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Fourteenth meeting

Sharm El-Sheikh, Egypt, 17-29 November 2018

Items 8, 10, 17, and 26 of the provisional agenda*

THE GLOBAL TAXONOMY INITIATIVE FORUM: REMOVING THE TAXONOMIC IMPEDIMENT FOR ALL CITIZENS

Note by the Executive Secretary

I. BACKGROUND

A. Purpose of the Global Taxonomy Initiative Forum

1. The Global Taxonomy Initiative Forum will consider the state of advancement in taxonomy and related deliverables to provide inputs for the formal and informal processes for the development of the post-2020 biodiversity framework with the goal of removing the taxonomic impediment for all citizens. The present document was prepared in consultation with the Coordination Mechanism for the Global Taxonomy Initiative and co-organizers¹ of the Forum. The purpose of the present document is to facilitate discussion at the Forum, which will be held on 16 November 2018 in Sharm El Sheikh, Egypt. The Forum takes place with generous financial support from the Government of Japan through the Japan Biodiversity Fund.

B. History of the Global Taxonomy Initiative under the Convention

2. At its second meeting, the Conference of the Parties noted the importance of scientific and technical work being undertaken by other international and intergovernmental organizations to the medium-term programme of work, and the Conference of the Parties expressed its awareness that such inputs had already contributed to advancing the work of the Subsidiary Body on Scientific, Technical and Technological Advice on publication and distribution of scientific and technical information (see decision II/2). Subsequently, at its fourth meeting, the Conference of the Parties endorsed the suggestions for action to develop and implement a Global Taxonomy Initiative (see decision IV/1). A Coordination Mechanism for the Global Taxonomy Initiative was established to assist the Executive Secretary in facilitating international cooperation and coordinating activities, and in using the Global Taxonomy Initiative as a forum for promoting the importance of taxonomy and taxonomic tools in the implementation of the Convention (see decision V/9). At its sixth meeting, the Conference of the Parties endorsed the programme of work for the Global Taxonomy Initiative, as annexed to decision VI/8.

* CBD/COP/14/1.

¹ ASEAN Center for Biodiversity, Consortium of European Taxonomic Facility, Global Biodiversity Information Facilities, International Barcode of Life (BIOSCAN), Nature & Science Foundation of Egypt, World Federation for Culture Collections.

3. The Conference of the Parties invited Parties, other Governments, regional and international organizations to take full account of the importance of taxonomic capacities in achieving the goals of the Convention, to support taxonomic activities to attain the 2010 target, and to provide all necessary support to national and, where appropriate, regional taxonomic centres of research and expertise (see decision VII/9, para. 2).
4. Following an in-depth review of the implementation of the programme of work for the Global Taxonomy Initiative, the Conference of the Parties at its eighth meeting noted that the taxonomic impediment was particularly serious in countries with mega-diversity and, among other things, adopted planned activities to support implementation of the programmes of work on mountain biological diversity, invasive alien species, protected areas, and island biological diversity (see decision VIII/3). Subsequently, at its ninth meeting, the Conference of the Parties, noting that taxonomic capacity-building activities could go beyond 2010, endorsed a number of outcome-oriented deliverables as relevant outputs of the programme of work on the Global Taxonomy Initiative (see decision IX/22).
5. Further to the decisions referenced above, the Conference of the Parties at its tenth session encouraged Parties and relevant organizations to make taxonomic and other necessary data and metadata from taxonomic and other relevant institutions and organizations easily accessible and their collections available, and it urged Parties and invited other Governments and organizations to increase the knowledge base on ecological range and the condition of the species in order to better meet user needs in respect of bioindication of ecological health (see decision X/39).
6. Following the adoption of the Strategic Plan for Biodiversity 2011-2020 (decision X/2, annex), the Capacity-building Strategy for the Global Taxonomy Initiative was welcomed by the Conference of the Parties at its eleventh meeting, and Parties and other Governments were invited to integrate, as appropriate, in a timely manner, the actions of the Capacity-building Strategy for the Global Taxonomy Initiative in their updated national biodiversity strategies and action plans (decision XI/29).
7. At its thirteenth meeting, the Conference of the Parties adopted the Short-term Action Plan (2017-2020) to Enhance and Support Capacity-Building for the Implementation of the Convention and its Protocols, which included organizing “training of trainers” courses on the application of molecular technology for species identification (see decision XIII/23, annex).
8. In accordance with decision V/9 and other relevant decisions mentioned above, the Global Taxonomy Initiative Forum will be held in Sharm El Sheikh, Egypt, on 16 November 2018 under the theme “Removing the taxonomic impediment for all citizens”. The Forum will review some selected activities and deliverables of the Global Taxonomy Initiative advanced under the Convention, in line with the Capacity-building Strategy, in particular: (a) enhanced use of existing tools and biodiversity informatics; (b) effective mechanisms of capacity development with integration of scientific and technical cooperation into national biodiversity strategies and action plans and their implementation; (c) biodiversity information use for decision-making, taking into account climate and land use changes and vital needs of ecosystem restoration; and (d) a sustainable taxonomic research programme with enhanced communication with Governments, including business and financial sectors, civil society organizations, and indigenous peoples and local communities, women and youth.
9. The outcome of the Forum is expected to contribute to the development of the post-2020 global biodiversity framework, which the community of the Global Taxonomy Initiative and its partners serve: evidence-based information on biodiversity, fostering capacity development and removing taxonomic impediments from Governments, organizations, businesses, biodiversity stakeholders and all other sectors of society.
10. In the present document, section II describes the state of advancement of taxonomy and its related deliverables, while section III highlights the points raised by the Global Taxonomy Initiative partners,

expert organizations and the Coordination Mechanism to remove the taxonomic impediment for all citizens.

