

Global Genome Biodiversity Network

Jonathan Coddington GGBN Executive Committee Member Smithsonian Institution

Members of the Interim Executive Committee

Global Genome Initiative





Preserving and Understanding the Genomic Diversity of Life

Just One Genome!





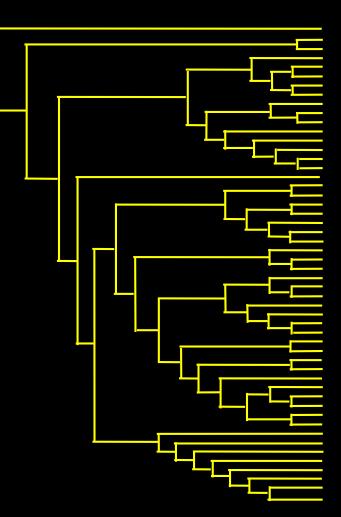


Tree of Life

94

- DOMAINS/KINGDOMS 3
- PHYLA / DIVISIONS
- CLASSES 364
- ORDERS 1413
- FAMILIES ~ 9654
- "GENERA"
- SPECIES
- >15,000,000?

~ 200,000



GGI Goals After



Before

Hard-to-find tissues	Public
Ambiguous quality	Genome-quality
Ambiguous ownership	Enterprise biorepositories
Individual scientists	Benefit-sharing & access
Expensive	Affordable
"Boutique"	Coordinated, strategic
Mostly model organisms	All branches of Life
Classical taxonomy	Gene-based identification
Experts only	Citizen technology
	Most organisms anywhere
Limits environmental monitoring,	Accurate, scalable, cheap tech to
conservation, biotech, basic	address important challenges
research	

GGBN Goals

- Standard for sharing tissue and DNA information
- Institutional directory (GRBio)
- Platform for aggregating member data and portal
- Best practices for management and stewardship of genomic samples
- Partners with different regional and taxonomic focus
- Identify global gaps in GGBN collections







Smithsonian Institution Forest Earth Observatory

Wytham Woods, UK

Haliburton Forest, Canada Wabikon Lake, WI

Wind River, WA

Yosemite, CA

Hawaii, USA

Panama

La Planada, Colombia Yasuni, Ecuador Amacayacu, Colombia Manaus, Brazil

all and the second

Harvard Forest, MA USA SERC, MD USA SCBI, VA

Luquillo, Puerto Rico

Korup, Cameroon Rabi, Gabon Ituri, Dem. Rep. Congo

Ilha do Cardoso, Brazil

Mo Singto, Thailand Doi Inthanon, Thailand

Huai Kha Khaeng, Thailand Khao Chong, Thailand Muchmalai, India

> Sinharaja, Sri Lanka Pasoh, Malaysia Bukit Timah, Singapore Madagascar

Xishuangbanna, China Dinghushan, China Changbaishan, China

> Tiantong, China Gutianshan, China Fushan, Taiwan Lienhuachih, Taiwan Nanjenshan, Taiwan Hong Kong, China

Palanan, Philippines Brunei Danum Valley, Malaysia Lambir, Malaysia

Wanang, PNG

NASA

Future Sites

GGBN

54 plots, 10,500 species, 4,346 genera ("trees") ~60% world total?













Chesapeake BaySequences572,290Species1,204Unknown40.9...91% correct for families; 85% for genera

Fort Pierce FL 409,613 1,391 28.3

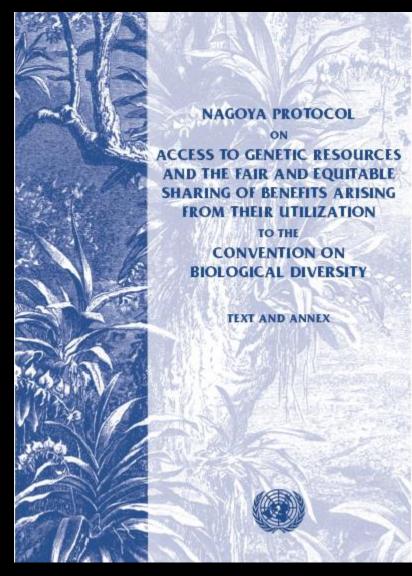


Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits

(Convention on Biological Diversity)

