GGBN 2023 CONFERENCE

17-20 OCTOBER, 2023

Universidad Autónoma de Aguascalientes
Aguascalientes, Mexico

#GGBNCONFERENCE2023

Global Genome Biodiversity Network

Welcome Address

We are delighted to announce the fourth international GGBN conference. Taking place in Aguascalientes, Mexico, from October 17th to 20th, 2023 and hosted by the Universidad Autónoma de Aguascalientes, the conference will focus on a wide array of topics, from basic databasing processes to environmental specimens and data analysis (sessions and workshops) and will include a discussion session on where we should head in the immediate future to reach GGBN's goals.

The GGBN 2023 conference expects to gather academic institutions and representatives of the private and public sectors, considering members and non-members of the GGBN community who are interested in preserving and studying our world's biodiversity. It does not matter the size of the attending institutions or collections, the conference will certainly bring new ideas, face-to-face interaction, and foster new collaboration opportunities that will enhance our understanding of life on Earth.

Besides the academic event, we look forward to hosting activities that will let the attendants interact with each other in a more relaxed environment. Those activities include tours around the city of Aguascalientes, which is one of the safest in the country, and will let you experience the culture and gastronomy of the central part of Mexico.

Thank you for your attendance!

On behalf of the Organizing Committee

Ole Seberg (NHM) / Denmark Executive Committee Chair	Katharine Barker (NMNH) / United States Program Manager, Secretariat	Jonas Astrin (LIB/ZFMK)/Germany Executive Committee Vice Chair

GGBN
Global Genome Biodiversity Network

OUR ORGANIZERS

Smithsonian

Natural History Museum

Universidad Autónoma de Aguascalientes

UNIVERSIDAD NACIONAL DE COLOMBIA

SANBI
Biodiversity for Life
South African National Biodiversity Institute

INECOL
El Instituto de Ecología

Botanischer Garten Berlin
Bo

UASLP
Universidad Autónoma de San Luis Potosí

SIGILLVM VNIVERSITATIS HAFNIENSIS

LIB Leibniz Institute for the Analysis of Biodiversity Change

UNIVERSITY OF LAGOS
IN DEED AND IN TRUTH

CONFERENCE COMMITTEE

Conference Organizing Committee

- Gilberto Ocampo, Universidad Autónoma de Aguascalientes
- Ana Lourdes Medrano-Cedillo Universidad Autónoma de Aguascalientes
- Jonas Astrin, Leibniz Institute for the Analysis of Biodiversity Change
- Jackie Mackenzie-Dodds, Natural History Museum London
- Katie Barker, GGBN/Smithsonian Institution, National Museum of Natural History
- Ole Seberg, Natural History Museum of Denmark
- Astrid de Mestier du Bourg, Botanical Garden and Botanical Museum

Local Organizing Committee

- Gilberto Ocampo, Universidad Autónoma de Aguascalientes
- Ana Lourdes Medrano-Cedillo, Universidad Autónoma de Aguascalientes
- Mónica Miguel-Vázquez, Universidad Autónoma de San Luis Potosí
- Patricia Hernández-Ledesma, Instituto de Ecología, A.C.
- Angie González, Universidad Nacional de Colombia

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GENERAL INFORMATION

“UAA Entre Las 200 Universidades Más Reconocidas de Latinoamérica.” UAA

CHECK IN IS FROM 8:00 AM TO 9:00 AM ON TUESDAY, OCTOBER 17 WITHIN THE VENUE LOBBY

SHORT TALKS

Please give your presentation in Powerpoint or pdf format to the technician in the break before the session via usb-stick. Please take care of the prescribed talktime.

POSTER EXHIBITION

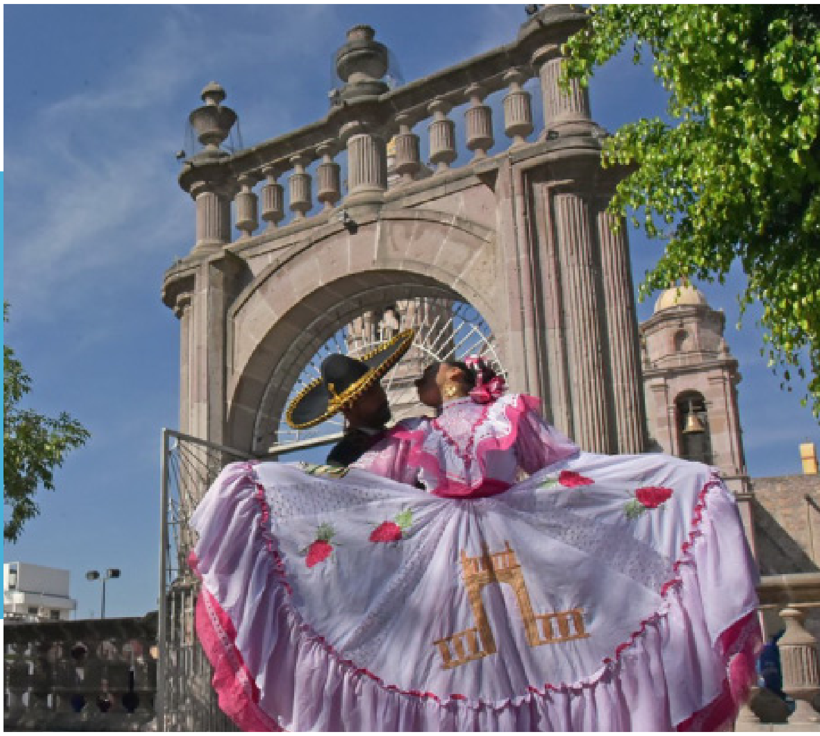
Posters are only accepted in A0 upright format and in English. The poster sessions are during the Coffee and Lunch breaks from October 17th to 19th. Please hang your posters up on October 17th during the morning coffee break from 10:30 to 11:00.

Venue Address

UNIVERSIDAD AUTÓNOMA DE AGUASCALIENTES,
AVENIDA UNIVERSIDAD 940, CIUDAD UNIVERSITARIA
20100 AGUASCALIENTES, AGS., MEXICO

- WiFi is available at the venue. The login data will be announced at the check in desk.
- The language of the meeting is English.
- We reserve the right to use any photograph/video taken at the event without the expressed written permission of those included within the photograph/video.

ADDITIONAL INFORMATION



Ferias y Festividades

RECOMMENDED RESTAURANTS

Near Hilton Hotel:

- Los Mixes
- Casa Fraile
- Miravelas Restaurante y Café

See more here

Near the University:

- Mi Playita, Taco Mar y Tierra
- La Miga y la Barriga Norte

See more here

Near Downtown Aguascalientes:

- La Saturnina
- Ragazzi Bistro

See more here

SERVICES NEARBY

Here, you will find essentials near the university, such as ATMs, exchange centers, pharmacies, convenience stores, and supermarkets.

Tourist Information

NEW TO AGUASCALIENTES? FIND GENERAL TOURIST INFORMATION HERE IN BOTH ENGLISDH AND SPANISH

Transportation

You can take a taxi or rent a car to go to the city (estimated cost to the hotel area, US $25). Also, you can take a ride using one of the following services: Bolt, Didi, and Uber. You can check the services that are available at the airport here.

If you'd rather take public transportation, you will find information about the routes you can use within the city of Aguascalientes here.

Conference Website

All announcements, documents, and information resources related to the GGBN 2023 Conference will be posted on the Conference Website: https://ggbn2023.weebly.com/. Please visit the website for the most current conference information.

Icebreaker

An icebreaker will take place on Monday, October 16, from 6:00 to 8:00 p.m., at the Cantina de Antaño. Complimentary drinks and snacks will be provided from 6:00 to 6:30 p.m. This will be first come, first served.

Activities

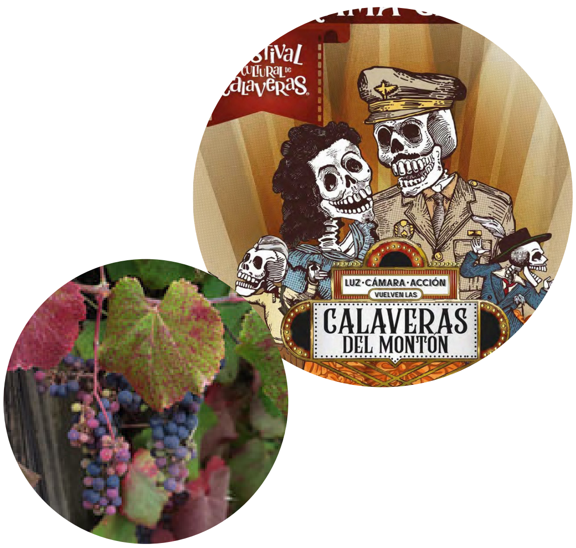
We will include planned activities such as tours around the city of Aguascalientes, which is one of the safest in the country, and will let you experience the culture and gastronomy of the central part of Mexico.

Monday, 16 October will include an icebreaker taking place at Cantina de Antaño

Tuesday, 17 October will include a group dinner. Signup and payment for conference dinner will take place at the check in desk from 7:30 AM to 9:00 AM on Tuesday. The estimated price for dinner is around $35 per person

Wednesday, 18 October will include a group activity and dinner. A bus will be leaving from Universidad of Aguascalientes at 6:00 PM and arriving back at 9:00 PM

Friday, 20 October will allow GGBN Conference participants a chance to see the heritage of Aguascalientes through the Local Culture Tour



Global Genome Biodiversity Network

SESSION DESCRIPTIONS

Tuesday, 17 October 2023

Session IA: Biodiversity Biobank Collections: Infrastructure. *Gilberto Ocampo and Ana Lourdes Medrano, Chairs*
Provides participants the opportunity to share information on their genetic collections, including facilities and infrastructure, interoperability, address issues related to long-term sustainability, address challenges around data and sample quality, present use cases.

Session IB: Biodiversity Biobank Collections: Sample Management. *Gilberto Ocampo and Ana Lourdes Medrano, Chairs*
Session on new insights regarding sample preservatives and preservation, DNA extraction, among others. Abstracts describing the use of classical museum samples in genomic projects (genome skimming, bait capture, draft genomes) are particularly (but not exclusively) encouraged.

Session II: Environmental Samples and Data. *Karen James, Rachel Meyer, Jackie Mackenzie-Dodds, Jonas Astrin, Chairs*
This session is open for abstracts and will look into the increasing importance of environmental samples in biodiversity collections (e.g. eDNA) and will explore links and synergies between Biodiversity Biobanks and Environmental Specimen Banks.

Wednesday, 18 October 2023

Session III: Cell Banking & Culture Collections. *Oliver Ryder, Jonas Astrin and Jackie Mackenzie-Dodds, Co-Chair*
Abstracts for this session may include presentations on protocols and techniques for collection, preservation, authentication and distribution for all types of culture collections and general considerations on ex-situ biodiversity conservation.

Session IV: Biobanking in Megadiverse Countries and the Southern Hemisphere. *Kim Labuschagne, Chair*
Despite several notable exceptions, biobanking activities are still comparatively scarce in the Southern Hemisphere. This stands in contrast to the actual need for biobanking in those regions of the world with particularly rich biodiversity, and to the general notion that all regions of the world should preserve autochthonous biodiversity ex-situ, including samples fit for molecular analysis. This is most relevant in areas currently undergoing strong anthropogenic change. This session will revolve around topics as: Which initiatives already exist and can be strengthened to help establishing biodiversity biobanks in megadiverse countries and the Southern Hemisphere? How is biobanking linked to public health programs and could this influence the effectiveness of building biodiversity biobanks? To what extent are indigenous perspectives being considered in biobanking to date?

Workshop I: Policies for Molecular Collections, GGBN Data Standard, and Workflows for Publishing Data Workshop. *Astrid de Mestier du Bourg, Chair*
Overview of the molecular collections handbook and workflows for publishing data. Participants can ask specific questions regarding publishing data to the GGBN.

SESSION DESCRIPTIONS

Thursday, 19 October 2023

Session V: Nagoya Protocol. *Gilberto Ocampo, Chair*

Biological collections and biobanks must be aware of Access and Benefit Sharing(ABS) to legally manage the biological material. Failure to comply can result in legal consequences. This session will provide, in an interactive way, key information about ABS; practical tools for researchers, collections and biobanks to deal with ABS measures and develop an ABS strategy; an update on the international discussions about Digital Sequence Information (DSI); and plenty of time for questions and discussion.

General Assembly Meeting. *Katie Barker and Jonas Astrin, Co-chairs*

Participants will be updated on the status of GGBN's activities around the current workplan. Results of the 2023 Community Survey and Stakeholder Analysis will be presented.

Workshop II: GGBN and the Future of Biodiversity Biobanking. *Katie Barker and Jonas Astrin, Co-chairs*

Participants will discuss how GGBN is meeting its mission, including identifying areas to improve or scale back certain services to the community. Results of this discussion will inform updates to GGBN's workplan.

GGBN TASK FORCES

Data Standards and Data Access for Genomic Samples

Gabi Droege, Botanic Garden and Botanical Museum Berlin-Dahlem (2011-present), Chair

- Development of a data standard for sharing DNA and tissue information
- Development and subsequent expansion of a global data platform for aggregating relevant data sources of genomic samples, vouchers, molecular analysis, publications, and images

Policies Related to Management and Stewardship of Genomic Samples

Amber Scholz, German Collection of Microorganisms and Cell Cultures GmbH (2020-present), Chair

Supports Member organizations’ work on Access and Benefits Sharing by:

- Raise awareness within the biodiversity biobank and genetic research communities
- Review and fill additional gaps in best practice and ABS resources as needed,
    - With partners (e.g., WFCC, CETAF, SPNHC, SYNTHESYS+)
    - Independently
- Develop additional use cases for management of permit/legal information
- Assess member’s progress on implementation of GGBN permit fields
- Implement Data Harvesting Tools (with Data Standards Task Force)

Biobank Procedures

Jonas Astrin, Zoological Research Museum A. Koenig (2016-present), Chair

- Improve biobank standard operating procedures and sample preservation by:
    - Conducting and publishing results on targeted sample preservation studies
    - Identifying and filling gaps in best practices related to the management of genomic samples

Document Library

Jackie Mackenzie-Dodds, Natural History Museum London, Chair

- Develop and strategically expand the GGBN Document Library for biodiversity biobanking

Communications and Outreach

Andrew Iloh, National Biodiversity Information Consortium, Biodiversity Education and Resource Center and Sheda Science and Technology Complex (2021-present), Chair

- Recruit new members and partners
- Identify strategic partners for increased cross-communication to target groups
    - Biobanks, researchers
- Expand GGBN online collections, fill in gaps with target projects
- Raise awareness of ABS and importance of genomic collections

Global Genome Biodiversity Network

INVITED SPEAKERS

- Adelita Tello San Vicente, SEMARNAT, MX
- Adepemi Ogundeji- Department of Microbiology and Biochemistry, University of the Free State, ZA
- Adrián Sestelo, Gobierno de la Ciudad de Buenos Aires, Buenos Aires, AR
- Adriana Díaz Flores, MX
- Ajith Seresinghe, CALeDNA & UC Santa Cruz, US
- Aleida R. Díaz-Castellanos, Centro de Investigación Científica de Yucatán, MX
- Andie Hall, Natural History Museum, London, UK
- Andrew Bentley, Biodiversity Institute, University of Kansas, US
- Angie Galindo Daniela Gonzelez-Departamento de Biología, Facultad de Ciencias, Universidad Nacional de Colombia, CO
- Astrid de Mestier, Botanical Garden and Botanical Museum, Berlin, DE
- Belen Escobari, Botanischer Garten und Botanisches Museum Berlin, Freie Universität Berlin, DE
- Ben Novak, Biotechnology for Bird Conservation Revive & Restore Sausalito, California, US
- Bernhard Bein, LOEWE Centre for Translational Biodiversity Genomics, DE
- Beth Kaplin, Center of Excellence in Biodiversity and Natural Resource Management, University of Rwanda, ZA
- Blagoy Uzunov, Sofia University "St. Kliment Ohridski", Faculty of Biology, Department of Botany, Sofia, BG
- Brian Dorsey, Ph. D. The Huntington, US
- Chris Armit, GigaScience, US
- Chuck Cook, Global Biodata Coalition, UK
- Cira Martinez, Comparative Genomics Lab, Institut de Biologia Evolutiva - CSIC UPF, Barcelona, ES
- Diego Paucar, Museo de Zoología QCAZ, Pontificia Universidad Católica del Ecuador, Quito, EC
- Eugenio Balch Pérez Molphe, Unidad de Biotecnología Vegetal, Centro de Ciencias Básicas, Universidad Autónoma de Aguascalientes, MX
- Francisco Pelegri, Departments of Genetics and Medical Genetics, University of Wisconsin, Madison, US
- Gilberto Ocampo, Universidad de Aguascalientes, MX
- Guadalupe Yesenia Hernández Márquez, International Indigenous Forum on Biodiversity and Ecosystem Services IIFBES, MX

Global Genome Biodiversity Network

INVITED SPEAKERS

- Gustavo Bravo, Instituto Alexander von Humboldt, Centro de Colecciones y Gestión de Especies, CO
- Ilio Montanari Jr, State University of Campinas, BR
- Ipek Kurtböke, WORLD FEDERATION OF CULTURE COLLECTIONS (WFCC), AU
- Jacqueline Mackenzie-Dodds, Natural History Museum, London, UK
- Jan Koschorreck, The German Environment Agency, Umweltbundesamt-UBA, Berlin, DE
- Janina Bornemann, Nagoya Protocol Compliance Officer, University of Bremen, DE
- John Williams, Department of Geography, University of Wisconsin, Madison, US
- Jonas Astrin, Museum Koenig, Bonn, DE
- Jörg Holetschek, Botanischer Garten Berlin, DE
- Julie Strand, Department of Animal and Veterinary Sciences, Aarhus University, Denmark, DE
- Kakha Nadiradze, Farmers Rights Defense, National Gene Bank Association of Georgia, US
- Karen James, University of Maine, Orono, Maine, US
- Kathryn R. Thomson, San Diego Zoo Wild Life Alliance, US
- Kim Labuschagne, South African National Biodiversity Institute (SANBI) Biobank, Foundational Biodiversity Sciences, ZA
- Kristian Ivanov, Sofia University “St. Kliment Ohridski”, Faculty of Biology, Department of Botany, 8 blvd. Dragan Zankov, Sofia, BG
- Kristian Meissner, Finnish Environment Institute, FI
- Luciana Franco, Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, BR
- Manuela Nagel, Cryo and Stress Biology Group, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Seeland, DE
- Manuela da Silva, Fiocruz, Oswaldo Cruz Foundation, BR
- Maria Jose J. Silva, Laboratório de Ecologia e Evolução (LEEV), Instituto Butantan, São Paulo, BR
- Maya-Stoyneva-Gärtner, Sofia University “St. Kliment Ohridski”, Faculty of Biology, Department of Botany, Sofia, BG
- Melania Muñoz Garcia, Leibniz Institute DSMZ German Collection of Microorganisms and Cell Cultures, DE
- Mudzuli Mavhunga, Biodiversity Biobanks South Africa, South African National Biodiversity Institute, Pretoria, ZA
- Mutegeki Alislam Said Musa, Tooro Botanical Gardens, Uganda, ZA

