a Party to the Convention.

The Nagoya Protocol is based on the fundamental principles of access and benefit-sharing as outlined in the CBD. These principles are based on potential users of genetic resources obtaining the Prior Informed Consent (PIC) of the country in which the genetic resource is located before accessing the resource and negotiating and agreeing on the terms and conditions of access and use of this resource through the establishment of Mutually Agreed Terms (MAT). This agreement includes the sharing of benefits arising from the use of the resource with the provider as a prerequisite for access to the genetic resource and its use. Conversely, countries, when acting as providers of genetic resources, should provide fair and non-arbitrary rules and procedures for access to their genetic resources. With the implementation of the Nagoya Protocol on Access and Benefit Sharing, which places responsibility for the control of and access to genetic resources with the importing country, obtaining samples from the wild has recently become a more difficult process. Thus, as a result of the Nagoya protocol, samples already collected (prior to October 2014) and stored in existing biobank collections have become increasingly valuable and in higher demand. Furthermore, negotiations around the Nagoya Protocol indicate a lack of consensus regarding the definition of 'biodiversity data' and thus the applicable ABS scope and obligations (Rohden and Scholz, 2022; von Wettberg and Khoury, 2022). With the lack of clarity and consensus, 'Digital Sequence Information' (DSI) has been used as a placeholder term in such discussions, despite its inadequacy in describing the types of sequence (genomics, transcriptomic, proteomic), provenance, and phenotypic data, or any other information that may be contained therein (Wynberg et al., 2021; Aubry et al., 2022). As part of the CBD Access and Benefit Sharing (ABS) frameworks, certain countries have already adopted domestic measures that regulate the access to, and use of, DSI from genetic resources. Data from biobanks would likely be covered by any new provisions, but there is not yet clarity on what data, if any, is covered. A range of resources have been developed to help biobank managers, researchers, and policy makers understand issues around ABS and DSI in the context of the Nagoya Protocol and other treaty frameworks as they pertain to research and conservation uses. The EAZA Nagoya guidance document and the Botanic Gardens Conservation International (BGCI) training documents for Nagoya and ABS are two such useful resources (See Supplementary.

The Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES), enacted in 1975 is an international agreement among governments to regulate the international trade of certain species. Animals and Plants are classified in three different Appendices with varying degrees of regulations based on threat levels the species face (See Supplementary). Species of wild flora and fauna that are listed and protected by CITES must be permitted for both export and import, including both live and dead animals and plants and their derivatives. A list of CITES protected specimens can be found in the CITES Appendices. Each Party to the agreement has established Management Authorities responsible for issuing CITES permits, as well as a group of Scientific Authorities advising said management. In 2002, a resolution was passed by Parties to the convention stating that CITES covers fungi and can indeed be included on the lists of protected species. Despite a discussion of caterpillar fungus during a workshop on the trade in medicinal plants at the 2012 CITES meeting, none of the 183 member states have come forward with a proposal so far, and as such no fungi are currently on the CITES lists of protected species.

Additionally, the standards for shipping biological specimens are globally regulated, particularly when they are considered dangerous goods. The International Air Transport Association (IATA) is a professional association devoted to the air transport industry and issues regulations on all matters concerning shipments. All major airlines including passenger and cargo transportation adhere to the safety guidelines of this association, which include proper material handling. Commercial shipping companies enforce packaging and labelling specimens according to IATA standards.

National and Regional:

Large variation exists among nations when regulating collection and in-country transportation of specimens for biobanking. Specimen collection is often regulated by both national level agencies and more regional level offices within a country. Differences will exist from nation to nation but also from species to species depending on their level of vulnerability and classification by CITES, IUCN Red Listing or any other national biodiversity regulations. To move specimens within a country, collection permits from both national and local authorities are needed, oftentimes also requiring local transportation permits. If an animal, plant, or fungal specimen has the potential to carry a pathogen that can cause disease in humans, a permit from a public health agency may be necessary. Likewise, if the biological sample has the potential to threaten agriculture, a permit from an agricultural agency may be necessary. In cases where a risk of harmful pathogens exist, special handling and storage protocols may be required. Import and export regulations also differ among countries and typically involve several different agencies. Often an agency in charge of natural resources provides permits for importing and exporting endemic species. If a plant or animal specimen has the potential to carry harmful pathogens, then agricultural or human health agencies may also require additional import or export permits.

Local:

When collecting specimens, permission or permits must be obtained from the landowner if the property is privately owned, or from the land management agency if the property is managed by a government authority. Local regulations also exist at the institution where specimens will be stored and managed. For vertebrate collections, animal welfare permits may need to be obtained from the biobank or research institution, and environmental health and safety regulations must be followed for the storage of those specimens.

4.1.1 Sample collection regulation

Research that involves the collection of biological samples, regardless of whether it originates from wildlife, plant material, funga or other organisms, may be regulated and therefore require permitting. The agencies in charge of such regulation span the breadth of governance and include international, federal, state, provincial, county, and local municipal agencies, as outlined above. Each relevant agency, with its specific remit, must be consulted for sample collection. For collectors who will handle and sample live vertebrates, additional permission may be required by the collector's institution to ensure

national standards of animal welfare to ensure animal welfare. This permitting typically comes from a research organisation's Institutional Animal Care and Use Committee (IACUC). In compliance with federal laws, regulations, and policy governing the use of non-human, vertebrate species for scientific research and/or instruction, the IACUC is responsible for reviewing research protocols to assure the humane treatment of vertebrate animals. This review is necessary for compliance with provisions of the Public Health Service (PHS) Policy on Humane Care and Use of Laboratory Animals, the Animal Welfare Act, federal granting agencies of the PHS, and all other applicable research animal welfare laws and regulations.

Prior to the initiation of any animal-related research activity, including sample collection, the IACUC must review and approve a completed Authorization to Use Animals in Research application detailing the technical or humane aspects of the proposed research. This is intended to certify that the applicant is familiar with and will comply with the legal standards of animal care and use established under federal and state laws and policies (e.g., PHS policy, Animal Welfare Act, the "Principles for the Utilization and Care of Vertebrate Animals Used in Testing, Research, and Training" and the standards set forth in the "Guide for the Care and Use of Laboratory Animals"). Additionally, the applicant must demonstrate that they are familiar with, experienced and technically capable of performing all animal manipulations and procedures described in the project application and that the responsibility for the supervision and training of any person who performs work on the project are knowledgeable and experienced people.

Traditionally, little attention has been paid to fungi in international meetings and conventions (such as the 26th session of the Conference of the Parties [COP26] of the UN framework Convention on Climate Change [UNFCCC], the 15th meeting of the conference of the Parties [COP15] to the Convention on Biological Diversity [CBD], and the IUCN World Conservation Congress); however, there has been a shift towards more inclusion. Nevertheless, national governments still fail to acknowledge fungi in conservation related legislation, missing the fundamental impacts that these protections may have on fungal sustainability. Moreover, regulations pertaining to harvesting, exportation, or importation of biological specimens for research and scientific purposes lacks language that specifically addresses this taxon in most of the relevant governmental agencies (e.g., Animal and Plant Health Inspection Services in the United States) (Oyanedel et al., 2022).



Tissue sampling. Photo: © Frank Rønsholt.

The IUCN has introduced globally accepted criteria and encourages the production of Red List assessments for threatened species, which are increasingly important instruments in national and international nature conservation. For instance, Chile became the first country in the world to protect fungi by law and include wild fungi in impact evaluation assessments for economic developments projects. Another example of significant legislative consequences of global listing comes from the United Kingdom, where globally threatened fungi were recently added as a criterion in official guidelines for the selection of sites to be considered for legal protection (Bosanquet et al., 2018; Sanderson 2018). According to these guidelines, all sites with valuable populations (lichens) or persistent fruiting populations (non-lichenised taxa) of fungi globally assessed as Critically Endangered (CR) should be considered for legal protection. Furthermore, similar protection should be extended to a subset of national sites for species with global assessments of Endangered (EN) and Vulnerable (VU). Around the world, it will be necessary to follow up on those fungal species already globally Red Listed to ensure that where there is legislative protection at national levels, species are formally proposed for inclusion under relevant national lists (Mueller et al., 2022). Thus, Global Red List assessments of fungi can be referenced and used by local land managers. They are especially useful where fungi are not included or are sparse in national and subnational conservation frameworks (Mueller et al., 2022).

The purpose of the regulations on sample collection can be varied but ultimately include protections for managing natural resources, fragile ecosystems, and endangered species. Oftentimes regulatory agencies are charged with reducing disease risks or invasive species introductions (Sikes and Paul, 2013). These regulations are therefore a necessity to maintain the integrity, ethics, and safety of sample collection from animals, plants and fungi as well as the chain of custody and use.



Sample from a blood draw of an African elephant (Loxodonta africana). Photo: © San Diego Zoo Wildlife Aliance.

4.2 Sample export and import

In addition to collection permits, permission is also typically required to export samples from the originating country and to import them to the destination country. CITES export and import permits, agricultural or health permits and natural resources agency permits are typically required by both exporting and importing countries. Exemptions, however, may be possible in cases of non-commercial loans, donations or exchange of museum, herbarium, diagnostic and forensic research specimens between CITES registered institutions. Special instructions on how samples are packaged and labelled may also be required by agencies of either country, such as for Animal By-Products. Animal By-Product regulation (ABP) pertains to the guidelines and rules governing the transportation, handling and disposal of biological materials and waste derived from animals. When it comes to shipping animal samples, adherence to these regulations is crucial to ensure biosecurity, prevent the spread of diseases, and comply with environmental standards. These regulations dictate how animal samples, such as tissues or blood, should be collected, stored, packaged, and transported to minimise contamination risks and uphold public health. Proper labelling, documentation, and containment measures are essential to prevent any potential human or environmental health hazards, protecting both those handling the samples and the environments they come into contact with. Adhering to animal byproduct regulations when shipping animal samples guarantees safe and responsible practices in research, diagnostics, and monitoring, thereby minimising health and ecological risks.

Often, these regulations are geographically limited. For example, in the United States, importation of avian samples from countries where highly pathogenic avian influenza or Newcastle's disease are prevalent, may be restricted or the samples may require treatment to ensure the neutralisation of the pathogen. This case falls under the regulatory purview of the USDA Animal and Plant Health Inspection Service (APHIS, Supplementary). In addition, the U.S. Centres for Disease Control and Prevention restrict African rodents, bats, civets, and small turtles from import due to disease concerns (See Supplementary).

In addition to species or geographic restrictions, certain biomaterial types may require additional permits. As an example, the EU Animal Health Law specifies the need for TRACES (Trade Control and Expert System) for certain biomaterials, dependent on their intended use and the national interpretation of the regulation by the exporting country. TRACES is a web-based platform established by the European Union (EU) to facilitate and regulate the movement of live animals, animal products, and germplasm (including live gametes) across national borders within the EU or imported from outside the EU (See Supplementary). TRACES requires users to register on the dedicated platform, notify the responsible authorities about the intended movement and provide all relevant information regarding sender, recipient, materials involved and nature of the transport. Health certificates are required for live specimens, whereas samples such as gametes and cell lines can fall outside of this requirement, depending on purpose and national interpretation. TRACES documentation, identity, and border inspections all must be successful in order to receive authorisation for transport. Compliance with TRACES regulations is essential to safeguard animal health, ensure traceability, and meet the regulatory requirements of the EU when transporting animal products across national borders. Failure to comply can lead to delays, fines, and other legal consequences. Therefore, it is crucial to work closely with the responsible national authorities and use the TRACES system to facilitate smooth and legal transport of specimens within the EU.

4.2.1 Considerations for proper sample shipping and transport

The sender must consider the physical environment that must be maintained during transit so that the specimens arrive as viable and intact as possible. Because some shipping conditions have the potential to degrade sample quality, precautions may be required including special packaging, labelling, permitting, and shipping timeframes. Finally, proper arrangements must be made for recipients and/

or customs agents. Thoughtful planning, well ahead of shipment, is necessary to ensure that collected specimens, some of which may be quite rare or valuable, arrive at their destination intact and are properly preserved.

4.2.2 Environmental (storage) conditions

Many specimens held in storage require special environments to ensure viability if and when removed from those storage conditions (i.e., during transportation). For example, plant seeds may require a low humidity, room temperature environment and can withstand these conditions for several weeks until processed for long term frozen storage, while cryopreserved tissues may require the ultra-cold environment of a dry shipper and require rapid transport. Depending on the temperature requirements, a continuous cold chain from origin to destination may involve ice packs, dry ice or a dry shipper to maintain the integrity of the sample. For specimens that require -80oC cold chains, dry ice is used in shipping to maintain sample quality, but these packages require special packaging and labelling (see below Section 4.3.2). The ISBER Recommendations for Repositories: Best Practices (See Supplementary) has an informative section on temperature requirements necessary to preserve specimen quality. Likewise, if samples must remain dry or at low humidity, a desiccant and adequate waterproofing may need to be added.

In the case of fungi, for long-term storage, dried macrofungi specimens are usually kept in herbarium boxes or packets and transported in the same way (Lodge et al., 2004). Fungi have been stored successfully on silica gel for up to 11 years (Smith and Onions, 1983) For permanent storage, lichen specimens should be placed in acid-free paper with 25% rag content and stored at room temperature (Buyck et al., 2010). They can, however, still deteriorate with time and green lichens may lose their colouration (Honegger, 2003). Ideally, lichen thalli and spores ejected from apothecia can be stored dried in vials at -20 °C without losing their macro and microscopic features. For fungal cultures, cryopreservation in liquid nitrogen and freeze-drying (lyophilization) are the methods recommended by the American Type Culture Collection for fungal repositories (Lee, 1991). Because both cryopreserved and lyophilized fungal cultures present problems of viability after reconstitution, it is very important to check viability before and after preservation independently of the technique used. The choice of preservation method depends on the species of concerns, the resource available, and the goal of the project (Nakasone et al., 2004).



Photo: © Hellabruun Zoo

4.2.3 Packaging and labelling

Depending on the classification of dangerous goods, specimens must be packaged in particular ways that are compliant with rules developed by IATA. For example, specimens shipped in liquids must have an appropriate amount of absorbent material and must be triple packaged and sealed. Similarly, potentially infectious material must be triple packaged to reduce exposures. Packages containing dry ice must include ventilation so that gaseous CO2 can freely escape the container. Use of dry ice must also be declared to the transporter and properly labelled with approved labelling (see Table 3). While dry shippers do not require special permitting or labelling, the shippers must be properly prepared. All liquid nitrogen used to charge the dry shipper must be absorbed; no free-standing liquid nitrogen can be left in the tank. Each dangerous good class requires specific packaging requirements as well as specific labelling on the outside of the package (see Table 3).

Designation	Code	Definition	Required Packaging	Required Label(s)
Biological substance category A	UN 2814	Infectious substances affecting humans	Triple packaged; IATA compliant	NFECTIOUS SUBSTANCE A CONTROL OF THE SUBSTANCE OF THE SUBSTANCE CATEGORY A
	UN2900	affecting animals		
Biological substance category B	UN3373	Infectious substances which do not meet the criteria to be classified as Category A	Triple packaged; IATA compliant	UN3373 BIOLOGICAL SUBSTANCE CATEGORY B
Patient exempt specimen	NA	Human or animal specimens where pathogen presence is not likely	Triple packaged	EXEMPT ANIMAL SPECIMEN
Dry Ice	UN1845 (class 9)	Dry ice is considered a hazardous material when shipping (explosion hazard)	Dry ice must not be sealed in any container with an airtight seal. Package must be of adequate integrity	UN1845 DRY ICE Net.Qtykg

Table 3. Hazardous goods shipment designations, codes, definitions, and labelling (Azdhs.gov, n.d.).

Once the packaging environment for sample integrity has been established, it is necessary to determine whether or not the package will require special handling and to classify what that handling may entail by the nature of the potential hazards to the public or to agriculture that are held within. If a hazard is determined to exist, then the package is considered a 'dangerous good' and is subject to packaging and shipping guidelines as determined by IATA (See Supplementary). As of December 2017, dangerous goods can no longer be hand carried on commercial airlines but must be shipped by cargo carrier and be compliant with the shipping regulations. Most commercial carriers (e.g., FedEx or DHL), as well as many research organisations such as universities, require proof of training for shipping and handling of dangerous goods. Certified training programs are available commercially and many

organisations offer in-house training programs. In addition to the guidance given by IATA, each nation's transportation authority may also have additional regulations for domestic or international shipping. Biological specimens are considered 'dangerous goods' to shipping authorities if they can harm people or other living organisms because they are toxic, flammable or contain infectious substances. The materials that a biorepository most often deals with that would be considered dangerous goods include toxic or flammable storage media such as formalin or ethanol. However, if only small quantities are being shipped, they are exempt from regulations. Check with IATA regarding volume limits and if the quantities being shipped are exempt from these regulations.

Some biobanked specimens may be suspected to have infectious pathogens, in which case they are also considered to be dangerous goods. Government agencies may declare that any biological specimen(s) from a certain species or a certain geographic origin may likely contain pathogens and thus are automatically classified as a dangerous good. It is imperative to check with the importing country's agricultural and public health administrations to determine if they have regulations regarding certain specimens.