- Entered into force Oct. 2014
- Greater legal certainty and transparency
- Promote and encourage research
- Awareness-raising & technology transfer
- In-country research capability and institutions

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GGBN Value Proposition One

- Make genomic collections discoverable for research through a networked community of biorepositories
 - Provide biorepositories with standardized methods for making genomic collections discoverable;
 - Provide biorepositories and contributors with community standards and best practices for the collection and data management of genomic samples;
 - Provide contributors with access to a community that provides storage facilities for and access to information on their genomic collections.

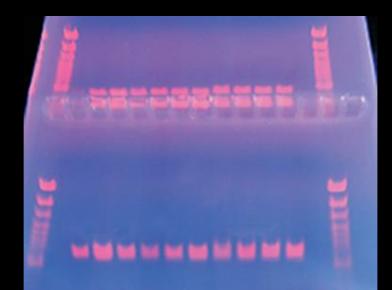




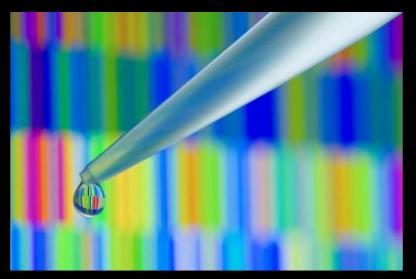


GGBN Value Proposition Two

- Provide trusted and transparent access to genomic samples for users and contributors through an ABS framework—supporting the trust from biodiversity-rich countries and organizations.
- Guide global biorepository growth strategically to preserve Life's genome



GGB





- Institutional Biorepositories plan to become core members and:
- Commit to preservation of genomic collections and associated metadata for research;
- Registered as a biorepository (GRBio);
- Enterprise level, reliable data system;
- Will contribute data to GGBN complying with GGBN standards

Core Membership

• An Associate Member that is contributing data to GGBN.

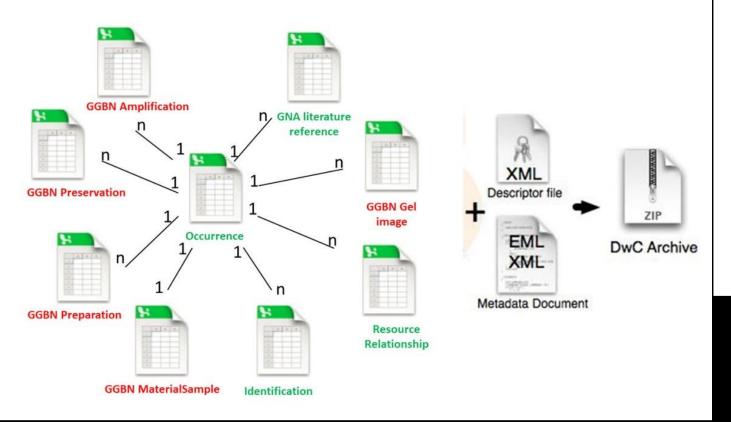
GGBN Data Portal Milestones

Oct 2011 1st Intl. workshop, DC July 2012 2nd Intl. workshop, Copenhagen 2013 BGI, China National Gene Bank, Ocean Sampling Day Spring 2013 NSF Workshop (USA,) August 2013: GGBN & DNA Bank Network sites merged Fall 2013 DFG Grant (3 FTE's 4 years) November 2014: Private beta release of GGBN Data Portal June 2015: 1st public release of GGBN Data Portal November 2015: Submit GGBN Data Standard to TDWG review and ratification process