INVITED SPEAKERS

- Natalia Bravo-Granados, Diversidad Taxonómica y Patrones de Distribución de Microorganismos en la Colección CBUDES: Biobanco de microorganismos del nororiente colombiano, CO
- Nico Franz, Arizona State University, US
- Ole Seberg, Natural History Museum of Denmark, DE
- Paulo Holanda, Bioquallis Consulting, Curitiba, Paraná, BR
- Rachel Meyer, University of California Santa Cruz, California, US
- Raymond Jansen, IUCN SSC Pangolin Specialist Group, c/o Zoological Society of London, London, UK
- Rebecca Pugh, National Institute of Standards and Technology, Chemical Sciences Division, Charleston, SC, US
- Riana Jacobs-Venter, National Collection of Fungi, ZA
- Rodrigo Taketani, Rothamsted Research, West Common, Harpenden, Hertfordshire, UK
- Ross Stewart, African Centre for DNA Barcoding (ACDB), Department of Botany and Plant Biotechnology, University of Johannesburg, ZA
- Thabo Tjikana, Directorate Genetic Recourses, Department of Agriculture Land Reform and Rural, Pretoria, ZA
- Tomàs Marquès, Comparative Genomics Lab, Institut de Biologia Evolutiva - CSIC UPF, Barcelona, ES
- Tullis Matson, Nature’s SAFE, Chapel Field Stud, Whitchurch, UK

Day 1 - 17 October 2023

08:00 - 09:00	**Arrival, check in**
09:05 - 09:35	**Urgency and Ethics: A Dilemma for Biobanking and Biodiversity Discovery - ***Oliver Ryder, San Diego Zoo Wildlife Alliance IUCN-SSC Animal Biobanking for Conservation Specialist Group*

Session IA - Biodiversity Biobank Collections: Infrastructure

Chairs - Gilberto Ocampo and Ana Lourdes Medrano

09:35 - 09:45	**The Vertebrate Genetic Resources Facility at the University of Kansas Biodiversity Institute** - *Andy Bentley, University of Kansas*
09:45 - 09:55	**Biological Collection of Tissues/DNA Host-Parasite Relationship: Infrastructure, Researcher Training and Visibility Strategies** - *Angie Gozález, Universidad Nacional de Colombia, Sede Bogota.*
09:55 - 10:05	**Biodiversity Biobanking at the Natural History Museum London – a Big New Facility at Thames Valley Science Park, Reading, UK. -** *Jackie Mackenzie-Dodds, National Museum of Natural History, London*
10:05 - 10:15	**Living Collections of the GermoLab Botanical Garden (CICY) -** *Aleida R. Díaz Castellanos, Centro de Investigación Científica de Yucatán*
10:15 - 10:30	**MORNING COFFEE BREAK**
10:30 - 10:40	**Managing Plant Repositories in Uganda amidst Limited Resources* -** *Mutegeki Alislam Said Musa, Tooro Botanical Gardens*
10:40 - 10:50	**UFS Yeast culture collection: Meeting the needs of researchers -** *Adepemi Ogundeji, University of the Free State, South Africa*
10:50 - 11:00	**The New Fiocruz Biodiversity and Health Biobank** - *Manuela da Silva, Fiocruz, Oswaldo Cruz Foundation*
11:00 - 11:10	**Conservation and sustainable use of plant genetic resources for food and agriculture: The South African Approach** - *Thabo Tjikana, Department of Agriculture Land Reform and Rural Development*
11:10 - 11:20	**Leibniz Institute DSMZ - German Collection of Microorganisms and Cell Cultures** - *Melania Muñoz García, Leibniz Institute*

(*) Zoom or pre-recorded

11:20 - 11:30	**Keeping it chilled: A South African catalogue of Wildlife Biodiversity -** *Kim Labuschagne, National Zoological Gardens of South Africa*
11:30 - 11:40	**LIB Biobank at Museum Koenig, Bonn, Germany -** *Jonas Astrin, Leibniz Institute for the Analysis of Biodiversity Change*
11:40 - 13:30	**LUNCH BREAK**

Session IB - Biodiversity Biobank Collections: Sample Management

Chairs - Gilberto Ocampo and Ana Lourdes Medrano

13:30- 13:40	**Rio de Janeiro Botanical Garden Tissue and DNA Collections' Management using the JABOT system*** - *Luciana Franco*
13:40 - 13:50	**Establishment and conservation of an in vitro Germplasm Bank of plant species from the arid zones of México** - *Eugenio Perez Molphe Balch, Universidad Autónoma de Aguascalientes*
13:50 - 14:00	**Unlocking collection treasures: Accessing museum samples for long read sequencing and genomic analysis** - *Bernhard Bein*
14:00 - 14:10	**Sample management in the DNA Bank of the Universidad Autónoma de Aguascalientes, Mexico** - *Gilberto Ocampo, Universidad de Aguascalientes*
14:10 - 14:20	**Establishing a Biobank at The Huntington -** *Brian Dorsey, The Huntington Botanical Gardens*
14:20 - 14:30	**Agrobiodiversity Index, Challenges, Opportunities and Trends -** *Kakha Nadiradze, Farmers Rights Defense, National Gene Bank Association of Georgia*
14:30 - 14:40	**Biomaterials Biobanking and BOLD Barcoding Benefits -** *Kim Labuschagne, National Zoological Gardens of South Africa*
14:40- 14:50	**Skimming at scale: bringing historic collections into the genomic era** - *Andie Hall, Natural History Museum, London*
14:50 - 15:00	**Collection of Medicinal and Aromatic Plants of the State University of Campinas** - *Ilio Montanari Jr., State University of Campinas*
15:00 - 15:20	**AFTERNOON COFFEE BREAK**

(*) Zoom or pre-recorded

Session II - Environmental Samples and Data

Chairs: Karen James, Rachel Meyer, Jackie Mackenzie-Dodds, Jonas Astrin

15:20 - 15:30	**Connecting environmental samples to a biodiversity information system to make data accessible*** - *Beth Kaplin, Center of Excellence in Biodiversity and Natural Resource Management, University of Rwanda*
15:30 - 15:40	**Towards inclusivity in molecular method standardization for biodiversity assessment***- *Kristian Meissner, Finnish Environment Institute, Syke*
15:40 - 15:50	**National Institute of Standards and Technology (NIST) Biorepository** - *Rebecca Pugh, National Institute of Standards and Technology, Chemical Sciences Division*
15:50 - 16:00	**Environmental specimen banks in research and regulation for a better environmental quality*** - *Jan Koschorreck, The German Environment Agency*
16:00 - 16:10	**Diversidad Taxonómica y Patrones de Distribución de Microorganismos en la Colección CBUDES: Biobanco de microorganismos del nororiente colombiano** - *Natalia Bravo-Granados, Diversidad Taxonómica y Patrones de Distribución de Microorganismos en la Colección CBUDES*
16:10 - 16:20	**Maine-eDNA: a case study for large-scale environmental sampling, metadata collection and data management in one of the world's fastest-warming ocean regions** - *Karen James, University of Maine*
16:20 - 16:30	**Summary of our experience in application of remote techniques for environmental sample collection** - *Blagoy Uzunov, Sofia University "St. Kliment Ohridski," Faculty of Biology, Department of Botany*
16:30 - 16:40	**CALeDNA: Environmental collections to enable landscape biodiversity surveys and models of community change -** *Rachel Meyer, University of California CALeDNA Program*
16:40 - 16:50	**Strengthening global-change science by integrating aeDNA with paleoecoinformatics* -** *John Williams, University of Wisconsin Madison*
16:50 - 17:00	**Diatoms, a model group for DNA Barcoding** - *Belen Escobari, Botanischer Garten und Botanisches Museum Berlin, Freie Universität Berlin*

(*) Zoom or pre-recorded

Day 2 - 18 October 2023

Session III: Cell Banking and Culture Collections

Chairs: Oliver Ryder, Jonas Astrin and Jackie Mackenzie-Dodds

09:00 - 09:13	**The UK Crop Microbiome Cryobank – Advancing Microbiome Research for Sustainable Agriculture*** - *Rodrigo Taketani, Rothamsted Research*
09:13 - 09:26	**Strategy for the Biobanking of Potato Genetic Resources at the IPK Genebank* -** *Manuela Nagel, Leibniz-Institut (IPK)*
09:26 - 09:39	**South African National Collection of Fungi: An established resource on the continent*** - *Riana Jacobs-Venter, National Collection of Fungi*
09:39 - 09:52	**The World Federation of Culture Collections and the Global Genome Biodiversity Network: Sharing the Same Mission for Sustainable Futures* -** *Ipek Kurtböke*, World Federation of Culture Collections*
09:52 - 10:05	**Establishing model lineage systems to study inter-species advanced reproductive approaches -** *Francisco Pelegri, University of Wisconsin, Madison*
10:05 - 10:18	**Important Considerations for Biobanking for Genetic Rescue of Endangered Species** - *Ben Novak, Revive and Restore*
10:18 - 10:33	**MORNING COFFEE BREAK**
10:33 - 10:46	**Introducing Nature's SAFE: a European Biobank for Conservation**- *Tullis Matson, Nature's Safe*
10:46 - 10:59	**Reproductive biotechnologies and Genetic Resource Banks Applied to Wildlife Conservation in Argentina* -** *Adrián Sestelo, Gerencia Operativa de Conservación y Gestión de Fauna*
10:59 - 11:12	**Projects at LIB Biobank Enabling Cell Banking and Protocol Collection -** *Jonas Astrin, Leibniz Institute for the Analysis of Biodiversity Change*
11:12 - 11:25	**PCRYOZOO Biobank of Animal Cell Lines* -** *Tomàs Marquès and Cira Martínez, Institut de Biologia Evolutiva*
11:25 - 11:38	**Organoids for Biobanking and Cellular Agriculture -** *Julie Strand, Aarhus University*
11:38 - 11:51	**Living algal collection of Sofia University "St. Kliment Ohridski" (ACUS)- Important Ex-Situ Biodiversity Conservation Facility, which Maintains High-quality Algal Strains-**
	Need for Biobanking of Algae in Bulgaria – a Country on the Balkan Peninsula with Extra Rich Biodiversity- *Maya Stoyneva and Kristian Ivanov, Sofia University "St. Kliment Ohridski"*
11:51 - 12:04	**Biobank of Megadiverse Fauna of Brazil -** *Maria José de Jesus Silva, Laboratório de Ecologia e Evolução*
12:04 - 13:30	**LUNCH BREAK**

(*) Zoom or pre-recorded

Session IV: Biobanking in megadiverse countries and the Southern Hemisphere

Chairs: Kim Labuschagne

13:30 - 13:45	**Pangolins: Cultural Use, Illegal Trade and the Scientific Importance of Biobanking Specimens in South Africa* -** *Ray Jansen, Zoological Society of London*
13:45 - 14:00	**Biobanking in a Megadiverse Country: a Brief review of Brazilian Current Initiatives* -** *Paulo Holanda, Bioquallis Consulting, Curitiba, Paraná*
14:00 - 14:15	**Biodiversity Biobanks South Africa: A Distributed Network of Repositories for South Africa's Rich Biodiversity -** *Mudzuli Mavhunga, Biodiversity Biobanks South Africa*
14:15 - 14:30	**The importance of the Humboldt Institute Tissue Collection for Biodiversity Research and Conservation in a Megadiverse Country -** *Gustavo Bravo, Instituto Alexander von Humboldt*
14:30 - 14:45	**Infrastructure and Management of a Large-scale Genome Bank in a Megadiverse Developing Country. A Case Study in Ecuador -** *Diego Paucar, Museo de Zoología*
14:45 - 15:00	**Using Biodiversity Biobanking to Enhance Plant Conservation in the Megadiverse Country South Africa* -** *Ross Stewart, African Centre for DNA Barcoding*
15:00 - 15:30	**AFTERNOON COFFEE BREAK**

Workshop I: Policies for Molecular Collections, GGBN data standard, and workflows for publishing data

Chair: Astrid de Mestier

15:30 - 15:45	**Management of Genetic Resources in Natural History Collections using Specify Collection Management Software -** *Andrew Bentley, University of Kansas*
15:45 - 16:00	**Symbiota-based Services for Publishing Genomic Collections Data* -** *Nico Franz, Arizona State University*
16:00 - 16:15	**Molecular Collections Handbook -** *Astrid de Mestier, Botanical Garden and Botanical Museum*
16:15 - 16:30	**GGBN Data Standard, and Workflows for Publishing data* -** *Jörg Holetschek, Botanischer Garten Berlin*

(*) Zoom or pre-recorded

Day 3 - 19 October 2023

Session V- The Nagoya Protocol in Practice: Does it Affect My Field Work and Associated Research?

Chair: Gilberto Ocampo

09:00 - 09:15	**Welcome / Interactive introduction to the Nagoya Protocol** - *Gilberto Ocampo and Melania Muñoz García, Universidad Autónoma de Aguascalientes and Leibniz Institute DSMZ*
09:15 - 09:30	**Why is the Nagoya Protocol important for GGBN Collections and Biobanks?** - *Manuela da Silva, Fiocruz, Oswaldo Cruz Foundation*
09:30 - 09:45	**The Nagoya Protocol in Mexico** - *Adelita San Vicente Tello, SEMARNAT*
09:45- 10:00	**The Nagoya Protocol and the EU ABS Regulation from a Users' Perspective* -** *Janina Bornemann, University of Bremen*
10:00 - 10:15	**International Indigenous Forum on Biodiversity and Ecosystem Services IIFBES & Universidad Iberoamericana -** *Guadalupe Yesenia Hernández Márquez & Adriana Flores Díaz, International Indigenous Forum on Biodiversity and Ecosystem Services IIFBES*
10:15 - 10:45	**MORNING COFFEE BREAK**
10:45 - 11:00	**The Nagoya Protocol: Where to start? Bild your ABS Strategy -** *Melania Muñoz García, Leibniz Institute DSMZ*
11:00 - 11:15	**Digital Sequence Information and Open Biodata Resources -** *Chuck Cook, Global Biodata Coalition*
11:15 - 11:25	**Q&A** **Chair - Gilberto Ocampo**
11:25 - 11:30	**Closing Remarks - Manuela da Silva**
11:30 - 12:00	**Conference Group Picture**
12:00 - 13:30	**LUNCH BREAK**
13:30 - 15:00	**General Assembly Meeting and Conference Close**
15:00 - 16:00	**Workshop II: GGBN and the Future of Biodiversity Biobanking**
16:00 - 17:00	**Executive Committee Meeting**

Posters

A Role for GigaScience Press in Tackling the Biodiversity Data Gap

Chris Armit, Gigascience

The GGBN Document Library – a Knowledge Base for Genomic Biodiversity Biobanking

Jackie Mackenzie-Dodds, Natural history Museum, London, UK

The Frozen Zoo® A Living Collection 50 Years in the Making

Kathryn R. Thomson, San Diego Zoo Wild Life Alliance

GGBN
Global Genome Biodiversity Network

CONFERENCE AGENDA

TIME BLOCK	DATES				
	MONDAY 16-Oct	TUESDAY 17-Oct	WEDNESDAY 18-Oct	THURSDAY 19-Oct	FRIDAY 20-Oct
9:00 - 12:00		Welcome/Official Opening Biodiversity Biobank Collections: Infrastructure/Sample Management	Cell Banking and Culture Collections	The Nagoya Protocol in practice: Does it affect my field work and associated research?	Local Culture Tour. Downtown Aguascalientes (self-guided) or town of Tequila (Jalisco)
		Coffee break (15 mins)	Coffee break (15 mins)	Coffee break (15 mins)	
13:30 - 17:00		Lunch/Posters/Task Forces	Lunch/Posters/Task Forces	Lunch/Posters/Task Forces	
		(11:40-13:30)	(12:15-13:30)	(12:00-13:30)	
		Biodiversity Biobank Collections: Sample Management	Biobanking in Megadiverse Countries and the Southern Hemisphere	General assembly meeting/Conference close Workshop II: GGBN and the Future of Biodiversity Biobanking Workshop	
		Coffee break (20 mins)	Coffee break (30 mins)		
		Environmental Samples and Data	Workshop I: Policies for Molecular Collections, GGBN Data Standard, and Workflows for Publishing Data	Executive Committee	
		End of day	End of day	End of day	
18:00 - 20:00	Welcome reception	Welcome dinner	Group outing	Group outing	

Abstract Book

Keynote

Urgency and Ethics: A Dilemma for Biobanking and Biodiversity Discovery

Oliver A. Ryder

San Diego Zoo Wildlife Alliance and IUCN-SSC Animal Biobanking for Conservation Specialist Group

With increasing urgency, efforts to identify biological specimens for characterizing biodiversity are underway, as a response to accelerated species population declines and increased rates of biological extinctions. These biomaterials represent the extant evolutionary heritage of all species on our planet and one of the greatest sources of information about life itself. The value of biobanking, and in particular living cell cultures is becoming recognized as an additional strategy for biodiversity discovery and species conservation, notably through genetic rescue. Yet, the number of species that have cryobanked cell cultures and/or gametes that comprise a sufficient sample of their genetic variation is miniscule, though nonetheless impactful.

Efforts for characterizing biodiversity are significantly enhanced with the remarkable advances in the field of comparative genomics that is addressing challenges in DNA extraction, sequencing library construction, generating whole genome sequencing data, assembling and aligning genomes, and providing equitable and open access to the vast amounts of data being produced. The rapid decrease in cost of accurate sequencing of long DNA molecules has been an encouragement to the large-scale comparative genomics projects such as Genome10K, the VGP (Vertebrate Genome Project) and the EBP (Earth Biogenome Project). As these and other projects move forward, the accumulation of biomaterials for biodiversity discovery overlaps with efforts to conserve biodiversity through biobanking.

The ambitions and actions of the sample data repositories and sequencing consortia such as GGBN (Global Genome Biodiversity Network) and the EBP are accountable to international treaties and national legislation for developing benefit sharing mechanisms, and embedding principles of inclusion, equity, diversity and justice and equitable engagement with local communities and Indigenous Peoples. Many valuable biomaterials have been collected without regard to emerging best practices. The urgency of moving forward with biobanking and biodiversity discovery through genome sequencing coexists with the urgency to utilize fair and equitable practices for access, recognition, authority, and collective benefit. These are challenges and opportunities we collectively face today. How human society addresses them are sure to shape the options for conserving a biodiverse planet Earth and the well-being of its inhabitants.

Session IA: Biodiversity Biobank Collections: Infrastructure

Chairs - Gilberto Ocampo Acosta and Ana Lourdes Medrano

The vertebrate Genetic Resources Facility at the University of Kansas Biodiversity Institute

Andrew Bentley

Biodiversity Institute, University of Kansas

The KUBI Genetic Resources Facility (GRF) is one of several key shared research facilities within KU's Biodiversity Institute. This facility houses 3 liquid nitrogen dewars for long term storage of all KUBI vertebrate tissue materials (Herpetology, Ichthyology, Mammalogy, and Ornithology). Collection managers for each division are responsible for the management and use of the genetic resources associated with their individual collections although funding is being sought for a centralized GRF manager. Collections data is managed through individual Specify databases and are searchable online. The facility currently houses almost 90,000 tubes of tissue and extracts across the four divisions encompassing more than 10,000 species from over 135 countries. The collections processes hundreds of national and international loans a year for phylogenetic and genetic research. The collections are growing rapidly through internal research expeditions as well as vouchering and gifts from other institutions and individuals. Each dewar has a capacity of approximately 90,000 individual samples stored in 2ml cryo tubes, within 81 tube cryo boxes in 15 box racks. These racks are maintained on a rotating circular platform above the liquid nitrogen in vapor phase. The dewars are supplied by 240-liter tanks through an automated monitoring system. The tanks are switched out by facility staff on a regular schedule based on LN2 use. The facility also contains multiple -80°C chest freezers used for processing and temporary housing of field samples and loan processing, along with a workstation and computer resources for processing of samples within the facility. All resources in the facility are monitored by an automated alarm system, while the air quality is monitored by an oxygen sensor for safety. Access to the facility is strictly controlled through card swipe access for security and safety. Safety training is carried out each year for all users of the facility in conjunction with the Environmental Health and Safety (EHS) office on campus. This talk will highlight the management and use of the facility and lessons learnt along the way.