II. STATE OF ADVANCEMENT OF TAXONOMY AND RELATED DELIVERABLES

A. Estimated global diversity of species

11. Global biodiversity plays a crucial role in maintaining human societies; its conservation and sustainable use therefore need to be addressed with a comprehensive view of its components. This section aims to explain the taxonomic knowledge accumulated to date and new technologies that can advance understanding global biodiversity, in accordance with Article 2 of the Convention, which states that “‘biological diversity’ means the variability among living organisms from all sources including, inter alia, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part”.

12. Past studies to estimate global biodiversity have provided a range of results from 5 million to 11 million species of Eukaryotes in which animals, plants, algae and fungi are classified, while microorganisms were incorporated in the studies with relatively high uncertainty (Chapman 2009; Mora et al. 2013; Costello M. et al. 2013).^{2, 3, 4} Recently, the species numbers of microscopic fungi and prokaryotes (bacteria and archaea) were estimated to be 1 trillion (10^{12}) by applying molecular analyses and statistical models (Locey et al. 2016).⁵

13. The estimated number of species in all domains of Eukaryota and Prokaryota globally is far greater than the number which are currently described by taxonomy (1.2 million described species after clearing out the synonyms⁶). This indicates that understanding global biodiversity still requires great advances in technology and societal change so as to accept new technologies that can accelerate research and discovery to resolve the lineages of life on Earth, as well as the great mass of species themselves, including microbial diversity. To date, the majority of entities of global biodiversity are known to be composed of prokaryotes that are not culturable but demonstrate their existence with their DNA sequence data (candidates of new taxa). In the natural environment, the interactions among those microbes in soil, water and other biomes, including gastrointestinal environments of animals, are critical to understand the various ecosystem functions and species interactions.

14. At many taxonomic institutes, DNA sequence analysis of preserved specimens has become a common practice by using genetic markers, for example, the cytochrome *c* oxidase subunit I gene (COI) for animals and other markers for plants. This technology is called DNA barcoding⁷ and currently DNA barcode are deposited in the public database Barcode of Life Data System (BOLD)⁸ hosted by the Centre for Biodiversity Genomics⁹ at the University of Guelph, Canada. Data on BOLD consisting of DNA sequences and metadata (such as taxonomy, locality, collectors, dates, host animals and plants, etc.) is shared freely with the public. The DNA barcoding community has contributed to the construction and sharing of DNA barcode libraries, and a series of international conferences have educated taxonomists on how best to apply DNA barcoding for their research purposes and is now stimulating major efforts to incorporate barcode-based identification in all forms of social use (e.g., BioAlfa (see para. 33 below)).

² <http://www.environment.gov.au/system/files/pages/2ee3f4a1-f130-465b-9c7a-79373680a067/files/nlsaw-2nd-complete.pdf>

³ <https://doi.org/10.1371/journal.pbio.1001127>

⁴ *Science* 2013:Vol. 339, Issue 6118, pp. 413-416 <http://science.sciencemag.org/content/339/6118/413>

⁵ PNAS 2016 vol. 113, no. 21 5970-5975 <http://www.pnas.org/content/pnas/113/21/5970.full.pdf>

⁶ The authors refer to the Species 2000 which is currently under the Catalogue of Life project (www.catalogueoflife.org/), the World's Register of Marine Species (www.marinespecies.org), the List of Prokaryotic Names with Standing in Nomenclature database (www.bacterio.cict.fr) and an additional information on the year of description of taxa was obtained from the Global Names Index database (www.globalnames.org).

⁷ <http://www.ibol.org/phase1/about-us/what-is-dna-barcoding/>

⁸ <http://www.boldsystems.org/>

⁹ <http://biodiversitygenomics.net>

Currently, DNA barcoding can be used to identify numerous species of organisms, and it can be applied to identify invasive alien species (including agricultural pests), endangered species, biological control agents, biodiversity prospecting subjects, and to advance understanding of understudied taxa in many parts of the world,¹⁰ especially the tropical regions where enormous numbers of undescribed species are yet to be encountered.

15. Recent taxonomic studies also apply high through-put DNA sequencing technologies to distinguish organisms by analysing some common marker genes that are broadly distributed among life on Earth (DNA barcoding is a good example in studies of animals, plants and fungi). The high through-put DNA sequencing technologies has facilitated analysis of microbial diversity, understudied groups of organisms, environmental DNA and the application of DNA barcoding for the identification of taxa from bulk samples (also known as DNA metabarcoding), which is empowering Parties to investigate biological specimens and species that are of concern to a particular country/region (e.g. invasive alien species, endangered species etc.) or societal guild. This applies especially to the societies in which substantial portions of the Earth's biodiversity remain and must be accepted by those societies for it to survive indefinitely.

16. Note that metagenomics in environmental and taxonomic studies to be mentioned in this section is using sequence information of just small regions of marker genes. It is a different approach from using genomics to discover and exploit functional components of genes.