IATA has categorised infectious substances into three groups, each with its own set of shipping requirements and permits. Category A infectious substances are capable of causing permanent disability, life threatening or fatal disease to humans or animals when exposure to them occurs. Category B infectious substances are infectious but do not meet the criteria for Category A. Exempt human/animal specimens are specimens in which it is not likely that a pathogen is present (Table 3) (Azdhs.gov, n.d.). Professional judgement must be used if a biological specimen is not specifically regulated; if you suspect the specimen may contain an infectious substance, it must be shipped accordingly. When shipping biological material, it is prudent to assume that shipping authorities will consider the sample as dangerous and to follow the appropriate shipping procedures (i.e., when in doubt, assume a sample may contain a pathogen, and handle it with the necessary precautions and follow IATA guidelines for packaging).

Additionally, some biological materials may be classified as 'select agents', with the potential to pose a more severe threat to public health and safety as well as to animal or plant health, and in such cases, additional shipping precautions or permitting may need to be undertaken.

If permits were required to collect, import, and export specimens, these must be included with the invoice, a packing list and waybill on the outside of the package. Shippers must notify receivers of incoming packages and provide them with a tracking number. Specimens should only be shipped early in the week to avoid arrival over the weekend when employees are absent. IATA details all the guidelines necessary for compliance (See Supplementary) and a thorough discussion of best practices in shipping banked specimens is provided by The ISBER Recommendations for Repositories: Best Practices. Biobanks must maintain regulatory compliance for all specimens in their care. CITES protected species require permits to hold samples from those species, including derived products such as DNA, but not urine or faeces.



Section 5: Data and databases

An important component of coordinating biobanking efforts is defining a minimum of metadata required for samples and collections for a particular taxon or sector. Implementing a common approach to metadata collection and management across sectors, regions and institutions would help to ensure that information and samples can be linked or shared, regardless of the specific database system used by individual institutions. Establishing data standards can provide guidance for new and emerging start-up collections to align with existing efforts (See Supplementary for an example of a metadata SOP). Since the information and samples in these biorepositories will potentially be around for decades to come, it is also important that these metadata requirements consider what information might be relevant to use the samples now, and in the future, and that the information remains organised, interpretable, searchable, accessible, interoperable, and reusable over time.

5.1 Database systems

There are currently a number of commercially available, widely accepted database management systems in use in the zoological, botanical, museum, and scientific sectors for the purposes of sample or object tracking and data management, including for use in biobanking. Outside of paid subscription-based systems, an individual entity may very well choose to use a self-developed system based on specific needs and resources available (i.e., paper/ hard copy system, excel spreadsheet, free open access software, etc.). Discrepancies between database management systems or operational definitions of data categories can lead to difficulties in data or specimen sharing or use. These discrepancies may require much more time and effort to reconcile different categories of data capture between two or more systems. Here we recognise and highlight examples of both commercially available and non-commercial database systems. It is imperative to choose a system that fits the needs and available resources of an organisation, but also be able to connect with other systems to facilitate collaboration.

The typical features of sample management and tracking ensure that all platforms can capture and track standard sample metadata (See Table 4). However, specific data fields do vary across sectors (e.g., flora vs. fauna), as do database platforms, depending on their primary use (e.g., managing specimens vs. live animals). Additionally, each platform's capabilities may vary, including their ability to track sample movement, store metadata (e.g., digital sequence information (DSI)), conduct statistics and issue reports. There are a number of considerations when choosing an existing management system versus developing a bespoke system, particularly with regard to metadata requirements, collaboration needs, and expense. There may be pros and cons for each system, but ultimately, selection and use are based on the needs and resources of the initiative and should align with the most widely used platform in their sector. A list of common biobanking data management systems for various sectors that practitioners may consider can be found in Table 5. Metadata should comply with existing standards, such as the Darwin Core format standard, the ABCD standard (Access to Biological Collection Data, 2005), the Multi-Crop Passport Descriptors (Alercia et al., 2015), ISBER Best Practices for Repositories: Data Standards (ISBER, 2023), or the GGBN data standard (Droege et al., 2016) to make data management standardised and compatible (Lawniczak et al., 2022; Schrade et al., 2024).

Examples of suggested minimum data for biobanking samples are outlined in the table below (Table 6) and it is also recommended to refer to well-established standardised metadata ontologies (e.g., Darwin Core terminology; see Supplementary), which can easily be adapted to custom systems. In particular, the use of a unique universal identifier (UUID) or globally unique identifier (GUID) is essential to enable identification of the original sample and its metadata (Triebel et al., 2018). Furthermore, considerations should be taken regarding potential sensitivity of some data that may limit how data can be shared. For example, the geographic location data that could identify sites of threatened species can often be under government jurisdiction and are not publicly available to prevent disturbance or poaching. Similarly, any data shared must first be agreed upon with the contributing institution, following the rules of prior informed consent and access and benefit sharing laid out in the Nagoya Protocol to the Convention on Biological Diversity (see Supplementary) (see Section 4: Legislation and Regulation).

5.2 Data sharing

The information stored in databases can also be used to inform population genetic management decisions and sampling for research as well as to strengthen overall partnerships and conservation outcomes of zoos, museums, botanic gardens, universities, and similar organisations. Where possible, a common database system should be used within a particular taxon, industry, or conservation network to facilitate and simplify the transfer of information and samples. At a minimum, databases should use defined terminology (e.g., Darwin Core standards) and data fields relevant to their field including metadata requirements for sample accession. Linking out to other database systems (e.g., genetic, and molecular databases or health records) is also recommended to increase the value and utility of

samples and information stored. For the purposes of biodiversity protection, the aim should be to work towards a data sharing network that communicates across key regions and supports incountry conservation efforts, including involvement of local communities and Indigenous Peoples in data sharing agreements and provision of benefit sharing. Similarly, a chain of custody should be implemented for data protection. Only when data (including all metadata) are recorded and shared in a standardised, fair and transparent way, can we make sure that they can be used optimally for conservation purposes (Leigh et al., 2024).

Taxon	Biobank Type (storage temperature)	Common Database Platforms (links)	Primary Use Case	Institution examples (in current use)
Fauna/ Flora/ Funga	Non-living cells ¹ • ambient • refrigerated • frozen	EMu Specify ZIMS ⁴	Museum specimen & collections management	Global use
Fauna/ Flora/ Funga	Living cells, seeds, & tissues² • desiccated-chilled; • frozen: -20°C to - 196°C	Freezer Works FreezerPro BRAHMS ⁵ GRIN Global GERMINATE Animal GRIN ZIMS ⁴ EMu	Preserved sample management	Smithsonian Institution (USA) Natural History Museum (UK) Kew Royal Botanic Gardens (UK) National Zoological Gardens Biobank (South Africa) Royal Botanic Gardens Trust (e.g., Australia: Plant Bank) USDA ⁶ & several CGIAR ⁷ genebanks Museums Victoria
Fauna	Living whole organisms ³ • Zoo & aquarium insurance populations	<u>Tracks®</u> <u>ZIMS</u> ⁴	Living population management (all aspects)	Many zoos & aquariums (WAZA members)
Flora	Living whole organisms Botanic Garden	PlantSearch IrisBG Hortis BG-Base	Tracking living collections across institutions	PlantSearch: Global database of living plant, seed and tissue collections (1,106,706 records)

Table 4. Common database and systems across sample types. The features of sample management and tracking apply to all examples. All examples are suitable for tracking metadata associated with biobanked samples, but specific feature sets vary among platforms depending on their Primary Use Case (e.g., research, reproduction/propagation, etc.)

¹ DNA fixed tissues. ² Germplams tissues. ³ Conservation breeding program species (mammals, birds, amphibians, reptiles, fishes, invertebrates (corals, molluscs). ⁴ There is an additional ZIMS module for biobanked samples for use in preserved sample management. ⁵ hBRAHM is also used for managing living seed banks. ⁶ USDA, United State Department of Agriculture. ⁷ CGIAR, Consultative Group on International Agricultural Research.

Common Database Platforms (link)	Benefits	Considerations
EMu	 Broad use across museums Can be exported into other databases 	 Costs of user licence & adding/modifying database metadata Not linked to pedigree data Can potentially be linked to Genbank data
FreezerWorks	 Broad use across museums; invoicing capability Can be exported into other databases Visualisation of freezer storage 	Costs of user licence & metadata editing
ZIMS	 Well-established, broad use across zoos Integration with PMx (for pedigree information) 	Costs of user licence & adding modules/modifying database metadata No ability to retain exclusive data rights
Tracks®	Ability to retain exclusive data rights (can run on own server)	Costs of licence & editing
BRAHMS	 Functionality tailored to seed banking of wild plant species Specimen records can link to living botanical collections 	Costs of licence
IrisBG	Stores many types of plant material (DNA, Seed, Herbarium) • Specimen records can link to living botanical collections	Costs of licence Not as specifically tailored to gene bank management
Specify	Open source software Uses Darwin Core Standards	Subscription fee to have access to training resources etc.
GRIN Global	Broad use across crop genebanks	GRIN Global developed out of USDA National Plant Germplasm System (NPGS); use is subsidized in global south by the Crop Trust
Animal GRIN	Broad use across livestock genebanks	 and CGIAR system Animal-GRIN is managed by the National Genetic Resources Program (NGRP) of USDA
Excel or Access	 No/minimal costs of users Good "starter" database for poorly resourced, small operations High accessibility to broad range 	 Not recommended for long-term use No automatic "versioning" capability Poor integration/interoperability Poor data security/compliance tracking – all or nothing editing access Poor workflow management – human error during sample check out/in
Bespoke Relational Database Systems	 High customisability to institution workflow Annual software fees minimal Can be configured with refined user permission for internal and external sharing 	 High initial development cost Funding for ongoing maintenance challenging Must be developed with global data standards in mind

Table 5. Potential benefits and considerations of common database platforms and systems for fauna.

Common metadata	Fauna	Flora	Funga
Sample/Specimen ID, type & history • temporal & locational data (date, time, GPS location) • taxonomic data • ecosystem parameters • links to field notes	Donor ID (global or local studbook no.) Date of birth, death, sample collection Ecological community at source (e.g., coral) Cell/tissue sample type (ejaculated or epididymal sperm; preovulatory or ovulated oocyte)	 Donor ID (sourced from living or preserved specimen), cell/tissue sample type (pollen, seed, spore), Life stage at sampling, aspect, elevation for sampling location, ecological community and population size at source number of maternal plants sampled (seed lots) 	Donor ID, egermination date, elife stage at sampling, ecological community at source
Sample functional data • objective assessment	• Ex. Sperm samples: Initial and post thaw sperm motility, longevity, DNA integrity, microbial culture (pos/neg)	Germination & propagation rate (Ex. pollen: viability assessments pre and post storage, longevity)	Colony formation on culture Germination and propagation rate
Sample Storage unique identifier (e.g., barcode) storage location storage conditions/medium	 Accession number/ unique sample identifier (e.g., barcode number) Storage medium Freezer ID, Tank/ canister/ cane/ box/ position number 	 Accession number/ unique sample identifier (e.g., barcode number) Storage medium Freezer ID, Tank/ canister/ cane/ box/ position number 	 Accession number/ unique sample identifier (e.g., barcode number) Storage medium Freezer ID, Tank/ canister/ cane/ box/ position number
Permits, Licences & Chain of Custodianship • name of institution with temporary or permanent custodianship of the sample • Traditional Custodian group/ Countrymen	 Traditional Custodian consent/approval Collection/Scientific Licences Collection relevant Ethics Approval 	Traditional Custodian consent/approval Collection/Scientific Licences	Traditional Custodian consent/approval Collection/Scientific Licences
Sample accession/ deaccession/ use	 Organisation accessioning sample Sample deaccession/use details 	Organisation accessioning sample Sample deaccession/use details	Organisation accessioning sample Sample deaccession/use details

Table 6. Key metadata across different taxa.

5.3 Other relevant software and programs

For banked samples destined for use in conservation breeding efforts, mate suitability is determined using various software, independent of the biobank database system (e.g., ENDOG [Gutierrez and Goyache, 2004], PMx [Lacy, et al., 2012]). However, pedigree and molecular data relevant to the sample donor can also be stored in the sample metadata, which is in turn entered into the aforementioned software programs along with pedigree/molecular data of the recipient, to determine a mate suitability index (and for molecular data - individual heterozygosity and allele representation). Full reporting of voucher/accession numbers of specimens sampled when DNA sequences are uploaded to platforms like GenBank (https://www.ncbi.nlm.nih.gov/genbank/) is also vital to avoid loss of links between the specimen, the sample, and the genetic sequence. There are several animal and plant initiatives that encompass large collaborations for tracking samples from various sources (museums, universities and breeding facilities) for genetics research (e.g., Bioplatforms Australia's Oz Mammals Genomics Initiative, the Genomic Observatories MetaDatabase, GEOME [See Resources]), which also offer useful guidance on genomics data fields and linkages to other datasets.

Modern database systems will have components that enable compliance tracking, reporting/ analytics, sample management, workflow management, data security and line of custodianship (e.g., Traditional Custodian/Indigenous groups) and sample use (Mc Cartney et al., 2022). Currently, global wildlife biobanks are characterised by a heterogenous and siloed approach that allows for minimal collaboration and sharing efforts. A global wildlife registry to which all biobanks could subscribe, and access would advance the concept of a global living and non-living genome biodiversity network. Short of this global registry, all efforts must be made, within reason and ability, to conform to accepted data capture standards and management systems within a sector to facilitate cooperation and information sharing and unite sectors under the goal of global biodiversity conservation efforts (Leigh et al., 2024).



Section 6: Creating a network

Biobanks play a crucial role in addressing the biodiversity crisis by providing access to banked biological samples and their associated metadata, facilitating timely and targeted conservation actions. Biobanking and database management should thus become integral components of conservation organisations' activities. While several biobanks and their overarching networks exist around the globe, few focus on wild species (see Section 2: Sample databases: Collection distribution and taxonomic representation), and fewer regularly interact and collaborate. This is partly because these initiatives are geographically and taxonomically diverse with varying missions and approaches to collection, processing, storage and sharing of biological specimens and associated metadata depending on sample availability and ease of collection (Zika et al., 2011). However, there are areas of overlap, expertise to share and synergies to explore when it comes to databases, access and use of samples and the long term persistence and growth of sample collections.

6.1 Connect and collaborate: the importance of networking

Firstly, common to all initiatives is that they manage a database of their specimen collection, ranging from simple to advanced, well-curated systems. It's crucial to have comprehensive knowledge of the locations where biological samples are stored, ensuring their visibility and accessibility for relevant studies pertaining to the species in question. Additionally, understanding the sampling gaps across species distribution ranges is essential (See Section 2: Gap analysis) to depict future sampling efforts, avoiding duplication and ensuring efficient use of resources. Currently, much of the information regarding sample collections is either inaccessible in a formal sense or available only informally to a select few researchers. Making sample information widely available would enhance dataset interoperability, facilitate biodiversity research, and enable better-informed management decisions, particularly in genetic management, at a faster pace. Notably, various communities, such as crop, zoos, botanic gardens and museums, already utilise databases to manage institutions holding material and the material itself. For instance, most zoos globally utilise the Zoo Information Management System (ZIMS), a closed database available to subscribers only. Similarly the botanical garden community also utilises a closed database, the PlantSearch by Botanic Gardens Conservation International, which has over one million plant records from more than a thousand botanical gardens. Additionally, many national genebanks contribute to Genesys, which hosts 4 million records of crops and crop wild relatives. Even though these databases are not visible outside their sectors, it would be strongly encouraged to make their collections of biobanked materials visible via their Data Portal (key fields), and encourage a partial set of standard fields be made publicly visible e.g. through GGBN and GBIF. As inspiration, several projects targeting the museum sector, such as the DiSSCo project, are making Museum collections increasingly visible and easily discoverable.

Secondly, it is also common to have well-defined policies and protocols in place for processing, storing, managing, and maintaining samples, as well as having a biospecimen access policy in place (see Section 3: Document harmonisation). The access policy usually specifies requirements that must be met for example to obtain samples for research, the level of expertise required to perform the proposed experiments or ethical and legal clearance. For these reasons, it is critical that biobank initiatives work together to facilitate more efficient collaborations and to empower understanding and adoption of best practices. Sharing knowledge and data, standardising methods, and processes, and communicating and collaborating in this way can help to ensure that important scientific biobank collections are not only well maintained but also expanded, covering taxonomical or geographical gaps and reducing costly duplication of efforts. Further, it can ensure that these valuable resources are actually put to use. Halting and reversing the biodiversity crisis requires collaboration and knowledge sharing among biobank initiatives to increase sample numbers and sample types available globally, and to streamline the access to those samples, which will enable higher-quality, and impactful research, while supporting legal and international regulations (e.g. CITES), obligations (e.g. CBD 2030 framework) and overall conservation outcomes.