Biological collection of tissues/DNA host-parasite relationship: infrastructure, researcher training and visibility strategies

Angie D. Gonzalez & [a], Nubia E. Matta[a]

[a]*Departamento de Biología, Facultad de Ciencias, Universidad Nacional de Colombia, Sede Bogota.*

Colombia has a great diversity of ecosystems, vertebrate and blood parasites that infect them. Biological collections of microorganisms are necessary for the taxonomic and evolutionary study of haemoparasites taxa of importance in wildlife, for epidemiological surveillance of potentially zoonotic parasites. The Host-Parasite Relationship Study Group collection has been studying the blood parasites from this country for 24 years, mainly through morphological analyses. Since 2010, we implemented molecular diagnosis and started a sub-collection for tissues and blood in preserving liquid. Currently, there are about 4,700 blood, tissue, or DNA samples extracted from mammals, birds, reptiles, and amphibians. From these samples it is possible to obtain DNA from the vertebrate and from Haemosporida, Adeleorina, Trypanosoma, and Nematoda parasites. Samples are safeguarded in cryoboxes in freezers from -80°C to -20°C. There is also an attached laboratory with the necessary equipment and reagents to develop nucleic acid extraction and PCR amplification. Vaucher information and molecular biology processes associated with samples are stored in a database with a cloud copy. The collection is mainly nourished by research projects and provide material for research and undergraduate and postgraduate thesis. Also, we develop courses and internships in order to train students and researchers about sampling and identification of hemoparasites in wildlife. Our findings are divulgated in scientific articles, photographic catalogs of the hosts, parasite species sheets, subcollections in SiB, GBIF, GGBN, and genetic information in BOLD, MALAVI and Genbank. Finally, to reach social appropriation of knowledge, the findings are published on the social networks of the Department of Biology of the National University of Colombia.

Biodiversity Biobanking at the Natural History Museum London – a Big New Facility at Thames Valley Science Park, Reading, UK.

Jackie Mackenzie-Dodds

Natural History Museum, London, UK

NHM's new 'Collections Archive and Digitisation & Research Centre' at Thames Valley Science Park, Reading, UK, opening later this decade, includes a large biodiversity biobank with increased capacity to receive, store and deliver genome quality material rapidly and at scale, to the global research community. Current molecular collections will be 'unlocked', digitised, and made accessible (FAIR data, CBD/NP compliant) via the NHM Data Portal, with new 'born digital' acquisitions expanding the resource from ~1.5M to >10M samples, including resources for 'omics, a comprehensive UK species reference collection from the Darwin Tree of Life, Bioscan and Biogenomics Europe projects expanding to all global eukaryotic species in the Earth Biogenome Project. The biobank will serve as an access point for sampling the museum's historic collections, and a hub for citizen science collections, addressing questions on biodiversity challenges across the planet and changes over longer temporal periods.

The biobank will be cross cutting and interdisciplinary across NHM Science, other research institutes, and biomedical partners worldwide, future proofing collaborations with new post-genomic 'living' viable resources (e.g., parasite cultures and animal cell lines in LN2) as well as traditional genetic material. The new business model will commit housing of research collections in the biobank post project, enabling access and re-use, extending to industry stakeholder applications e.g., environmental monitoring and impact assessments. Partnerships with other global data centres will ensure data is available via multiple interoperable data portals including GenBank, NBN, GBIF, OBIS and GGBN, accessed by researchers in academia, as well as government, industry, educators, and the public.

The biobank aims for ISO20387 accreditation aligning with clinical biobanks for better comparative biodiversity studies and will provide expertise and training in best practice molecular sample collection, curation, and preservation of taxa across the tree of life and habitats (animals, plants, fungi, soil, water, and air). New specimens will be correctly identified and validated by NHM's world class taxonomists, reconciling increasing numbers of difficult and new-to-science species using the NHM's historical collections, thereby improving the robustness of datasets shared with the global taxonomic community.

The biobank facility will be central to the NHM's wider molecular pipeline with automated sample and data workflows integrated with adjacent research, biomedical, microbiology laboratories and ancient DNA facility. It will provide molecular loans plus short and long-term sample storage services for internal and external users as part of an integrated package of standardised and cost efficient in-house modular molecular pipeline processes offering a full range of options from field to data (including reference genome provision), data analysis and informatics.

The biobank will be a state-of-the-art modern suite of secure restricted (archival) and regular (working collections) storage access for users, employing a mixed economy of storage formats: 4°C, -20°C, automated ultracold (-80°C) and cryo- (-196°C LN2) freezers, plus ambient storage at room temperature (humidity controlled cabinets, FTA and silica gel systems), prioritising cost benefit analysis recommendations to phase towards a majority of cryo- plus ambient storage in line with a net-zero strategy, with regularly reviewed rolling replacement plans optimising energy efficiency.

Living Collections of the GermoLab Botanical Garden (CICY)

Aleida R. Díaz Castellanos, Sigfredo Escalante Rebolledo, Ramón Souza Perera and Ricardo Alvarez Espino

Centro de Investigación Científica de Yucatán

The regional laboratory for the study and conservation of germplasm GERMOLAB, has the mission to study, conserve and maintain available plant germplasm of species from the Mesoamerican region with emphasis on those related to the Mayan culture. To do so, we carry out research schemes focused on identifying the appropriate protocols for the conservation of germplasm for each species studied. There is currently an orthodox seed bank where species with different uses, categories of protection and endemism are conserved; various field collections, a botanical garden and nurseries have also been established that allow for the reproduction of both orthodox and recalcitrant seed species. The latter are particularly abundant in the wetter areas of the Yucatan Peninsula and their long-term ex situ conservation requires in-depth research, infrastructure and protocols different from those of a conventional seed bank. In this context, interest arose in establishing other forms of long-term germplasm conservation, so we participated in the call for BGCI-GGI awards for botanic gardens, obtaining partial funding to develop a plant tissue conservation project. This initiative seeks to conserve DNA samples from plant families and genera that are under-represented or unrepresented in GGBN's biorepositories. For this reason, we sought the support of the DNA Bank of the Autonomous University of Aguascalientes (ADNUAA), the only biorepository associated with GGBN in Mexico, to start a collaboration that would allow us to collect species present in the botanical garden of GERMOLAB, and to conserve these samples in the long term in the ADNUAA. The aim is to conserve leaf tissue samples for future research, from a set of rare, endemic and threatened species of the Yucatan Peninsula. More than fifty target species were selected. So far, we have collected and sent to ADNUAA leaf tissue samples of 31 species, and we are adapting collection protocols for some species in particular. Back-up herbaria will be uploaded to the CICY Herbarium in Yucatan. This project will strengthen inter-institutional collaboration for research and conservation of genetic resources.

Managing Plant Repositories in Uganda amidst Limited Resources.

Mutegeki Alislam Said Musa

Tooro Botanical Gardens, Uganda, Africa

Although Uganda is one of the most biodiverse countries in Africa and rich in genetic diversity, plant genomic research is still underdeveloped due to several limitations. Most repositories focus on health care, agriculture; horticulture, veterinary, forensic, environment, aquatic sciences, wildlife and education which are majorly housed and coordinated by some Universities and government institutions.

There are very limited efforts for plant repository development towards preservation, research, studying of the native plant diversity for conservation and restoration; The Uganda National Council for Science and Technology developed Biobanking Guidelines that provide a framework for establishing, certification and operation of the biobanks in health care, agriculture; horticulture, veterinary, forensic, environment, aquatic sciences, wildlife and education. However, there is still limited advocacy and adoption by the general conservation practitioners and institutions!

This has serious implications for Uganda's long-term plant repository development. There is limited capacity in non-government biorepositories and financing is particularly restricted.

The existing plant repositories concentrate on plants for food, agricultural development and there are less efforts to adopt to native plant diversity that is highly threatened in the wild and cultivation hence increasing threat issues to their conservation. This poses a great danger on the future of plant genomic research and conservation.

The Tooro Botanical Gardens, plant repository houses thousands of native plant seeds, voucher specimens and DNA tissue samples with increased accessions annually promoting native plant conservation amidst several limitations; During the BGCI/GGI-Awards program 2020, Tooro Botanical Gardens promoted initiatives that enhance collection and preservation of threatened and non-threatened tree species and contributed to data to the GGBN network;

This project impacted tremendously biodiversity conservation, increased the gardens specimen accessions with additional 34 genera of 36 species of 22 families, 6 species were globally threatened while 9 species were nationally threatened and 21 species high value species in nationally. A total of 264 voucher Specimens and 264 DNA tissue samples collected making up a total of 528 samples that were shared to the GGBN network and to date under tree conservation and forest restoration in Uganda program with my conservation and research team we continue collecting threatened and non-threatened rare and social-ecomically important tree species specimens for the TBG repository.

It is with this background I submit my abstract to attend the GGBN international Conference to share our experiences, learning from diversity of experts, open more grounds, capacity and opportunities of preserving global biodiversity, increasing individual and institutional capacity in collections', data basing, Analysis and connecting with a wide GGBN community.

There is an urgent need to better coordinate plant genomic repository efforts, increase standard best practices and adoption amidst limited resources. The need to strengthen the gene bank infrastructure, enabling the use of modern biotechnological tools and equipment's, advanced ex situ conservation methods, identifying gaps in collections, developing core collections, and linking data with international databases a transitional output I envisage at the international conference.

UFS Yeast culture collection: Meeting the needs of researchers

AO Ogundeji & CH Pohl

University of the Free State, South Africa

The starting point for the development of microbiological technologies most certainly is extensive culture collections. A huge responsibility lies on each and every one working with microbes to isolate, identify, preserve and exploit the advantages of microbes, and also grant access to researchers and industries. Hence, the establishment of the Yeast culture collection, located at the University of the Free State, Bloemfontein South Africa. The Yeast Culture Collections and its associated services underpin the initiative of Biodiversity Biobank South African (BBSA) on increasing the range and quality of biodiversity samples stored, and increasing and improving access for research and development, through a single, centralised data portal, which will also allow more strategic collection of samples, thus becoming a national asset for researchers and industries.

The Yeast culture collection was set-up in 1980's by Prof. Johannes van der Walt, and is the largest yeast collection in Africa with more than 3000 strains in its depository. The yeast culture collection has been mostly used for research regarding taxonomy, discovery of new compounds produced by yeasts, bioconversion, biofuels and heterologous proteins expression systems. However, a new vision has been provided through the BBSA initiatives, which is to serve the academic, industrial and government agency research community through provision of high-quality yeast cultures, characterization information, and expertise, for use in educational, research and industrial applications.

Currently, the BBSA Yeast culture collection is working towards meeting the requirements of BBSA, such as by aligning with national and international standards and procedures such as quality control, permits acquisition, standard SOP, data management, etc. This strategy is being implemented to ensure that the Yeast Culture Collection services provided are professional and according to global standard.

The New Fiocruz Biodiversity and Health Biobank

Manuela da Silva, Carlos Roberto Sobrinho do Nascimento, Paulo de Carvalho Villas Bôas & Gustavo Stefanoff.

Fiocruz, Oswaldo Cruz Foundation

In the context of Covid-19 pandemic, Oswaldo Cruz Foundation (Fiocruz), with the support of the Brazilian Health Ministry, built a biobank that initiated its activities with the virus Sars-CoV-2 and human biological material related to Covid-19. This initiative aims to provide an adequate infrastructure for the safe, reliable, ethical, legal and traceable storage of approximately 1,5 million biological materials and associated data, in accordance with the regulations in force, and following strict quality, biosafety and biosecurity requirements defined in the ISO 20387:2018 standard. Considering that this infrastructure is a legacy for research, development, and innovation in health care, its scope is being expanded to other types of biological materials, which resulted in its new name. From Fiocruz Covid-19 Biobank it changed to Biodiversity and Health Biobank (Fiocruz-BBS from the name in Portuguese: Biobanco da Biodiversidade e Saúde da Fiocruz). The services offered by Fiocruz-BBS are performed by a highly qualified technical team and provided for public and private institutions, including deposit, isolation, identification, preservation, and supply of biological materials. In order to assure a long-term sustainability, the following guidelines are being stablished: a) Development of a Comprehensive Business Plan; b) Diversification of Funding Sources; c) Ensuring Ethical and Legal Compliance; d) Implementation of strict quality control procedures; e) Investment in Infrastructure; f) Establishment of partnerships; and g) Benchmarking and Best International Practices.

Conservation and sustainable use of plant genetic resources for food and agriculture: The South African Approach

Thabo T. Tjikana

Directorate Genetic Recourses, Department of Agriculture Land Reform and Rural Development

The conservation and sustainable use of plant genetic resources for food and agriculture (PGRFA) are vital for ensuring global food security, preserving biodiversity, health, employment opportunities and building resilient agricultural systems in the face of challenges like climate change and population growth. This document seeks to present the approach adopted by the Department of Agriculture Land Reform and Rural Development of the South African Government to manage national PGRFA. The South African Plant Genetic Resources Centre (NPGRC) coordinates national conservation and sustainable use of PGRFA activities related to *in situ* and *ex situ* conservation, which include collection of seeds, multiplication, characterization, documentation and gene bank management. The NPGRC (aka national gene bank) further ensures the availability of landrace seeds or plant genetic resources through its programmes that are designed to work with formal and informal institutions.

The collection of plant genetic resources is from local farmers, following scientifically accepted methods incorporated with cultural practices and traditional knowledge to ensure a holistic conservation approach. The collection of PGRs are managed in the NPGRC using adopted techniques of biotechnology for improved management of orthodox seeds, recalcitrant seeds and vegetatively propagated species. These PGRs are either managed and/or conserved in the field, shade house, freezers, and in tissue culture laboratory, depending on the storage requirements or type of the species. The collected PGRs conserved *ex situ* in the NPGRC are currently at 6357 accessions.

The *ex-situ* conservation activities involves processing of the PGR, morphological characterization, multiplication and documentation of accessions. As part of supplementing the *ex-situ* conservation of PGRFA activities, the NPGRC had established *in situ* conservation activities that includes the *on farm* conservation and multiplication of PGRFA projects in both Northern Cape and Free State Provinces, as well as the community seed banks in three provinces (Limpopo, Eastern Cape and North West Provinces). Both the *on farm* and the community seed banks are being managed by the participating farmers. The NPGRC has further expanded the *in-situ* conservation of PGRFA activities by introducing the repatriation of PGRFA to the Kwa Zulu Natal farmers affected by the 2022 floods.

Germplasm of the NPGRC can be accessed through a signed Material Transfer Agreement for research purposes and freely to restore and repatriate crops or species lost during natural disasters and lose through crop production improvement programmes.

Leibniz Institute DSMZ - German Collection of Microorganisms and Cell Cultures.

Melania Muñoz García; Amber H. Scholz; Jörg Overmann

Leibniz Institute DSMZ German Collection of Microorganisms and Cell Cultures, Germany

The Leibniz-Institute DSMZ is the German competence center for the research, provision and application of microbial diversity. DSMZ hosts more than 35,000 bacterial cultures, 8,000 fungi and a total of more than 84,000 bioresources, making the DSMZ one of the world's leading microbiological resource centers. The technical equipment includes PacBio Sequel IIe single-molecule real-time (SMRT) sequencing, Oxford Nanopore GridION Mk1, Illumina NextSeq 2000 and MiSeq sequencer, flow cytometry with single cell sorting, MALDI-TOF, and a Biolog Gen-III. DSMZ has a track record of microbial genome analysis and been involved in the sequence analysis of so far ~3500 bacterial genomes. DSMZ has also developed The Bacterial Diversity Metadatabase (BacDive; https://bacdive.dsmz.de) which represents the largest database for standardized bacterial phenotypic data and has become a frequently used resource with over 30,000 different users per month. The additional microbial key databases SILVA, BRENDA, TYGS, and LPSN are now all hosted by the DSMZ and are currently interlinked to create one large, integrated knowledge database platform *DSMZ Digital Diversity (https://www.dsmz.de/research/digital-diversity/).*

As a leading research infrastructure in Europe, we closely follow up international fora and the decisions made on biodiversity conservation, sustainable use and benefit-sharing. The Science Policy team works in both directions: bringing the voice of scientists to international negotiations, ensuring scientific knowledge supports decision-making; and bringing policy decisions into practice in the research community. As a large biological resource center which receives deposits from dozens of countries, sends biological material out to nearly a hundred countries, and many of our on-going research projects involve international collaborations, we work to ensure compliance with international legal frameworks that govern use and transfer of biological material (genetic resources), in particular, the UN Convention on Biological Diversity (CBD) and its Nagoya Protocol, under which the DSMZ became the first registered collection under Regulation (EU) No 511/2014.

Keeping it chilled: A South African catalogue of Wildlife Biodiversity

Kim Labuschagne

South African National Biodiversity Institute (SANBI) Biobank, Foundational Biodiversity Sciences, P O Box 754, Pretoria, 0001

The South African National Biodiversity Institute (SANBI) Biobank is a collection dedicated to the long-term curation of wildlife biomaterials. The ''Biological annihilation" of species from the past few decades has increased the need for these well-managed global collections of biodiversity samples. The SANBI Biobank currently curates approximately 200 000+ samples from more than 85 000 individual animals, representing over 1 000 species. This collection ensures access for research and technological applications, including forensic sciences, comparative genomics, nutrition, epidemiological surveys, reproductive technologies, genetics and pathology diagnoses for the national and international science communities. This platform also supports project management and coordination of samples, including permit applications, optimal storage of samples from collection to analysis, data management, sampling protocols and procedures, as well as serving the bigger biodiversity biobank community with the setting up and running of well managed collections. With the launch of the Biodiversity Biobanks South Africa (BBSA) project, the SANBI Biobank has also positioned itself as a repository rescuing orphan collections from where both staffing and infrastructure capacity is lacking, thereby ensuring these invaluable samples are not lost, but curated for many years to come.