17. One notable difference between the new approach in barcoding and metagenomics, and traditional taxonomic studies that include nomenclature, is the material that generates the taxonomic conclusions. Although nomenclature of taxonomy for animals, plants, fungi and bacteria/archaea requires the deposit of type specimens/type cultures in collections, a new approach in systematics using bioinformatics (grouping organisms based on the similarity of DNA sequences) is increasingly used in biodiversity observation in the field, as well as laboratory, and it is a powerful tool for discovering and observing understudied and very species-rich taxa. The DNA barcoding community publicly shares its information on the preserved barcode voucher specimens and information on BOLD. This ensures that taxonomic collaboration for species description can occur wherever there is motivation.

B. Sharing taxonomic tools, knowledge and their use

18. The taxonomic infrastructure that is created by taxonomists in natural history museums, science centres and botanical gardens through their collections, research laboratories and other biodiversity explorers serves: (a) research in taxonomy (species discovery, assigning scientific name and description) and (b) biodiversity sciences for many other scientific disciplines that incorporate species concepts and biodiversity as central elements. This taxonomic infrastructure and the taxonomic expertise play a key role in documenting and understanding biodiversity, and research on collections contributes to such issues as sustainable development or climate change and climate change modelling (CETAF 2018).¹¹

19. Access to the digital information and specimens in natural history collections, including environmental data captured when the specimens were collected is increasing as a result of the deployment of new tools and techniques that mobilize digital images of specimens and their associated data (Glopp RE. 2018)¹². Efforts to mainstream specimen digitization have taken root and have accelerated traditional taxonomic studies as well as distribution modeling and global change research. Emerging imaging technologies such as microcomputed tomography and confocal laser scanning microscopy are changing how morphology and anatomy can be investigated (Short AEZ, et al 2018).¹³

¹⁰ <https://dnabarcodes2017.org/wp-content/uploads/2017/11/iBOL-2017-Conference-Abstracts.pdf>

¹¹ <https://cetaf.org/taxonomic-facilities/collections>

¹² BioScience, Vol. 68, Issue 1, 2018, pages 3–4 <https://doi.org/10.1093/biosci/bix155>

¹³ Annual Rev Entomol :2018 63 513-530 <https://www.annualreviews.org/doi/abs/10.1146/annurev-ento-031616-035536>

1. Global Biodiversity Information Facility

20. The Global Biodiversity Information Facility (GBIF)¹⁴ is an international network and research infrastructure funded by the world's governments aimed at providing anyone, anywhere, with open access to data about the occurrence of all types of life on Earth. The GBIF network of participating countries and organizations, working through participant nodes, provides data-holding institutions around the world with common standards and open-source tools that enable them to share information about where and when species have been recorded. GBIF provides a platform currently sharing more than 150 million preserved specimen records contributed by its participant nodes and data publishers of the world (accessed November 2018). In this section, some selected accessible biodiversity data, tools and capacity-building activities for Parties to use biodiversity information are reviewed in the context of outcome-oriented deliverables for the Global Taxonomy Initiative annexed to decision IX/22 and Aichi Biodiversity Targets in the Strategic Plan for Biodiversity 2011-2020 (decision X/2).

21. The GBIF Backbone Taxonomy¹⁵ is a single synthetic management classification of global biodiversity assembled from checklists provided by expert taxonomic organizations, which has provided global checklist for names of 2.8 million biodiversity components (5.6 million records with 2.2 million synonyms). However, regional or national level checklists are also needed to assist local management needs (e.g. information on infraspecific levels matters in local management of biodiversity).

22. Regarding biodiversity occurrences on Earth, it is notable that over one billion records became available on the GBIF portal in 2018, published by more than 1,300 institutions in over 120 countries. Users who download individual data sets or search results and use them in research or policy agree to cite them using a Digital Object Identifier (DOI), enabling credit to be returned to institutions publishing the data, and supporting transparency and reproducibility of research results. The breakdown of biodiversity occurrence data, as of November 2018, is as follows:

Animalia:	757,392,691
Plantae:	231,165,545
Fungi:	14,940,711
Chromista:	9,666,456
Bacteria:	1,278,150
Protozoa:	677,089
<i>incertae sedis</i> :	60,766
Archaea:	19,304
Viruses:	1,553

23. In addition, the GBIF platform shares 108 taxonomic tools for: collection management; taxonomic data management; observation data management; data use for geospatial analysis, among others. Based on tracking of research literature by the GBIF Secretariat, 696 peer-reviewed articles cited substantive use of GBIF-mediated data during 2017. There is high potential for use of the data available through the GBIF platform for use in biodiversity management.

24. The second meeting of the Global Biodiversity Informatics Conference, held in Copenhagen from 24 to 27 July 2018, agreed to establish a lightweight alliance for biodiversity knowledge aimed at transforming and aligning diverse efforts to observe, measure and model the living planet, thus helping to fill existing information gaps and responding to needs of the Convention, the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), the Food and Agriculture Organization of the United Nations (FAO), conservation bodies, and many other user communities. Details of the roadmap

¹⁴ <http://www.gbif.org>

¹⁵ <https://www.gbif.org/dataset/d7dddbf4-2cf0-4f39-9b2a-bb099caae36c>

to establish the alliance for biodiversity knowledge can be found at <https://www.biodiversityinformatics.org/>.