Lastly, sample collection and long-term curation is often resource-intensive and time-consuming in terms of e.g. equipment, staffing and maintenance. As such, individual and networked biobanking systems usually incorporate some form of partial cost recovery, and require at least partial public or government funding, while some have private or institutional funding. To use resources effectively, it is important for biospecimen repositories to try to eliminate duplicated or redundant efforts where possible. Collaborative initiatives that pool resources and knowledge can enable faster identification of knowledge and sampling gaps, as well as prioritisation and funding needs. Moreover, networking and collaboration accelerate the learning curve for biobanking for restoration and conservation efforts, leading to more rigorous and timely evaluation of resource use, successes and failures to meet conservation actions.

6.2 Opportunities for collaboration

Within IUCN and across other conservation orientated partners it is critical to cultivate and prioritise active collaborations. Within IUCN Species Survival Commission several Specialist Groups (SGs) exist which rely on biobanking activities and have experts within their groups, such as the Conservation Genetics SG, Seed Conservation SG, Amphibian SG, Animal Biobanking for Conservation SG, Fungal Conservation Committee and Mushroom, Bracket and Puffball SG. Recently, the Species Survival Commission identified a need to standardise approaches and facilitate biobank synergies across SGs and Members, with a newly established SSC Center for Species Survival in Biodiversity Banking hosted by San Diego Zoo Wildlife Alliance. Several IUCN Specialist Groups (SGs) are ideally placed to help drive collaborations. The taxon SGs can play a pivotal role in liaising with the Conservation Genetics SG for prioritising species for sampling drives and biobanking as well as providing taxon specific protocols, techniques and methodologies. The Conservation Genetics SG and other institutions from the zoo and botanic garden communities (e.g., EAZA, AZA, WAZA, BGCI) may advise on the structuring of databases, handling of sensitive information (such as precise geolocation details) and acquisition and loans protocols for research and management as decided by the groups themselves in order to help facilitate the creation of collaborative networks.

Conservation planning can benefit from incorporating biobanking, whether through use of biological material to enable molecular genetic studies of genetic diversity including inbreeding, relatedness, and adaptations, as well as for disease monitoring, or the use of cryopreserved samples such as gametes or cell lines for a species breeding programme or action plan, especially linking in situ and ex situ efforts, in line with the One Plan Approach (Ryder and Onyma, 2018; IUCN resolution WCC 2020 Res 079 | IUCN Library System). The IUCN SSC Conservation Planning SG is one potential expert group that could help evaluate the needs and potential uses of banked samples in species conservation efforts; other experts, Specialist Groups and networks such as regional wildlife veterinary associations or the Food and Agriculture Organization (FAO) of the United Nations could provide input on overarching conservation issues, particularly within the One Health framework, such as resilience and sustainability of food resources as it relates to wild crop relatives.

Beyond IUCN, many conservation-oriented partners with extensive biobanking expertise and knowledge exist, such as FAO, EAZA, individual zoos, botanical gardens and museums and many more (see Supplementary for examples). Bridging initiatives and fostering active collaboration in a global network is key to drive positive biodiversity conservation.

6.3 Developing key competencies for collaboration

Developing key competencies for effective collaboration is essential in both professional and research settings. Open communication, resource sharing and leveraging diverse expertise can enhance an initiative's capabilities, refine objectives, and help to identify critical needs and gaps to be filled. By developing these competencies, individuals and teams can forge strong, productive collaborations with impactful outcomes, both within and across different initiatives. Table 7 lists examples of key competencies and how to develop them:

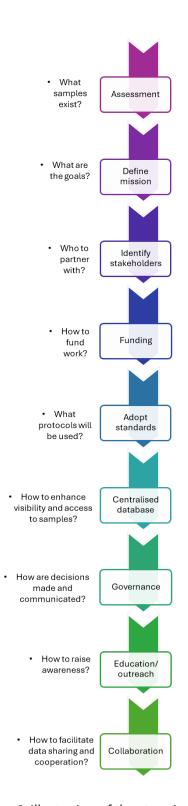
6.4 How to develop a network

Establishing a global network for biodiversity conservation and biobanking will enhance collaborations, optimise resources and accelerate research, but requires coordinated efforts and strategic planning, including defining the structure and modes of interaction of such a network, a clear mission, and concrete aims and goals. Figure 9 lists a set of steps towards creating such a network.

		Practising active listening, asking clarifying questions
	Enhanced communication	Providing feedback to ensure understanding amongst stakeholders
		Clear and concise articulation of ideas
2	Trust building	Be reliable and consistent in fulfilling commitments Demonstrate integrity, honesty, and accountability in all interactions
3	Respect of privacy and confidential information	Adhere to data protection standards
	Project	Set clear objectives, prioritise tasks, and well-defined timelines
4	4 management skills	Build on communication and trust to streamline projects
5 Conflict		Approach conflicts with problem-solving mindset
	Conflict resolution	Respect differing viewpoints
	Fostering of an	Embrace diversity
6	6 inclusive environment	Encourage creativity and innovation

Table 7. Examples of key competencies





1. Conduct a comprehensive global assessment:

- · Focused efforts to evaluate existing biobanks and their collections
- Enhance visibility and accessibility for incorporation into relevant research priorities.
- Integrate biobanking and database management into mainstream conservation activities for plant, animal, and fungal specimens.
- Encourage continuous curation of samples across geographic ranges to quide future efforts.

2. Define mission, goals and key activities:

 Outline vision and identity of the initiative to help guide strategic action plans.

3. Identify and engage (likeminded) stakeholders:

- Including biobanks, research institutions, museums, conservation organisations and policy makers for potential collaborations.
 - Foster partnerships among diverse parties.
- Promote initiatives aligned with international agreements like the CBD and Nagoya.

4. Establish funding mechanisms:

- . To support network development, infrastructure, and capacity building.
- ldentify various funding sources such as international or government grants, corporate responsibility/sponsorship, research grants, membership fees or fee-for-service and public engagement initiatives.

 Consider operating under an existing organisational structure (e.g., zoo or
- Consider operating under an existing organisational structure (e.g., zoo of botanic garden association).

5. Establish and adopt common standards and protocols:

- Including for sample and data collection, storage, and management to ensure interoperability and data sharing across the network.
- Ensure compliance with permitting, regulations and protocols for material transfers
- Ensure uses are Nagoya-compliant and that Access and Benefits Sharing of samples, and associated digital sequence information, is accounted for (Rohden and Scholz et al., 2022; see Section 3: Legislation and Regulations).

6. Develop an accessible, centralised, global database/data portal:

- To catalogue searchable samples and research interests to facilitate collaboration between biobanks and other stakeholders.
- Consider adopting or adapting existing databases from similar institutions like seed banks, zoos, botanical gardens and museums to streamline the process.

7. Establish governance structures and communication channels:

- To facilitate coordination and decision-making among network members.
- To ensure transparent communication and effective governance and maintain network integrity and functionality.
- Consider establishing committees with diverse representatives to vote on strategic plans and establish fora for communications.

8. Provide education and outreach:

- To raise awareness about the importance and benefits of participating in a global biobanking network for species conservation efforts.
- Collaborate with organisations like zoos, botanical gardens, museums, universities and major NGOs to reach target audiences effectively.

9. Promote international collaboration:

- Engage in international research initiatives and facilitate data and sample sharing
- Provide access to and help network sample collections, expertise and research opportunities to enhance global conservation efforts.

Figure 9: Illustration of the steps involved and to be considered for creating a global network for biodiversity conservation and biobanking

6.5 Examples of collaborative biobanking initiatives

In order to illustrate various approaches to collaborative biobanking, five initiatves will be presented on the following pages

Case study: CryoArks - a UK-wide consortium

CryoArks is a consortium of academic institutions, museums, and zoos, with links to the Frozen Ark and EAZA biobank (Pérez-Espona, 2021) (Figure 10). Coordinated by Cardiff University, partner institutions worked together to establish the UK's first comprehensive zoological biobank. Originally funded by the BBSRC (Biotechnology and Biological Sciences Research Council) and established in 2018, CryoArks addresses the need to provide a sustainable, publicly visible and accessible biological resource for researchers and conservation practitioners. The initiative developed the physical and bioinformatics infrastructure needed to connect the diverse and disconnected collections of animal frozen material held in zoos, aquariums, museums, research institutes, and universities across the country. As a national coordinated biobank, CryoArks utilise existing freezer capacity (-196°C and -80°C) at the Molecular Collections Facility of the Natural History Museum (NHM) in London and added new freezers (-80°C) at the National Museums Scotland and at the Royal Zoological Society of Scotland.

CryoArks uses the open-source Specify Software (see Table 4) to make custom key data fields collated across the sectors involved in CryoArks to develop a comprehensive, web-enabled sample database. CryoArks operates as a centralised system to receive and process sample requests avoiding the need to contact each partner institution individually. Applications to borrow samples from CryoArks can be made by completing and submitting a sample request form. Sample requests are reviewed by the CryoArks Sample Acquisition and Loans Committee and supplied at the discretion of institutional collections managers once the necessary paperwork (e.g., MTAs) is completed. As more institutions join the initiative, visibility of existing sample collections increases, which facilitates access to a wide range of samples and taxa, reducing the need to re-sample from the field. This is extremely important at a time when species are under increasing threat and direct sampling becomes ever more difficult, due to e.g. theimplementation of the Nagoya Protocol on Access and Benefit Sharing of Genetic Resources. Organisations interested in joining the CryoArks community can either donate samples to be stored and curated in one of the CryoArks hubs or make their collection accessible by supplying sample metadata that will be added to the CryoArks database under a Data Transfer Agreement (DTA). CryoArks has developed various resources and guidance documents available to the biobanking community. The resources are of particular use to researchers collecting samples with accessibility and long-term storage in mind or to anyone that is responsible for a frozen collection. While BBSRC funding has ended in 2022, the CryoArks network aims to continue to expand its activities in the future to be able to support more UK institutions with collection audits, establish further partnerships, integrate more collections, also searchable via the database, and ensure long-term financial sustainability.

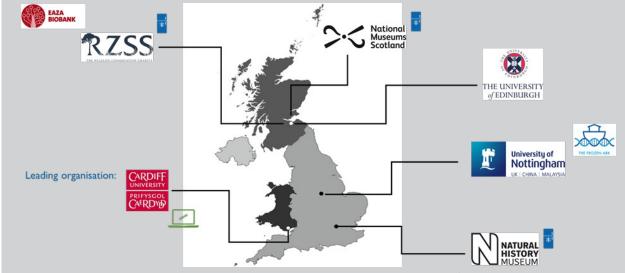


Figure 10. CryoArks Consortium in 2018. Consortium coordinated by Cardiff University in partnership with the Natural History Museum (NHM) of London, National Museums of Scotland (NMS), the Royal Zoological Society of Scotland (RZSS), The Frozen Ark, University of Nottingham, and the University of Edinburgh. Cardiff University hosts the CryoArks website and database. CryoArks biobanking core hubs are based at NHM, NMS, and RZSS.

Case study: The EAZA Cryopreservation Network: Collaboration Towards a Common Goal

In 2016, the European Association of Zoos and Aquariums (EAZA) established dedicated biobanking facilities for its Members in Europe, Western Asia and beyond. The EAZA Biobank is be a primary resource for in situ population management, conservation and wildlife health research by banking biological samples collected by EAZA members (DNA Biobanking: e.g., tissue, blood, serum). Currently, there are four official EAZA Biobank "hubs" where biological samples are physically held, and each hub has a geographical responsibility for sample receipt as defined in the 'EAZA Biobank Vision' document. Cryopreservation, or cryobanking, of "living" reproductive or somatic cells allows for yet another useful tool for population management and conservation research, including maintenance of genetic diversity or even revival of lost genetic lines. For population management programmes like the EAZA Ex situ Programmes (EEP), the collection and use of living cell samples has the potential to increase the success of these programmes considerably, especially when they have roles that require longterm persistence (e.g., Ark and insurance populations). Furthermore, it may allow additional EEPs with important conservation roles to be established, ones that currently may not be feasible to manage without these tools. As such, cryopreservation can play a key role in the conservation of numerous species. Examples of EEP species include the Amur leopard, Sumatran tiger, Somali wild ass, Socoro dove, Pileated gibbon, pupfishes, European mink, mountain chicken frog, Cherry-crowned mangabey and Lac Alaotran gentle lemur. The EAZA Biobank recognises the need for cryopreservation within the EAZA community but is not currently able offer these specific services. However, a Cryopreservation Interest Group (CIG) has been established under the EAZA Biobank with the remit of providing expertise and guidance in cryopreservation to the EAZA membership. To achieve this, an EAZA Cryopreservation Network has been launched by the EAZA Biobank and the CIG, in collaboration with in collaboration with other key bodies of EAZA.

The EAZA Cryopreservation Network is composed of external cryobank partners with liquid nitrogen storage capacity and expertise in cryopreservation techniques, and who also prioritise conservation goals, including ex situ conservation and population management. The EAZA Biobank, via the CIG, oversees the onboarding process of any candidate cryobank partner that is interested in joining this network (Figure 11). A Memorandum of Understanding (MoU) between the partner and EAZA is required, stating the intent to collaborate, to collect and store high-quality living cell samples and ensuring provision of appropriate infrastructure and protocols for sample storage, or development of in vitro cell lines for the purposes of non-commercial conservation management and research, in line with the 'One Plan Approach' and EEPs' population management strategies. Where possible, the cryobank partners' research, development and use of the samples provided by the EAZA membership will be applied to the continuing development and progression of EAZA's EEPs.

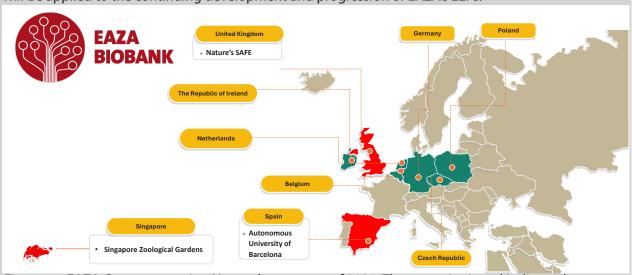
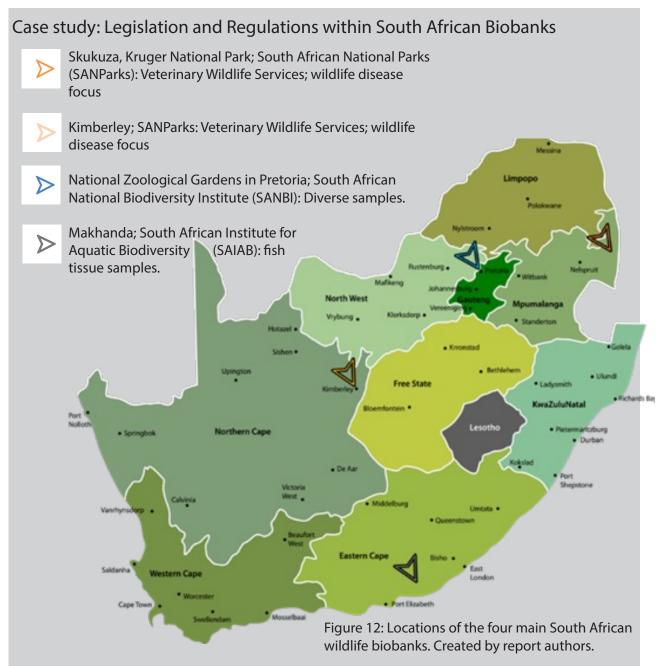


Figure 11. EAZA Cryopreservation Network current as of 2025. The countries in red indicate the presence of at least one official Cryonetwork Partner and countries in green indicate negotiations with potential new Cryonetwork Partners,



There are four main wildlife biobanks in South Africa that provide samples for research purposes (Figure 12) and a specific workflow to request and transport those samples (Figure 13). The scope and vision is to facilitate the increased use of samples for research and conservation purposes, to share samples globally/increase the access for experts and to advanced facilities/technologies in order to develop knowledge and inform decision-making about conservation and management of biodiversity.

Pertinent legislation/regulations:

1. Animal Disease Control Act (1984): Legislation that covers biosecurity in South Africa. Biobanks with animal tissues or microbes must be certified and the distribution of samples is strictly controlled.

2. Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits: Biodiversity Access and Benefit Sharing (BABS) Regulations under the National Biodiversity Act were published in 2015 stating any export of genetic resources for non-commercial research purposes requires a permit and a Material Transfer Agreement (MTA) between the supplying institution and the recipient. The applicant for an export permit must be South African or specify a South African collaborator. While the focus of this agreement is on bioprospecting and commercialisation, it also includes research. Globally, there is increasing pressure to ensure that research using material from other countries complies with the Nagoya Protocol and customs officials of signatory countries may

also start checking for relevant permits.