LIB Biobank at Museum Koenig, Bonn, Germany

Jonas J. Astrin

Museum Koenig, Bonn, Germany

The Museum of Nature Hamburg (ZMH) and Zoological Research Museum A. Koenig in Bonn (ZFMK) recently (in 2021) merged to form the Leibniz Institute for the Analysis of Biodiversity Change, LIB, together holding ~15M collection objects and employing around 300 staff. LIB research focuses on the diversity of (mostly) animal species, their evolution and ecology, and on underlying genetic processes. The LIB Biobank stores environmental samples (mostly DNA), animal tissue samples—both fixed and viable—and extracted nucleotides. It is linked to the morphological collections in Bonn and Hamburg and serves requests / deposits samples for the international research community. Currently, arthropods and vertebrates as well as mixed eDNA or community DNA samples constitute the majority of the samples held by the LIB Biobank, with a geographic focus on Central Europe, and through collaborative projects also on the Caucasus, parts of Africa, and beyond. The LIB Biobank uses the Diversity Workbench open source collection database to which we adapted the BioCode LIMS plugin available for the Geneious software. Through the database, we share or upload data to/with GGBN, GBIF, BOLD (-> GenBank) and the institute's collection portal. In 2024, the LIB Biobank will move to a new facility on Bonn University campus where almost all storage (including DNA) will be happening in liquid nitrogen gas phase, with capacity for millions of samples and with new labs, including a designated cell culture lab.

We participate in biobank networks as the International Society for Biological and Environmental Repositories; IUCN's Animal Biobanking for Conservation Specialist Group; the European, Middle Eastern & African Society for Biopreservation and Biobanking; the Frozen Ark; or the Alliance of German Cryobanks. The LIB Biobank also interacts closely with the Biodiversity Genomics Europe, German Barcode of Life, Caucasus Barcode of Life, and the Earth Biogenome projects, among others.

Session IB: Biodiversity Biobank Collections: Sample Management

Management of genetic resources in natural history collections using Specify collection management software.

Andrew Bentley

University of Kansas

The Specify Collections Consortium currently services more than 340 collections at 101 institutions in 20 countries through our Specify 6 and 7 software packages and numerous data management and conversion services. In response to the genomic revolution in natural history collections, the ever increasing unique management needs of tissue collections and genetic resources along with the establishment of the Global Genome Biodiversity Network (GGBN) data portal, Specify collections management software (http://www.specifysoftware.org/) has extended its data model and tools to more effectively manage, publish, and integrate tissue and DNA extract data. We have achieved this by adding support for more genetic specific fields and tables along with items specific to the GGBN data schema. Specify's database design now includes a number of data fields and tables proscribed in GGBN standard vocabularies. We also realigned some of the underlying table relationships to address the needs of specimen curation and collection transactions for extract and tissue samples. Specify now also supports "Next Generation" sequencing metadata with fields to record NCBI SRA ID numbers for web-linking tissue and extract metadata to entries in the NCBI SRA databases. Specify also facilitates the linking and integration of data in support of the Extended Specimen ideal with the ability to link to Genbank sequence records in NCBI and vice versa.

With the ongoing evolution of the TDWG Darwin Core (DwC) standard for specimen data exchange, Specify has also increased Specify 7's data publishing capabilities to export collections data to any DwC or other standards-based, exchange schema. This generic, external schema mapping capability enables Specify collections to design and map data packages to publish their data to any community aggregator or collaborative project database based on Darwin Core while taking advantage of the ever-expanding DwC extensions. The development of these versatile new integration capabilities was in collaboration with, and through financial support from GGBN. This talk will showcase Specify's capabilities while highlighting the above changes in the context of delivery of museum tissue and extract data records to the GGBN data portal for aggregation.

Rio de Janeiro Botanical Garden Tissue and DNA Collections' Management using the JABOT system

Luciana Franco; Luís Alexandre Estevão
Instituto de Pesquisas Jardim Botânico do Rio de Janeiro

The Jardim Botânico do Rio de Janeiro (JBRJ) has, among others, the mission to conserve, curate and showcase plant diversity in its alleys and beds. Initially created as a place to experiment with plants sent from other Portuguese provinces, the Rio de Janeiro Botanical Garden plays a pivotal role in garden science and plant conservation activities. With a considerable biological diversity, the living collection, composed of the Arboretum and Thematic Collections, still maintains historical collections that date from its creation.

In 2018, prioritizing taxa absent from other biorepositories, some of them unique to JBRJ, a genome-quality tissue sample collection, the "RBtecido" (RBtissue), was initiated, with funds received from the GGI-Gardens Partnership Award. This collection, together with samples from the institution's DNA Bank (RBdna), has been made discoverable through the GGBN data portal as a result of the 2018 GGBN-GGI Awards Program funding.

The biological collections housed at the Jardim Botânico do Rio de Janeiro also include herbarium exsiccates, a wood collection, a carpological collection, a seed bank, and an ethnobotany collection. Together, these different collections add up to almost one million specimens, contributing substantially towards the neotropical flora knowledge.

Since 2005, considering the need to make these botanical collections and associated information more accessible, the Rio de Janeiro Botanical Garden developed a database system for botanical collections management known as the JABOT system (http://jabot.jbrj.gov.br). In its second version, functionalities were created to assist in curating collections correlated to the herbarium and the living collection.

In this presentation, an overview of the JABOT system and some functionalities used in the RBtecido and RBdna collections' management will be shown.

Establishment and conservation of an *in vitro* Germplasm Bank of plant species from the arid zones of México

Eugenio Pérez Molphe Balch; Lucía Isabel Chávez Ortiz; Ma. de Lourdes de la Rosa Carrillo; Yenny Adriana Gómez Aguirre

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Mexico has a large number of plant species native to the arid and semi-arid zones of the country, standing out the species belonging to the Cactaceae and Crassulaceae families, as well as several genera of the Asparagaceae family. In these groups there are species of great ecological interest, many of which are endemic. They are also important from an economic point of view, since a large number of high-value products are obtained from these plants, as well as being highly prized as ornamental species. Other aspects that make this group of plants especially interesting is their natural ability to survive in environments with low water availability, and their resistance to high temperatures, which makes them an option to face climate change. Unfortunately, many species within these groups are currently threatened, mainly due to overexploitation of wild populations and destruction of their habitat. Therefore, at the Autonomous University of Aguascalientes, protocols have been developed for the establishment and in vitro propagation of species of the aforementioned families. In addition to this, a germplasm bank has been established that preserves viable tissues established in vitro. For this, a slow growth system is used, this in order to prolong the time between subcultures and thus reduce the maintenance costs of the cultures. Retarded growth is achieved by adding osmotic agents, such as mannitol and sorbitol, to the culture media. This reduces the availability of water so that the growth rate of the preserved tissues is significantly reduced. When complete plants of any of the conserved species are required, they are only removed from the slow growth system and multiplied through previously developed in vitro propagation protocols. Currently, this in vitro germplasm bank preserves 48 species or varieties of the Agave genus, 4 of Yucca, 170 species or subspecies of the Cactaceae family (with 48 genera represented, some native to South America), 10 species of the Crassulaceae family (of the genera Echeveria, Graptopetalum, Pachyphytum and Sedum), 4 species of Beaucarnea, 4 of Dasylirion and 3 of Nolina. The first species were established in this bank in 1998, and their tissues are still viable and capable of regenerating whole plants. In vitro regeneration is always performed from meristematic tissues to minimize the risk of somaclonal variation. This germplasm bank has provided plants to be used in reforestation projects, establishment of arid gardens in schools and other institutions, as well as educational activities. The bank also provides tissues for the development of research projects in genomics, phytochemistry and other areas of biotechnology, such as the generation of transformed roots and cell suspension cultures for the production of metabolites of interest. This demonstrates that massive propagation, coupled with in vitro germplasm conservation, are a viable alternative for the conservation and rational use of these species.

Unlocking Collection Treasures: Accessing Museum Samples for Long Read Sequencing and Genomic Analysis

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In the wake of the current biodiversity crisis, natural history collections are becoming important libraries storing thousands of specimens of rare or extinct species otherwise inaccessible to researchers. Apart from morphological and ecological data, collections are a potential source for biodiversity genomics. While target-capture or short-read whole genome sequencing were shown to work well on museum specimens, assembling high-quality genomes with long read sequencing technologies is notoriously difficult, as museum samples often exhibit DNA degradation and damage. Here, we utilize PacBio High Fidelity (HiFi) sequencing, providing longer and more accurate sequencing also for moderately fragmented DNA, to assemble highly contiguous genomes from museum specimens. Extracting DNA from dozens of vertebrate specimens stored in ethanol, we found that DNA fragment size does not correlate with storage time and, importantly, even older vertebrate samples preserved at room temperature often contained kilobase-sized DNA fragments. In all cases selected for sequencing, an amplification step was necessary to produce enough input DNA to allow for HiFi sequencing. For most specimens, we succeeded in sequencing endogenous genomic DNA with average read N50 values of over 5,000 bp. For the endangered maned sloth (*Bradypus torquatus*), we sequenced to 30X HiFi coverage and obtained an initial assembly, but noticed persisting assembly gaps likely due to PCR bias during the amplification step. By integrating data obtained with less-biased polymerases, we obtained drastic improvements of assembly completeness and contiguity. Finally, adding HiC data, we obtained a chromosome level assembly of the maned sloth. These results provide an important proof-of-principle for high-quality genome sequencing of museum specimens. In ongoing work, we are optimizing this new protocol, applying it to other vertebrates. Ultimately, our work could establish natural history collections as a key resource for biodiversity genomics.

Sample management in the DNA Bank of the Universidad Autónoma de Aguascalientes, Mexico

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Universidad de Aguascalientes,

The DNA Bank of the Universidad Autónoma de Aguascalientes (ADNUAA) was founded in 2017 to hold plant (vascular plants and bryophytes *s.l.)* and lichen genomic material. A set of goals were established to reach the appropriate quality standards to manage our samples at every level, from sample collecting in the field to shipping the material to other facilities around the world. Therefore, a group of seven operational activities was established to manage our samples: plant sample collection, plant tissue storage, DNA extraction, DNA extraction/quality evaluation, extracted DNA storage, DNA bank database, and DNA bank sample transference. Plant material collection is performed in the field and the tissue is stored in silica gel bags; a voucher is always linked to that sample and the specimen is identified, processed, and integrated to the herbarium HUAA. The dry tissue is incorporated into our DNA bank, using a catalog number which links the sample to the herbarium material. All specimens are stored in the dry collection (ca. 2,300 samples; room temperature/-20°C freezer), although some go through a DNA extraction process; the latter depends on the availability of plant material (quantity and quality) and if the taxon is a native/rare species. The samples are extracted using modified CTAB protocols, depending on the taxon (e.g., cacti, mosses, lichens), and later evaluated through spectrophotometry or gel electrophoresis. The extracted material is further stored in a -80°C ultrafreezer, using the same catalog number as the dry material collection to keep the integrity of the information. Herbarium specimen data and DNA sample collection information (dry and extracted) will be incorporated in the immediate future into a MySQL database, which will be hosted by the University's servers, so both collections can simultaneously work with the database. The database uses the Darwin Core standard and by the end of the year the DNA collection will be uploaded to both GGBN and GBIF platforms. Finally, to facilitate the exchange of material with other genomic collections, researchers, or students, we established a material transference agreement document, which is a tool that formalizes the request and shipment of plant material for scientific purposes. Although all those steps are fully functional, there are still areas of improvement that can be explored and implemented, in such a way that our collection complies with national and international standards to preserve plant biodiversity, mainly from central Mexico.

Establishing a Biobank at The Huntington

Brian L. Dorsey, Ph.D.
The Huntington

The Huntington's botanical gardens include over 80,000 plants from more than 27,000 taxa (including cultivars). This broad and historic collection is an important resource of genomic diversity that has only been utilized opportunistically in the past. The GGBN has been a welcome stimulus for us to develop our tissue and DNA banks and a platform to make this resource known and available to the broader research community. This process is in its beginning stages at The Huntington, but we have made some good progress in the last few years. In this talk, I will discuss our experience so far with starting a biobank, including lessons learned and challenges we are still facing. Specific issues include storage space, staffing, data wrangling, and extraction protocols – topics likely common to all biobanks. It is my hope that we may provide some insights for others beginning their own biobanks and contribute to a discussion of best practices for all.

Agrobiodiversity Index, Challenges, Opportunities and Trends

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In this rapidly changing world, we are facing an escalating climate breakdown, biodiversity loss and the decline of ecosystems and current studies and research has confirmed that deforestation, desertification, soil erosion, droughts and flooding across the world are developing more rapidly because of climate change. The paper highlights the Agrobiodiversity Conservation Methodologies and Standards for Gene Banks by FAO. The Agrobiodiversity Conservation policies and regulations of a region can form major impediments to or provide opportunities for alternative methods of conservation. These overarching rules not only vary worldwide but also often within a country's administrative zones. The positive experiences, areas for improvement, and strategies for promoting legislative change will be discussed during the GGBN Conference in Mexico. Conserving genetic Agrobiodiversity is also important for supporting future breeding and selection efforts. One crucial way to safeguard and improve access to genetic resources is through gene banks. Many Local Breeds of Georgia's Agrobiodiversity face extinction if we do not act now. Rare farm animals represent an irreplaceable piece of South Caucasus Agrobiodiversity and offer an incredible variety that may be needed for future Gene Banks and Breeding on farms – robust health, high immune resistance, foraging, and the ability to thrive in a changing climate. Local Agrobiodiversity is a vital part of ensuring food security for our planet – now and for the future. Animal agriculture, though an important source of nutrition and wealth, can exacerbate the challenges posed by climate change, disease emergence, and economic shocks.

The loss of Agrobiodiversity and Genes Erosion of Local Livestock Breeds is a challenge, that calls for innovative solutions to provide the Embryos Cryopreservation to accelerate the novel technologies, Livestock Gene Bank Standards, including sustainable use, digitalization of Data and innovative technologies and necessary infrastructure & knowledge management.

Conservation organizations and Gene Banks worldwide will highlight the threats to genetic diversity in their respective countries and the question is how we measure Agrobiodiversity and the Index of Agrobiodiversity by collecting data on biodiversity across the often-disconnected domains of Nutrition, Agriculture, and Genetic Resources. Besides measuring the status of agrobiodiversity, the Index identifies actions, risks, and opportunities to increase its use and conservation. The Agrobiodiversity Index also is a very important Index to determine the effectiveness of Global conventions and treaties to monitor how well countries are doing with their commitments towards agrobiodiversity and the performance of Gene Banks, Policy Makers and agriculture companies, and make appropriate decisions to provide the Data Management and Open Science Performance.

Cryopreservation of Local Livestock Breeds overcomes the problems of the most valuable Genes and DNA that allow selective breeding and stock improvement and enable the conservation and future sustainable use. One of the emerging requirements for cryopreservation of Embryos can be used by local breeders for evolving new DNA samples. The out washed embryos of Local varieties that has been produced are based on the gene bank collections. Agrobiodiverse Livestock Breeds suffer from Climate Change, Heat waves, poor feeding and over pasturing and the fact that at present it is possible to cryopreserve only Using only purebred cattle that are all sourced from a single breed will create a very homogeneous uniform cattle herd. They will all have the same environmental adaptations. for finfish eggs and embryos. However, the recent report on the freezing of shrimp embryos. However, the recent Research provided by the AFRD in Georgia on the freezing of Livestock Cryopreserved Embryos looks promising.

Therefore, it is essential that gene banking of Embryo will be undertaken by local breeders and livestock for Farmers sharing the Genetic Resources. The effective Gene Banking of local livestock Breeds requires the collecting the Data of Genetic assessments of populations, cryopreservation protocols for varying Embryos and publicly-accessible database that provides a mechanism by which to monitor the inventory and inform stakeholders about which samples are maintained in the collection. As well as the full Genetic assessments have largely been performed using either pedigree and/or genomic information. The collected samples can be useful in evaluating the various landscape of genomics. Combining genetic/genomics and geographic differences can assist in evaluating genetic differences within and among populations.

Biomaterials Biobanking and BOLD Barcoding Benefits

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With the ever-increasing human population expected to reach 8.5 billion by 2030, life on earth for all species is becoming a greater global concern due to habitat transformation, fragmentation, and unsustainable levels of resource exploitation. These declines have also been exacerbated by climate change, biological invasions, and illegal trade. South Africa is considered one of the megadiversity countries, with high levels of species richness and endemism. With more species being placed on the International Union for Conservation of Nature (IUCN) Red List, the importance of collecting and storing biomaterials from this natural heritage is critical. Without these collections, access to disappearing species *in situ* will become more challenging, and research questions more difficult to answer. The advent of the DNA barcoding initiative including the creation of species reference libraries through the Barcode of Life Data Systems (BOLD) has however contributed significantly to biodiversity assessments globally. DNA barcoding is a method for rapidly identifying organisms to the species level using DNA sequence data of a standardized barcode gene region. By adding layers to ordinary sample collection, including photographs serving as e-vouchers, metadata not limited to collection date and locality, but including every detail about the collecting event, these samples can also be used to set up reference libraries to contribute significantly to species verification and biodiversity assessments globally. These libraries are important in South Africa and have been used in the identification of evidence in forensic science cases, in the food industry to minimize food piracy, the detection of invasive species and for taxonomic research among others. It is therefore important to define biobanking workflows and associated metadata (whilst identifying biobanking gaps), to ensure maximum use of biomaterial resources for the establishment of a comprehensive species collection that will be available to the wider research community.

Skimming at scale: bringing historic collections into the genomic era

Andie Hall, Ben Price, William Marsh, Joana Cristavao, Oliver White, Silvia Salatino, Ian Barnes

Natural History Museum, London, UK

It has been estimated that global natural history collections contain over 1 billion specimens. Vast numbers of specimens were collected before the structure and function of DNA was known, long before we learned to sequence it. These specimens are witnesses to global change and in many cases the only known representatives of the species. They have been patiently waiting to reveal their secrets, and this is now becoming feasible at scale. Our approach has been to combine minimally destructive and ancient DNA extraction methods with ssDNA library preparation, and to scale these methods down to suit small tissue samples, reducing consumable costs while enabling robotics to increase throughput.

We tested a number of DNA extraction and Illumina library preparation methods using DNA ladder, entomological and herbarium specimens. Extraction method significantly impacted recovery of fragments typical in museum specimens, including the choice of magnetic bead for bead-based methods. Library building protocol was found to significantly impact endogenous content, aligned read length distribution, library complexity and collapsed read proportion. The best column and bead-based DNA extraction method had no significant effect on these parameters, there were slight differences in overall yield and fragment length of the DNA extracted.

Combined with highly multiplexed sequencing the cost per specimen drops to the point where museum samples can be incorporated into a myriad of studies. We therefore drafted an automatable high-throughput pipeline for genome skimming of museum specimens which we are refining via a variety of projects with different tissue types, many over 100 years old.

COLLECTION OF MEDICINAL AND AROMATIC PLANTS OF THE STATE UNIVERSITY OF CAMPINAS

Ilio Montanari Jr.

State University of Campinas, Brazil

The Collection of Medicinal and Aromatic Plants (CMAP) is kept at the Pluridisciplinary Center for Chemical, Biological and Agricultural Research - CPQBA, research center that belongs to the State University of Campinas-UNICAMP located the city of Paulínia-SP, Brazil. CPQBA plays a very important role in the national scientific scenario, as a reference in natural products (plants and microorganisms), biotechnology and environment. As the name indicates, CMAP is a thematic collection, with medicinal and aromatic species from four continents. CMAP has the goal of preservation, research, education, exchange of materials and dissemination of collections. "In vivo" conservation, seed bank, a laboratory of "in vitro" preservation, herbarium and germplasm banks are part of the collection's context. The CMAP team, made up of agronomists and biologists, has the expertise of species preservation, domestication and acclimatization of medicinal and aromatic plants, as well as the development of crop technology.