GGBN

November 2015: 2nd public release of GGBN Data Portal

GGBN Data Standard



Extensions for Darwin Core Archives

Class dwc:Occurrence properties

Class dwc:occurrence properties: dwc:occurrenceID - the identifier column that will ink Occurrences and Samples. dwc:colatolgNumber (UnitDUnitD) - will be in the associated Occurrence record. dwc:collectionCode (UnitSourceID) - will be in the associated Occurrence record. wc:institutionCode (Unit/SourceInstitutionID) - will be in the asso warks (Unit/Notes) - dwo already has this term, no need to add it.

mple propertie

proposed identifier for the Sample class. IIIDate - Date until ordering of sample is blocked, year-month-day (e.g. 2012-10-26) marks - Description of why the sample is blocked, e.g. feedback on use required from original ion valu

ionUnit - Unit of DNA concentration, e.g. notul nDate - Date of DNA extraction (DNA only)

Method - Method or extraction protocol used for DNA extraction (DNA only n who carried out DNA extraction (DNA only) od - Method or protocol used for secondary purification of already extracted g

any which delivered or donated the DNA samp

ef for borb DNA and tassue Mother - Date winn quality parameters were determined, used for both DNA and basue whanec280, 230 - Ratio of absorbance at 300 nm and 230 nm assessing DNA purity (mostly versame, incloades many EDTA, canorhydrate, prevano, (DNA samples or many EDTA) whanec280, 280 - Ratio of absorbance at 250 nm and 280 nm assessing DNA purity (mostly dary measure, indicates mainly EDTA, carbohydrates, phenol), (DNA samples only) mpleType - tissue, DNA, RNA

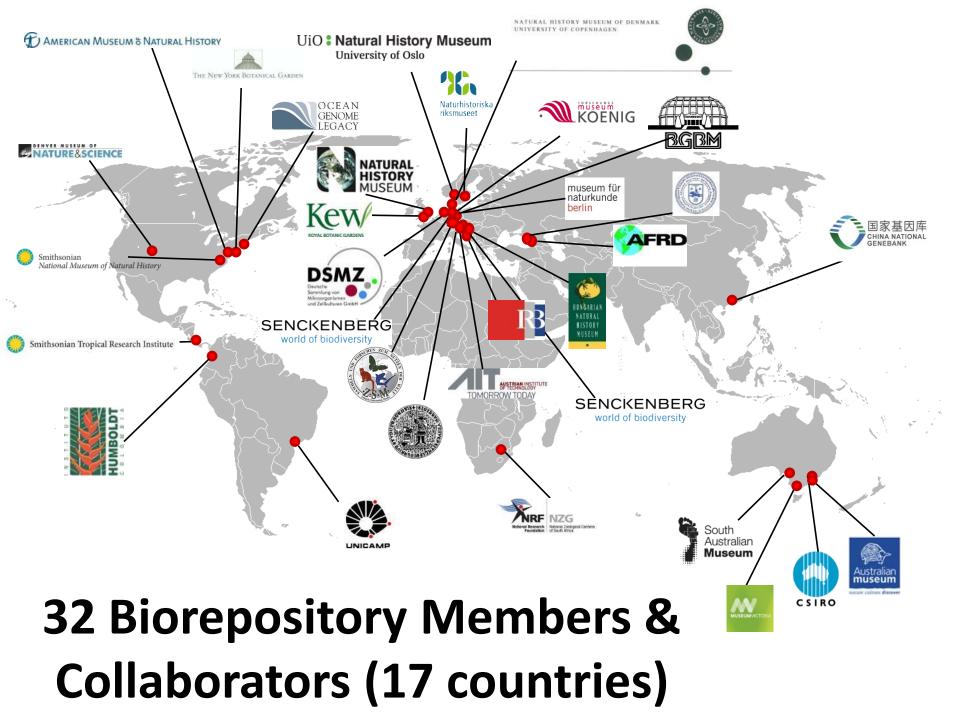
ndOfUnit - muscle, blood, oDNA (specify based on controlled vocabulary ollectingPermit- Controlled vocabulary: not required, yes, no, unknow ollectingPermitURL- URL to document