2. *Biodiversity Heritage Library*

25. Biodiversity Heritage Library (BHL)¹⁶ is the world's largest open access digital library for biodiversity literature and archives. It operates as a worldwide consortium of natural history, botanical, research, and national libraries working together to digitize the natural history literature held in library collections from across the globe and making it freely available via open access as part of a global "biodiversity community." Since its launch in 2006, 143,179 titles, 235,862 volumes and 55,612,697 pages have been made digitally available online by the BHL and its partners (accessed November 2018).

26. It is essential that the species names embedded in the BHL become linked to DNA barcodes and other forms of genetic data that are already beginning to characterize survival of wild biodiversity through its incorporation into the societies that care for it.

Barcode of Life Data Systems

27. Regarding DNA barcoding, the Barcode of Life Data Systems (BOLD; www.boldsystems.org) at the Centre for Biodiversity Genomics (<http://biodiversitygenomics.net/>), University of Guelph, Canada provides a high-powered informatics platform that supports interdisciplinary genomics research and practical use of DNA barcodes through big data management workflows, analytical tools, and publication pathways. BOLD supports over 1,000 institutions in 94 countries by the secure sharing of biodiversity and DNA sequence data. Currently, 6.4 million barcode records for 600,000+ species in animals, plants and fungi are accessible, along with their specimen information. BOLD has matured to an essential interactive platform for multi-authored and multi-process collaborations that prepare complex wild biodiversity for all possible non-damaging uses across society. This platform is essential for handling hundreds of thousands of species-level records for highly diverse tropical communities that lack morphology-based identifications for most species.

28. Some experts have found that BOLD platform serves as a model for a collaboration workbench, allowing teams from different countries and different disciplines to collaborate on analyses, especially incorporating taxonomy with ecology and biogeography (Basset et al. 2017)¹⁷. The BIN system of species identification with a unique identifier and the related BOLD tools and barcodes, have become a powerful way around some parts of the 'taxonomic impediment' (Miller et al. 2016)¹⁸. A BIN - a Barcode Index Number -- is an indexing system for clusters of barcode sequences that has been developed to facilitate species identification especially in species-rich and understudied settings such as tropical ecosystems. To conduct a metagenomics approach, DNA sequence libraries become an essential tool. Integration of DNA barcode sequences from all parts of the world, especially in mega-diverse tropical regions to a platform such as BOLD systems, is critically important to increase the applicability of DNA barcoding among all groups of organisms, and especially to make that information available to all citizens.

Clearing-house Mechanism

29. The Global Registry of Introduced and Invasive Species (GRIIS, <http://www.griis.org>) developed under the Global Invasive Alien Species Information Partnership by the efforts of country editors, the IUCN-Invasive Species Specialist Group, and the GBIF, is connected to the Country Profile page of the CBD Clearing-house Mechanism (<https://www.cbd.int/countries/>). Occurrence information of invasive alien species with valid taxonomic names has become accessible through the Clearing-house Mechanism

¹⁶ <https://www.biodiversitylibrary.org/>

¹⁷ Ecol Evol. 2017 Oct 22;7(23):9991-10004. doi: 10.1002/ece3.3515. eCollection 2017 Dec
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5723595/>

¹⁸ Phil. Trans. R. Soc. B 371: 20150339. <http://dx.doi.org/10.1098/rstb.2015.0339>

as an external source of shared scientific information with the taxonomic labeling consistent with the GBIF. Once barcoded, these species also become visible in all the various nation-level barcoding activities.

30. The deliverables of the Global Taxonomy Initiative under the biodiversity informatics category (planned activity 7 of the Programme of Work) have made significant progress. However, the use of such publicly available biodiversity information for analysis and planning for biodiversity management is currently at an early stage and varies enormously among Parties. At its 22nd meeting of Subsidiary Body on Scientific, Technical and Technological Advice, a new web tool, the UN Biodiversity Lab (<https://www.unbiodiversitylab.org/>), was launched for the purpose of building partnerships among data providers and data users to ensure that governments have access and capacity to use cutting-edge spatial data to make key conservation and development decisions. It is vital to supply available biodiversity information from taxonomic institutions to user-friendly data platforms.

C. Capacity-building activities in taxonomy

31. This section summarizes capacity-building activities to support access to, and generation of taxonomic information with trainings, projects or the publication of taxonomic literature (planned activity 5 of the Programme of Work).

Belgium

32. The Global Taxonomy Initiative in Belgium has issued grants for the following eligible countries: Algeria, Benin, Burkina Faso, Burundi, Cabo Verde, Cambodia, Cote d'Ivoire, Democratic Republic of Congo, Gambia, Ghana, Guinea, Guinea Bissau, Kenya, Laos, Liberia, Mali, Morocco, Mozambique, Niger, Nigeria, Palestinian Territory, Rwanda, Senegal, Sierra Leone, Tanzania, Thailand, Togo, Uganda and Vietnam. Belgium has also produced a series of peer-reviewed manuals dedicated to capacity building in zoological and botanical taxonomy, in collection management, and in good practices for taxonomic and curatorial research, called *Abc Taxa*. This can be downloaded at <http://www.abctaxa.be/volumes>.