Maintaining plants in the "in vivo" collection allows important observations to be made, such as: flowering period, vegetative growth, seed production, seed viability, insect visitation, occurrence of pests and diseases, studies of the influence of environmental factors, studies on biology and reproduction. The collection offers material for botanical identification, cytological and molecular characterization, propagation tests, multiplication and storage of seeds, contributing to genetic conservation programs and the exchange of genotypes between research Institutions.

The CMAP herbarium contains exsiccates from the "in vivo" collection. Through them we can obtain information regarding the morphology, systematics, geographic distribution, habitat, taxonomy, and plant uses, which are the basis for carrying out work in the fields of botany and ethnobotany.

In the micropropagation laboratory, the "in vitro" cultivation technique guarantees the production of uniform plants, which could not be obtained by seed cultivation in allogamous plants, due to the risk of finding variability among descendants. It is also a widely used technique for the production of virus-free plants.

The seed bank contains seeds collected in the "in vivo" collection. The seeds of perennial species are stored at a temperature of – 20 °C for ten years and annual seeds are stored at 4 °C and renewed every 5 years. The team conducts germination and health tests periodically. The collection is managed using records on number of generations each species has been in the field to infer the degree of inbreeding once the active principles of these plants are produced as a function of their genetic code.

CMAP also has several cultivation fields of germplasm banks of medicinal and aromatic plants of greater economic and ecological interest that are used in domestication and genetic improvement programs with the purpose of creating cultivars that can be inserted into production systems and can develop new agricultural options.

Session II: Environmental Samples and Data

Chairs – Karen James, Rachel Meyer, Jackie Mackenzie-Dodds, Jonas Astrin

Connecting environmental samples to a biodiversity information system to make data accessible

Beth Kaplin, Venuste Nsengimana, Mapendo Mindje

Center of Excellence in Biodiversity and Natural Resource Management, University of Rwanda

Repositories of biological material are untapped resources that are exceedingly relevant for countries today as we face biodiversity loss along with the challenges of climate change which affect food security, species distributions, and disease spread, among others. Rwanda sits within a biodiversity hotspot, the Albertine Rift, where there are still many exciting biodiversity discoveries being made, and where biodiversity information are often scattered and not readily accessible. We have developed the Rwanda Biodiversity Information System which currently hosts over 140,000 observation records of species, to make biodiversity data available for researchers, policymakers, and land use and conservation planning. Linking environmental samples with this information system is the next step in exploring strategies to ensure samples, for example from eDNA studies, can be efficiently curated, accessible, and linked to ecosystem types and biodiversity data in the country. In this talk we will present the information system and the strategies we employ to connect specimen data with observation data in the information systems. Because of the challenges of costs and capacity, networks are one of the best strategies to develop effective environmental samples storage.

Towards inclusivity in molecular method standardization for biodiversity assessment

Kristian Meissner; Tiina Laamanen; Veera Norros
Finnish Environment Institute, Syke

The global decline in biodiversity has significant impacts on human well-being and can worsen the negative aspects of climate change. Biological monitoring data is crucial for detecting biodiversity loss and assessing the effectiveness of conservation efforts, but many regions lack standardized protocols for monitoring. This is particularly challenging for countries in the Global South, which host a significant portion of global biodiversity. Molecular methods, like eDNA, could help support biodiversity conservation goals and align with the targets of the UN Global Biodiversity Framework but very few standards on their use exist.

International standardization, led by organizations like ISO, can help countries without the capacity to develop their own protocols and ensure compatibility of results. However, efforts to standardize minimum requirements of molecular monitoring methods for biodiversity should be more inclusive, equally involving both the Global North and South.

To promote coordination and inclusivity, task forces like the IUCN's GLOSAM and the International eDNA Standardization Task Force (iESTF) have been established to standardize molecular methods and procedures.

This talk will summarize recent advances in improving inclusivity and standardization for molecular biodiversity monitoring. In particular, it will summarize developments made during the autumn of 2023 at the Science Summit at the UN general Assembly 78 and at the GEO BON conference.

The National Institute of Standards and Technology (NIST) Biorepository

Rebecca Pugh; Debra Ellisor, Jen Hoguet, Amanda Moors,and Jennifer Ness

National Institute of Standards and Technology, Chemical Sciences Division, Charleston, SC USA

The National Institute of Standards and Technology (NIST) has been involved in long-term banking of biological and environmental specimens for over 40 years. Frozen tissue and fluid specimens representing over 20 taxonomic Orders are archived at the NIST Biorepository, Hollings Marine Laboratory, Charleston, South Carolina, USA, with more recent collections focusing on marine fauna, including mammals, seabirds, sea turtles, bivalves and fish. Biospecimens originally intended for monitoring geographic and temporal trends in emerging contaminants as well as changes in transport and accumulation of legacy contaminants have increased value today because of adherence to standardized protocols and best practices. Biobanking operations, including biospecimen collection, processing, storage, and shipping, as well as the accuracy of the data collected throughout the lifetime of the biospecimen and how that data is curated, ensures a high quality, homogenous and stable aliquot is provided for downstream analyses. These biospecimens are an invaluable resource to the scientific community. An overview of the NIST Biorepository and many of the best practices that are utilized by NIST will be presented.

Environmental specimen banks in research and regulation for a better environmental quality

Jan Koschorreck

The German Environment Agency, Umweltbundesamt-UBA, Berlin, Germany

Environmental specimen banks (ESBs) systematically store high quality samples from the environment and human populations in support of environmental management and innovative research for a better environmental quality. ESBs are operated by environment agencies as part of the national long-term environmental research infrastructure or by environmental research institutes. With new monitoring methods, there is a large potential to make better use of ESB samples in research and chemicals regulation.

ESB sampling is already ongoing for up to 50 years at regular intervals in the freshwater, marine and/or the terrestrial compartment. Some ESBs also sample human populations. ESB operations are guided by strict protocols for sampling, processing and archiving. The samples are stored at low or ultra-low temperatures in the archives which provides for their long-term biological and chemical integrity.

There are around 30 ESBs in the world, of which around 20 are located in Europe. The specimens are used to monitor the quality of the environment and the efficacy of regulatory efforts to control known hazardous substances like metals, PAHs, PBDEs, dioxins and other organochlorines. However, the main objective of ESBs is retrospective analysis of chemicals of emerging concern (CECs): ESB samples allow for spatio-temporal analysis of substances which were unknown, not known to be hazardous or not analytically detectable at the time of sampling. Recent examples are new PFAS, new flame retardants, chlorinated paraffins, nanomaterials and pharmaceuticals.

The systematic use of high quality ESB data and samples has the potential to significantly increase our understanding of the fate of regulated and non-regulated contaminants in the environment. ESB data is already being used to some extent to identify persistent organic pollutants (POPs) under the Stockholm Convention and potential persistent and bioaccumulative compounds in REACH legislation. However, consistent and interdisciplinary approaches that make better use of high quality ESB samples can overcome the reluctant use of monitoring data in chemicals risk assessment.

The application of cutting-edge analytical methods to ESB samples is a win-win situation for the value of ESB samples and our understanding of the quality of the environment. Scientific progress and decreasing costs now make it possible to study archived environmental samples using molecular biology methods. Population genomics can be used to study microevolution and adaptation in the genomes of archived biological samples in response to environmental stressors. In addition, DNA metabarcoding and metagenomics can examine community DNA associated with the samples in both non-biological and non-biological matrices, such as soils and tree leaves. And when samples are stored at extremely low temperatures, RNA can be used for transcriptomics to gain insights into physiological responses to anthropogenic and other stressors.

These fascinating new molecular tools not only provide much-needed temporal trends in biodiversity over recent decades. They also offer interdisciplinary links to other areas of environmental monitoring research and a better understanding of the evolution of ecosystem health and services.

Global Genome Biodiversity Network

Taxonomic diversity and microorganism distribution patterns at CBUDES collection: Biobank of microorganisms from northeastern Colombia

Natalia Bravo-Granados; Juanita Trejos-Suárez

Diversidad Taxonómica y Patrones de Distribución de Microorganismos en la Colección CBUDES: Biobanco de microorganismos del nororiente colombiano

La Colección Biológica CBUDES (RNC:280) de la Universidad de Santander, alberga 2583 microorganismos, compuesta por 2511 bacterias y 72 hongos. Su objetivo principal es preservar, documentar y estudiar un biobanco de microorganismos del nororiente colombiano obtenido a través de diversas investigaciones en muestras humanas, animales y ambientales en el entorno de una sola salud a través de cuatro departamentos de Colombia. Para ello se ha desarrollado una metodología para la gestión del conjunto de datos con el procesamiento y visualización de estos, que se da como un factor crucial en su análisis, tornándolos accesibles, interpretables y procesables para una amplia audiencia. Se implementó un proceso de evaluación previa para asegurar la calidad de los datos, detectando posibles errores o ausencias. Se recurrió a herramientas de integración, visualización, análisis y colaboración de datos para su limpieza. Mediante OpenRefine y Species Matching del GBIF se realizó Data wrangling, facilitando la organización de datos y la validación de nombres taxonómicos. OpenRefine identificó 120 ausencias en las coordenadas geográficas, atribuidas a falta de especificación por los investigadores. La visualización y exploración de datos se efectuó con Power BI. Dentro de la colección, el 95% (2455) de los 2583 especímenes se clasificaron taxonómicamente hasta nivel de especie, mientras que el 5% (128) se limitó al nivel de género. Predominando, el filo *Proteobacteria*, el cual abarcó el 94.81% (2449) de los microorganismos, con el 85.91% de ellos aislados e identificados en Bucaramanga. *Escherichia* fue el género más abundante, representando el 90.67% (2342) de los especímenes, mayormente hallados. Su presencia en el Área Metropolitana de Bucaramanga fue significativa al compararla con otros municipios de la región. A menor escala, el filo *Zygomycota* presentó dos organismos, uno del género *Absidia* y otro de *Mucor*, ambos aislados en Valledupar. El 91% de los microorganismos fueron identificados mediante métodos moleculares y el 4% restante empleó microbiología clásica. La utilización de herramientas como mapas, tablas y gráficos proporcionó información valiosa sobre patrones de diversidad, interacciones entre organismos y distribuciones geográficas, anteriormente inobservable en hojas de cálculo. Estos recursos resaltaron puntos críticos de biodiversidad. Se observó la importancia de la visualización de datos en la difusión y promoción de acceso abierto a datos científicos, contribuyendo así al paradigma de ciencia abierta. El análisis riguroso y la integración de herramientas tecnológicas en la manipulación de datos biológicos promueven la comprensión y utilización efectiva de los recursos biológicos almacenados en la Colección Biológica CBUDES.

Maine-eDNA: a case study for large-scale environmental sampling, metadata collection and data management in one of the world's fastest-warming ocean regions

Karen James[1]; Steven Allers[1]; Keijaoh Campbell[1]; Chaofan Chen[1]; Lauren Crofton-Macdonald[1]; Beth Davis[1]; Laura Jackson[1]; Benjamin King[1]; Darren Ranco[1]; Samantha Silverbrand[1,2]; Jennifer Smith-Mayo[1]; Geneva York[1]; Melissa Kimble[1]; Andrew Rominger[1,3]; Kate Beard[1]

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Maine-eDNA is a 5-year research, education, and outreach program that seeks to transform our understanding and the sustainability of Maine's coastal ecosystems via environmental DNA (eDNA) innovations that unlock new scales of inference and collaboration. Central to Maine-eDNA is an initiative to collect, extract DNA from, metabarcode, analyze and archive thousands of eDNA samples across four adjacent, interconnected lake-to-coast transects in the Gulf of Maine region from 2019 through 2023. The integration and analysis of this Big Data resource and associated spatiotemporal and environmental data is supported by *medna-medatada*, a FAIR (Findable, Accessible, Interoperable, and Reusable), open-source data management system for tracking environmental DNA samples and field, lab and bioinformatic metadata to enable hypothesis-testing about spatial and temporal differences in aquatic communities and potential drivers of change. Integrated into *medna-metadata* are Local Contexts Biocultural Notices and Labels (BC Labels), enacting CARE (Collective Benefit, Authority to Control, Responsibility and Ethics) principles in the context of Maine-eDNA samples and metadata, which are collected from unceded lands of the four Wabanaki Confederacy nations: the Mi'kmaq, Maliseet, Passamaquoddy and Penobscot.

Summary of our experience in application of remote techniques for environmental sample collection

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In the last decades, algal strains are increasingly gaining the attention of the scientific community due to their diverse applications in biotechnology, medicine, pharmacy, cosmetics, etc. In this respect, phycoprospecting gets raising awareness, with need not only for seeking new, original algal strains, but for application of methods which can fasten the field work and ensure its financial optimization. Among the important current innovations in algal collection and sampling is the use of remote vehicles, and of the drones especially.

The presentation documents our experience in use of two drone types in collection of algae from two ecological groups in different regions of Bulgaria with demonstration of both advantages and shortages of the method. In June 2018, we applied the drone DJI Mavic Pro for observation and documentation of the aquatories of nine lakes and reservoirs in Bulgaria with the idea to identify the hot spots of algal blooms and collection of harmful planktonic algae (Stoyneva-Gärtner et al. 2019). In July of the same year, the same drone was used for identifying sites for collection of algae from a thermal spring water body (Stoyneva-Gärtner & Uzunov 2019). In 2019 and 2021, a drone supplied by thermo-camera for surface water temperature measurement DJI Mavic 2 Enterprise Dual Pro was applied for sampling of planktonic algae in 42 small and large waterbodies, situated at different altitude in the inland and coastal parts of Bulgaria (Radkova et al. 2020; Stefanova et al. 2020; Stoyneva-Gärtner et al. 2021, 2022, 2023; Uzunov 2021 a,b; Valskys et al. 2022). In 2022 and 2023, the same drone was used for identification of sampling sites from ancient megaliths in South Bulgaria (Projects 80-10-47/10.05.2022 and 80-10-88/26.04.2023 with SF-SU). Despite the shortage of dependence on the environmental conditions and impossibility to use the drones during strong winds, as well as in regions with unstable satellite connections and internet cover, the results obtained from all these attempts strongly confirm the advantages of use of remote instruments in field algal collection, which saves time, fuel and efforts.

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CALeDNA: Environmental collections to enable landscape biodiversity surveys and models of community change

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The CALeDNA program has nearly 7 years of environmental collections, where every year thousands of 2mL tubes are collected from soils and sediments, or where water is filtered and preserved in buffer, and deep frozen as a public research resource. Collections are mainly from California but the program is expanding to have global reach. CALeDNA collections are paired with detailed metadata including photographs, and for the ~5000 of these collections, environmental DNA (eDNA) has been extracted and metabarcoded to describe biodiversity that shed DNA into the sample. Our Metabarcoding method includes 6 loci to profile bacteria, fungi, plants, algae, protists, and animals. To enable collections and their data to be visible, analyzed by diverse people with different creativity and expertise, and reanalyzed over time as reference DNA databases improve, we created the eDNA Explorer to host and process the raw data. In this talk, I will describe the links between the physical collection, the permissions, metadata, NCBI SRA sequence data, and taxonomic inventory outcomes. Many challenges exist to link these components of the extended specimen, and we are working to scale up tools and work with different organizations to ensure collections are accessible research resources for the future.

Strengthening global-change science by integrating aeDNA with paleoecoinformatics

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Ancient environmental DNA (aeDNA) from sedimentary archives is transforming our understanding of the patterns and drivers of past biodiversity dynamics, by enabling the study of formerly invisible taxa and whole clades at unprecedented taxonomic resolution and spatiotemporal extent. Examples include the detection of climate refugia during past climate change, the shifting effects of historic land use, the responses of communities to past climate variability, and the rebuilding of biodiversity in deglaciated lands. To date, however, early-stage aeDNA research has focused on method development and generating individual site-level records. Now, as the number of sites quickly grows worldwide, aeDNA research is at the cusp of supporting regional- to global-scale analyses of the distribution and diversity of life. Achieving this scientific goal requires data systems capable of integrating many individual aeDNA records with each other, other paleoecological and paleoenvironmental proxies, and modern genetic reference libraries. Because aeDNA-derived inferences are changeable and methods are evolving, these systems must support expert data governance, dynamic taxonomic inferences, dynamic age inferences, and precise depth positioning. aeDNA data systems can be accelerated by building upon and interlinking existing resources in bioinformatics (e.g. EMBL/NCBI) and paleoecoinformatics (e.g. Neotoma Paleoecoinformatics, LinkedEarth). Specific recommendations include focusing first on supporting metabarcoding-based taxonomic inventories, beginning test uploads and integrations with existing paleoecoinformatic resources, harmonizing aeDNA bioinformatic workflows, and building structures for community data governance. These advances will enable transformative insights into global-scale biodiversity dynamics during large environmental and anthropogenic changes.

Diatoms, a model group for DNA Barcoding

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Diatoms are one of the most important indicator groups for water quality analysis. Traditionally, features visible under a light microscope were usually used to identify the taxa. As part of the project German Barcode of Life (GBOL, https://www.bolgermany.de/) a reference library for diatom DNA barcodes (18SV4, rbcL) was set up, which expands the features to be used for species identification. The taxonomic validation of the barcodes was achieved by using traditional identification process, namely light and scanning electron microscopy to document and identify clone cultures that were specially isolated from water bodies of different trophism and morphometry.

DNA Barcoding Reference Library for Diatoms

The aim of monitoring methods that work with molecular characteristics is to improve standardization of the methods and the processing of larger amounts of samples in less time with a greater depth of identification. The precision of the method relies on very well-documented reference sequences, which are compared with sequence data from the environmental DNA. The DNA Barcoding Reference Library therefore comprises not only sequence data and scientific names, but also the entire documentation, which ensures full compatibility of molecular and morphological analyzes as far as possible. The core of the GBOL2 project was therefore the creation of a reference library. A sustainable research infrastructure was created by depositing specimens in the Herbarium Berolinense (B), in the DNA bank of the BGBM and by fully documenting all data in publicly accessible databases (INSDC, GGBN, AlgaTerra, collection database at the BGBM). It is equally suitable for recording biodiversity and answering taxonomic questions as well as for finding diatom species in the environment. A specially developed automated modular eDNA data analysis pipeline is available for the analysis of diatom species communities in environmental samples using eDNA metabarcoding for water quality assessment. As an example, more than 400 indicator species from more than 80 genera were completely documented with the help of more than 1,300 clonal cultures. With the GBOL2 diatom project, a best-practice application example for the documentation and making available of barcode reference libraries was created, which provides valuable results for the further development of methods and standards. The analysis of diatom communities in environmental samples using eDNA metabarcoding enables the highest possible resolution and reproducibility when assessing water quality. The GBOL2 data are supplemented by other cultures (approx. 500 from Europe, approx. 600 from Mexico, approx. 750 mainly from both Koreas, Vietnam and Canada). The reference library is constantly being expanded to include taxa from Iraq and Antarctica in order to examine the suitability of these floras for biomonitoring purposes in these regions in addition to basic taxonomic research.