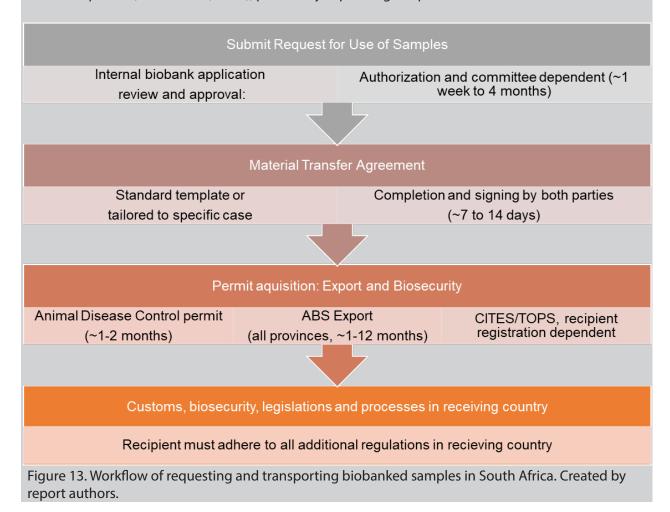
- 3. CITES (1973): allows for exemption for scientific exchange of materials from listed species, and while South African legislation states that this activity is exempt from permitting, ordinary export permits are still required. Both the supplying and receiving institutions must be registered with CITES.
- 4. Threatened and Protected Species (TOPS) (2007): further regulates the permit system involving listed threatened or protected species, to regulate how specific restricted activities may be carried out.

Required permits:

- 1. Section 20 permit: under the Animal Disease Control Act, which applies to "investigation, experiment or research".
- 2. Export permit: required if the species is on the TOPS list under the TOPS Regulations of the Biodiversity Act. The BABS Regulations state that export permits must be issued by the province from which the material was collected (i.e., if samples are collected from several provinces, a permit must be obtained from each province). In the case of CITES and TOPS, it is unclear whether this is the province from which the sample was originally collected, or the province in which the biobank is located.

Additional considerations:

- Applications/permits processing time(s) are variable.
- Finding information about/completing permit requirements may be a time-consuming challenge. Allocate time accordingly in order to adhere to all pertinent regulations.
- Consulting biobank staff about permit requirements, forms and contact information for relevant authorities may expedite access to samples.
- Legislation, regulations, and policies may change over time. In South Africa, a new policy on the
 conservation and sustainable use of South Africa's biodiversity that recognises the need to address
 the negative impact of the permitting requirements on research for conservation purposes is in
 development (Hamer et al., 2021), potentially expediting the process.



Case study: The Millennium Seed Bank Partnership (MSBP)

Th MSBP is coordinated by the Royal Botanic Gardens, Kew, stands as the largest ex situ plant conservation programme in the world. Launched in 1996, its mission is to provide an "insurance policy" against the extinction of plants in the wild by storing seeds for future use. The MSBP works with over 100 partner institutions across more than 95 countries, forming a robust network dedicated to seed conservation. These partnerships enable countries to meet international conservation objectives, such as the Global Strategy for Plant Conservation and the Millennium Development Goals of the United Nations Environment Programme. Key collaborations include major partnerships in Africa, the Americas, Asia, Europe, and Oceania, where efforts focus on collecting, conserving, and researching seeds from diverse plant species.

In practice, the MSBP ensures that seed collections are maintained in their country of origin whenever possible, with duplicates sent to the Millennium Seed Bank for long-term storage. This strategy not only preserves genetic diversity but also supports local conservation initiatives and capacity building. For instance, in Australia, the MSBP collaborates with national and regional seed banks to safeguard native flora against threats such as climate change and habitat loss. In Africa, partnerships with botanical gardens and research institutions focus on conserving economically and ecologically important species.

By April 2007, the MSBP had banked its billionth seed, and by October 2009, it had achieved its initial goal of banking 10% of the world's wild plant species. As of June 2015, the bank housed 34,088 wild plant species and 1,980,405,036 seeds, representing over 13% of the world's wild plant species. The MSBP's comprehensive approach combines seed collection, storage, and research. This includes studying seed biology, developing germination protocols, and researching plant adaptation to climate change. Through its global network, the MSBP facilitates knowledge exchange and training, This extensive global effort underscores the importance of international collaboration in achieving significant conservation milestones and safeguarding biodiversity for future generations.



Case Study: Coral Biobanking in Partnership with Indigenous Stakeholders

The Great Barrier Reef is of immense cultural and ecological significance, particularly to First Nations peoples who, as Traditional Custodians, have maintained a deep connection to their sea Country for thousands of years. In response to the threats posed by climate change, initiatives like the Australian Coral Reef Resilience Initiative and the Reef Restoration and Adaptation Program, a major transdisciplinary and multi-agency program, aim to safeguard coral biodiversity through different interventions, including cryopreservation and biobanking (Daly et al., 2024).

While samples are collected under the appropriate permits, until recently, this work was done without consultation with, or permission from, Traditional Custodians. New partnerships and projects aim to change these practices.

The Woppaburra Coral Project

A key example of Indigenous collaboration in conservation, the Woppaburra Coral Project aims to deliver key knowledge for reef restoration and adaptation science, while training future leaders and building capacity in Woppaburra Country (Figure 14). An important component of this project involved the collection and cryopreservation of living coral genetic material during an on-Country spawning event, where participants gained hands-on experience in the biobanking process. The collection of a total of 150 samples from 40 corals was undertaken with the free, prior, and informed consent (FPIC) of the Woppaburra Traditional Custodians, providing opportunities for knowledge sharing between Indigenous and non-Indigenous communities working in reef conservation (Daly et al., 2024).

Cultural Safety and Governance

The project highlighted the importance of cultural issues in conservation and biobanking practices, recognizing the spiritual connection that First Nations people maintain with their sea Country—including biological samples. Subsequently, a Biobanking Cultural Safety event was held at Taronga Conservation Society Australia's Institute of Science and Learning, to foster discussions on ensuring the enduring cultural connection to stored coral samples and set a precedent for future projects to uphold Indigenous rights and authority.

Impact and Future Directions

This collaboration demonstrates how Western science and Indigenous knowledge systems can work together to support biodiversity and reef resilience. The development of governance frameworks, such as the CryoDiversity Bank Materials Transfer Agreement, ensures that Traditional Custodians retain decision-making power over the use of biobanked materials. These efforts establish a model for wider equitable and sustainable reef restoration practices and serve as the basis of a best-practices approach to biobanking activities in other regions and fields.

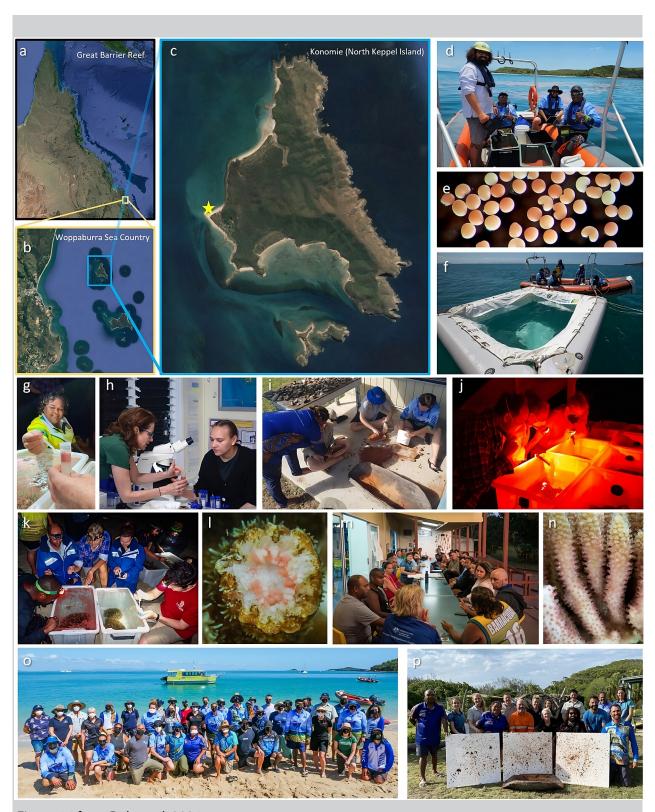


Figure 14 from Daly et al. 2024

6.6 The way forward: A global network with centralised sample data

Biobanking of appropriately collected biological specimens that may provide a suitable resource for biodiversity conservation studies, including population management and potential genetic rescue and assessment of current and ongoing conservation status, offer a context for development of policies that can contribute to knowledge-based biodiversity assessments, monitoring, and actions. To progress conservation of global biodiversity, a robust global biobanking network to serve as a primary resource for supporting the success of conservation efforts and goals is an urgent need. Various biobanking initiatives at different stages of development already exist and range from startups to well-established, in different regions of the world, spanning representation of many taxa, at many levels. Biobank institutions may network and collaborate solely within a geographic region (i.e., within a country), or based on sample type (e.g., cell cultures) or taxonomy of samples of interest (e.g., amphibian-specific biobanks). Regardless of how collaborations take place, or criteria for establishing a network, sample collections may be listed and made visible to one another through a global database. With an accessible global database, initiatives more easily have the potential to explore collaborations outside of their region, taxonomy or sample type and accelerate novel research. These stakeholders will need to actively pursue cooperation to create fruitful collaborations and strive to operate under a unifying model where each institution maintains its own collections but agrees to list some level of data regarding their collections on a centralised, shared database. Several taxonomic or biomaterial focused, and transboundary spanning initiatives exist, such as the EAZA Biobank and Cryopreservation Network, the Frozen Ark, the UAMH Centre for global microfungal biodiversity, the WI-KNAW culture collection, the Millenium Seed Bank, several rooted within IUCN SSC Specialist Groups, and many more including the past ENSCONET initiative for European Native plants, and projects aiming to digitise collections like RBG Kew and Natural History Museum of London (see Supplementary for more biobanking initiatives).

Current lack of information, especially regarding genetic assessments, can be ameliorated through such a global network of biobanking facilities and shared information. Three major open-source platforms include GGBN, GENESYS and GBIF with its Global Registry of Scientific Collections (GRSciCOII (see Section 2; See Supplementary), which serve as globally networked databases aiming to provide centralised sites where collections can be catalogued, and information and samples requisitioned in accordance with internationally equitable and legal stipulations. GGBN, GENESYS and GBIF provide a centralised searchable access point to numerous collections from a range of museums, governments, and research facilities and more. These can be searched in a variety of ways and contain within them both overlapping and complementary data on a diverse array of living and non-living samples. Searches can be conducted by institution name and type (museum, university, botanical garden, zoo, or research facility, etc.), taxonomic representation of the samples housed in each collection (microorganisms, fungi, plant or animal), the type of sample (living cells, e.g., gametes, etc., or nonliving, e.g., DNA, blood, etc.) and the storage/preservation of the sample. They also incorporate digital collections and, in some cases, though this is more prominent in GBIF than GGBN and Genesys, have more data on more specialised repositories that target specific resources, such as, eDNA repositories, and blood, cell, and tissue from specific taxonomic groups.

Currently, not all biobanks use the same database and data management processes. One of the challenges that hinders immediate collaboration, is that data is not collected or registered in a standardised manner, making sharing of databases and potential incorporation into global databases very difficult (Zika et al., 2011). Following the best practices outlined in Section 3: Document Harmonisation would enable data sharing within the global network. There can also be cultural obstacles, where people do not want to share data. Thus, to allow sample and data sharing for the greater good, a cultural shift needs to take place away from more guarded, secretive practices towards a more open and collaborative spirit. Biodiversity will not gain from having samples sit in a freezer unused. To help facilitate global networking and collaborations of biobanks, a non-biased regulatory body could be appointed or set up to help guide the direction of this field for flora, fauna, and fungi.

Additionally, more collections can be digitised, which would be extremely valuable for accessing and using data from a collection without physically accessing it. Taxon specialist groups, whether those of IUCN, regional zoo and aquarium associations, botanical gardens, or regional or national equivalents locally, are ideally positioned to monitor databases on their taxon of interest and to help provide guidance or actively pursue closing of sampling gaps. Disciplinary Specialist Groups (such as the IUCN SSC CGSG) or taxa-specific genetics subcommittees or advisors can help advise on sample types suitable for the species research needs. Commitments to justice, equity, diversity, and inclusion are key components of the developing network, including consideration of the Nagoya Protocol and full collaborative participation of local communities and Indigenous peoples (see Section 4: Legislation and Regulations). A global network embracing inclusiveness and fostering knowledge and data sharing, would provide a solid unified effort for progressing biodiversity conservation.

References

Abeli, T., Dalrymple, S., Godefroid, S., Mondoni, A., Müller, J. V., Rossi, G., & Orsenigo, S. (2020). Ex situ collections and their potential for the restoration of extinct plants. Conservation biology: the journal of the Society for Conservation Biology, 34(2), 303–313. https://doi.org/10.1111/cobi.13391

Alercia, A., Diulgheroff, S., Mackay, M. (2015). FAO/Bioversity multi-crop passport descriptors V.2.1. Food and Agriculture Organization of the United Nations (FAO), Bioversity International. Rome, Italy.

American Veterinary Medical Association (AVMA). (2008). One Health—a new professional imperative. One Health Task Force. http://www.avma.org/onehealth/purpose.asp. Accessed online 13 June 2011

Amstislavsky, S., Lindeberg, H., Aalto, J. & Kennedy, M. (2008), Conservation of the European Mink (Mustela lutreola): Focus on Reproduction and Reproductive Technologies. Reproduction in Domestic Animals, 43: 502-513. https://doi.org/10.1111/j.1439-0531.2007.00950.x

Antonelli*, A., Fry*, C., Smith*, R.J., Eden*, J., Govaerts*, R.H.A., Kersey*, P., Nic Lughadha*, E., Onstein*, R.E., Simmonds*, M.S.J., Zizka*, A., Ackerman, J.D., Adams, V.M., Ainsworth, A.M., Albouy, C., Allen, A.P., Allen, S.P., Allio, R., Auld. T.D., Bachman, S.P., Baker, W.J., Barrett, R.L., Beaulieu, J.M., Bellot, S., Black, N., Boehnisch, G., Bogarín, D., Boyko, J.D., Brown, M.J.M., Budden, A., Bureš, P., Butt, N., Cabral, A., Cai, L., Cano, J.A., Chang, Y., Charitonidou, M., Chau, J.H., Cheek, M., Chomicki, G., Coiro, M., Colli-Silva, M., Condamine, F.L., Crayn, D.M., Cribb, P., Cuervo-Robayo, A.P., Dahlberg, A., Deklerck, V., Denelle, P., Dhanjal-Adams, K.L., Druzhinina, I., Eiserhardt, W.L., Elliott, T.L., Enquist, B.J., Escudero, M., Espinosa-Ruiz, S., Fay, M.F., Fernández, M., Flanagan, N.S., Forest, F., Fowler, R.M., Freiberg, M., Gallagher, R.V., Gaya, E., Gehrke, B., Gelwick, K., Grace, O.M., Granados Mendoza, C., Grenié, M., Groom, Q.J., Hackel, J., Hagen, E.R., Hágsater, E., Halley, J.M., Hu, A.-Q., Jaramillo, C., Kattge, J., Keith, D.A., Kirk, P., Kissling, W.D., Knapp, S., Kreft, H., Kuhnhäuser, B.G., Larridon, I., Leão, T.C.C., Leitch, I.J., Liimatainen, K., Lim, J.Y., Lucas, E., Lücking, R., Luján, M., Luo, A., Magallón, S., Maitner, B., Márquez-Corro, J.I., Martín-Bravo, S., Martins-Cunha, K., Mashau, A.C., Mauad, A.V., Maurin, O., Medina Lemos, R., Merow, C., Michelangeli, F.A., Mifsud, J.C.O., Mikryukov, V., Moat, J., Monro, A.K., Muasya, A.M., Mueller, G.M., Muellner-Riehl, A.N., Nargar, K., Negrão, R., Nicolson, N., Niskanen, T., Oliveira Andrino, C., Olmstead, R.G., Ondo, I., Oses, L., Parra-Sánchez, E., Paton, A.J., Pellicer, J., Pellissier, L., Pennington, T.D., Pérez-Escobar, O.A., Phillips, C., Pironon, S., Possingham, H., Prance, G., Przelomska, N.A.S., Ramírez-Barahona, S.A., Renner, S.S., Rincon, M., Rivers, M.C., Rojas Andrés, B.M., RomeroSoler, K.J., Roque, N., Rzedowski, J., Sanmartín, I., Santamaría-Aguilar, D., Schellenberger Costa, D., Serpell, E., Seyfullah, L.J., Shah, T., Shen, X., Silvestro, D., Simpson, D.A., Šmarda, P., Šmerda, J., Smidt, E., Smith, S.A., Solano-Gomez, R., Sothers, C., Soto Gomez, M., Spalink, D., Sperotto, P., Sun, M., Suz, L.M., Svenning, J.-C., Taylor, A., Tedersoo, L., Tietje, M., Trekels, M., Tremblay, R.L., Turner, R., Vasconcelos, T., Veselý, P., Villanueva, B.S., Villaverde, T., Vorontsova, M.S., Walker, B.E., Wang, Z., Watson, M., Weigelt, P., Wenk, E.H., Westrip, J.R.S., Wilkinson, T., Willett, S.D., Wilson, K.L., Winter, M., Wirth, C., Wölke, F.J.R., Wright, I.J., Zedek, F., Zhigila, D.A., Zimmermann, N.E., Zuluaga, A., Zuntini, A.R. (2023). State of the World's Plants and Fungi 2023. Royal Botanic Gardens, Kew. DOI: https://doi. org/10.34885/wnwn-6s63

Aubry, S., Frison, C., Medaglia, J.C., Frison, E., Jaspars, M., Rabone, M., Sirakaya, A., Saxena, D. & Van Zimmeren, E. (2022). Bringing access and benefit sharing into the digital age. Plants, People, Planet, 4(1), pp.5-12.