ssBenefitSharing- Controlled vocabulary: not required, yes, no unknown esBenefitSharing (BL -) (BL to document) nefftSharingUL-URL to docubulary: not required, yes, no unknown nefftSharingURL-URL to docuburnt exMethod - used for both DNA and tissue ne - fboolenyi, thus if source is gone ecularWeight (Mof/Weight) - Controlled vocabulary: yes, no (DNA only),

onProcess - Process used in preparing the specimen or sample arationMaterials - Materials and chemicals used in the preparation of the specimen redBy - Person and/or institution responsible for or effecting the preparation rationDate - Date of preparation, year-month-day (e.g., 2012-10-26)

July 2014: Released for Public Review, implemented in **IPT/DwC-A and BioCASE/ABCDDNA**

November 2015: Submit GGBN Data Standard to **TDWG review and ratification process**



GGBN **Taxa and Samples Per Year** --Samples Taxa

White Paper on Data Portal



Nucleic Acids Research Advance Access published November 19, 2013 Nucleic Acids Research, 2013, 1–6 doi:10.1093/nar/gkt928

The Global Genome Biodiversity Network (GGBN) Data Portal

Gabriele Droege^{1,*}, Katharine Barker², Jonas J. Astrin³, Paul Bartels⁴, Carol Butler², David Cantrill⁵, Jonathan Coddington², Félix Forest⁶, Birgit Gemeinholzer⁷, Donald Hobern⁸, Jacqueline Mackenzie-Dodds⁹, Éamonn Ó Tuama⁸, Gitte Petersen¹⁰, Oris Sanjur¹¹, David Schindel² and Ole Seberg¹⁰

¹Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Berlin 14195, Germany, ²National Museum of Natural History Smithsonian Institution, Washington DC 20013, USA, ³Zoological Research Museum Alexander Koenig, Bonn 53113, Germany, ⁴Wildlife & Environment Society of South Africa, Pretoria 0001, South Africa, ⁵National Herbarium of Victoria, Royal Botanic Gardens Melbourne, South Yarra, VIC 3141, Australia, ⁶Molecular Systematics Section, Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey TW9 305, UK, ⁷Systematic Botany, Justus-Liebig-Universität, Giessen 35392, Germany, ⁸Giobal Biodiversity Information Facility (GBIF), Copenhagen Ø DK-2100, Denmark, ⁹Department of Zoology, The Natural History Museum, London SW7 5BD, UK, ¹⁰Natural History Museum of Demmark, Copenhagen K DK-1307, Denmark and ¹¹Smithsonian Tropical Research Institute, Balboa Ancon, Unit 0948, Panama

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ABSTRACT

The Global Genome Biodiversity Network (GGBN) was formed in 2011 with the principal aim of making high-quality well-documented and vouchered collections that store DNA or tissue samples of biodiversity, discoverable for research through a networked community of biodiversity repositories. This is achieved through the GGBN Data Portal (http://data.ggbn.org), which links globally distributed databases and bridges the gap between biodiversity repositories, sequence databases and research results. Advances in DNA extraction techniques combined with next-generation sequencing technologies provide new tools for genome sequencing. Many ambitious genome sequencing projects with the potential to revolutionize biodiversity research consider access to adequate samples to be a major bottleneck in their workflow. This is linked not only to accelerating biodiversity loss and demands to improve conservation efforts but also to a lack of standardized methods for providing access to genomic samples. Biodiversity biobank-holding institutions urgently need to set a standard of collaboration towards excellence in collections stewardship, information access and sharing and responsible and ethical use of such collections. GGBN meets these needs by enabling and supporting accessibility and the efficient coordinated expansion of biodiversity biobanks worldwide.