Session III: Cell Banking and Culture Collections

Chairs- Oliver Ryder, Jonas Astrin, and Jackie Mackenzie Dodds

The UK Crop Microbiome Cryobank – Advancing Microbiome Research for Sustainable Agriculture

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Plant microbiomes are critical to crop health, improved yields, and food quality. However, most research on this subject tends to focus on a single aspect of this complex network of interactions and ecological processes. Thus, the UK Crop Microbiome Cryobank (UKCMC) project is developing a unique, integrated, and open-access resource to enable the development of solutions to improve soil and crop health. The project objectives encompass providing accessible cryopreserved microbial isolates, samples origin datasets with complete metadata, comparing soil and crop sample communities, and establishing standardized protocols for complex soil microbiota. Six of the UK's key crops and 11 sampling sites across the UK were targeted, and the methods and data outputs will underpin research activity both in the UK and internationally. Soils from these 11 locations (three contrasting soil types) were used to grow wheat, barley, oats, potato, Fava beans, oil seed rape crops in controlled glasshouse experiments with bare soils as controls. The rhizosphere soils from these pots were used for the isolation of micro-organisms (mostly bacteria), 16S rRNA gene and ITS metabarcoding and metagenome sequencing. All data generated will be made available on the AgMicrobiome Base website (https://agmicrobiomebase.org/). Currently, ~37,000 isolates have been collected, of these ~23,000 were tested for multiple plant-growth-promoting characteristics such as nutrient solubilization and stress resistance. Microbial communities from these samples underwent taxonomic sequencing, including bacterial (16S) and fungal (ITS - wheat only) communities. Shotgun metagenomic sequencing is in progress for wheat and fava bean communities, alongside de novo whole-genome sequencing of selected cultivable isolates. Robust data analysis pipelines were devised to handle the high-throughput data outputs. We believe that the model created is transferable to different crop and soil systems, acting not only as a mechanism to conserve biodiversity, but as a potential facilitator of sustainable agriculture systems that mitigate against climate change.

Global Genome Biodiversity Network

Strategy for the biobanking of potato genetic resources at the IPK genebank

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The federal *ex situ* collection of agricultural and horticultural plants at IPK houses about 152,000 accessions of more than 3,000 species. Dependent on the specific storage requirements, most accessions (145,000 accessions) are stored as desiccation tolerant seeds. About 2,600 accessions are maintained in the field; 2,900 are kept in vitro under slow-growth storage conditions; and 2,400 accessions, predominantly shoot tips of potato, mint and *Allium* genetic resources, are cryopreserved.

Potato genetic resources include four cultivated potato species mainly clonally propagated and 107 wild potato species maintained as true potato seed. As the maintenance of this potato diversity requires a complex conservation management including field, in vitro and cryopreservation and seed storage, a comprehensive sample management has been established in the IPK genebank. In addition to sample and data management, including passport data and legal information, a reference collection, phytosanitary certificates, distribution of >600 potato accessions (out of a total of 19,000 distributed accessions) and the duplicate storage at Svalbard Global Seed Vault is organized. The presentation will focus on the specific sample handling, data storage and global material exchanges and provide insight into the challenges of preserving different materials.

South African National Collection of Fungi: An established resource on the continent

Riana Jacobs-Venter, A

National Collection of Fungi

Fungi are an extremely diverse and abundant group of microbes and are particularly important – having an impact on human, plant and animal health as well as the functioning of natural ecosystems. They are some of the most overlooked organisms, despite making up 25% of the world's biomass and more than 90% of the estimated 3.8 million fungi in the world are currently unknown to science.

The South African National Collection of Fungi (SANCF) has for the past 115 years documented South African fungal diversity. The first accounts on the fungal diversity of the country are from European botanical explorers collecting Southern African fungi for scientific study, venturing to the subcontinent in the late 1700s. This was followed by sporadic reports until I.B. Pole Evans was officially appointed as the first mycologist by the British government. His appointment served as the first official recognition of mycology as a distinct branch of research in the country. In 1905, he became the Head of Mycology and Plant Pathology in the newly established Transvaal Department of Agriculture, and Chief of the Division of Botany for the whole of South Africa. In the same year he established a plant-pathological reference collection, the forerunner for the current National Collection of Fungi.

The basic goals of the SANCF remained integral throughout, although various phases in terms of research focus, are recognised over the past 115 years. These include an emphasis on the collection and the recording of fungal pathogens, followed by a focus on mycotoxins and recently to the documentation of biodiversity. There is also an increasing demand for information and diagnostics surrounding plant pathogens. Currently, research at the NCF focus on the surveys of native and agricultural ecosystems, molecular phylogenetics and species identification.

The SANCF currently form part of two national initiatives namely the Biodiversity Biobanks of South Africa and the Natural Science Collection Facility. These platforms are meant to co-ordinate activities within the South African Biobank and natural Science collection to ensure alignment with international standards. The collection further focus the preservation of 35 000 strains as lyophilised material, cryopreserved in glycerol and agar slants. Migration to the data management tool, SPECIFY is also underway.

DNA barcoding is a routine tool used for quick and reliable identification of fungal species, but the results are only as reliable as the robustness of the reference dataset. Towards this goal, the SANCF has started a project to generate DNA Barcodes for all isolates housed in the PPRI living fungal collection of the SANCF, as well as documenting all DNA sequence data generate for material housed in the PREM fungorium. Not only does these DNA Sanger sequences serve as verification for the morphological identification, it may indicate species where further taxonomic work is required to resolve species boundaries. As these are all made available via international databases (NCBI GenBank and BOLD) it contributes to the international and local efforts to improve the diagnoses of fungal plant pathogens.

The World Federation of Culture Collections and the Global Genome Biodiversity Network: Sharing the Same Mission for Sustainable Futures

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The World Federation for Culture Collections (WFCC) plays a major international role in all matters related to culture collections such as the operation and management of culture collections as well as addressing issues in a wider context such as the importance of (i) standardization and best practice guidelines, (ii) networking, capacity building and education, (iii) postal, quarantine and safety regulations (iv) IP, patent and commercialization, (v) access, policies and legal frameworks and (vi) sustainability of endangered collections. Moreover, WFCC in the era of molecular advancements places emphasis on genome level characterization of the microorganisms as well as defining criteria to ensure type strain integrity as well as its preservation in a genetically stable form. WFCC interacts with different global organizations to promote the importance of culture collections with emphasis placed on the contributions and impact culture collections make on science, health, education, and society. One of such organization is the Global Genome Biodiversity Network (GGBN) and their interest is also “long-term preservation of genomic samples representing the diversity of non-human life on Earth. GGBN provides a platform for biodiversity biobanks across the world and provides its members with the primary benefit of making their DNA and tissue collections discoverable for research through a networked community of biodiversity biobanks. In doing so, GGBN provides trusted and transparent access to genomic samples for all, through an access and benefit sharing framework”. The two organizations thus share the same mission of collaborating with member collections to ensure quality standards, improve best practices for the preservation and use of samples either live cultures or molecular level samples and related information. They also work to harmonize exchange and use of material in accordance with national and international conventions.

This presentation will communicate overlapping and shared mission between to organizations. With the advances in the field of molecular biology true potential of microorganisms are continuously being revealed the hidden biotechnological potential preserved in their cryptic genes. Microbial culture collections have been providing biological resources including the living organisms to many different sectors as well as offering preservation services to microbiologists working in different fields ranging from education to environment, agriculture, health and biotechnology. In the post-genomic era supply of information at the genome level has been imperative and GGBN’s role is complementary to the WFCC and vice versa.

Biotechnology has capitalized on diverse metabolic capabilities of microorganisms and delivered solutions for the benefit of the mankind such as bioremediation, microbial immobilization and detoxification of the pollutants, bio-restoration of mine sites, bio-clean-up of the oil spills, biodegradation of waste, biological control of pests and pathogens, production of useful chemicals including enzymes that can be used in textile, detergent and food industries, as well as production of different kinds of medicines. They are alternative sources of energy and will provide more solutions to current global problems in parallel to the technological advancements. Microbial biotechnologies will play a vital part in the near future. However, the effective use of microorganisms will depend on the preservation of their key properties as well as generating information on their genomes and full molecular aspects and as a result, WFCC and the GGBN will thus be an integral source for microbial biotechnology.

Establishing model lineage systems to study inter-species advanced reproductive approaches

Francisco Pelegri

University of Wisconsin, Madison

Current efforts aiming at the biopreservation of biological materials imply the ability to reintroduce genetic diversity present in biopreserved samples in the future, as needed for proper management of animal population health. Such reintroduction will depend on the regeneration of individuals corresponding to the endangered species through advanced reproduction methods, such as cloning or germ cell transfer, using biological material from biopreserved samples. Such advanced methods require surrogate individuals and/or organs, e.g. eggs and surrogate mothers for cloning, and somatic hosts for germ cell transfer. In principle, such methods could be carried out using surrogate eggs/individuals from the same species as the biopreserved samples, e.g. from a captive population, however it is likely that in many cases related to endangered species, corresponding captive populations will not be available to provide such egg/individual surrogates. An important alternative will therefore be to implement advanced reproductive methods using of eggs/individual surrogates from closely related species, which may be able to allow the production of unaltered individuals from the biopreserved samples. The success of such methods will likely closely follow phylogenetic relatedness: the more closely related species are, the more likely inter-species reproductive approaches will be successful. We use the well-studied developmental genetics model organism the zebrafish, Danio rerio, and closely related species within the Danionin clade to systematically assess the success of inter-species reproductive technology in relation to phylogenetic relatedness. Our initial studies assess the success of inter-species nucleocytoplasmic hybrids (cybrids), relevant to the feasibility of cloning, in particular with regards to mitochondrial-nuclear interactions for energy production and the activation of the zygotic genome for the initiation of development. Additionally, we are gearing up to use the same system to assess the success of inter-species germ cell transfer. We are additionally aiming at establishing similar approaches in Mantellidae (anuran) and Estrildidae (avian) lineages.

Important Considerations for Biobanking for Genetic Rescue of Endangered Species

Ben Novak, Pete Miraglia, Jackie Mountcastle

Revive & Restore

Following the successful cloning of endangered black-footed ferrets and Przewalski's horses from decades-old biobanked cell lines, Revive & Restore has begun a pilot program with the United States Fish & Wildlife Service (USFWS) to biobank high-quality cell lines and tissues for native endangered species for future recovery uses. Owing to limited cell culture methods and biological considerations for many species, this program has started with mammals. The premise seems simple enough - collect at least one male and one female tissue sample non-lethally for cell culturing and cryopreservation for each of approximately 25 endangered, threatened, or candidate species under ESA review. In addition to cryopreserving cell lines, platinum-quality reference genomes are being assembled. The pilot program's first cell lines are established and the reference genome is in process for the endangered Mexican wolf, but other species in the program are posing unique challenges. This program is serving to uncover the pinch points and growing pains for scaling up effective biobanking for recovery applications, as USFWS aims to make biobanking a broader practice across recovery plans for the 1,500 and counting listed threatened and endangered native species. A number of lessons have come to light regarding the necessary sample input parameters, greatly impacted by the need to collect tissues non-lethally and safely, and their impact on future short-term and long-term output applications. These include tissue sample size and its relation to potential cell culture yields, which can limit potential genome sequencing approaches. Sample size and tissue type can also limit the number of viable cell passages for various in vitro research purposes. In addition to the pilot work with mammals, our research regarding non-mammalian taxa reveals significant technical challenges to be addressed for strategic biobanking. For some taxa, such as passerine birds, lampreys, and some flies, the germline possesses additional germ-cell specific chromosomes (called germ-line restricted chromosomes), meaning the complete genome cannot be obtained from somatic samples. If the greater biobanking and conservation community plan to establish biobanked populations useful for future recovery purposes, these limitations and unknowns need to be addressed. In this talk, we outline our pilot program, the white space for research and development for biobanking across animal taxa, and several major considerations for biobanking and relevant strategies to account for them to ensure biobanked resources will be useful for future genetic rescue purposes.

Introducing Nature's SAFE: a European Biobank for Conservation

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The charity Nature's SAFE is a UK-based living biobank of cryopreserved viable cells and tissues from deceased endangered zoo animals and native wildlife. With anthropogenic activities causing extinction rates to accelerate to levels far greater than natural, *ex situ* and *in situ* conservation programmes need additional support to save species. Cryobanking followed by assisted reproductive technologies may be the only way to save some species and therefore is vital for long-term conservation planning. Nature's SAFE was the first approved cryo-network partner of the European Association of Zoos and Aquaria (EAZA) providing a free cryopreservation and storage service for zoos and conservation charities to minimise financial barriers to conservation. Importantly, the Nature's SAFE working model ensures the ownership of the samples remains with the institution from which they came. Nature's SAFE works with international experts to advise on best practice and optimal solutions. This proactive approach is helping answer scientific questions and applying this knowledge to make real-life impact on conservation today. Nature's SAFE plans to establish a network of global sample collection sites, and in parallel, scale up cryopreservation capacity and expertise with new living biobank hubs in locations strategic for sample collection. To date, Nature's SAFE collaborates with nearly 20 UK zoological collections, including Chester Zoo, Zoological Society of London, Longleat Safari Park and Paignton Zoo, resulting in a repository of multiple samples from over 200 species and is finalising their first European hub: Nature's SAFE Ireland. In Collaboration with external research partners, Nature's SAFE is working to develop induced pluripotent stem cell lines from multiple endangered taxa and is developing *in vitro* ovarian tissue culture protocols. As the scientific network of expertise expands, the research strategy will broaden to include *in vitro* testicular tissue culture and coral cryopreservation. The full potential of Nature's SAFE will only be reached when there are preserved samples from all endangered species around the world; until then, replication and upscaling is imperative.

Reproductive biotechnologies and Genetic Resource Banks applied to wildlife conservation in Argentina

Adrián J. Sestelo
Gerencia Operativa de Conservación y Gestión de Fauna

It´s well known that our planet is living actually a non-precedent ambient crisis principally doubt by our own bad utilization of natural resources, fact that have pulled the species extinction rate to values 1000 times more elevated than natural evolution.

Natural habitats are more and more fragmented which produce wildlife populations reduction and isolation, generating consanguinity and biodiversity lack. However, that process could be easily reverted through the incorporation of new genetic. This is the main reason the use of reproductive biotechnology and creation of genetic resources banks was suggested as tools for wildlife populations management (captives or free range).

As an answer to these needs, since the last 30 years we are working on the Reproductive Biotechnology Laboratory for Wildlife Conservation and the development of the Genetic Resources Bank (or Biobank), where thanks to the cooperative work with lot of national and international institutions we develop and apply reproductive technologies, also making the first Argentinian Genetic Resource Bank entirely dedicated to wildlife, especially those autochthonous and endangered. This kind of activities have positioned our laboratory as a research and scientific education pole in wildlife reproduction topics as well as a Wildlife Genetic Resources Reservoir.

The Reproductive Biotechnology Laboratory develop different research lines and application of reproductive biotechnologies (Artificial Insemination, In Vitro Fertilization, Intra-Cytoplasmic Sperm Injection, Embryo Transfer, Nuclear Transfer or Cloning), Mesenquimal Stem Cells regenerative therapies in endangered birds, cooperative population management though studbook coordination and, finally, the creation and maintenance of the Biobank, where we preserve viable biological materials as spermatozoa, oocytes, embryos, cells, tissues, etc.

Actually the Biobank is composed by 4 different Repositories: Genetic Resources Repository with more than 8600 samples from more than 800 individuals from 123 different species. Bone Repository with more than 250 individuals. Entomological Repository a worldwide representation of more than 1440 individuals. Anatomopatological Repository with formulated samples of veterinary diagnosis interest with 155 samples.

Socially, a legacy is thus left for future generations, comprised of the stored genetic material, research developed and specially the community awareness.

Projects at LIB Biobank enabling cell banking and protocol collection

Camilla B. Di Nizo[1]; Carolina Corrales[1]; Jonas J. Astrin[2]

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[2]*the LIB Biobank team*

Cryopreserved living cells are a reproducing resource and offer high-quality DNA, RNA and access to chromosomes. Besides enabling the deep characterization of biological diversity, cells can also be a powerful tool for conservation strategies. While not trivial to preserve, biobanked cells guarantee the best possible suitability for any future applications.
The Leibniz Institute for the Analysis of Biodiversity Change (LIB) at Museum Koenig in Bonn, Germany established a first cell culture lab in 2019 (soon to be replaced by a new facility). This was enabled mostly by FOGS (Forensic Genetics for Species Protection; https://fogs-portal.de/en/), a project that focuses on combating illegal wildlife trade through developing combined molecular markers (SNP+STR). As a complementary ex-situ conservation approach, FOGS cryopreserves vertebrate somatic cells. Since 2023, also the BGE project (Biodiversity Genomics Europe; https://biodiversitygenomics.eu/) is starting to channel samples into the cell bank at LIB. The tissues that have so far given best results are skin and eye (for mammals, birds, and reptiles) and fins (for fishes). In BGE we are starting to experiment with invertebrate, particularly arthropod cell culture. To date, the LIB Biobank has been able to freeze almost 600 samples representing 73 vertebrate taxa (mammals, birds, reptiles, fishes, and amphibians), including vulnerable, endangered, and critically endangered species, as well as two species extinct in the wild (all confirmed via DNA barcoding). We have furthermore been able to freeze primary tissues from another 91 species for later initiation of cell culture. Many of these samples originate from zoos, but a considerable number also represents German wildlife. We have started to collect cell culture samples also in the Caucasus. In addition to actively cryopreserving new samples, we took over a legacy collection of mostly viable tissues from almost 120 fish species predominantly from the North Sea and NE Atlantic and made these publicly available. The cell lab of the LIB Biobank offers karyotyping as a service in joint projects.

Within the SYNTHESYS+ (https://www.synthesys.info/) project, the LIB Biobank coordinated the collection of information on a wide range of biodiversity biobanks and their protocols and practices. A considerable proportion of this information includes viable samples. The resulting open access handbook (https://doi.org/10.3897/ab.e101876) gives an overview to field sampling, preservation, and storage of biomaterials for animals, plants, fungi, and protists.

CRYOZOO Biobank of Animal Cell Lines

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The CRYOZOO project of the Barcelona Zoo is an Animal Cell Line Biobank with the purpose tocreate a stable, international, and permanent biobank of cell lines from a wide variety of animals, giving priority to endangered species worldwide. The Biobank is a project created by the Barcelona Zoo Foundation, managed by the Institute of Evolutionary Biology (IBE) UPF-CSIC, and supported by the Barcelona Zoo, the European Molecular Biology Lab (EMBL) and the Museum of Natural Science of Barcelona. Specifically, the CRYOZOO has as main priorities: the conservation of viable cell lines with priority to the most threatened vertebrates according to the IUCN red list, the characterization of the molecular phenotypes for these cell lines, such as genome, epigenome, and transcriptomics information, the study and promote research in cell reprogramming techniques for the creation of IPS cells (induced pluripotent stem cells).Even though the project started only four years ago, we have currently received more than400samples from different zoos and aquariums, we have been able to generate200cell lines from different species (including mammals, birds, amphibians, reptiles, and fish), establish 50karyotypes,30 whole genome sequencesandgenerate7iPSClinesof different species some of them classified as a critical endangered and extinct in the wild. Future challenges are elaborate protocols for establishing not describes viable cell lines from many reptiles and amphibian's species, the latter currently being the most threatened group of vertebrates, research on the generation of cell lines from invertebrates, as well as the continuation of research on the generation of induced pluripotent stem cells from critically endangered species, considered one of the last ex situ resources to help species conservation.