Costa Rica

33. A growing team of Costa Rican parataxonomists has conducted 35 years of biodiversity inventory from Area de Conservacion Guanacaste (ACG) in Costa Rica for the caterpillars, their food plants, and their parasitoids. They have, in collaboration with Center of Biodiversity Genomics in Canada, barcoded 450,000 for 43,000 species in Costa Rica. These parataxonomists have proven very capable of absorbing and working around the additional complexity and requirements for accuracy and detail that are generated by adding DNA barcoding to the field base of the ACG inventory (Janzen and Hallwachs 2011, 2016)¹⁹. Generous funding from Japan International Cooperation Agency has allowed the information to be used for biomonitoring to assess impact of building a geothermal industrial facility in the natural forest. Costa Rica has set the goal of their application of DNA barcoding - bioliteracy for all citizens through the project BioAlfa²⁰, which plans to achieve sequencing DNA barcodes of 1 million eukaryote species in the entire nation in 10 years and promote their “non-damaging biodevelopment” for their conservation through a combination of national sweat equity by all, coupled with external funding and international collaborations with taxonomic institutions.

United Kingdom

34. The Darwin Initiative supported by the United Kingdom has funded 1,123 projects in 159 countries since 1992 to address threats to biodiversity, such as habitat loss or degradation, climate change,

¹⁹ PLoS ONE 6(8): e18123. <https://doi.org/10.1371/journal.pone.0018123> ; dx.doi.org/10.1139/gen-2016-0005

²⁰ <https://www.cbd.int/side-events/2837>

invasive species, over-exploitation, pollution and eutrophication. The initiative has supported at least 50 projects including elements addressing the taxonomic impediment in developing countries.

Association of Southeast Asian Nations (ASEAN)

35. The ASEAN Center for Biodiversity has undertaken Taxonomic Capacity Building Project 2010–2016 with the Japan-ASEAN Integration Fund (JAIF). A series of JAIF training workshops and internship programs on various species and families were conducted to enhance the capabilities of not only scientists but also officials and staff of ASEAN Heritage Parks and other protected areas. Experts from the ASEAN region and Japan took the lead in discussing the nomenclature and application of taxonomic methods and principles. The hands-on activities provided actual experiences with the collection, identification, and management of specimens. A total of 449 participants completed the training workshops (388) and internship programs (61), including the training workshops for management planning of selected ASEAN Heritage Parks. Six training manuals on corals, dicots, monocots, CITES species, Freshwater/Brackish Water Fishes and Data Organization and Mapping of Taxonomic information were produced. Four field guides were developed, printed, and distributed. The trainees served as contributing authors of the field guides listed below:

(a) Selected Monocot Plants of Northern Thailand and Southeast Asia: A Field Guide. (Fernando, E. S., Pollisco Jr., F. A., & M. T. Uriarte, Editors).

(b) Ho, B. C., Tan, B. C. & Luong, T. T. 2015. Guide to the Bryophytes in the Limestone Glass House of Queen Sirikit Botanic Garden. ACB Field Guide Series No.1. (Fernando, E. S., Miwa, H., & Pollisco, Jr., F. A., Editors). ASEAN Centre for Biodiversity and Japan-ASEAN Integration Fund. Los Baños, Philippines. 108p.

(c) Callado, J. R. C., Adjie, B., Suksathan, P., Lestari, W. S., & Darnaedi, D. 2016. Field Guide to the Pteridophytes of Chiang Mai, Thailand. ACB Field Guide Series No. 2. (Fernando, E. S., Miwa, H., Pollisco, Jr., F. A., Editors). ASEAN Centre for Biodiversity and Japan-ASEAN Integration Fund. Los Baños, Philippines. 174 p.

(d) Julia, S., Ngau, J. W. Robi, N. J., Tanaka, N., & Anak, Amin, V. L. 2017. Field Guide to the Plants of the Deer Cave Trail, Gunung Mulu National Park, Sarawak. ACB Field Guide Series No.3. (Fernando, E. S., Miwa, H., Pollisco, Jr., F. A., Editors). ASEAN Centre for Biodiversity and Japan-ASEAN Integration Fund. Los Baños, Philippines. 164 p.

Consortium of European Taxonomic Facilities (CETAF)

36. This pan-European association of natural history museums, science centres and botanical gardens, with 59 members from 21 countries, promotes taxonomy and taxonomy training, as well as taxonomic publishing, within and across Europe. CETAF is home to the Distributed European School of Taxonomy (DEST) (<http://taxonomytraining.eu/>) that provides field and theoretical courses to university students, with a focus placed on encouraging participation from individuals from non-European countries via grant provision. CETAF also endorses the European Journal of Taxonomy, a Diamond Open Access journal that specializes in publishing taxonomic works (<http://www.europeanjournaloftaxonomy.eu/index.php/ejt>). Since 2011 the European Journal of Taxonomy has published 1261 new species or infra-specific taxa, 9 new families, subfamilies and tribes, and 116 new genera and subgenera in a total of 13,579 pages. CETAF runs a number of successful working groups that focus on specific topics that are of interest to the community, and that promote capacity building for taxonomy, namely:

(a) The CETAF Strategy group developed the CETAF Strategy and Strategic Development plan 2015-2025 that outlines with the objectives and targets of the association, including for the promotion and support of taxonomy and systematics in Europe (https://ns309467.ip-188-165-193.eu/sites/default/files/final_strategy_and_strategic_development_plan.pdf). CETAF is currently

defining its Joint Research Agenda for Biodiversity and Geodiversity Sciences in Europe and is specifically focusing on integrating taxonomy into the European research agenda;

(b) The CETAF Collections Group focuses on the management and enhancement of natural history collections, establishing best practices, management guides and common collections policies as well as collaborating with the Society for the Preservation of Natural History Collections on cross-cutting issues.