INTRODUCTION

Genome sequencing for biodiversity analysis is at the forefront of innovation and discovery due to technological advances and the sequencing of whole genomes in the last 10 years. Information generated from biodiversity genomics will revolutionize our approach to taxonomy, phylogeny, conservation, ecological monitoring, wildlife management, agriculture, drug development, zoonotic disease forecasting and even aspects of national security. Consequently, the demand is rapidly increasing for professionally preserved, managed and documented samples that yield high-molecular weight DNA and RNA from throughout the tree of life [e.g. (1,2)]. Many ambitious projects with the potential to revolutionize biodiversity research are finding access to adequate samples needed for genome sequencing to be a major bottleneck in their workflow. Examples of these projects include the Ten Thousand Vertebrate Genomes Project (Genome10 K),

*To whom correspondence should be addressed. Tel: +49 20 838 50 139; Fax: +49 30 838 50 186; Email: g.droege@bgbm.org Present address:

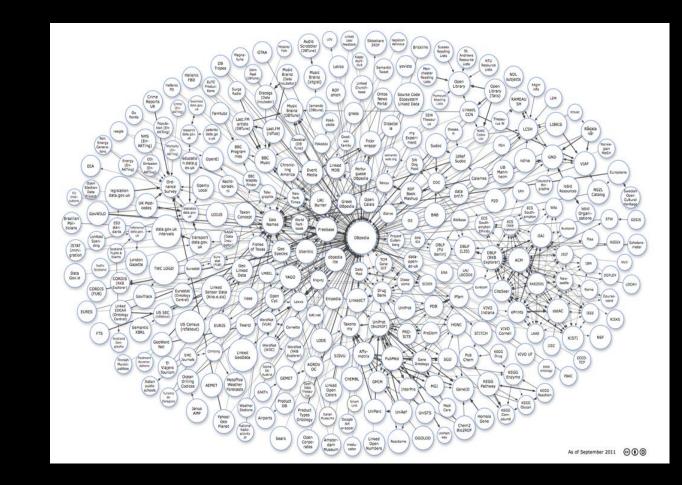
Gabriele Droege, Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Berlin, 14195; Germany.

The authors wish it to be known that, in their opinion, the first two authors should be regarded as Joint First Authors.

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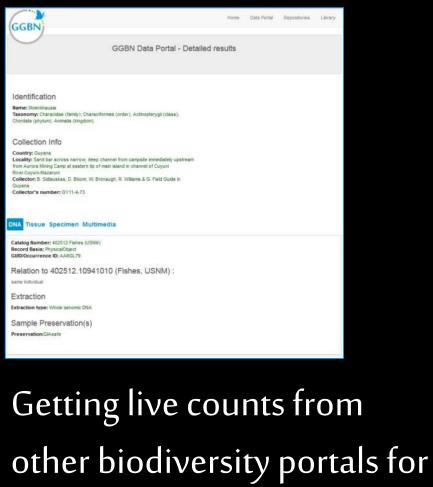
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Linked Data and Stable Identifiers

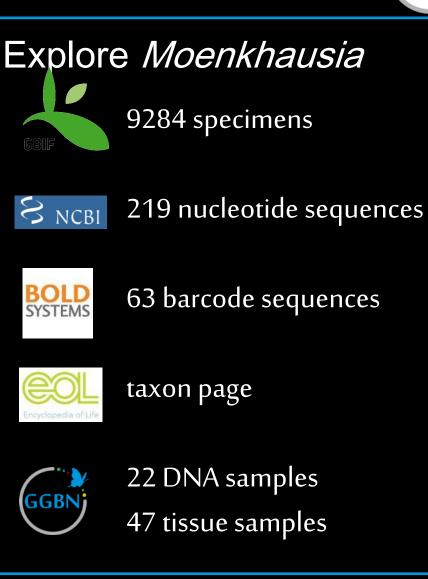


GGBN collaborates with other stakeholders and across domains to reach this goal.

Aggregate multiple sources



each record



GGB



2nd GGBN International Conference









Berlin June 2013 w SPNHC





Next Steps

GGBN

- Begin concrete USA collaborations
 - -Specify
 - -Arctos
 - -Recruit new Associate/Core Members
- IDigBio Working Group?
- Other suggestions?