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DNA BARCODING AND THE INTERNATIONAL BARCODE OF LIFE INITIATIVE – STATUS UPDATE (2014-2015)

Note by the Executive Secretary

INTRODUCTION

1. The Executive Secretary is circulating herewith, for the information of participants in the nineteenth meeting of the Subsidiary Body on Scientific, Technical and Technological Advice, a note received from the International Barcode of Life Initiative (iBOL) on the above-mentioned subject. The information is provided in the form and language in which it was received by the Secretariat.

* UNEP/CBD/SBSTTA/19/1.

DNA BARCODING AND THE INTERNATIONAL BARCODE OF LIFE INITIATIVE – STATUS UPDATE (2014-2015)

Notes for Secretariat of the Convention on Biological Diversity

DNA Barcoding is a novel cross-disciplinary area of biological science that uses patterns of variation in short standardized gene regions (DNA barcodes) to assess the biological diversity of living organisms and to provide fast, cheap and reliable species-level identifications. Originally proposed at the University of Guelph in Canada in 2003, this approach has gained worldwide scientific recognition that has led to the development of the International Barcode of Life initiative (iBOL¹) – a global alliance of researchers and practitioners aimed at coordination and information exchange on conceptual and methodological advances and the creation of a global openly accessible reference library of DNA barcodes from taxonomically authenticated specimens that can be used to identify unknown organisms. This is a summary of the progress made by the DNA barcoding community since the publication of the SBSTTA 18 Information Document 20².

Research publications. Since the first paper came out in 2003, the annual number of research publications dealing with DNA barcoding has been steadily increasing, peaking at 789 in 2014 and exceeding 450 in the first half of 2015, with the total number of publications approaching 4.7K. The cumulative number of citations has seen exponential growth, currently exceeding 85K. Importantly, DNA barcoding enjoys proportionally higher and increasing research contributions from developing countries, compared to some older and larger technology-intensive disciplines, such as Genomics (Adamowicz and Steinke, in review).

Growth of the barcode library. The DNA barcode library hosted by the Barcode of Life Data System (BOLD)³, contains over 4.5 million barcode sequences from nearly 500K distinct genetic clusters representing over 164K formally described species of animals, 62K plants, and 20K fungi. This represents a nearly 45% increase over the past 1.5 years. The number of BOLD users in this same period increased from 13K to 16K. Certain organism groups of global concern are well represented; for example, the coverage for species from the IUCN ISSG Invasive Alien Species list is 88% for animals and 94% for plants. This makes the BOLD reference library readily applicable in addressing practical needs of meeting Aichi Biodiversity Targets, particularly Target 9.

Research progress and technological advancements. There are clear indications that in recent years DNA barcoding has advanced beyond pure academic research and proof-of-concept studies towards applications. This is manifested by growing involvement of non-academic researchers and an increasing level of participation from government regulators, business-oriented organizations, the industry sector and even citizen scientists who are keen to apply this technology. To address these emerging new needs, new informatics tools are being deployed that facilitate access to DNA barcoding technology by the broad user community. An example of such recently developed platforms is Lifescanner⁴.

Although standard DNA barcoding protocols rely on 'traditional' Sanger-based DNA sequencing technologies, a growing body of research demonstrates the utility of other analytical methods, particularly next-generation sequencing approaches (e.g., metagenomics and eDNA), in certain

¹ <http://ibol.org>

² UNEP/CBD/SBSTTA/18/INF/20; 13 June 2014

³ <http://boldsystems.org>

⁴ <http://www.lifescanner.net/>

applications. These cutting-edge technologies are capable of delivering ultra-high volumes of genomic data necessary for rapid detection of organisms of key economic importance and for large-scale monitoring and biosurveillance at the ecosystem level. At the same time, there is growing interest in cheap PCR-based diagnostic solutions ready for field deployment by businesses and regulators. Recent advances in nanopore sequencing technologies mark a breakthrough in developing a portable DNA sequencing device that could be readily applicable in performing in situ identifications using DNA barcodes.

Important events. The 6th International Barcode of Life Conference⁵ was hosted by the University of Guelph in Ontario, Canada, on August 18-21, 2015. It brought together 601 delegates from 51 countries, surpassing by far all preceding barcoding conferences. Its 34 parallel sessions, one poster session, and 30 keynote and plenary talks covered a broad range of topics related to basic and applied research, technological advancements and policy developments. This important event marked five years since the formal launch of the International Barcode of Life initiative (iBOL) and demonstrated a rapidly growing interest in the discipline, as well as increased involvement of researchers from diverse backgrounds, government regulators, and people outside academia.

The conference had a strong research focus, covering basic research questions, such as classical DNA barcoding, taxonomy, biodiversity, ecology, agroecosystems, evolution, bioinformatics, molecular analytical tools, next-generation sequencing, and conservation. At the same time, it showcased a remarkable breadth of successful practical applications ranging from medicinal plants, biosurveillance, biomonitoring, detection of environmental DNA, identification of agricultural pests, invasive species parasites and disease vectors to general questions pertaining to food safety, ecosystem services, education, ethics and international policy.

Global capacity building efforts. Recent advances in DNA barcoding research and application were made possible due to concerted efforts of 27 iBOL member nations and research teams around the world to engage researchers and the user community in building the reference libraries and operationalizing analytical pipelines. A key component of these efforts is sharing the technological advances between teams, specialized training of experts and building analytical capacity in biodiversity rich and technologically under-resourced countries. It is important to acknowledge the important role of financial support from organisations focused on international development, such as IDRC and DFATD (Canada), Japan Biodiversity Fund (Japan), CBOL (United States) and others. This support has led to increased global participation in the DNA barcoding initiative and to the decentralization of research projects that are increasingly driven by principal investigators within developing nations. The collaborative models and best practices developed in this process can serve as an example for building international partnerships to address Aichi Biodiversity Targets in line with the provisions of the Nagoya Protocol.

An important recent development in this regard is the Global Taxonomy Initiative Training Course on Rapid Identification of Invasive Alien Species for Achieving Aichi Biodiversity Target 9 using DNA Barcoding Techniques and Methodologies launched in partnership between the SCBD and iBOL. This project aims to aid CBD Parties in the implementation of the Strategic Plan for Biodiversity 2011-2020 (decision X/2) and the Capacity-building Strategy for the Global Taxonomy Initiative (decision XI/29). Its particular focus is empowering developing countries to identify invasive alien species using rapid DNA-based approaches. It facilitates capacity building, technology transfer and information exchange related to identification and monitoring

⁵ <http://dnabarcodes2015.org/>

of prioritized invasive alien species. It was made possible, thanks to support from the Government of Japan and the Japan Biodiversity Fund (JBF).