(c) The CETAF Information Science and Technology Commission aims to develop common infrastructures and common standards that facilitate biodiversity data connectivity and interoperability. This group recently produced the CETAF stable identifiers for natural history collections that are being implemented across member institutions.

(d) The CETAF Digitization Group is currently working on definitions and best practices in specimen digitization. They act as a platform for information sharing and as a forum for exchange thus promoting cooperation between digitization initiatives and coordination between different collection digitization-based projects to ensure continuity.

(e) The CETAF Earth Sciences Group aims to integrate Earth sciences into biodiversity research efforts providing rich, deep-time data on evolution, and on past changes in both biodiversity and the climate that are essential for understanding the evolution of life on Earth as well as for mitigating natural disaster risks and seeking responses to climate change issues.

(f) The CETAF Legislations and Regulations Group provides information and tools on European and international regulations that affect both collections and taxonomic research. This group produced the CETAF Code of Conduct and Best Practices for Access and Benefit Sharing (https://cetaf.org/sites/default/files/final_cetaf_abs_coc.pdf) that is widely used across Europe to guide collections-based institutions in their compliance with the Nagoya Protocol.

(g) The CETAF Training and e-Learning Group focuses on the delivery of taxonomy training within Europe and the exploration of distance learning techniques with the aim of creating a Virtual Learning Environment in Taxonomy. Their current project Talent in Biodiversity (BioTalent) (<http://biotalent.myspecies.info/content/eu-conference>) delivers a blended e-learning biodiversity training programme which contributes to raising the level of biodiversity literacy for both teachers and students.

(h) The CETAF Taxonomic Publishing Group focuses on facilitating and promoting taxonomy publishing. It has recently produced the CETAF guidelines and best practices in taxonomy publishing and Open Access to facilitate the citation of taxonomic names and open access publishing.

(i) The CETAF European Biodiversity Monitoring Group aims to employ the scientific expertise of the European taxonomic facilities to create an inventory of the rich European biodiversity with a focus on individual species in order to provide a tool for policy making in conservation.

Global Biodiversity Information Facility – Biodiversity Information for Development

37. Biodiversity Information for Development (BID) is a programme funded by the European Union and led by the Global Biodiversity Information Facility since 2015 with the aim of increasing the amount of biodiversity information available to support decision making in the nations of sub-Saharan Africa, the Caribbean and the Pacific. The programme has supported 63 projects from 50 countries in the three target regions, including 40 projects from Africa, eight from the Caribbean and five from the Pacific Islands. Through developing a community of practice in biodiversity informatics in these regions, BID had by September 2018 enabled the mobilization of 309 datasets through the GBIF.org platform, including 690,000 species occurrence records and involving institutions in many countries that had never previously shared biodiversity data.

The GTI-DNA-tech trainings in developing countries

38. In response to decision XI/29 and XIII/23 and with the generous financial support from the Government of Japan through Japan Biodiversity Fund, the Secretariat of the CBD organized a series of training courses on rapid species identification, in collaboration with the Centre for Biodiversity Genomics, University of Guelph, Canada, between 2015 and 2018. During this period 52 individuals were trained in the application of DNA barcoding through online courses delivered from the University of Guelph (<https://courses.opened.uoguelph.ca/>). From these individuals, 29 participants were invited to take laboratory and bioinformatics training at the University of Guelph to gain the experience needed to become trainers of DNA barcoding (2015-2016). In 2017 the trained trainers received project development training via a Webinar and remote consultation on project proposal writing and communication with CBD national focal points. The call for proposals to organize the GTI-DNA-tech training was sent to all Parties²¹.

39. As a result of these preparatory steps, ten GTI-DNA-tech training workshops were organized in 2018 by the trained trainers from: Belarus and Moldova, Bhutan, Colombia, Nigeria, Philippines, Sri Lanka, Suriname, Tunisia, Turkey, and Uruguay. All projects were designed for supporting the national implementation of the National Biodiversity Strategies and Action Plans (NBSAPs) and development of collaborative work relationships among the respective Government(s), research institutes, protected areas managers and others. International technical support from the University of Guelph, Canada and Naturalis, Netherlands and host institutions have also provided in-kind contributions to maximize the GTI-DNA-tech training opportunity for the implementation of the NBSAPs and achieving their national targets. The outcomes of each training event will be presented at the Expert Kiosk on Taxonomy and Invasive Alien Species during the UN Biodiversity Conference in Sharm El Sheikh, Egypt.

40. The GTI-DNA-tech standard manual containing techniques on sampling, specimen collection management, DNA barcoding, bioinformatics and potential scale up of the technology for wider taxonomic groups was shared among the trainers and all the training events were conducted with the standard manual. By the end of 2018 around 200 trained trainers gained expertise in DNA barcoding, most of them (166 trainees) during the GTI-DNA-Tech 2018 events which produced a total of 510 records of locally collected samples uploaded and shared on the BOLD platform.