Azdhs.gov; (n.d.). Category A & B Shipping Examples. https://www.azdhs.gov/documents/preparedness/state-laboratory/category-a-and-b-shipping-examples.pdf

Bertola, L. D., Brüniche-Olsen, A., Kershaw, F., Russo, I. M., MacDonald, A. J., Sunnucks, P., Bruford, M. W., Cadena, C., Ewart, K., de Bruyn, M., Eldridge, M., Frankham, R., Guayasamin, J., Grueber, C., Hoareau, T., Hoban, S., Hohenlohe, P., Hunter, M., Kotze, A., Kuja, J., Lacy, R.C., Laikre, L., Lo, N., Meek, M.H., Mergeay, J., Mittan-Moreau, C., Neaves, L.E., O'Brien, D., Ochieng, J.W., Ogden, R., Orozco-terWengel, P., Paez-Vacas, M., Pierson, J., Ralls, K., Shaw, R. E., Sogbohossou, E. A., Stow, A., Steeves, T., Vernesi, C., Watsa, M. & Segelbacher, G. (2023). A pragmatic approach for integrating molecular tools into biodiversity conservation. Conservation Science and Practice, e13053. https://doi.org/10.1111/csp2.13053

Bertram, M. G., Costi, M. P., Thoré, E. S. J., Sabo-Attwood, T., & Brooks, B. W. (2024). One Health. Current Biology, 34(11). https://doi.org/10.1016/j.cub.2024.04.025

Blesbois, E. (2007). Current status in avian semen cryopreservation. World's Poultry Science Journal. 63. 213 - 222. 10.1017/S0043933907001419.

Bolton, R.L., Mooney, A., Pettit, M.T., Bolton, A.E., Morgan, L., Drake, G.J., Appeltant, R., Walker, S.L. Gillis, J.D. & Hvilsom, C. (2022). Resurrecting biodiversity: advanced assisted reproductive technologies and biobanking. Reproduction and fertility 3(3): R121–R146. https://doi.org/10.1530/RAF-22-0005

Bosanquet, S., Ainsworth, M., Cooch, S., Genney, D. & Wilkins, T. (2018). Non-Lichenised Fungi. In Guidelines for the Selection of Biological SSSIs. Part 2: Detailed Guidelines for Habitats and Species Groups; Joint Nature Conservation Committee: Peterborough, UK.

Bragg, J.G., Cuneo, P., Sherieff, A., and Rossetto, M. (2019). Optimizing the genetic composition of a translocation population: Incorporating constraints and conflicting objectives. Mol Ecol Resour. 20: 54–65. https://doi.org/10.1111/1755-0998.13074

Bragg, J.G., Yap, J-Y.S., Wilson, T., Lee, E., and Rossetto, M. (2021). Conserving the genetic diversity of condemned populations: Optimizing collections and translocation. Evol Appl. 14: 1225–1238. https://doi.org/10.1111/eva.13192

Brandies, P., Peel, E., Hogg, C.J. & Belov, K. (2019). The value of reference genomes in the conservation of threatened species. Genes, 10:846.

Burbano, H. A., & Gutaker, R. M. (2023). Ancient DNA genomics and the renaissance of herbaria. Science, 382(6666), 59-63.

Burgin, S. (2008). BioBanking: An environmental scientist's view of the role of biodiversity banking offsets in conservation. Biodiversity and Conservation. 17. 807-816. 10.1007/s10531-008-9319-2.

Buttke, D.E., Decker, D.J., & Wild, M.A. (2015). The role of one health in wildlife conservation: a challenge and opportunity. Journal of Wildlife Diseases. 51(1):1-8. Doi: 10.7589/2014-01-004.

Buyck, B., Laessoe, Th., Meyer, M., & Hofstetter, V. (2010). Collecting the forgotten kingdom: Guidelines for the field mycologist with emphasis on the larger fungi. In: Eyman, J., Degreed, J., Häuser, C.L., Moje, J.C., Samyn, Y., Van de Spiegel, D. (Eds) Manual on Field Recording Techniques and Protocols for All taxa Biodiversity Inventories (ATBIs), Abc Taxa. Brussels, Belgium, 653 pp.

Byers, O., Lees, C., Wilcken, J. & Schwitzer, C.. (2013). The One Plan approach: The philosophy and implementation of CBSG's approach to integrated species conservation planning. WAZA Magazine. 14. 2-5.

Carroll, E.L., Bruford, M.W., DeWoody, J.A., Leroy, G., Strand, A., Waits, L. & Wang, J. (2018). Genetic and genomic monitoring with minimally invasive sampling methods. Evolutionary Applications 11, 1094–1119.

Castañeda-Álvarez, N. P., Khoury, C. K., Achicanoy, H. A., Bernau, V., Dempewolf, H., Eastwood, R. J., Guarino, L., Harker, R. H., Jarvis, A., Maxted, N., Müller, J. V., Ramirez-Villegas, J., Sosa, C. C., Struik, P. C., Vincent, H., & Toll, J. (2016). Global conservation priorities for crop wild relatives. Nature plants, 2, 16022. https://doi.org/10.1038/nplants.2016.22
Convention on Biological Diversity (2022). https://www.cbd.int/doc/decisions/cop-15/cop-15-dec-04-en.pdf

CITES (n.d.). https://cites.org/eng

Clulow, S., Clulow, J., Marcec-Greaves, R., Della Togna, G., & Calatayud, N. E. (2022). Common goals, different stages: the state of the ARTs for reptile and amphibian conservation. Reproduction, fertility, and development, 34(5), i–ix. https://doi.org/10.1071/RDv34n5_FO

Comizzoli, P., & Wildt, D.E. (2017). Cryobanking Biomaterials from Wild Animal Species to Conserve Genes and Biodiversity: Relevance to Human Biobanking and Biomedical Research. In: Hainaut, P., Vaught, J., Zatloukal, K., Pasterk, M. (eds) Biobanking of Human Biospecimens. Springer, Cham. https://doi.org/10.1007/978-3-319-55120-3_13

Convention on Biological Diversity, CBD. (2011). Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization. Montreal, Canada.

Corrales, C., & Astrin, J.J. (2023). Biodiversity Biobanking – a handbook on Protocols and Practices. Advanced Books Monograph. https://doi.org/10.3897/ab.e101876

Cowie, R.H., Bouchet, P. & Fontaine, B. (2022). The sixth Mass Extinction: fact, fiction or speculation? Biological reviews, 97(2): 640–663. https://doi.org/10.1111/brv.12816

CPC (2019). Center for Plant Conservation Best Plant Conservation Practices to Support Species Survival in the Wild. Center for Plant Conservation, Escondido, CA. https://saveplants.org/wp-content/uploads/2020/12/CPC-Best-Practices-5.22.2019.pdfCrespo, M.J., Abarca, M.L. & Cabanes, F.J. (2000). Evaluation of different preservation and storage methods for Malassezia spp. Journal of Clinical Microbiology, 38: 3872–3875. https://doi.org/10.1128/jcm.38.10.3872-3875.2000

Cunningham, A. A., Daszak, P. & Wood, J.L.N. (2017). One Health, emerging infectious diseases and wildlife: two decades of progress? Phil. Trans. R. Soc. B, 372, 20160167. http://dx.doi.org/10.1098/rstb.2016.0167

Curry M. R. (1995). Cryopreservation of semen from domestic livestock. Methods in molecular biology (Clifton, N.J.), 38, 189–197. https://doi.org/10.1385/0-89603-296-5:189

Daly, J., Van Issum, H., Cummins, M., Evans-Illidge, E., Randall, C. J., Boyd, S., Cveticanin, L., Dundas-Hargraves, K., Liddell, B., Hobbs, R. J., O'Brien, J. K. (2024). Cross-cultural approach to biobanking of living coral cells on Woppaburra sea Country in the southern inshore Great Barrier Reef. Australasian Journal of Environmental Management, 32(1), 6–21. https://doi.org/10.1080/14486563.2024.2401567

Day, J. G., & Stacey, G. N. (2007). Cryopreservation and freeze-drying protocols. Totowa, NJ: Humana Press.

Day, J. G., & Stacey, G. N. (2008). Biobanking. Molecular Biotechnology, 40: 202–213.

Della Togna, G., Howell, L. G., Clulow, J., Langhorne, C. J., Marcec-Greaves, R., & Calatayud, N. E. (2020). Evaluating amphibian biobanking and reproduction for captive breeding programs according to the Amphibian Conservation Action Plan objectives. Theriogenology, 150, 412–431. https://doi.org/10.1016/j.theriogenology.2020.02.024

Droege, G., Barker, K., Seberg, O., Coddington, J., Benson, E., Berendsohn, W.G., Bunk, B., Butler, C., Cawsey, E.M., Deck, J., Döring, M., Zhou, X. (2016). The Global Genome Biodiversity Network (GGBN) Data Standard specification. Database 2016: baw125. https://doi.org/10.1093/database/baw125

Espinel-Ingroff, A., Montero, D. & Martin-Manzuelos, E. (2004). Long-term preservation of fungal isolates in commercially prepared cryogenic microbank vials. Journal of Clinical Microbiology, 42: 1257–1259. https://doi.org/10.1128/jcm.42.3.1257-1259.2004

FAO. (1996). FAO focus. Biodiversity preserved: in situ and ex situ; CGIAR. FAO, Rome, Italy. http://www.fao.org/focus/e/96/04-e.html.

FAO. (2010). The second report on the state of the world's plant genetic resources for food and agriculture. FAO, Rome, Italy.

Farquharson, K. A., Hogg, C. J., & Grueber, C. E. (2018). A meta-analysis of birth-origin effects on reproduction in diverse captive environments. Nature communications, 9(1), 1055. https://doi.org/10.1038/s41467-018-03500-9

Frankham, R., Ballou, S. E. J. D., Briscoe, D. A., & Ballou, J. D. (2002). Introduction to conservation genetics. Cambridge University Press.

Fu, Y.-B. (2017). The Vulnerability of Plant Genetic Resources Conserved Ex Situ. Crop Science, 57: 2314-2328. https://doi.org/10.2135/cropsci2017.01.0014

Gollin, M. (2008). Biopiracy started with a bounce. Nature 451, 1055. https://doi.org/10.1038/4511055a

Guerrant, E. O., Havens, K., Maunder, M., & Havens, K. (Ed.) (2004). Ex Situ Plant Conservation: Supporting Species Survival in the Wild. Island Press.

Gutierrez, J. P. & Goyache, F. (2004). A note on ENDOG: a computer program for analysing pedigree information. 122, 172–176.

Hamer, M., Behr, K., Engelbrecht, I., & Richards, L. (2021). Permit requirements, associated challenges and recommendations for biodiversity collections and research in South Africa. S Afr J Sci. 117(9/10) ,Art. #11765. https://doi.org/10.17159/sajs.2021/11765

Hawksworth, D.L., & Lücking, R. (2017). Fungal diversity revisited: 2.2 to 3.8 million species. Microbiology Spectrum, 5(4), FUNK-0052-2016. https://doi.org/10.1128/microbiolspec.FUNK-0052-2016

Herrick J. R. (2019). Assisted reproductive technologies for endangered species conservation: developing sophisticated protocols with limited access to animals with unique reproductive mechanisms. Biology of reproduction, 100(5), 1158–1170. https://doi.org/10.1093/biolre/ioz025

Hewitt, R., & Watson, P. (2013). Defining biobank. Biopreservation and biobanking, 11(5), 309–315. https://doi.org/10.1089/bio.2013.0042

Hildebrandt, T. B., Hermes, R., Goeritz, F., Appeltant, R., Colleoni, S., de Mori, B., Diecke, S., Drukker, M., Galli, C., Hayashi, K., Lazzari, G., Loi, P., Payne, J., Renfree, M., Seet, S., Stejskal, J., Swegen, A., Williams, S. A., Zainuddin, Z. Z., & Holtze, S. (2021). The ART of bringing extinction to a freeze - History and future of species conservation, exemplified by rhinos. Theriogenology, 169, 76–88. https://doi.org/10.1016/j. theriogenology.2021.04.006

Hoban S. (2019). New guidance for ex situ gene conservation: Sampling realistic population systems and accounting for collection attrition, Biological Conservation, 235, 199-208.

Hoban, S., Archer, F.I., Bertola, L.D., Bragg, J.G., Breed, M.F., Bruford, M.W., Coleman, M.A., Ekblom, R., Funk, W.C., Grueber, C.E., Hand, B.K., Jaffé, R., Jensen, E., Johnson, J.S., Kershaw, F., Liggins, L., MacDonald, A.J., Mergeay, J., Miller, J.M., Muller-Karger, F., O'Brien, D., Paz-Vinas, I., Potter, K.M., Razgour, O., Vernesi, C. & Hunter, M.E. (2022). Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. Biological Reviews 97: 1511–1538. https://doi.org/10.1111/brv.12852.

Hohenlohe, P.A., Funk, W.C., & Rajora, O.P. (2021). Population genomics for wildlife conservation and management. Mol Ecol. 30: 62–82. https://doi.org/10.1111/mec.15720

Howard, J. G., Lynch, C., Santymire, R. M., Marinari, P. E., & Wildt, D. E. (2016). Recovery of gene diversity using long-term cryopreserved spermatozoa and artificial insemination in the endangered black-footed ferret. Animal Conservation, 19(2), 102-111.

Hu, Y., Fan, H., Chen, Y., Chang, J., Zhan, X., Wu, H., Zhang, B., Wang, M., Zhang, W., Yang, L., Hou, X., Shen, X., Pan, T., Wu, W., Li, J., Hu, H., & Wei, F. (2021). Spatial patterns and conservation of genetic and phylogenetic diversity of wildlife in China. Science advances, 7(4), eabd5725. https://doi.org/10.1126/sciadv.abd5725

Hvilsom, C., Segelbacher, G., Ekblom, R., Fischer, M.C., Laikre, L. Leus, K, O'Brien, D. Sahw, R. & Sork, V. (2022). Selecting species and populations for monitoring of genetic diversity. ISBN: 978-2-8317-2204-7. https://doi.org/10.2305/IUCN.CH.2022.07.en

Intergovernmental Science-Policy Platform on Bidiversity and Ecosystem Servces (IPBES). (2019). Global assessment report of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services, Brondízio, E. S., Settele, J., Díaz, S., Ngo, H. T. (eds). IPBES secretariat, Bonn, Germany. 1144 pages. ISBN: 978-3-947851-20-1

International Organization for Standardization (ISO). (2018). ISO 20387: 2018 – General requirements for biobanking [online]. Geneva [Cited 14 April 2022]. https://www.iso.org/standard/67888.html.

The International Society for Biological and Environmental Repositories (ISBER). (2023). Best Practices: Recommendations for Repositories (5th Edition). Retrieved from: https://cdn.ymaws.com/www.isber.org/resource/resmgr/best_practices/ISBERBestPractices-5thEditio.pdf

IUCNSSC. (2014). IUCN Species Survival Commission Guidelines on the Use of Ex situ Management for Species Conservation. https://portals.iucn.org/library/node/44952

Jackson, J. (2008). The thief at the end of the world: Rubber, power, and the seeds of Empire. Penguin Books.

Jang, T. H., Park, S. C., Yang, J. H., Kim, J. Y., Seok, J. H., Park, U. S., Choi, C. W., Lee, S. R., & Han, J. (2017). Cryopreservation and its clinical applications. Integrative medicine research, 6(1),

Jensen, E. L., Díez-del-Molino, D., Gilbert, M. T. P., Bertola, L., Borges, F., Cubric-Curik, V., de Navascués, M., Frandsen, P., Heuertz, M., Hvilsom, C., Jiménez-Mena, B., Miettinen, A., Moest, M., Pečnerová, P., Barnes, I., & Vernesi, C. (2022). Ancient and Historical DNA in Conservation Policy. Trends in Ecology & Evolution, 37(5), 420-429. https://doi.org/10.1016/j.tree.2021.12.010

Kier, G., Kreft, H., Lee, T. M., Jetz, W., Ibisch, P. L., Nowicki, C., Mutke, J., & Barthlott, W. (2009). A global assessment of endemism and species richness across island and mainland regions. Proceedings of the National Academy of Sciences of the United States of America, 106(23), 9322–9327. https://doi.org/10.1073/pnas.0810306106

Kulak, V., Longboat, S., Brunet, N. D., Shukla, M., & Saxena, P. (2022). In Vitro Technology in Plant Conservation: Relevance to Biocultural Diversity. Plants (Basel, Switzerland), 11(4), 503. https://doi.org/10.3390/plants11040503

Lacy, R., Ballou, J. & Pollak, J. (2012). PMx: software package for demographic and genetic analysis and management of pedigreed populations. Methods Ecol. Evol. 3, 433–437.