Organoids for biobanking and cellular agriculture

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Organoids are the next generation research resources. With the ability to self-organize as 3D tissue structures, organoids are able to mimic key functions, structure, and the biological complexity of an organ. They are typically derived from stem cells (pluripotent, fetal or adult), and compared to 2D cultures they are able to recapitulate the specificity of in vivo structures and function in an *in vitro* system (Zhao et al., 2022). Compared to 2D cell cultures, organoids have a variety of features that makes them far superior in terms of specificity and resemblance to the original tissue or organ. Organoids are self-organizing multicellular structures developing from stem or progenitor cells which exhibit *in vivo* organ architecture. They are able to replicate *in vivo* processes and are genomically stable over multiple passages. Moreover, they are self-renewing and can be propagated, cryopreserved and resuscitated without compromising the genetic identity (Kumari et al., 2020).

Organoids have essential properties that in light of the biodiversity crisis need to be addressed as well as a focus point for further biobanking strategies. Because organoids can be amplified *in vitro* and cryopreserved they can be used for multiple experiments within many different research aspects. Organoids provides models to investigate host-microbe interactions, virus-bacteria and parasite infections, studies on nutrient absorptions, genome editing, cellular agriculture, agricultural bioactive compound screenings, climate - veterinary and biomedical sciences ect (Beaumont et al., 2021). Developing organoids from different organs of animal species constitute a highly sophisticated model system that has the potential to reduce animal experiments significantly (Csukovich et al., 2022).

Climate change is playing an increasingly important role in the decline of biodiversity. Climate change has altered marine, terrestrial, and freshwater ecosystems around the world. It has caused the loss of local species, increased diseases, and driven mass mortality of plants and animals, resulting in the first climate-driven extinctions.

In our lab we focus on cellular agriculture from a climate perspective - moreover the production of animal sourced products from cell culture. Rather than farming animals, we can cultivate cells to create the same products and thereby support sustainable food production, where far less livestock would be needed. As animal agriculture is the second largest contributor to human-made greenhouse gas emissions and thereby one of largest drivers when it comes to climate changes, innovation in the form of for example cellular agriculture is highly needed.

Living algal collection of Sofia University “St. Kliment Ohridski” (ACUS) - important ex-situ biodiversity conservation facility, which maintains high-quality algal strains

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The collection of living algae of the Department of Botany, Faculty of Biology of the University of Sofia ‘St Kliment Ohridski’ was registered under № 965 in the World Data Base of Microorganisms (WFCC-MIRCEN World Data Centre for Microorganisms, Japan) on 13.04. 2010 with the acronym ACUS (Uzunov et al. 2012 - https://www.academia.edu/15763711/ACUS_the_new_collection_of_living_aeroterrestrial_algae_of_the_University_of_Sofia_St_Kliment_Ohridski). The presentation follows briefly the history of the collection since its first development in 60s of 20th century with transformation of the methods applied in cultivation from liquid to solid agar cultures, the new methods used in the collection of the materials (e.g., Gärtner et al. 2010: chrome-extension://efaidnbmnnnibpcajpcglclefindmkaj/https://www.zobodat.at/pdf/BERI_96_0027-0034.pdf), and its recent content, enriched by algae from different ecological groups The core of the collection comprised the aeroterrestrial algae from different regions and habitats of Bulgaria, but it keeps also materials from Asia Minor, Antarctic and Central Europe (Uzunov et al. 2012). In addition, nowadays ACUS stores algae from aquatic habitats and thermal springs. Currently, more than 150 species represented by 231 strains from different taxonomic phyla (Cyanoprokaryota, Chlorophyta, Streptophyta, Ochrophyta) are kept in living state on solid agar, enriched by Bold Basal Medium (BBM). In the frame of the current SUMMIT project (Contract 70-123-11/ 27.02.2023 with Sofia University “St. Kliment Ohridski”) the collection equipment is undergoing renovation. Moreover, nowadays, when phycoprospecting which searches for original valuable algae, is gaining serious scientific awareness, the original algal strains of ACUS, have been increasingly subjected to molecular-genetic, biochemical and biotechnological investigations. For example, three original strains of the streptophyte genus *Klebsormidium* have been genetically investigated (Stoyneva-Gärtner et al. 2019). The role of one of them, *Klebsormidium nitens* ACUS00207, for sustainable phosphorus management in wastewater treatment plants was demonstrated (Valchev et al. 2021) being compared with that of the chlorophyte *Desmodesmus* sp. (ACUS00808) (Valchev et al. 2019). Later, the strain ACUS00207 and the strain *Tetradesmus obliquus* (ACUS00220) were used in screening the resource recovery potential of onsite technology that involves algae-based post-treatment in the last steps of the conventional biological domestic wastewater treatment (Valchev et al. 2023). The phylogenetic and biochemical analysis of five *Visheria/Eustigmatos* strains revealed a rich and diverse carotenoid content, which showed their great biotechnological potential, but also enlarged the knowledge on the pigment composition of the ochrophyte class Eustigmatophyceae (Stoyneva-Gaertner et al. 2019; Stoykova et al. 2019). Genetic-molecular investigations were conducted on mixed environmental samples from more than 43 Bulgarian wetlands, revealing interesting toxin-producing cyanoprokaryotic strains from the genera *Microcystis* and *Cuspidothrix* (Radkova et al. 2020; Stoyneva-Gärtner et al. 2021, 2022, 2023; Uzunov 2021 a,b). We strongly believe, that future studies in such aspects will reveal the great industrial potential of algae cultivated in ACUS.

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Biobank of Megadiverse Fauna of Brazil

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The Cell Bank established about 40 years ago by Dr. Yatiyo Yassuda and his research group - of which I was part developing scientific initiation, master's, doctorate and postdoctoral projects - is currently under my responsibility at LEEV, Butantan Institute. We keep samples frozen in liquid nitrogen of amphibians, reptiles, rodents, bats, marsupials, carnivores, and primates collected in different Brazilian biomes for biodiversity conservation purposes. Financial support is provided by FAPESP, CNPq, and CAPES.

Session IV: Biobanking in Megadiverse Countries and the Southern Hemisphere

Chair- Kim Labuschagne

Pangolins: cultural use, illegal trade and the scientific importance of biobanking specimens in South Africa

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Pangolins (Order: Pholidota) are considered the most heavily poached and illegally traded group of mammals on Earth. In recent years, the primary source of pangolins traded mainly to Asia has been from the African continent. West African countries being the epicenter, in particularly Nigeria. Prior to this demand from Asia, pangolins where harvested for bushmeat in central and West Africa where they are still considered a delicacy. To a lesser extent, their body parts, in particularly their scales, are used for spiritual and cultural medicine purposes. In South Africa, the resident Temminck's pangolins are culturally used for a number of spiritual and medical remedies such as the bringers of good luck, warding off evil or bad omens and the bringer of rains and helping to alleviate various medical conditions. This use of pangolins is very small and considered insignificant as a threat to the species. However, the illegal trade has increased significantly as the Asian demand and high prices offered has reached local communities in South Africa. Police intelligence operations have been successful in many cases and arrests since 2017 involved 479 suspects intercepted and arrested with 237 pangolins. A number of these pangolins are so compromised they do not survive medical treatment and rehabilitation. These mortalities are housed at the SANBI Biobank in Pretoria where they are carefully logged into the system with police case numbers, medical records and any other history. It is here that scientists can gain access to this biological material of a rare and endangered species of which very little is known to science. Further studies on this material include fields of science such as evolutionary history, molecular taxonomy, anatomy, and parasitology and contributed significantly towards a better understanding the origin of the species, its taxonomy, anatomical adaptation towards digging, its unique parasite community and reproductive anatomy. In its role as a repository for (often rare) biological material, SANBI's relatively new but modern biobank has contributed significantly towards scientific investigations in a relatively understudied genera and serves as molecular bank for South Africa biodiversity.

Biobanking in a megadiverse country: a brief review of Brazilian current initiatives.

Paulo Holanda

Bioquallis Consulting, Curitiba, Paraná – Brazil

Biobanks play a very important role in preserving and making available biological resources derived from humans, animals, plants and microorganisms for scientific research and other purposes. In Brazil, they are fundamental in underpinning research and sustainable development, making biological material and associated data available to the scientific community and strategic sectors such as health, environment, agriculture and industry. Furthermore, by preserving biological resources representative of Brazilian biodiversity they greatly contribute to the understanding and conservation of species and ecosystems. However, Brazilian biobanks face major challenges in biobanking, such as legal, political, and cultural issues related to access/use of biological material itself and the knowledge generated from these resources that represent the autochthonous biodiversity. Even so, some Brazilian institutions have been promoting relevant and very promising initiatives, contributing significantly to biobank activities that results in innovation, environmental sustainability, improvement of public health and well-being of the population. These initiatives range from strengthening (or organizing networks of) Brazilian biobanks that represent the genetic diversity of biological material used for scientific and technological research, conservation and provision of services to newly and modern gene banks aiming to preserve biodiversity, stimulating the bioeconomy and valuing the knowledge of local communities through the use of blockchain technology. Finally, Brazilian biobanking initiatives are crucial not only for the conservation of the indigenous biodiversity, but also for significant advances in several areas of knowledge globally and, to this end, it is essential to continually pursue ways to continue supporting and strengthening these initiatives, thus ensuring the conservation and responsible use of biological resources.

Biodiversity Biobanks South Africa: A distributed network of repositories for South Africa's rich biodiversity.

*Mudzuli Mavhunga & Michelle Hamer

Biodiversity Biobanks South Africa, South African National Biodiversity Institute

From land to ocean, South Africa is recognised for its high levels of faunal and floral species richness and is considered one of the 17 megadiverse countries of the world. Eight of the world's 36 biodiversity hotspots are found on the African continent, and three of these, namely the Cape Floristic Region, the Succulent Karoo, and the Maputaland-Pondoland-Albany are found in South Africa. Habitat loss and fragmentation, invasive alien species and unsustainable harvesting are among some of the major threats to biodiversity in the country. The National Red List assessments indicate that 10% of South Africa's birds and frogs, 20% of its mammals and 13% of its plants are threatened, with some species extinct in the wild. In addition, South Africa's microbial diversity has potential for use in bioprospecting for a range of industries, and the country also has indigenous livestock breeds and crop cultivars that are adapted to local conditions. Guaranteeing that there is a comprehensive representation of this biodiversity in national biobanks by ensuring storage and distribution of quality samples for research and development is crucial for the preservation of iconic and highly endangered species.

South Africa has a wide range of biomaterials collected over 20 or more years and distributed across several biobanks and research institutions. These biobanks have however been largely managed independently, with no nationally accepted standards or practices for collection, storage, and distribution of biomaterials. In recognition of the need for a national biodiversity biobanking research infrastructure that is accessible to all researchers, the Biodiversity Biobanks South Africa (BBSA) was established by the Department of Science & Innovation as one of several South African Research Infrastructure Roadmap projects. This research infrastructure provides a platform for co-ordinated and collaborative networking across existing biodiversity biobanks that represent all components of South Africa's biodiversity. The objectives of the BBSA include increasing the range of samples deposited and stored across the network, ensuring the biomaterials are readily accessible and made available to all researchers; ensuring that biobanks render services that align with national, regional, and international standards; facilitating training for biobank staff and users; and actively contributing to national, continental, and global initiatives. Participation in the BBSA is either as Core- or Affiliated-biobanks. Core biobanks support open access to biomaterials, adopt and implement standardised procedures and guidelines, while Affiliated biobanks participate only in some activities and initiatives and are not bound by the standards and procedures agreed upon by Core facilities. The network currently comprises over 20 biobanks, storing and managing collections of frozen plant and animal tissues, DNA extracts, microbial cultures and much more.

The Importance of the Humboldt Institute Tissue Collection for biodiversity research and conservation in a megadiverse country

Gustavo A. Bravo[1*], Kevin Borja[1], Amalia Díaz[1], Sandra P. Galeano[1], Mailyn González[1], Angela L. Gutiérrez[1], Luis M. Leyton-Ramos[1], Angela M. Mendoza-Henao[1], Jhon C. Neita[1], Luz Eneida Ochoa[1,2], Nicolás Reyes-Amaya[1], Socorro Sierra[1], Eduardo Tovar[1], *Shairy Vergara Sandoval*[123] Carolina Gómez-Posada[1]

[*]*Speaker*

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The tissue collection of the Humboldt Institute is a natural legacy of Colombia's genetic biodiversity available to society. Its mission is to preserve long-term genetic samples of the biodiversity of Colombian fauna and flora as a source of information for studies that contribute to the inventory of biodiversity in a mega-diverse country, and provide tools for its adequate knowledge, management, and conservation. The collection currently has approximately 45,000 catalog numbers, with plants (ca. 43%) and birds (ca. 25%) being the best-represented groups. Close to 36,000 tissues (ca. 80%) have voucher specimens and the collection is available for on-line consultation in CEIBA-Humboldt, SIB Colombia, and GBIF. Thanks to the support of GGBN, we were able to synchronize and update the information of ca. 10,000 samples in the tissue database with the databases of the plant, vertebrate, and invertebrate collections of the Humboldt Institute, which will facilitate their incorporation into the GGBN data network. Currently, the main sources of genetic data from the collection are barcoding/metabarcoding analyses and phylogenetic studies targeting specific groups. The Humboldt Institute team is now focusing on improving field and laboratory protocols to ensure the quality of the information and obtaining high-quality DNA and RNA for genomic and transcriptomic studies. Furthermore, following the One Health framework, efforts will be directed toward studies aiming to alleviate the triple planetary crisis - climate change, biodiversity loss, and degradation of natural ecosystems. Samples in the collection are available for today's science and will be available for tomorrow's science.

Infrastructure and management of a large-scale genome bank in a megadiverse developing country. A case study in Ecuador

*Diego A. Paucar; Santiago R. Ron

**Speaker*
Museo de Zoología QCAZ, Pontificia Universidad Católica del Ecuador, Quito, Ecuador

The tropics are home to the majority of the world's biodiversity, however not many tropical countries hold large-scale biocollections, few make an effort to preserve genetic resources and even fewer make their resources easily accessible to the public. One notable exception is the specimen collection and genome bank of the Pontificia Universidad Católica del Ecuador (PUCE). The PUCE genome bank currently houses 85949 tissue samples and 8403 DNA extracts comprising animals, plants, and fungi, making it the largest genome bank in Ecuador and one of the largest in Latin America. Its core biocollections focus on Ecuadorian species but also include samples collected worldwide, product of donations and exchanges with international institutions. The Division of Herpetology of the Museum of Zoology QCAZ at PUCE spearheaded the development of the infrastructure and database currently in use for the genome bank. Along with the implementation of strict preservation protocols and over two decades of increased collection efforts of amphibians and reptiles, the Division of Herpetology is responsible for nearly 70% of the genome samples held at PUCE. Herein, the QCAZ herpetology collections are discussed as a case study of the management of a large-scale genome bank in a megadiverse developing country. All live specimens that arrive to the QCAZ herpetology collection have liver and muscle samples extracted and preserved in cryovials with 96% ethanol as part of the standard preservation protocol. The cryovials have a position assigned in cardboard freezer boxes coded with an alphanumeric coordinate system and are stored at -80°C in ultra-low temperature freezers. The specimen and genome bank records are publically accessible through BIOWEB and the GGBN database. The BIOWEB database includes information on collection data and voucher specimens; the administrative internal database has additional information on preservation and laboratory procedures for the specimens, tissue samples, DNA extracts, and cryovial coordinates. PUCE is a core member of the Global Genome Biodiversity Network.

Using biodiversity biobanking to enhance plant conservation in the megadiverse country South Africa.

Ross D. Stewart & Michelle van der Bank

African Centre for DNA Barcoding (ACDB), University of Johannesburg

South Africa is recognized as one of the world's biodiversity hotspots, particularly regarding plant diversity. It boasts an estimated 24,000 vascular plant species, a significant proportion of which are exclusive to its three biodiversity hotspots: the Cape Floristic Region, Succulent Karoo, and Maputaland-Pondoland-Albany. Despite the wealth of botanical riches, the utilization of biodiversity biobanking remains surprisingly limited, particularly among local researchers. This presentation will explore the valuable contributions made by the African Centre for DNA Barcoding (ACDB) in the effort to collect and document the plant life of southern Africa. Over the past 15 years, ACDB has accumulated 11,562 plant specimens, representing an array of 2,019 genera and spanning 349 families. ACDB has also put considerable effort into safeguarding the African cycads (*Encephalartos*; Zamiaceae), recognizing their extreme vulnerability and threat of going extinct. Investing in our DNA bank has not only allowed us to contribute to understanding South Africa's botanical knowledge but also provided other researchers with material to help conserve our country's biodiversity.

Workshop I: Policies for Molecular Collections, GGBN Data Standard, and Workflows for Publishing Data

Chair- Astrid De Mestier

Management of genetic resources in natural history collections using Specify collection management software.

Andrew Bentley
Biodiversity Institute, University of Kansas, Lawrence, USA

The Specify Collections Consortium currently services more than 340 collections at 101 institutions in 20 countries through our Specify 6 and 7 software packages and numerous data management and conversion services. In response to the genomic revolution in natural history collections, the ever increasing unique management needs of tissue collections and genetic resources along with the establishment of the Global Genome Biodiversity Network (GGBN) data portal, Specify collections management software (http://www.specifysoftware.org/) has extended its data model and tools to more effectively manage, publish, and integrate tissue and DNA extract data. We have achieved this by adding support for more genetic specific fields and tables along with items specific to the GGBN data schema. Specify's database design now includes a number of data fields and tables proscribed in GGBN standard vocabularies. We also realigned some of the underlying table relationships to address the needs of specimen curation and collection transactions for extract and tissue samples. Specify now also supports "Next Generation" sequencing metadata with fields to record NCBI SRA ID numbers for web-linking tissue and extract metadata to entries in the NCBI SRA databases. Specify also facilitates the linking and integration of data in support of the Extended Specimen ideal with the ability to link to Genbank sequence records in NCBI and vice versa.

With the ongoing evolution of the TDWG Darwin Core (DwC) standard for specimen data exchange, Specify has also increased Specify 7's data publishing capabilities to export collections data to any DwC or other standards-based, exchange schema. This generic, external schema mapping capability enables Specify collections to design and map data packages to publish their data to any community aggregator or collaborative project database based on Darwin Core while taking advantage of the ever-expanding DwC extensions. The development of these versatile new integration capabilities was in collaboration with, and through financial support from GGBN. This talk will showcase Specify's capabilities while highlighting the above changes in the context of delivery of museum tissue and extract data records to the GGBN data portal for aggregation.

Symbiota-based services for publishing genomic collections data

Nico M. Franz, Edward E. Gilbert, Azhar Husain, Rosie Liao, M. Andrew Johnston, Katelin D. Pearson, Gregory Post, Laura D. Steger, Lindsay J. Walker & Kelsey M. Yule.