D. Citizen science

41. Participatory science projects engaging citizen scientists have been emerging into taxonomic works for many decades. For example, the herbaceous plants of Sweden were mapped by school children long before the internet. More than half of the records available through GBIF are contributed by initiatives involving volunteer observers²², including major global platforms such as eBird²³ (contributing 361 million records) and iNaturalist²⁴ (contributing 5.8 million records) and a wide range of national and thematic citizen science platforms, of which the largest by volume are Sweden's Artdataportalen²⁵ (64.5 million records), the Danish Ornithological Society²⁶ (19.3 million records), the Norwegian Species Observation Service²⁷ (19.2 million records) and the Southern Africa Bird Atlas Project²⁸ (15.7 million records).

²¹ <https://www.cbd.int/doc/notifications/2017/ntf-2017-110-gti-en.pdf>

²² Chandler *et al.* (2016) Contribution of citizen science towards international biodiversity monitoring. Biological Conservation. Elsevier BV. Available at: <https://doi.org/10.1016/j.biocon.2016.09.004>.

²³ <https://ebird.org/home>

²⁴ <https://www.inaturalist.org/>

²⁵ <https://www.artportalen.se/>

²⁶ <http://www.dof.dk/>

²⁷ <https://www.artsdatabanken.no/>

²⁸ <http://sabap2.adu.org.za/>

42. Citizen science projects can capture large data sets on a scale not otherwise possible. A web platform, MicroPlant (<http://microplants.fieldmuseum.org/>) had participation by around 8,000 individuals in 2017. The website provided an opportunity for non-experts to measure taxonomic characteristics on digital images. The project coordinator reported that non-expert users can measure defined morphological characteristics rapidly. After eliminating erroneous records, the preliminary analysis of the results generated by non-experts were comparable to those of the experts. The data generated in these authentic experiences are contributing to research on the morphological diversity of a hyper diverse liverwort genus, *Frullania*, as well as generating underlying data associated with the individual specimens. The online tool is aiding in accelerating biodiversity discovery and documentation, connecting scientific collections to a broader audience, and encouraging similar activities in other organisms (von Konrat et al 2018).²⁹

43. In Malaysia, there is an urgent need for biodiversity monitoring and public engagement with wildlife to raise awareness of biodiversity loss and to begin to reverse it. The participants in the “Peninsular Malaysia Butterfly Count” project collected butterfly legs for species identification through DNA barcoding. Fifty-seven citizens took part in the butterfly count. Collectively, the participants sampled 220 butterfly legs from 26 mostly urban and suburban sampling localities. Although the primary purpose of the Peninsular Malaysia Butterfly Count was to promote awareness and engage the public with biodiversity, the Butterfly Count did produce some ecologically interesting findings. The sampled butterflies revealed that widely distributed, cosmopolitan species, often recently arrived at the Peninsula or with documented "invasive" potential, dominate the habitats sampled by the participants. Data from the first Butterfly Count helps establish a baseline for monitoring changes in butterfly communities in Peninsular Malaysia (Wilson JJ. et al. 2015)³⁰

44. In Costa Rica parataxonomists have been identifying caterpillars since 1978, creating today’s 900,000 individual caterpillar rearing records (<http://janzen.sas.upenn.edu>). BioAlfa’s intent to barcode the entire eukaryote biota of Costa Rica is already relying very heavily on mass collections made by members of the lay public, particularly by installing Malaise traps widely, just as has been the case with Canada; one year of Malaise trapping by Canadian school children caught more species of insects than were known for the entire country

III. Removing the taxonomic impediment for all citizens

45. The Global Taxonomy Initiative works as a forum to remove or ameliorate the ‘Taxonomic Impediment’ for the Convention (decision V/9). This section summarizes some of the lessons learned and suggests ways forward based upon advice from expert organizations for development of the post-2020 biodiversity framework. The Global Taxonomy Initiative Forum will further discuss and refine these key messages to convey to the formal and informal processes of the framework.

46. The Partners actively working on behalf of the Global Taxonomy Initiative, composed of taxonomic institutions, biodiversity expert organizations, expert users of taxonomic information, and trainers of capacity building projects of the world. They have recognized the following taxonomic needs, implying that such needs will continue in the post-2020 period:

(a) Taxonomic knowledge, whether morphology-based or sequence based, or both, backed by vouchered specimens and annotated with temporal, geospatial, ecological and socio-economic observations on biodiversity is fundamental for evidence-based decision making about the measurement and complexity of the impact of climate change, land-use change and ecosystem restoration, conservation, and “non-damaging biodiversity bio-development”, among many other kinds of sustainable biodiversity management and exploitation;

²⁹ <https://onlinelibrary.wiley.com/doi/full/10.1002/aps3.1023> <https://doi.org/10.1002/aps3.1023>

³⁰ Biodiversity Data Journal 3. E7159 <https://doi.org/10.3897/BDJ.3.e7159> <https://bdj.pensoft.net/articles.php?id=7159>

(b) Taxonomic knowledge is essential for every sector and its citizens, including indigenous peoples and local communities, women and youth, to become aware of the status, nature and needs of biodiversity on which they continue to rely or need to know, and wish to safeguard;

(c) Taxonomic knowledge is necessary for regulatory bodies to detect invasive alien species, pests, pathogenic agents, endangered species and other regulated species and specimens, in order to prevent negative impacts on biodiversity and human well-being, and facilitate safe and sustainable international trade, economy and development with and around biodiversity;

(d) Taxonomic knowledge is required in all assessments, surveillance and management measures of biodiversity, including biodiversity indicators to monitor the progress of biodiversity targets in the post-2020 period, and needs to be factored into their planning and compilation;