Langhof, H., Kahrass, H., Sievers, S. & Strech, D. (2017). Access policies in biobank research: what criteria do they include and how publicly available are they? A cross-sectional study. European Journal of Human Genetics, 25(3): 293–300. https://doi.org/10.1038/ejhg.2016.172

Lawniczak, M.K.N., Davey, R.P., Rajan, J., Pereira-da-Conceicoa, L.L., Kilias, E., Hollingsworth, P.M., Barnes, I., Allen, H., Blaxter, M., Burgin, J., Broad, G.R., Gaya, E., Holroyd, N., Lewis, O.T., Crowley, L.M., McTaggart, S., Mieszkowska, N., Minotto, A., Shaw, F., Sivess, L.A.S., Richards, T.A. (2022). Recording sample metadata for the Darwin Tree of Life Project. Sample manifest Standard Operating Procedure v. 2.4 in: https://raw.githubusercontent.com/darwintreeoflife/metadata/main/DToL_METADATA_SOP_v.2.4.pdf

Lee, J.J. (1991). American Type Culture Collection Preservation methods: freezing and freezedrying. The Journal of Protozoology, 39(5): 651.

Leigh, D. M., Hendry, A. P., Vázquez-Domínguez, E., & Friesen, V. L. (2019). Estimated six per cent loss of genetic variation in wild populations since the industrial revolution. Evolutionary applications, 12(8), 1505–1512. https://doi.org/10.1111/eva.12810

Leigh, D. M., Vandergast, A.G., Hunter, M. E., Crandall, E.D., Funk, W. C., Garroway, C.J., Hoban, S., Oyler-McCance, S.J., Rellstab, C., Segelbacher, G., Schmidt, C., Vázquez-Domínguez, E., & Paz-Vinas, I. (2024). Best practices for genetic and genomic data archiving. Nature Ecology & Evolution. https://doi.org/10.1038/s41559-024-02423-7

Li, Z., Sun, X., Chen, J., Liu, X., Wisely, S.M., Zhou, Q., Renard, J.P., Leno, G.H. & Engelhardt, J.F. (2006). Cloned ferrets produced by somatic cell nuclear transfer. Developmental biology, 293(2), pp.439-448.

Lodge, D.J., Ammirati, J.F., Odell, T.E., Mueller, G.M., Hundorf, S.M., Wang, C.J., Stokland, J.N., Schmit, J.P., Ryvarden, L., Leacock, P.R., Mata, M., Umaña, L., Wu, Q.X.F., & Czecerpiltz, D.L. (2004). Terrestrial and lignicolous macrofungi. In: Mueller, G.M, Bills, G.F. & Foster, M.S. (Eds) Biodiversity of Fungi: Inventory and Monitoring Methods. Academic Press.

Maxted, Nigel. (2001). Ex Situ, In Situ Conservation. Encyclopedia of Biodiversity. 683-695. 10.1016/B0-12-226865-2/00115-2.

Mc Cartney, A.M., Head, M.A., Tsosie, K.S., Sterner, B., Glass J.R., Paez, S., Geary, J., & Hudson, M. (2023). Indigenous peoples and local communities as partners in the sequencing of global eukaryotic biodiversity. npj biodivers. 2, 8. https://doi.org/10.1038/s44185-023-00013-7

McKenney, B. & Kiesecker, J. (2009). Policy Development for Biodiversity Offsets: A Review of Offset Frameworks. Environmental management. 45. 165-76. 10.1007/s00267-009-9396-3.

Mondal, R., Kumar, A., & Gnanesh, B.N. (2023). Crop germplasm: Current challenges, physiological-molecular perspective, and advance strategies towards development of climateresilient crops. Heliyon. 9(1):e12973. doi: 10.1016/j.heliyon.2023.e12973. PMID: 36711267; PMCID: PMC9880400.

Moore, S. G., and Hasler, J. F. (2017). A 100-Year Review: Reproductive technologies in dairy science. Journal of dairy science, 100(12), 10314–10331. https://doi.org/10.3168/jds.2017-13138

Millenium Seed Bank (MSB). (2015). Seed Conservation Standards for Millennium Seed Bank Partnership Partnership Collections. https://brahmsonline.kew.org/Content/Projects/msbp/resources/Training/MSBP-Seed-Conservation-Standards.pdf

Mueller, G.M., Martins-Cunha, K., May, T.W., Allen, J.L., Westrip, J.R.S., Canterio, C., Costa-Rezende, D.H., Dreschler-Santos, E.R., Vasco-Palacios, A., Ainsworth, A.M., Alves-Silva, G., Bungarts, F., Chandler, A., Gonçalves, S.C., Krisai-Greilhuber, I., Irsenaite, R., Bjarne, J.J., Kosmann, T., Lendemer, J., Try-McMulin, R., Mesic, A., Motato-Vásquez, V., Ohmura, Y., Reese, R.N., Perini, C., Saar, I., Simijaca, D., Yahr, R. & Dahlberg, A. (2022). What do the first 597 Global Fungal Red List Assessments tell us about the threat status of fungi? Diversity, 14:736. https://doi.org/10.3390/d14090736

Nakasone, K.K., Peterson, S.W. & Shung-Chang, J. (2004). Preservation and distribution of fungal cultures. In: Mueller, G.M, Bills, G.F., Foster, M.S. (Eds) Biodiversity of Fungi: Inventory and Monitoring Methods. Academic Press.

Niskanen T, Lücking R, Dahlberg A, Gaya E, Suz LM, Mikryukov V, Liimatainen K, Druzhinina I, Westrip JRS, Mueller GM, Martins-Cunha K, Kirk P, Tedersoo L, Antonelli A (2023) Pushing the frontiers of biodiversity research: Unveiling the global diversity, distribution, and conservation of Fungi. Annu Rev Environ Resour 48:149–176. https://doi.org/10.1146/annurevenviron-112621-090937

OECD Policy Highlights (2016). Biodiversity Offsets: Effective design and implementation. https://www.oecd.org/environment/resources/Policy-Highlights-Biodiversity-Offsets-web.pdf.

Overmann, J. & Smith, D. (2017). Microbial resource centers contribute to bioprospecting of bacteria and filamentous microfungi. In Paterson, R & Lima, N (Eds.), Bioprospecting: Success, Potential and Constraints (pp. 51–79). Cham, Switzerland: Springer International Publishing. https://doi.org/10.1007/978-3-319-47935-4_4

Oyanedel, R., Hinsley, A., Dentiger, B.T.M., Milner-Gulland, E.J. & Furci, G. (2022). A way forward for wilf fungi in international sustainability policy. Conservation Letters, 15(4): e12882. https://doi.org/10.1111/conl.12882Palacios, X.F. (1998). Contribution to the estimation of countries' interdependence in the area of plant genetic resources. Background study paper no 7 rev 1, FAO Commission on Genetic Resources for Food and Agriculture, Rome.

Panis B. (2009). Cryopreservation of Musa germplasm: 2nd edition. Technical Guidelines No. 9 (F. Engelmann and E. Benson, eds). Bioversity International, Montpellier, France.

Paoli, D.P. (2005). Biobanking in microbiology: From sample collection to epidemiology, diagnosis and research. FEMS Microbiol Rev., 29(5): 897–910. https://doi.org/10.1016/j.femsre.2005.01.005

Paton, A., Antonelli, A., Carine, M., Forzza, R.C., Davies, N., Demissew, S., Dröge, G., Fulcher, T., Grall, A., Holstein, N., Jones, M., Liu, U., Miller, J., Moat, J., Nicolson, N., Ryan, M., Sharrock, S., Smith, D., Thiers, B., Victor, J., Wilkinson, T. & Dickie, J. (2020). Plant and fungal collections: current status, future perspectives. Plants People Planet, 2:499–514. doi: 10.1002/ppp3.10141

Platform on Biodiversity and Ecosystem Services, Brondízio, E. S., Settele, J., Díaz, S., Ngo, H. T. (eds). IPBES secretariat, Bonn, Germany. 1144 pages. ISBN: 978-3-947851-20-1

Prescott-Allen, R. & Prescott-Allen, C. (1990). How many plants feed the world? Conservation Biology 4: 365–374

Ritter, C.D., Dunthorn, M., Anslan, S., De Lima, V., Tedersoo, L., Nilsson, R.H. & Antonelli, A. (2020). Advancing biodiversity assessments with environmental DNA: Long-read technologies help reveal the drivers of Amazonian fungal diversity. Ecologu and Evolution, 10(14): 7509–7524. https://doi.org/10.1002/ece3.6477

Robert, A. (2009). Captive breeding genetics and reintroduction success. Biological Conservation, 142, 2915-2922.

Robinson, J. A., Ortega-Del Vecchyo, D., Fan, Z., Kim, B. Y., vonHoldt, B. M., Marsden, C. D., Lohmueller, K. E., & Wayne, R. K. (2016). Genomic flatlining in the endangered island fox. Current Biology, 26(9), 1183–1189. https://doi.org/10.1016/j.cub.2016.02.062

Rohden, F. & Scholz, A.H. (2022). The international political process around Digital Sequence Information under the Convention on Biological Diversity and the 2018–2020 intersessional period. Plants, People, Planet, 4(1), pp.51-60.

Royal Botanic Gardens, Kew (2023). Species Fungorum Plus. Checklist dataset https://doi. org/10.15468/ts7wsb accessed via GBIF.org on 2024-05-19.

Roycroft, E., MacDonald, A. J., Moritz, C., Moussalli, A., Portela Miguez, R., & Rowe, K. C. (2021). Museum genomics reveals the rapid decline and extinction of Australian rodents since European settlement. Proceedings of the National Academy of Sciences of the United States of America, 118(27), e2021390118. https://doi.org/10.1073/pnas.2021390118

Ryan, M.J., McCluskey, K., Verkleij, G., Robert, V. & Smith, D. (2019). Fungal biological resources to support international development: Challenges and opportunities. World Journal of Microbiology and Biotechnology, 35(9): 139. https://doi.org/10.1007/s11274-019-2709-7

Ryder, O.A. & Onuma, M. (2018). Viable Cell Culture Banking for Biodiversity Characterization and Conservation. Annu Rev Anim Biosci. Feb 15;6:83-98. doi: 10.1146/annurevanimal-030117-014556. PMID: 29447472.

Ruta, C., Lambardi, M. & Ozudogru, E.A. (2020). Biobanking of vegetable genetic resources by in vitro conservation and cryopreservation. Biodivers Conserv 29, 3495–3532. https://doi.org/10.1007/s10531-020-02051-0

Sanderson, N., Wilkins, T., Bosanquet, S. & Genney, D. (2018). Lichens and Associated Microfungi. In Guidelines for the Selection of Biological SSSIs. Part 2; JNCC: Peterborough, UK, 31p.

Sandler, R.L., Moses, L. and Wisely, S.M. (2021). An ethical analysis of cloning for genetic rescue:

case study of the black-footed ferret. Biological Conservation, 257, p.109118.

Scarascia-Mugnozza, G.T., and Perrino, P. (2002). The history of ex situ conservation and use of plant genetic resources. In: J.M.M. Engels, V. Rao Ramanatha, A.H.D. Brown, M.T. Jackson, editors, Managing plant genetic diversity. CABI Publishing, Wallingford, UK. p. 1–22.

Schrade, L., Mah, N., Bandrowski, A., Chen, Y., Dewender, J., Diecke, S., Hiepen, C., Lancaster, M.A., Marques-Bonet, T., Martinez, S., Mueller, S.C., Navara, C., Prigione, A., Seltmann, S., Sochacki, J., Sutcliffe, M.A., Zywitza, V., Hildebrant, T.B., and Kurtz, A. (2024). A Standardized Nomenclature Design for Systematic Referencing and Identification of Animal Cellular Material. Animals. 2024; 14(11):1541. https://doi.org/10.3390/ani14111541

Segelbacher, G., Bosse, M., Burger, P., Galbusera, P., Godoy, J. A., Helsen, P., Hvilsom, C., lacolina, L., Kahric, A., Manfrin, C., Nonic, M., Thizy, D., Tsvetkov, I., Veličković, N., Vilà, C., Wisely, S. M., & Buzan, E. (2022). New developments in the field of genomic technologies and their relevance to conservation management. Conservation Genetics, 23(2), 217-242. Advance online publication. https://doi.org/10.1007/s10592-021-01415-5

Sherman, J.K. (1980). Historical Synopsis of Human Semen Cryobanking. In: David, G., Price, W.S. (eds) Human Artificial Insemination and Semen Preservation. Springer, Boston, MA. https://doi.org/10.1007/978-1-4684-8824-1_16

Sikes, R. S., & Paul, E. (2013). Fundamental differences between wildlife and biomedical research. ILAR journal, 54(1), 5–13. https://doi.org/10.1093/ilar/ilt015

Smith, D., & Onions, A.H. (1994). The preservation and maintenance of living fungi (No. Ed. 2). CAB International.

Smith, D. & Ryan, M.J. (2003). Current status of fungal collections and their role in biotechnology. In: Handbook of fungal biotechnology Marcel Dekker, New York 527–538.

Smith, D., Abeli, T., Bruns, E. B., Dalrymple, S. E., Foster, J., Gilbert, T. C., Hogg, C. J., Lloyd, N. A., Meyer, A., Moehrenschlager, A., Murrell, O., Rodriguez, J. P., Smith, P. P., Terry, A., & Ewen, J. G. (2023). Extinct in the wild: The precarious state of Earth's most threatened group of species. Science (New York, N.Y.), 379(6634), eadd2889. https://doi.org/10.1126/science.add2889

Species Fungorum. (2020). Coordinated by the Royal Botanic Gardens, Kew. Retrieved from https://www.speciesfungorum.org/Names/Names.asp (2020).

Thormann, I., Dulloo, M.E., Engels, J.M.M. (2006). Techniques of ex situ plant conservation. In: Plant conservation genetics. Centre for Plant Conservation Genetics, Southern Cross University. The Haworth Press Inc, Lismore, Australia, pp. 7–36.

Tiersch, T. R., Yang, H., Jenkins, J. A., & Dong, Q. (2007). Sperm cryopreservation in fish and shellfish. Society of Reproduction and Fertility supplement, 65, 493–508.

Triebel, D., Reichert, W., Bosert, S., Feulner, M., Okach, D.O., Slimani, A., Rambold, G. (2018). A generic workflow for effective sampling of environmental vouchers with UUID assignment and image processing. Database 2018: 1–10. https://doi.org/10.1093/database/bax096

Turghan, M. A., Jiang, Z., & Niu, Z. (2022). An Update on Status and Conservation of the Przewalski's Horse (Equus ferus przewalskii): Captive Breeding and Reintroduction Projects. Animals: an open access journal from MDPI, 12(22), 3158. https://doi.org/10.3390/ani12223158

Upton, C. (2020). Conserving Natures? Co-producing Payments for Ecosystem Services in

Mongolian Rangelands. Development and Change, 51: 224-252. doi: 10.1111/dech.12549

Verlinden, M., Nys, H., Ectors, N., & Huys, I. (2014). Access to biobanks: harmonization across biobank initiatives. Biopreservation and biobanking, 12(6), 415–422. https://doi.org/10.1089/bio.2014.0034

Verma, O.P., Kumar, R., Kumar, A., and Chand, S. (2012). Assisted Reproductive Techniques in Farm Animal - From Artificial Insemination to Nanobiotechnology. Vet. World. 5(5):301-310. doi: 10.5455/vetworld.2012.301-310

von Wettberg, E. & Khoury, C.K. (2020). Access to crop digital information and the sharing of benefits derived from its use: Background and perspectives. Plants, People, Planet, 2(3), pp.178-180.

Wade, E. M., Nadarajan, J., Yang, X., Ballesteros, D., Sun, W., & Pritchard, H. W. (2016). Plant species with extremely small populations (PSESP) in China: A seed and spore biology perspective. Plant diversity, 38(5), 209–220. https://doi.org/10.1016/j.pld.2016.09.002

Walters, E., Benson, J., Woods, E., & Critser, J. (2009). The history of sperm cryopreservation. In A. Pacey & M. Tomlinson (Eds.), Sperm Banking: Theory and Practice (pp. 1-17). Cambridge: Cambridge University Press. doi:10.1017/CBO9781139193771.002

Walters, C., & Pence, V. C. (2021). The unique role of seed banking and cryobiotechnologies in plant conservation. Plants, People, Planet, 3(1), 83-91. https://nph.onlinelibrary.wiley.com/doi/full/10.1002/ppp3.10121

Wilson, E.O. (1992). The Diversity of Life. Penguin, London, UK, pp 421.

