III EXECUTIVE SUMMARY

DNA barcoding, the use of sequence diversity in a standardized gene region(s) to identify species, is revolutionizing biodiversity science by shifting key practices, especially those linked to species identification and species discovery**.** DNA barcoding has also proven to be a valuable tool in strengthening the audit trail for sequence data submitted to the INSDC. It exerts this impact by ensuring the retention of voucher specimens so that taxonomic assignments can be validated, by adding geospatial information, and by preserving the trace files that underpin each sequence record. DNA barcoding is also gaining application in fields ranging from environmental monitoring to marketplace surveillance and forensics. The full realization of DNA barcoding's impacts and its extension into more domains of science requires a concerted research effort. This is the motivation that underpinned the first planning efforts in 2007 to activate the International Barcode of Life project (www.iBOL.org).With the core mission of building a DNA-based identification system for all multi-cellular organisms, and a projected operating budget of $150M across its 25 participating nations over its first six years (2009-2015), iBOL represents the largest initiative ever undertaken in biodiversity genomics. Reflecting this fact, iBOL has already gained integration into global endeavours, as indicated by its recent adoption as a collaborative program with the Convention on Biological Diversity.

The advance of DNA barcoding from concept to major international research program in less than a decade reflects large investments in both research infrastructure and data acquisition, particularly in Canada. Support ($10M) from the Canada Foundation for Innovation (CFI) and the Ontario Research Foundation (ORF) allowed construction of the world's first barcoding core facility in 2006, the Canadian Centre for DNA Barcoding (CCDB). A second award ($15M) from the same agencies is now enabling expansion of the CCDB; the new space (40,000 sq ft) will support key elements of iBOL research and administration. Reflecting more than $40M in additional research support from several organizations, particularly Genome Canada, the CCDB oversees both an efficient sequencing facility and the BOLD informatics platform which is the primary repository for barcode data, the workbench for major projects, and the delivery system for barcode-based identifications. This funding package has also provided the support necessary to build the administrative teams needed to oversee both national research activity and to create the Secretariat required to co-ordinate work across the iBOL Project

The application reviewed by Genome Canada in early 2009 requested $25M to aid Canada's involvement in iBOL over a 6-year period. Approximately 10% of this total was targeted for expansion of the CCDB, while the balance was directed towards the core sequencing facility, towards BOLD, and towards the administrative teams needed to ensure smooth operations of the CCDB, the Canadian Barcode of Life Network and the iBOL Project. It was recognized that funding beyond that available from Genome Canada was required to support these activities, and several additional funders have now contributed. As noted above, the CFI and the ORF have provided $15M to expand the CCDB. The Ontario Ministry of Research and Innovation has also provided $13M to aid barcode research, particularly BOLD. As a consequence of these investments, our nation is well positioned to aid the rise of iBOL. Although Canada was the first to provide major awards for iBOL participation, six other nations (Argentina, Brazil, China, India, Mexico, USA) have now each committed more than $5M and research agencies in three other nations (Australia, Germany, Norway) are considering similar investments.

The iBOL application to Genome Canada described several key scientific deliverables, but the plan to build a DNA barcode reference library with records from at least 500K species by 2015 provided the grand challenge. The proposal set the specific goal of obtaining a barcode record from 1M specimens before December 2010 and this target was exceeded by a comfortable margin of 80,000 records. Providing barcode coverage for 153,000 species (32% of the six-year goal), the progress in library construction reflects the mobilization of collection programs across iBOL; specimens have derived from192 countries. It also reflects expansion of the BOLD platform so that it can support new gene regions and the development of an automated protocol allowing the assignment of newly analyzed specimens to a barcode cluster, an advance required to support rapid data release. Growth of the barcode library has been accompanied by the achievement of other milestones – a mirror site for BOLD has been established in China and progress toward comprehensive barcode coverage for species at certain sites has been more rapid than projected.

Because of these accomplishments, iBOL has met all of the formal milestones described in its 2009 proposal. The balance of this report provides additional details for each of the five iBOL themes, emphasizing progress since July 2009, proposed shifts in orientation, and challenges that await resolution. The most detailed updates relate to library construction, sequencing and informatics platforms, and on the development of new approaches for the application of DNA barcode data. This report does not aim to summarize the results of the more than 100 publications generated by members of the iBOL Project since July 2009. However, there are three general points that can be made. Firstly, the strong performance of DNA barcodes in species identification has been validated for a growing diversity of taxonomic groups. Secondly, the results of DNA barcode analysis have gained an increasingly important role in species discovery. Thirdly, DNA barcode libraries are already gaining new applications in environmental surveillance and in ecological investigations, such as probing food web structure.

With this brief consideration of scientific achievements, the remainder of this Executive Summary considers progress in developing iBOL's governance and management structure and the administrative systems needed to ensure that project deliverables are met and that cohesion is fostered. Both the iBOL secretariat and the administrative team needed for smooth operations of the Canadian core facility are in place. IBOL's Board of Directors has met on a quarterly basis over this interval and now gained representation from seven nations (Argentina, Canada, China, Mexico, Norway, South Africa, USA). As well, iBOL's Scientific Steering Committee has met twice - first in Mexico City (November 2009) and subsequently in Guelph (September 2010). The latter meeting was the first to assemble all of iBOL's organizational components – its scientific leaders, board, advisory committees and management. This consultation focused attention not only on the success of the capacity-building phase, but also identified the need to extend capacity through the central, regional and national nodes, to explicitly link this emergent capacity to the scientific goals of the Project, and to integrate the GE^3LS research component with the other five themes of the project, creating six Themes and 26 Working Groups. While the Working Groups associated with compiling the DNA barcode library (WG 1.1 – 1.10,) methods development (WG 2.3) and informatics resources (WG 3.1) have understandably been the most active to date, global development and replication of technology platforms, and a research focus on applications of barcoding and articulation of its socio-economic benefits, are gaining importance. As participation in iBOL increases, the ability of Working Groups 5.1 and 5.2 to provide strong project management and internal communications support across all nodes and working groups will be critical. Equally, the more centralized governance, advisory, management and outreach functions must deliver the necessary strategic cohesion for iBOL to sustain its successful trajectory.