THE CANADIAN BARCODE OF LIFE NETWORK

Robert H. Hanner, Robert T. Dooh and *Paul D. N. Hebert
Canadian Barcode of Life Network, Biodiversity Institute of Ontario, Department of Integrative Biology, University of Guelph, Guelph, ON, N1G 2W1, Canada

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INTRODUCTION

The goal of the Canadian Barcode of Life Network, and of the large international consortium of which it is a part, is to develop an accurate, rapid, cost-effective and universally accessible DNA-based system for species identification. The DNA barcoding paradigm had its conceptual birth in Canada (Hebert et al., 2003a; Hebert et al., 2003b), which has become the first country to establish a national research network dedicated to the assembly of DNA barcodes on a large scale. The goal of the national network is to continue work on animals while extending the DNA barcode paradigm to the remainder of eukaryotic life, including fungi, plants and protists.

CANADA'S DNA BARCODING AGENDA

Following the coining of the term "DNA barcoding", a considerable amount of momentum has been generated for applying a standardized single-gene analytical approach to cataloguing biodiversity. In response to the emergence of this new global community, the Consortium for the Barcode of Life (CBOL) was established in 2004 and has since commissioned several working groups which address key issues in the development of DNA barcoding. This international movement now consists of members from over 80 organizations in 33 countries, across six continents.

The Canadian Barcode of Life Network represents the first network dedicated to barcoding all biodiversity within national boundaries and involves researchers and funding support from a broad range of institutions across the country (Table 1). Our previous work (e.g., Hebert et al., 2004; Hebert et al., 2003a; Hebert et al., 2003b; Hogg and Hebert, 2004; Lorenz et al., 2005; Smith et al., 2005) has demonstrated that a DNA barcode derived from a 648 base pair segment of the mitochondrial cytochrome *c* oxidase subunit I gene will enable a highly efficient system for the identification and discovery of animal life. This goal is now being pursued under four taxonomic themes:

- Animal Diversity — about 100K animal species will need to be barcoded to complete the national survey. At least10K species will be barcoded within 5 years.
- Protist Diversity — research will target macroalgae, microalgae, and ciliates, with some emphasis on their possible roles as bioindicators of ecosystem health.
- Plant Diversity — barcoding of the approximately 5,600 species of plants present in Canada will proceed with emphasis on optimizing protocols for identifying roots, pollen, seeds and spores.
- Fungi Diversity — research will proceed with initial emphasis on barcoding known pathogens within ecosystems.

While the ultimate objective is to barcode all species, our initial target is to establish a database of DNA barcodes for economically, socially, and environmentally important organisms from the Canadian biota. In addition to the pursuit of a national biodiversity research agenda, our researchers are playing lead roles in a number of international barcoding movements, including the Fish Barcode of Life Initiative (FISH-

BOL), and the All Birds Barcoding Initiative (ABBI). Through the pursuit of these goals, the Canadian Barcode of Life Network will make important contributions to global biodiversity research as a whole.

TAKING A LEAD ROLE ON THE GLOBAL STAGE

The logistical challenges of barcoding biodiversity at this scale are considerable, and a robust strategy is required to coordinate the flow and processing of both specimens and their data. Key areas requiring attention include laboratory processing, information management, and the coordination of the efforts of all stakeholders. In this regard, the Canadian Barcode of Life Network has lead development of protocols for large-scale DNA barcoding.

The refinement of laboratory protocols occupies a central role in the whole barcoding process, and is a primary focus for a fifth research theme (Analytical Platforms) in our Network. The core analytical facility for the Canadian Barcode of Life Network has pioneered the optimization of laboratory techniques for high-throughput DNA barcoding (Figure 1). Moreover, we have demonstrated that production targets of 100K barcode records are feasible for single analytical facilities (Hajibabaei et al. 2005). This production rate can be achieved in an environment with a multitude of specimen sources and other collaborative relationships, while delivering specimen information to a centralized database system. In order to facilitate and coordinate the rapid assembly of this database across a national (or international) research network, we have developed a suite of web-accessible tools to aid in the management and assembly of DNA barcodes. The Barcode of Life Database (BOLD) presents varied collaborative tools for data management, from specimen collection records, to taxonomy, to the DNA barcodes themselves. In addition, BOLD offers a universally accessible DNA-based system for species identifications. As an extension of this, we are pursuing the development of a portable, rapid identification instrument that can be used in biodiversity monitoring.

CONCLUSION

DNA barcoding offers a highly promising approach to resolve the 'taxonomic impediment' that constrains global biodiversity research. Through the efforts of a determined network of researchers, and support from diverse organizations, Canada will make important contributions to a biological research program whose goal is as ambitious as it is important: an understanding of the full diversity of life.

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Further Information

Barcode of Life: www.barcodinglife.org
Canadian Barcode of Life Network: www.bolnet.ca
Fish Barcode of Life: www.fishbol.org

TABLE 1: Partners in research, funding and in-kind support.

CANADIAN BARCODE OF LIFE PARTNERSHIPS
Agriculture and Agri-Food Canada, Applied Biosystems, Bio-Rad Laboratories, Beckman-Coulter Canada, Brock University, Canada Foundation for Innovation, Concordia University, Dalhousie University, Department of Fisheries and Oceans, Environment Canada, Genome Canada, Laurentian Forestry Centre, McGill University, McMaster University, Mount Allison University, Natural Resources Canada, NSERC, Ontario Genomics Institute, Parks Canada, The Alfred P. Sloan Foundation, The Biodiversity Institute of Ontario, The Gordon and Betty Moore Foundation, The Royal Ontario Museum, Université du Québec à Rimouski, University of British Columbia, University of Guelph, University of Laval, University of Lethbridge, University of New Brunswick, University of Toronto, University of Western Ontario, University of Windsor, VWR International, York University

FIGURE 1: Conceptual diagram of the high throughput flow of specimens and data into a universally accessible database.