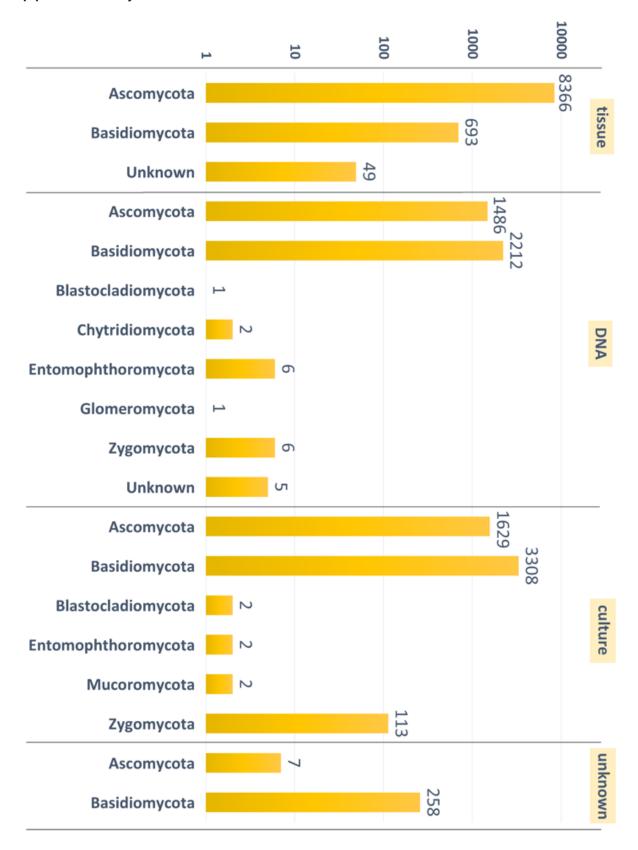
Witzenberger, K.A. & Hochkirch, A. (2011). Ex situ conservation genetics: a review of molecular studies on the genetic consequences of captive breeding programmes for endangered animal species. Biodivers Conserv 20, 1843–1861. https://doi.org/10.1007/s10531-011-0074-4

Wu, B., Hussain, M., Zhang, W., Stadler, M., Liu, X., & Xiang, M. (2019). Current insights into fungal species diversity and perspective on naming the environmental DNA sequences of fungi. Mycology, 10(3), 127-140.

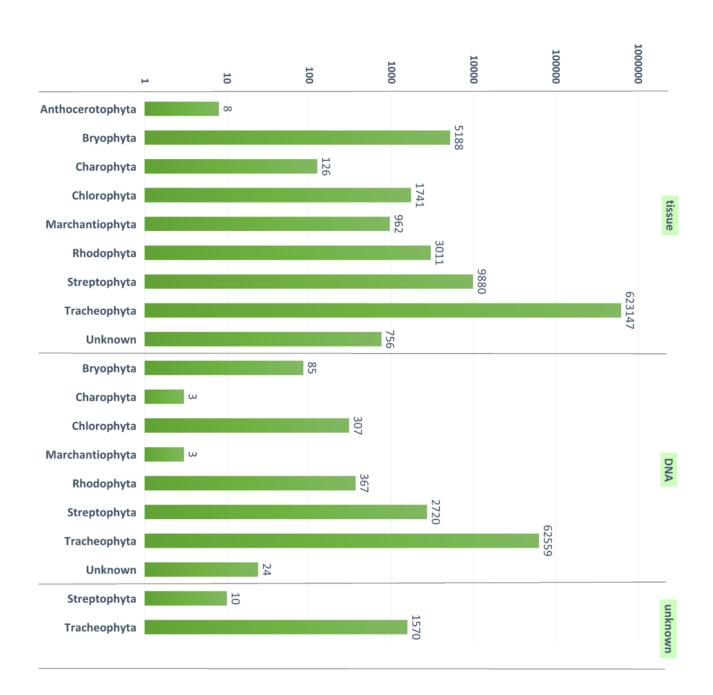
Wynberg, R., Andersen, R., Laird, S., Kusena, K., Prip, C., & Westengen, O. T. (2021). Farmers' rights and digital sequence information: Crisis or opportunity to reclaim stewardship over agrobiodiversity? Frontiers in Plant Science, 12, 686728. https://doi.org/10.3389/fpls.2021.686728

Yuille, Martin. (2013). Yuille M. Advanced biobanking and good management. In "Zukunft der Biobanken-Forschung in Deutschland: Vernetzung, Kollaborationen und Strukturaufbau" eds M. Hummel, T. Illig, R. Jahns, M. Kiehntopf, M. Krawczak, P. Schirmacher, S.C. Semler. Pp. 73-96. Akademische Verlagsgesellschaft AKA GmbH, Berlin. ISBN 978-3-89838-691-3.

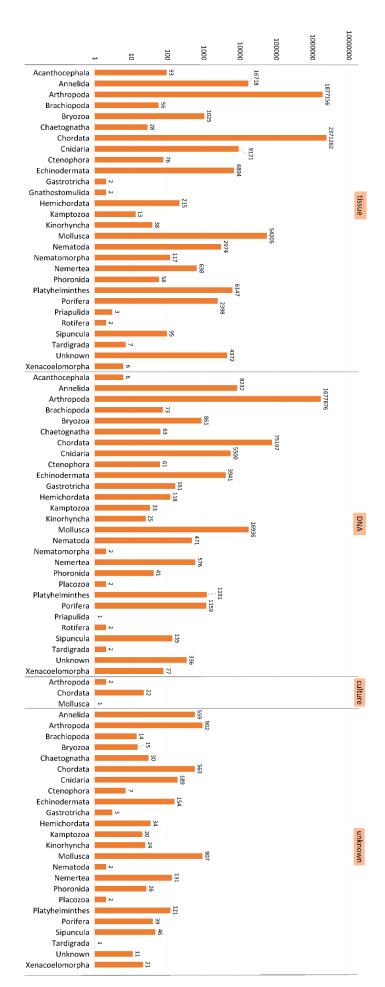
Supplementary



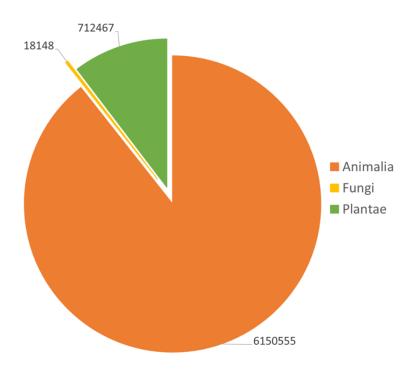
Supplementary Figure 1: Funga samples per phylum grouped by GGBN sample type categories: Tissue, DNA, Culture and Unknown. Unknown category is miscellaneous physical samples, not identified by the contributor. Y-axis in logarithmic scale. Created by report authors.



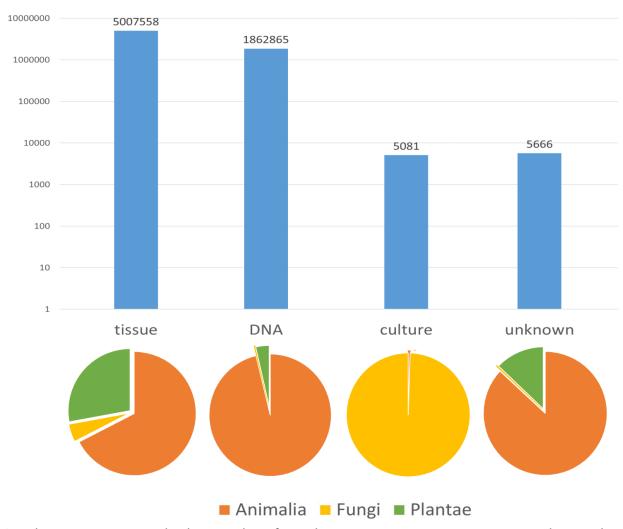
Supplementary Figure 2: Flora samples per phylum grouped by GGBN sample type categories: DNA, Tissue and Unknown. Unknown category is miscellaneous physical samples, not identified by the contributor. Y-axis in logarithmic scale. Created by report authors.



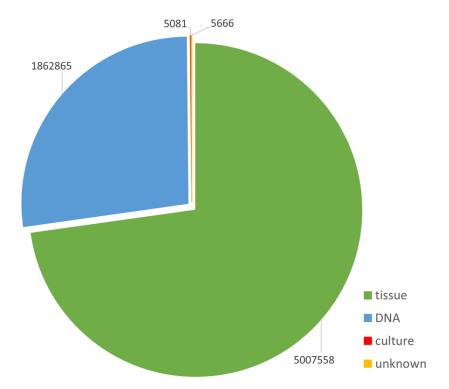
Supplementary Figure 3: Fauna samples per phylum grouped by GGBN sample type categories: Tissue, DNA, Culture and Unknown. Unknown category is miscellaneous physical samples, not identified by the contributor. Y-axis in logarithmic scale. Created by report



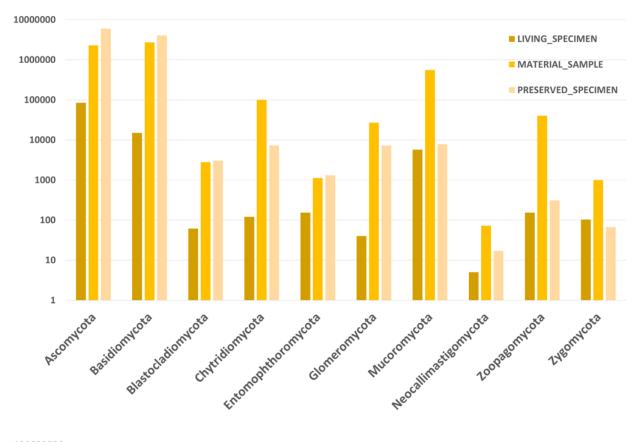
Supplementary Figure 4: Figure shows the total GGBN sample pool relative to each of the kingdoms. Created by report authors.

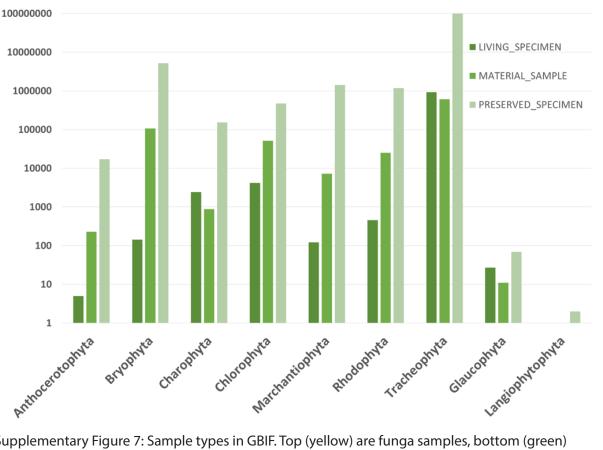


Supplementary Figure 5: Absolute number of samples per GGBN category: tissue, DNA, culture and unknown, and overall representation per kingdom. Unknown category is miscellaneous physical

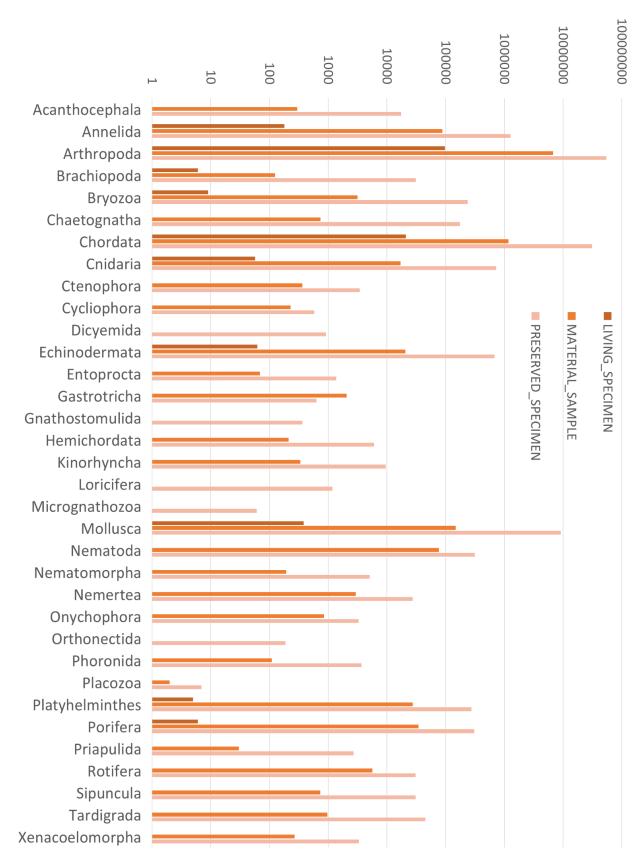


Supplementary Figure 6: Absolute number of samples per GGBN category: tissue, DNA, culture and unknown relative to each category. Unknown category is miscellaneous physical samples, not identified by the contributor. Created by report authors.

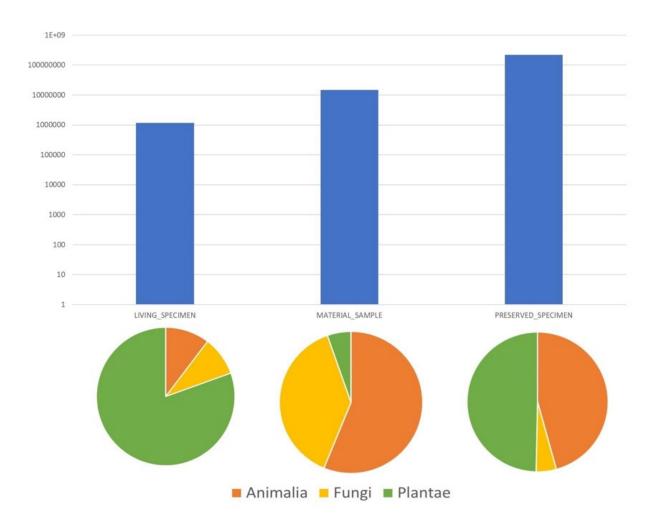




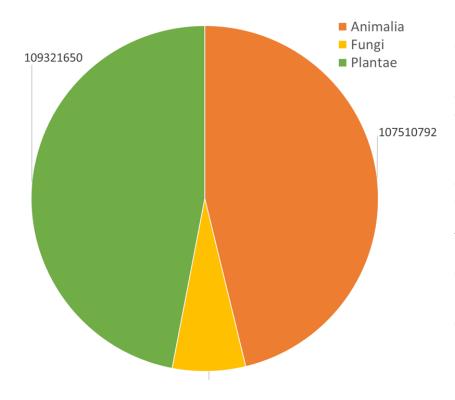
Supplementary Figure 7: Sample types in GBIF. Top (yellow) are funga samples, bottom (green) are flora samples grouped by phylum. Each phylum group is divided into Material Sample, Living Specimen or Preserved Specimen. Material Sample covers miscellaneous samples that are deemed different from the two other categories by the contributor. Living Specimen is a sample that is living i.e., a plant in a botanical garden or a living animal in a zoo. Preserved Specimens are samples stored in a preserving agent, dried, or on an herbarium sheet. Y-axis in logarithmic scale. Created by report authors.



Supplementary Figure 8: Animalia sample types in GBIF grouped by phylum. Each phylum group is divided into Material Sample, Living Specimen or Preserved Specimen. Material Sample covers miscellaneous samples that are deemed different from the two other categories by the contributor. Living Specimen is a sample that is living i.e., a plant in a botanical garden or a living animal in a zoo. Preserved Specimens are samples stored in a preserving agent, dried, or on an herbarium sheet. Y-axis in logarithmic scale.



Supplementary Figure 9: Figure shows the total GBIF sample pool relative to each of the kingdoms.



Supplementary Figure 10: Absolute number of samples per GBIF category: Material Sample, Living Specimen and Preserved Specimen, and overall representation per kingdom. Material Sample covers miscellaneous samples that are deemed different from the two other categories by the contributor. Living Specimen is a sample that is living i.e., a plant in a botanical garden or a living animal in a zoo. Preserved Specimens are samples stored in a preserving agent, dried, or on an herbarium sheet. Y-axis in logarithmic

		Fauna	Flora	Fungi
Asia	Tissue	126881	51144	394
	DNA	14096	1825	113
	Culture	23	0	156
	Unknown	369	189	0
Europe	Tissue	762011	298610	6137
	DNA	174568	26658	2128
	Culture	1	0	3638
	Unknown	472	392	265
lorth America	Tissue	3042130	97339	542
	DNA	1547666	8079	246
	Unknown	2870	80	0
	Culture	0	0	186
outh America	Tissue	266044	44285	970
	DNA	6110	7047	52
	Culture	0	0	77
	Unknown	0	160	0
ntarctica	Tissue	9698	2	26
	DNA	5025	0	0
	Culture	0	0	9
Oceania	Tissue	49915	10276	296
	DNA	27067	2313	239
	Culture	0	0	14
	Unknown	61	136	0
frica	Tissue	50541	78719	363
	DNA	10506	18267	110
	Unknown	11	225	0
	Culture	o	0	52

Supplementary Table 1: GGBN sample registrations for geographical continents.

