Centre for Biodiversity Genomics, Biodiversity Institute of Ontario
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Biological Material Transfer Policies

Biological Material (hereafter referred to as the 'Material') includes biological specimens (whole collection vouchers, tissue samples, and/or bulk samples), as well as Genetic Material (sensu Nagoya Protocol; see www.cbd.int/abs/) contained therein, transferred to the Centre for Biodiversity Genomics (CBG, hereafter referred to as the Recipient) for DNA analysis.

By signing this BMTA, the Provider (individual and/or institution) acknowledges the following:

• The Provider holds legal ownership/custodianship rights over the Material and has authority to transfer it to the Recipient for molecular analyses. The Provider shall inform the Recipient of any third-party restrictions on the storage and utilization of the Material, including those imposed by external permit-issuing authorities.

• Unless repatriation of specimens/tissues and/or genomic DNA has been requested in this BMTA under Special Conditions, any Material (including Genetic Material) remaining after analysis will be permanently stored by the Recipient as a permanent loan from the Provider, to ensure reproducibility of analytical results and/or taxonomic verification. If repatriation has been requested, the Provider shall assume applicable cost-recovery fees valid on the date of the request.

• If donation has been requested in this BMTA under Loan Conditions, it is agreed the Provider intends to donate the Material to the Recipient. By signing this document, the Provider transfers its right of ownership of the collection materials and all their unmodified derivatives to the Recipient, thereby giving the Recipient full rights to use them for non-commercial research or teaching purposes, to transfer them to other non-profit organizations, without the need for authorization.

• The Provider acknowledges that the original material is free of known biological or other hazards to minimize potential health risks to individuals who may be exposed to this material during shipment and/or processing. The Provider also acknowledges that the original material has been properly preserved in 95% ethanol and housed at -4°C away from light or that an otherwise stated method of adequate preservation has been decided between the Provider and Recipient to minimize the potential of specimen and DNA degradation.

• The Material has been obtained under appropriate collection and animal care permits in its country of origin; where appropriate, Indigenous and local communities were consulted and provided prior informed consent for its collection and transfer; Material shipments are in compliance with all applicable shipping regulations; necessary export/import documentation required by relevant customs and conservation authorities has been provided; and, where governed by local regulation, the collection and transfer of the Material complies with the provisions of the Nagoya Protocol (see www.cbd.int/abs/).

• The Recipient acknowledges that the original material and its derivatives will not be used in human subjects, in clinical trials, or for diagnostic purposes involving human subjects and will not be used for commercial purposes or forwarded to commercial organizations for the purpose of making profit. Any prospective uses of biological materials for purposes other than non-commercial academic research and/or teaching shall be negotiated with the provider under a separate agreement.

• The Recipient will DNA barcode or metabarcode samples at their discretion; analysis may involve a combination of multiple sequencing techniques (ex. Individual specimen SMRT sequencing and bulk sample metabarcoding). Unless otherwise negotiated, samples will remain in the CBG's hold-up freezer storage until funds become available for their analysis. As such, the Recipient cannot guarantee when samples will be analyzed or when results will be available.

Data Sharing Policies

The CBG is committed to the principles of rapid release and open sharing of reference DNA barcode data (including genomic data, specimen provenance information, and images) within the international research community. Contributors are encouraged to initiate pre-publication release of their data. Records will be released publicly in compliance with best practices established under CBG's Data Release Policy (see https://biodiversitygenomics.net/wp-content/uploads/2026/08/DataReleasePolicy_Aug2026.pdf); data release will commence upon data publication, or after 12 months from the date the sequence was generated. Additional costs may apply for data to remain private, please contact your CBG representative.

All sequence data contained in BOLD (including unpublished projects) are used by the BOLD Identification Engine https://id.boldsystems.org/ to provide DNA-based taxonomic identifications to public users. Reports generated by the BOLD Identification Engine include similarity scores and tree-based identification with branch labels containing detailed taxonomy and broad geographic localization (to country level). Information on individual specimens (sample or BOLD process IDs, museum catalogue numbers and place of voucher deposition) and their detailed geographic origin are not disclosed through the BOLD Identification Engine. Once specimen data have been submitted to BOLD, provenance information and images become partially available to the public online through the BOLD Taxonomy Browser at https://boldsystems.org/data/taxonomy-page/. This information is used to generate summary statistics and illustrative distribution maps and does not disclose the contents of individual research projects and specimen data records.

Non-target sequence (NTS) records are DNA barcode sequences that are not the intended subject of the sequencing process. NTS records reflect the complexity of biological samples and the sensitivity of modern sequencing technologies and are automatically generated as part of the DNA barcoding workflow. NTS records might reflect genuine biological or unrelated co-occurrences. Under subsidized rates these records are automatically retained on BOLD and can be subject to data review and validation by CBG researchers.