Arizona State University, US

We review and forecast the prospects of the Symbiota software platform in the context of managing and publishing standard-compliant genomic biocollections data. Symbiota (https://symbiota.org) is an open-source biodiversity data management software that allows natural history and similar collections to actively manage and publicly share collections data following the Darwin Core data standard. More than 1,900 collections worldwide contribute to 56 Symbiota-based data portals, each of which serves as an aggregator of biodiversity occurrences connected by a shared taxonomic, institutional, geographic, or thematic focus. Symbiota portals increasingly support the Digital Extended Specimen Network as features have been developed to directly link specimen, sample, and observational occurrence records to a wide variety of ancillary information; including trait data, associated resources and publications, material samples, species checklists, datasets, and more. Genetic and genomic data can currently be linked to samples and specimens as associated resources, and ongoing Symbiota development aims to fully implement the GGBN data standard to facilitate discoverability and interoperability of sample-associated genomic data. The National Ecological Observatory Network (NEON) Biorepository and its complementary Symbiota data portal (https://biorepo.neonscience.org) are an early testbed for creating these linkages in the context of a large-scale, ecologically focused biobank. The NEON Biorepository archives nearly 100,000 samples and specimens annually, collected across 81 terrestrial and freshwater aquatic sites throughout the United States. Of the 400,000 samples and specimens archived to date, the NEON Biorepository has received and made available over 74,000 genomic extracts, 36,000 frozen tissue samples, and 96,000 frozen microbial samples. Many of these samples are already linked (i.e., extended) to derived NEON data products, which include externally managed metagenomic and barcode sequencing data. New frontiers for the NEON Biorepository and other Symbiota portals focus on automated integrations with other software components of the genomic data pipeline that will enable open, reciprocal and scalable data workflows. These components include biobanking software for biosample management, cloud computing and sequence data storage, bioinformatics pipelines for genome assembly and QA/QC, and systems for brokering submissions of genomic data to public repositories. Additional development is needed to ensure that the genomic data made available through these Symbiota portals conform to not only FAIR, but also CARE data principles, including the application of Traditional Knowledge and Local Contexts labels to genomic collections and sample data.

Policies handbook for molecular collections

Astrid de Mestier
Botanical Garden and Botanical Museum

Molecular collections, including tissues, cell cultures, environmental samples and nucleic acid (RNA/DNA) are increasing both in number and size worldwide. They provide crucial resources for researchers by making available a growing amount of data. Nevertheless, such collections need to be managed according to policies already in place, regarding how material can be acquired, used, shared, donated and disposed of.

A review of the “policies handbook in molecular collection”, published at the beginning of the year will be presented here. The handbook was produced in the context of the SYNTHESYS+ project and involved scientist from various institutions in Europe. Its purpose is to provide guidelines and recommendations to improve the management of biocollection databanks and to help institutions and researchers to navigate the legal and administrative procedures. It focusses on workflows to put in place, when sending material to other institutions or receiving it and on establishing guidelines to track data and permits associated to the collection’s items.

In this talk, we review the various chapters of the handbook, especially regarding the documents and legal information that can be associated to a collection item. How to best manage them in order to comply with ABS obligations? Here, we acknowledge the need for procedures and best practices and we provide clear, simple and efficient guidelines to facilitate it.

GGBN data standard and workflow for publishing data

Jörg Holetschek
Botanischer Garten und Botanisches Museum, Berlin, Germany

The FAIR principles (findable, accessible, interoperable, reusable) are increasingly applied to molecular collections, thus providing the scientific community with a growing amount of data. This data sharing requires the establishment of agreed community data standards as well as easy-to-use software implementations for data providers. This part of the workshop will provide an overview of the approaches to facilitate FAIR data sharing for molecular collections. We will discuss the basic principles of data sharing in biodiversity networks and introduce common community data standards, give an overview of the available tools and the steps required for potential data providers to publish their data to a network such as GGBN.

Session V: The Nagoya Protocal in Practice: Does it Affect my Field Work and Associated Research?

Chair- Gilberto Ocampo

Why is the Nagoya Protocol important for GGBN Collections and Biobanks? *Ex situ* collections best practices for benefit sharing.

Manuela da Silva

Fiocruz, Oswaldo Cruz Foundation

All nations have the sovereign right to manage their biodiversity and national systems for regulating access to genetic resources and associated traditional knowledge. The regulatory framework for research is defined by Access and Benefit Sharing (ABS) legislation, however other instruments, such as best practices and codes of conduct, are essential for its effective and sustainable implementation. Biological Collections and Biobanks, as important repositories and providers of genetic resources and associated information, play a central role in promoting Nagoya Protocol on Access and Benefit Sharing. The staff of these infrastructures need to be aware of the legislation of the country of origin of the genetic resources they use and distribute, in order to comply with it. GGBN Collections and Biobanks have engaged in these discussions to understand fully and appreciate the spirit and the letter of the laws and obligations being established. The result was the development of tools to manage ABS, including a best practice to ensure legitimate exchange and use of genetic resources. The GGBN Best Practice on ABS gives practical guidance for the day-to-day work of the institution, so that: a) it can understand its rights and responsibilities under the national laws implementing appropriate treaties and relationships with Providing Countries of biological material; b) its staff, authorized visitors and associates abide by appropriate laws and regulations when working in or on behalf of the institution; c) biological material entering the collections and biobank is obtained with appropriate legal certainty and can legally be retained; and that d) it manages effectively obligations and legal contracts entered into with Providers. Not all parts of this practice may be relevant or applicable for all institutions to implement. For more information visit: https://wiki.ggbn.org/ggbn/ABS_Fact_Sheet_and_Answers_to_Frequently_Asked_Questions

El Protocolo de Nagoya en México

San Vicente Tello, Adelita; Rojo Horta, Joel; Chamorro-Cobaxin, Baruch Xocoyotzin; Cheé-Santiago, Jocelyn

SEMARNAT, Mexico

La implementación de Protocolo de Nagoya (PN) en México ha significado un gran reto dada la gran riqueza biocultural de nuestro país. La actual administración, en congruencia con los principios que la rigen, ha desarrollado principios de política en torno a la soberanía de sus recursos naturales. Asimismo, elaboró con el Grupo de Trabajo Intersecretarial los Criterios de la Política Nacional sobre Recursos Genéticos y Conocimiento Tradicional asociado. Los retos que se enfrentan es el logro de objetivo del PN que se refiere Acceso justo y equitativo de los beneficios (ABS por sus siglas en inglés). Para lo cual, se trabaja en instrumentos regulatorios para armonizar las acciones de los proveedores y usuarios bajo un enfoque de respeto, protección y distribución justa y equitativa de los beneficios en un contexto de tecnologías e innovaciones emergentes.

The Nagoya Protocol and the EU ABS Regulation from a Users’ Perspective

Janina Bornemann

University of Bremen

If you are working with European partners or are considering doing so, you should be aware of the Nagoya Protocol and the EU ABS Regulation on compliance measures for users of genetic resources. For each EU Member State, a designated Competent National Authority (CNA) checks whether users of genetic resources comply with their obligations under the Nagoya Protocol and the EU ABS Regulation. In Germany, the newly introduced position of a "Nagoya Protocol Compliance Officer (NPCO)" helps researchers at their institutions to deal with the challenges of comply with the ABS regulations.

My presentation will introduce the EU ABS Regulation from a user's perspective. The Regulation was developed with the aim of ensuring due diligence under the Nagoya Protocol in the European Union. In Germany, there are frequent inspections by the German CNA, the Federal Agency for Nature Conservation (BfN). If the BfN finds users to be non-compliant, fines of up to $53,000 can be imposed, as well as orders to stop research, confiscation of material, and prohibition/withdrawal of publications. These sanctions are in addition to the sanctions in the provider countries, which are also notified by the BfN.

The day-to-day work of an NPCO deals with all the challenges posed to researchers by the Nagoya Protocol and the EU ABS Regulation, such as dealing with the many different legislations in the provider countries, the length and complexity of the processes for obtaining permits, and various challenges in communication with provider countries. Sometimes also the scope of the EU ABS Regulation differs from the scope of the legislation in the provider countries, making due diligence even more difficult.

In my role as NPCO, I will talk about the different challenges of the Nagoya Protocol and the EU ABS Regulation for researchers, how best to deal with them and give you tips on how to be compliant.

Community protocols as the rules to access and benefit sharing of genetic resources and traditional knowledge associated to genetic resources at the local level

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Community protocols, biocultural community protocols, etc. are new instruments supported by an international binding agreement or Nagoya Protocol on access to genetic resources (GR) and benefit sharing from their utilization, which is part of the Convention of Biological Diversity. Nagoya Protocol rules not just the genetic recourses, but also traditional knowledge (TKAGR) from indigenous peoples and local communities (IPLC) associated to these genetic resources. Traditional knowledge is defined as *"a living body of knowledge that is transmitted from one generation to another in the same community. It is usually part of the cultural and spiritual id replace with ratified entity of the community"*[1] and its importance relays on being the first primary source of information on the existence of genetic resources[2] saving time and money in bioprospecting activities. For many decades, TK has been the base of the chemical and biotechnological industry in the world. Before accessing to GR and TKAGR any person or institution interested in these kinds of activities, such as researchers and businesspersons (users) shall follow the rules under Nagoya Protocol. Other international instruments and legislation on access and benefit sharing (ABS) and national legislation on ABS, to obtaining the consent from the TKAGR holders and, in many cases, the access to genetic resources belonging to indigenous territories and agreed how the benefit sharing will be trough Mutually Agreed Terms.

Nagoya Protocol Art. 12 stablishes community protocols are one of the customary laws that parties in accordance with national legislation, shall take into consideration among other obligations in regard to the TKAGR. Community protocols, biocultural community protocols, and so on, are new instruments that regulates the relationship between communities and external agents, through the documentary recognition of customary law and the forms of internal organization of the communities. These instruments have been developed by using diverse participative methods, and in full respect for the collective decision-making processes of the stakeholders and associated networks. These instruments constitute a new way to approach communities not just to access GR but also different interventions that could be harmful to the communities.

Regarding the research of genetic resources, community protocols play a critical role, as a new approach for academics and businesspersons who must follow these customary rules before uptake bioprospecting or research initiatives, allowing to engage with IPLC in a more equitable manner and share benefits, embedding ethical rules and principles for TK manage.

The experience of Oaxacan micro-regional biocultural protocol shows how communities' rules future engagement with academia, business sector, NGOs, governments, etc. to protect Agave Sp. Genetic resources, as well as to promote local organization and joint research, self-access for GR and TKAGR, helping on addressing bioprospecting and GR utilization initiatives. It is important to know these procedures and apply them to have compliance with the national and international regulations on GR and TKAGR.

The Nagoya Protocol: Where to start? Build your ABS Strategy

Melania Muñoz García & Amber H. Scholz

Leibniz Institute DSMZ German Collection of Microorganisms and Cell Cultures

You have heard about the Nagoya Protocol, but are not sure where to start? The German Nagoya Protocol HuB is here to help!

The "access and benefit-sharing" principle, or ABS for short, is about the commitment of giving benefits to the countries where the biological materials come from, and it is part of the global targets on conservation, restoration and sustainable use of biodiversity.

The Nagoya Protocol establishes the international bases to implement the ABS principle, however, the regulations differ among countries and understanding the legal obligations can be complex even for experienced professionals. That is the reason why the GNP-HuB develops easy-to-understand materials and tools to help researchers to comply with the Nagoya Protocol.

Biological collections and biobanks, which receive, keep and distribute biological material all around the world, must be aware of ABS to legally manage the biological material. Failure to comply can result in legal consequences.

During this talk, a hands-on activity will help researchers to be prepared for their ABS processes, including the preliminary steps: what to do before starting with the ABS process; defining your research needs: the "red line" for any negotiations; working out what types of benefits that can be shared; and exploring options for future research. Keeping in mind all the details during the process will save you time in the future.

The GNP-HuB project will help you to navigate the ABS world. You can get more information on the HuB project website, check it out here: https://www.nagoyaprotocol-hub.de/.

Digital Sequence Information and open biodata resources

Chuck Cook & Guy Cochrane

Global Biodata Coalition, University of Cambridge

Can you imagine conducting research in a world with restricted access to genomic sequences and databases? Decisions made in international fora could adversely affect access to data and scientists must be aware of this.

Life scientists have for decades shared research data through open-access databases that now form a global infrastructure of thousands of interlinked resources, providing access to deposited and curated data across all life science domains. These biodata resources are critical to biological, life science, and biomedical research across academia and industry; they have substantial impacts both in fundamental and applied research, and they underpin and amplify the research investments made by funders. Restricting the open availability of data in these resources would adversely affect life sciences research worldwide.

The UN Convention on Biological Diversity (1992) established the principle of access and benefit sharing, in which users of genetic resources must share benefits with the source countries of biological materials. “Genetic resources” originally referred only to physical samples, and the Nagoya Protocol established the basis for a bilateral system to guarantee benefits. In recent years, though, benefit sharing from the use of digital sequence information (DSI) has become an important topic during international negotiations. DSI is a policy term referring broadly to genomic sequences and other related digital data deposited in global databases.

Any benefit sharing regime risks inhibiting free and open access to biological data: restrictions on access to sequence information will have knock-on effects for the thousands of other data resources using that information to enhance their own services.

The principle of “fair and equitable sharing” aims to ensure that the benefits of DSI, whether monetary or non-monetary, should be shared with the originating country under the assumption that DSI is mostly used by high-income countries, and that benefits should flow unilaterally to provider countries. However, recent work by Scholz and collaborators (2021) has shown that all countries use DSI, with data exchanged multi-laterally across the globe, so any system of benefit sharing will need to accommodate this global usage.

Participation of the scientific community in the discussions has been crucial in highlighting the importance of open access to DSI and to advocating a multilateral approach that will ensure benefit sharing without hindering research and development.

In 2022, at the Kunming-Montreal COP15, the Parties agreed to develop a solution for the sharing of benefits arising from the use of DSI and also recognized that a multilateral approach has the potential to meet the criteria identified by the parties.

The current COP agreement recognizes the importance of open data but is likely to demand more information, such as sample provenance, from data submitters—including biobanks and biodiversity projects—to allow usage tracking. The involvement of the scientific community in international discussions on DSI is key to ensuring that the multilateral mechanism for benefit sharing from DSI is designed according to scientific practices and does not hinder research and development. The DSI Scientific Network (www.dsiscientificnetwork.org) provides an opportunity for researchers to be involved in this process.

Global Genome Biodiversity Network

Poster Session

The GGBN Document Library – a Knowledge Base for Genomic Biodiversity Biobanking

Jackie Mackenzie-Dodds, *Natural History Museum, London, UK*

The GGBN 'Document Library' serves as a one stop shop knowledge exchange platform for biodiversity biobanks, researchers, and institutions via software for secure and compliant (copyright, restricted/open access permissions) online document archiving. Created in 2014, tested and developed ever since, this resource now holds >1K papers and enables scientists to perform full text searches, tagging of documents, publications, use cases, and biodiversity biobanking information in the following areas:

- Biobank Management (including Governance, Business Models, Health and Safety).
- Curation Protocols (including specimen and sample field collection, sample preparation, shipping, laboratory curation and storage methods) for Animals, Plants and Microorganisms.
- Education and Training Tools (including workshop documents and publications, interactive session protocols and technology).
- GGBN Conferences (Conference documents archive).
- GGBN Information (GGBN-specific information and GGBN-produced materials).
- Information and Data Management Systems (Data standards, data workflows, pipelines, portals, database interoperability).
- Regulation and Legislation: ABS: Documents and publications regarding access to genetic resources and benefit sharing (ABS), including examples/templates for Permits/PIC/MAT/MTA/How To publications/case studies across the globe), Non-ABS (CITES etc), and Shipping Regulations.
- Research Protocols (including laboratory specimen and sample analysis: e.g., species-specific extraction, amplification, sequencing for fresh and archival/ancient material).
- Biobanking Programme/Initiative Publications including CryoArks, Darwin Tree of Life and SYNTHESIS.

Members of the GGBN Document Library team will be present in person at the Poster Sessions and we welcome all GGBN 2023 conference delegates to visit and learn from live demos and hands on tuition how to search the library, upload their own documents and much more. Please first request a GGBN Document Library account (free for everyone) by contacting library@ggbn.org and bring your login details with you on the day.

The Frozen Zoo® – A living collection 50 years in the making

Kathryn R. Thomson

San Diego Wild Life Alliance

Founded by Dr. Kurt Benirschke in the 70's, the Frozen Zoo® is the largest collection of its kind today. Housing viable cell lines from nearly 11,000 individuals of almost 1,300 vertebrate taxa, this ever expanding repository is a wealth of potential for various applications. In addition to the impressive collection of viable cell lines, the Frozen Zoo® also contains reproductive cells and tissues, and plant tissues.

All samples are taken opportunistically, whether shortly after the animal has died, or during a routine medical exam. An average of 245 new individuals are added into the collection in a given year, approximately 40 of which represent new species. Each new accession into the Frozen Zoo® is a welcome addition and increases the potential for species conservation.

The species and subspecies represented in this collection account for about 5.4% of all threatened birds, amphibians, reptiles, and mammals classified by the IUCN Red List. There are also approximately 700 more threatened species occurring within current zoo and aquarium collections that, if banked, could increase this representation to over 16% (Mooney et al. 2023). Currently, three of the species in the Frozen Zoo® are extinct, and there are an additional six extinct in the wild species represented.

The increasing demand for high quality genomic resources and prospects for species genetic rescue highlight the importance of cell line collections such as the Frozen Zoo®. These living cells can be expanded for applications beyond what is possible with stored non-viable tissue and DNA such as the development of stem cell technology and tissue engineering, genomics, and assisted reproduction.

Viable cells from this collection have been used in a variety of different research projects. Samples have been provided to numerous institutions for projects that lend a conservation benefit. Over the last 10 years alone, approximately 230 cell lines have been sent out to researchers at over 25 institutions throughout the United States.

A Role for GigaScience Press in Tackling the Biodiversity Data Gap

Chris Armit, Mary Ann Tuli, Yannan Fan, Nafisa Qazi, Christopher I Hunter, Scott Edmunds & Laurie Goodman

GigaScience

The alarming decline in biodiversity is a global issue, and capturing and sharing biodiversity data is crucial in tackling this issue and in combating vector-borne diseases, which account for one quarter of all human infectious disease worldwide. From a data perspective, there is a huge data gap between the biodiversity hotspots of the planet, and the proportionately small amount of environmental specimen data that we have from these regions. This has a massive impact on our understanding of global health.

To tackle the data gap, in 1999 the Organisation for Economic Co-operation and Development (OECD) created the organisation Global Biodiversity Information Facility (GBIF) as a central repository for archiving and accessing biodiversity data. Digitisation of museum and academic collections is a key component of this repository, but there is also a need for occurrence records and supporting BioBank facilities for physical specimens and the supporting genomic sequence data.

A unique opportunity in 2022 was the partnership between GigaScience Press, the Global Biodiversity Information Facility (GBIF), and the TDR, the Special Programme for Research and Training in Tropical Diseases hosted at the World Health Organization (WHO). The focus of this partnership was the publication of new datasets that present biodiversity data for research on Vectors of Human Diseases. Data Release papers from this partnership on vectors of human disease were published in *GigaByte* Journal as part of a thematic series, which mobilised more than 500,000 occurrence records and 675,000 specimens from more than 50 countries. Due to the international nature of the vector-borne disease data, the thematic series was published in multiple languages.

The role of the GigaDB team in this partnership was to assist the data peer review process, and to provide the necessary support for Data Release papers that required curation. This involved data auditing and providing a data review for each submission, and ensuring the data were open and FAIR (Findable, Accessible, Interoperable and Reusable). We report on use case scenarios that combine occurrence records with genomic sequence data, and how this can increase our understanding of the global transmission of vector-borne human disease. In addition, we highlight our potential to incentivise the digitisation and open publication of other data catalogues, such as BioBank sample catalogues.

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