			Four				E	a a i				loro	
			Faur	ıa		Fungi			Flora				
	Culture	DNA	Tissue	Unknown	Total	Culture	DNA	Tissue	Total	DNA	Tissue	Unknown	Total
Australia	0	5,963	18,009	0	23,972	4	16	70	90	575	2,832	114	3,521
Brazil	0	582	16,496	0	17,078	51	39	214	304	5,993	11,574	88	17,655
China	23	1,506	6,334	0	7,863	12	1	14	27	498	11,355	52	11,905
Colombia	0	234	11,006	0	11,240	3	0	64	67	22	2,111	3	2,136
Democratic Republic of the Congo	0	200	2,535	0	2,735	2	0	0	2	11	1	0	12
Ecuador	0	2,288	66,702	0	68,990	2	0	270	272	105	3,292	1	3,398
India	0	347	1,772	0	2,119	14	0	4	18	43	3,326	3	3,372
Indonesia	0	605	32,601	1	33,207	7	10	11	28	114	2,446	10	2,570
Madagascar	0	709	2,564	0	3,273	1	2	11	14	181	23,299	10	23,490
Malaysia	0	671	3,124	0	3,795	3	36	37	76	42	2,103	5	2,150
Mexico	0	1,051	40,076	0	41,127	6	7	47	60	151	7,978	24	8,153
Papua New Guinea	0	2449	4107	0	6556	4	3	194	201	139	3085	13	3,237
Peru	0	418	64193	0	64611		0	16	16	102	6230	20	6,352
Philippines	0	1,991	10,255	208	12,454	4	0	38	42	32	1,747	4	1,783
South Africa	0	4,594	12,636	0	17,230	21	0	114	135	10,492	6,188	16	16,696
United States	0	29,846	1,312,435	2,867	1,345,148	122	174	156	452	3,222	34,234	19	37,475
Venezuela	0	609	1,191	0	1,800	1	12	75	88	17	2,335	4	2,356

		Fauna	Flora	Fungi
Asia	Living specimen	669	112528	18111
	Material sample	581312	98945	566864
	Preserved specimen	10410654	14281167	498464
Europe	Living specimen	147383	215895	21751
	Material sample	1171935	285964	3103899
	Preserved specimen	20108397	18387216	4189699
North America	Living specimen	165	62610	4982
	Material sample	4725883	125735	725371
	Preserved specimen	42607035	28329403	3503016
South America	Living specimen	1715	69605	4035
	Material sample	265591	49616	612126
	Preserved specimen	8055700	18164951	545760
Antarctica	Living specimen	1	124	89
	Material sample	11886	5829	8755
	Preserved specimen	318958	36871	30990
Oceania	Living specimen	3057	49703	17759
	Material sample	713615	25871	321891
	Preserved specimen	8597998	8261044	607576
Africa	Living specimen	3832	39438	418452
	Material sample	896663	548322	206503
	Preserved specimen	13586187	808721	19142361

	Fauna			Fungi			Flora					
	Living	Material	Preserved	Total	Living	Material	Preserved	Total	Living	Material	Preserved	Total
Australia	3,055	560,342	6,047,508	6,610,905	8,328	165,374	375,486	549,188	43,107	12,808	6,202191	6,258,106
Brazil	28	52,676	3,193,164	3,245,868	1,214	249,565	297,022	547,801	3,283	15,335	10,699,408	10,718,026
China	69	69,155	458,980	528,204	390	84,884	68,566	153,840	18,760	19,504	5,041,113	5,079,377
Colombia	105	25,578	1,391,530	1,417,213	658	177,782	47,149	225,589	33,082	14,087	1,695,380	1,742,549
Democratic Republic of the Congo	0	5,155	433,266	438,421	275	28,940	17,748	46,963	662	632	584,375	585,669
Ecuador	3	16,278	528,293	544,574	150	388	22,411	22,949	4,187	1,137	1,235,289	1,240,613
India	12	21,715	376,007	397,734	2,022	99,479	38,480	139,981	10,439	17,402	424,672	452,513
Indonesia	5	101,094	994,487	1,095,586	522	6,702	11,221	18,445	6,169	3,995	833,761	843,925
Madagascar	1	50,522	508,656	559,179	24	37,576	4,698	42,298	1,427	2,393	903,605	907,425
Malaysia	5	107,365	307,680	415,050	827	18,843	11,033	30,703	3,692	1,374	425,537	430,603
Mexico	27	76,680	5,594,152	5,670,859	111	180,019	148,779	328,909	6,768	12,935	4,739,712	4,759,415
Papua New Guinea	1	68,267	581,652	649,920	216	85,528	26,105	111,849	3,025	5,339	515,504	523,868
Peru	22	12,117	566,779	578,918	186	3,043	13,396	16,625	9,970	2,608	1,130,923	1,143,501
Philippines	2	16,586	859,986	876,574	107	23	35,151	35,281	2,289	547	399,943	402,779
South Africa	2,193	369,712	1,316,291	1,688,196	1,215	53,942	38,686	93,843	3,160	13,666	1,547,245	1,564,071
United States	109	490,881	23,966,234	24,457,224	2,533	305,751	2,543,728	2,852,012	20,184	33,017	17,347,410	17,400,611
Venezuela	4	3,101	437,361	440,466	121	116	27,328	27,565	1,056	314	513,616	514,986

Supplementary Table 4: Sample registrations in GBIF for the 17 megadiverse countries.

Category	Name	Region	Discipline	Link
Biobanking Netw	orks and Associated Guidance			
Network	Australian Plant Conservation Network	Australia	Plants (Wild)	<u>link</u>
Best Practices	Plant Germplasm Conservation in Australia	Australia	Plants (Wild)	<u>link</u>
Network	Biobanking and Biomolecular Resources Research Infrastructure – European Research Infrastructure Consortium (BBMRI- ERIC)	Europe	Human clinical	<u>link</u>
Best Practices	BBMRI-ERIC Knowledge Base	Europe	Human clinical	<u>link</u>
Policy/Regulatory Guidance		Europe	Human clinical	<u>link</u>
Network	Botanic Gardens Conservation International (BGCI)	International	Plants (Wild)	<u>link</u>
Policy/Regulatory Guidance		International	Plants (Wild)	<u>link</u>
Database	BGCI Databases of Plant Records, Gardens, Expertise	International	Plants (Wild)	<u>link</u>
Network	Canadian Tissue Repository Network	North America	Human clinical	<u>link</u>
Best Practices	Biobank Resource Centre Standard Operating Procedures	North America	Human clinical	<u>link</u>
Network	Center for Plant Conservation (CPC)	North America	Plants (Wild)	<u>link</u>
Best Practices	CPC Rare Plant Academy: Best Practices and Learning Modules	North America	Plants (Wild)	<u>link</u>
Network	Consultative Group on International Agricultural Research (CGIAR)	International	Plants (Agriculture)	<u>link</u>
Best Practices	CGIAR Genebank Platform	International	Plants (Agriculture)	<u>link</u>
Best Practices	A European Genebank Integrated System (AEGIS)	Europe	Plants (Agriculture)	<u>link</u>
Best Practices	Crop Genebank Knowledge Base	International	Plants (Agriculture)	<u>link</u>
Best Practices	The International Plant Genetic Resources Institute (IPGRI) - Guidelines	International	Plants (Agriculture)	<u>link</u>
Database	Genesys	International	Plants (Agriculture)	<u>link</u>
Network	CryoArks	UK	Animals (Wild)	<u>link</u>

Category	Name	Region	Discipline	Link
Best Practices	CryoArks Training Resources	UK	Animals (Wild)	link
Network	European Association of Zoos and Aquaria (EAZA) Biobank	Europe	Animals (Wild)	<u>link</u>
Best Practices	EAZA - Biobank Sampling Protocols, Strategy Documents	Europe	Animals (Wild)	<u>link</u>
Policy/Regulatory Guidance	EAZA - Nagoya Protocol Guidance (appendix to Population Management Manual)	Europe	Animals (Wild)	<u>link</u>
Network	European Genebank Network for Animal Genetic Resources (EUGENA, formerly ERFP)	Europe	Animals (Agriculture)	<u>link</u>
Policy/Regulatory Guidance		Europe	Animals (Agriculture)	<u>link</u>
Network	Food and Agriculture Organization of the United Nations (FAO)	International	Cross disciplinary (Agriculture)	<u>link</u>
Best Practices	FAO - Cryoconservation of Animal Genetic Resources FAO - Molecular Genetic Characterization of	International	Animals (Agriculture) Animals	<u>link</u>
Best Practices Best Practices	FAO - Genebank Standards for Plant Genetic	International International	(Agriculture) Plants (Agriculture)	<u>link</u>
Network	International Society of Biological and Environmental Repositories (ISBER)	International	Cross disciplinary	<u>link</u>
Best Practices	ISBER Best Practices	International	Cross disciplinary	<u>link</u>
Training	ISBER Webinars	International	Cross disciplinary	<u>link</u>
Network	IUCN SSC Animal Biobanking for Conservation Specialist Group	International	Animals (Wild)	<u>link</u>
Network	IUCN SSC Seed Conservation Specialist Group	International	Plants (Wild)	link
Network	Millennium Seed Bank Partnership (MSBP)	International	Plants (Wild)	<u>link</u>

Category	Name	Region	Discipline	Link
Database	Millennium Seed Bank Data Warehouse	International	Plants (Wild)	<u>link</u>
Best Practices	MSBP Resources	International	Plants (Wild)	<u>link</u>
Network	Smithsonian's National Zoo & Conservation Biology Institute Coral Biobank Alliance	International	Animals (Wild)	<u>link</u>
Training	Coral Cryopreservation Training Course	International	Animals (Wild)	<u>link</u>
Network	United States Department of Agriculture- Agricultural Research Service (USDA-ARS) National Animal Germplasm Program	United States	Animals (Agriculture)	<u>link</u>
Best Practices	USDA-ARS National Animal Germplasm Tools for Decision Support	United States	Animals (Agriculture)	<u>link</u>
Network	United States Department of Agriculture- Agricultural Research Service (USDA-ARS) National Plant Germplasm System	United States	Plants (Agriculture)	<u>link</u>
Training	USDA-ARS GRIN-U Learning Platform	United States	Plants (Agriculture)	<u>link</u>
Additional Biodiv	versity Collections Networks, Standards,	and Resource	es	
Data Standards	Population Genomics Sample Metadata for the BGE Project (Produced by Biodiversity Genomics Europe (BGE) and ERGA (European Reference Genome Atlas)	Europe	Cross disciplinary	<u>link</u>
Data Standards	Darwin Core	International	Cross disciplinary	<u>link</u>
Database	Distributed System of of Scientific Collections (DiSSCo)	Europe	Cross disciplinary	<u>link</u>
Database	Genomic Observatories MetaDatabase (GEOME)	International	Cross disciplinary	<u>link</u>
Network	Global Biodiversity Information Facility (GBIF)	International	Cross disciplinary	<u>link</u>
Database	GBIF Data Portal	International	Cross disciplinary	<u>link</u>
Database	Global Registry of Scientific Collections (GRSciCOLL)	International	Cross disciplinary	<u>link</u>
Network	Global Genome Biodiversity Network (GGBN)	International	Cross disciplinary	<u>link</u>
Database	GGBN Data Portal	International	Cross disciplinary	<u>link</u>
Data Standards	GGBN Data Standard	International	Cross disciplinary	<u>link</u>

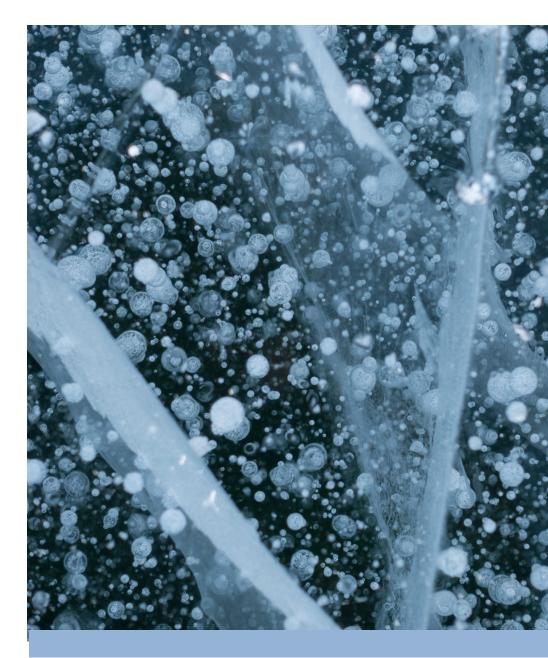
Category	Name	Region	Discipline	Link
Database	National Specimen Information Infrastructure	China	Cross disciplinary	link
Databases	South African National Biodiversity Institute (SANBI) Infobases	South Africa	Cross disciplinary	<u>link</u>
Network	Synthesis+ (Synthesis of Systematic Resources)	Europe	Cross disciplinary	<u>link</u>
Best Practices	Biodiversity Biobanking – a Handbook on Protocols and Practices	International	Cross disciplinary	<u>link</u>
Network	Oz Mammals Genomics Consortium	Australia	Animals (Wild)	<u>link</u>
Database	Natural History Museum Data Portal	International	Cross disciplinary	<u>link</u>
Database	Atlas of Living Australia	Australia	Cross disciplinary	<u>link</u>
Database	Registro Nacional de Colecciones	Colombia	Cross disciplinary	<u>link</u>
Network/Database	Integrated Digitized Biocollecitons (iDigBio)	North America	Cross disciplinary	<u>link</u>
Database	Sistema de Información sobre la Biodiversidad Brasileña [SIBBr]	Brazil	Cross disciplinary	<u>link</u>
Database	NIH - National Cancer Institute Biospecimen Research Database	United States	Human clinical	<u>link</u>
Regulatory Authory biobanking net	orities & Guidance (see also regulatory co. works above)	mpliance guida	nce created	
Policy/Regulatory Guidance	AUTM Material Transfer Agreement Templates and Toolkit	International	Cross disciplinary	link
Policy/Regulatory Guidance	Drafting Biological Material Transfer Agreement: A Ready-To-Sign Model for Biobanks and Biorepositories	International	Human clinical	<u>link</u>
Policy/Regulatory Guidance	European Union Trade Control and Expert System (TRACES)	Europe	Cross disciplinary	<u>link</u>
Policy/Regulatory Guidance	The International Air Transport Association (IATA) Manuals	International	Cross disciplinary	<u>link</u>
Regulatory Authority	Programa de Conservacion de Especies en Riesgo (PROCER)	Mexico	Cross disciplinary	<u>link</u>
Regulatory Authority	United Nations	International	Cross disciplinary	<u>link</u>
Policy/Regulatory Guidance		International	Cross disciplinary	<u>link</u>

Category	Name	Region	Discipline	Link
Policy/Regulatory Guidance	Convention on Biological Diversity (CBD) and the Nagoya Protocol on Access and Benefits Sharing (ABS)	International	Cross disciplinary	<u>link</u>
Policy/Regulatory Guidance	Agreement under the United Nations Convention on the Law of the Sea on the Conservation and Sustainable Use of Marine Biological Diversity of Areas beyond National Jurisdiction (BBNJ)	International	Cross disciplinary	<u>link</u>
Policy/Regulatory Guidance	,	International	Cross disciplinary	<u>link</u>
Policy/Regulatory Guidance	, ,	International	Cross disciplinary	<u>link</u>
Policy/Regulatory Guidance	· · · · · · · · · · · · · · · · · · ·	International	Plants (Agriculture)	<u>link</u>
Policy/Regulatory Guidance	US Centers for Disease Control and Prevention (CDC) Animal Product Guidance	United States	Animals	link
Policy/Regulatory Guidance	United States Department of Agriculture Animal and Plant Health Inspection Service (APHIS) Guidance	United States	Cross disciplinary	<u>link</u>

Supplementary Table 5. Additional resources that include a non-exhaustive list of biobanking networks, biological collections initiatives, and regulatory authorities and their associated guidance documents, templates, and tools.

Organisation	Country	Organism(s)	Link
Australian Wildlife Biobank at Museums Victoria	Australia	Animals (Wild)	<u>link</u>
Brazilian Threatened Fungal Species Collection (Coleção de Fungos Ameaçados do Brasil - CFAB Mind. Funga)	Brazil	Fungi	<u>link</u>
CryoDiversity Bank at the Taronga Institute of Science & Learning	Australia	Animals (Wild)	<u>link</u>
Oswaldo Cruz Foundation	Brazil	Cross disciplinary	<u>link</u>
Smithsonian's National Zoo and Conservation Hiology Institute Center for Species Survival's Genome Resource Bank	United States	Animals (Wild)	<u>link</u>
Royal Botanic Gardens Kew	United Kingdom	Plants (Wild), Fungi	link
San Diego Zoo Wildlife Alliance Frozen Zool® and Wildlife Biodiversity Bank	United States	Animals (Wild), Plants (Wild)	<u>link</u>
South African National Biodiversity Institute (SANBI) Wildlife Biobank	South Africa	Animals (Wild), Plants (Wild)	<u>link</u>
Xishuangbanna Tropical Plant Germpleam Bank	Chine	Plants (Wild)	link

Supplementary Table 6. Examples of long term biobanking institutions specialising in the biobanking of wild species identified by contributing IUCN SSC members as potential collaborators for species in need.





INTERNATIONAL UNION
FOR CONSERVATION OF NATURE

WORLD HEADQUARTERS Rue Mauverney 28 1196 Gland, Switzerland mail@iucn.org Tel +41 22 999 0000 Fax +41 22 999 0002 www.iucn.org