(e) ‘Big’ and accessible taxonomic knowledge, data and information are already available to most sectors and citizens, but to retrieve their needed data and analyze the data for themselves, more tools, learning opportunity and technical support with respect to conservation are necessary in all parts of the world;

(f) Analysing big biodiversity data and addressing the identified and emerging gaps of biodiversity data can be carried out by biodiversity experts and by the lay public, primarily within a country but not limited to them. If the GTI community continues to expand, the relevant international collaborations can be further facilitated. This is critical, particularly for mega-diverse tropical countries where the great bulk of wildlife is still undiscovered;

(g) Understudied organisms lead to gaps in management capacity for some biomes. These include aquatic biodiversity (marine and terrestrial), soil biodiversity, invertebrate animals, microscopic plants, fungi and the vast majority of unculturable microorganisms;

(h) Existing human resources in taxonomy to support biodiversity management is reportedly increasing in a few places, but communication and collaboration is weak between taxonomic expertise and governments (national and local), business sectors, lay citizens and international bodies. All citizens may assist in taxonomic work to be used for conservation and through appropriate development processes minimizing detrimental impacts on biodiversity. More effective and widespread communication between taxonomists/taxonomic knowledge holders and users of taxonomic knowledge across society should be enhanced;

(i) International collaboration among governments as well as specialists should be enhanced, so that global knowledge on biodiversity can be increased and the unbalanced distribution of taxonomic knowledge holders and the capacity gap between the North and the South can begin to be removed.

47. Partners in the Global Taxonomy Initiative have a high potential and willingness to resolve the needs mentioned above, envisioning that taxonomic science and technology will further advance in the post-2020 period, and its application to the post-2020 strategy will grow:

(a) Robust computing technologies and a genomics approach can reveal massive amount of global cryptic biodiversity, and the relationships of the components of biodiversity;

(b) The assets behind taxonomic knowledge (physical biological specimens/cultures, digital information on biodiversity, including specimen images, heritage libraries, DNA barcode libraries) are growing and a significant amount of collateral digital information backed by biological specimens is becoming available to the Governments and the public. Nevertheless, tools development and training on the tools for users are critically important to allow all sectors and guilds of society to be able to identify and record the components of biodiversity, so as to become “bio-literate”;

(c) Another asset behind taxonomy is an increasing number of taxonomists, parataxonomists and citizen scientists in taxonomic studies in some parts of the world. This reaction can navigate society

into higher awareness of biodiversity and therefore carry out participatory implementation of the Convention in all stakeholders;

(d) Thanks to the donor Governments, expert organizations and individual taxonomists, the legacy of BioNET INTERNATIONAL, the Global Invasive Species Programme and many other international programmes strengthened taxonomic capacity during the pre-2010 period. The legacy has continued through the international collaboration undertaken by taxonomic institutions in the form of powerful national, regional or global projects of biodiversity information facilities, DNA barcoding, and citizen-science, among others;

48. The partners of the Global Taxonomy Initiative take steps to:

(a) Continue to further enhance international collaboration to address the information gap, especially on understudied taxa and regions, especially in tropical and polar regions, marine, freshwater environments and soil. Taxonomic knowledge about them should continue to be shared in a free and open manner for the use to develop the post-2020 biodiversity framework and further advance biodiversity science. DNA technologies, such as DNA barcoding can meet this need for conservation and sustainable use of biodiversity and advance in non-commercial researches;

(b) Develop and support innovative and effective capacity building by using advanced technologies in taxonomy, such as DNA barcoding and metagenomics for all citizens rather than just the scientific community; assure everyone directly understands them, especially for the tropical mega-diverse countries and regions rich in unexplored biodiversity;

(c) Develop user-friendly interfaces and downloadable materials on taxonomic knowledge, species occurrences and associated information that are in a format suitable for the user, to enhance the use of biodiversity data for conservation and social use, as well as biodiversity research in support of the Convention and all other sectors;

(d) Enhance collaboration within the broad scientific community, including the communities in ecological research, *in silico* biodiversity research, geospatial analysis and socio-economic studies and projects, taking into account the impact of climate change, rapid land-use change, industrial impacts, and needs for planning and implementing of ecosystem restoration;

(e) Further improve technologies for rapid species identification and its application to priority species, such as invasive alien species, pests, pathogenic agents, endangered species, crop wild relatives and species for food security, biological control agents, among others, so as to support national and regional regulatory purposes; note that much more data coverage in barcode libraries are necessary for identifying close relatives and species that are not yet sufficiently studied in barcode marker regions;

(f) Support and enhance citizen science and in-country technical and scientific capacity development to increase public awareness and non-damaging use of biodiversity, for all members in the society, including indigenous peoples and local communities, women and youth;

(g) Undertake actions to sustain taxonomic research projects with innovative approaches and services to broad communities, including business and other sectors that are traditionally viewed as distant from environmental considerations;

(h) Recall article 8 of the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity, and continue to comply with laws and regulations set by Parties to access and utilize biological specimens, enhance productive international collaborations in non-commercial scientific research relevant to taxonomy, so that the global benefit on understanding biodiversity, sharing and use of biodiversity data will be increased. Most importantly, taxonomic knowledge will be transferred effectively, and capacity development will be assured in countries where technical capacity is limited.