October 2024

# TERRESTRIAL ARTHROPOD MONITORING PROGRAM

## METABARCODING REPORT – BC PARKS

Collections Unit, Centre for Biodiversity Genomics (CBG), University of Guelph

# Field Collection

In 2023, two Malaise traps were deployed in each of nine sites across British Columbia as part of the Terrestrial Arthropod Monitoring Program (Figure 1; Supplementary File Tab 1). Six sites were within the Pacific Maritime ecozone, and three sites were within the Montane Cordillera ecozone, with one site (GS) repeated from a previous study conducted by CBG in 2014. Traps collected samples for 14 weeks from May to September 2023 and photos were taken of each trap during deployment.

All traps were serviced bi-weekly by either BC Parks staff, or Discover Parks Ambassadors stationed at each park. A grand total of 116 samples were collected over seven bi-weekly cycles. A summary of all collected samples including collecting dates, wet weights, and analysis comments is provided in Supplementary Tab 2.

For more details on field sites and activities, see the BC Parks Field Report and Trap Images.

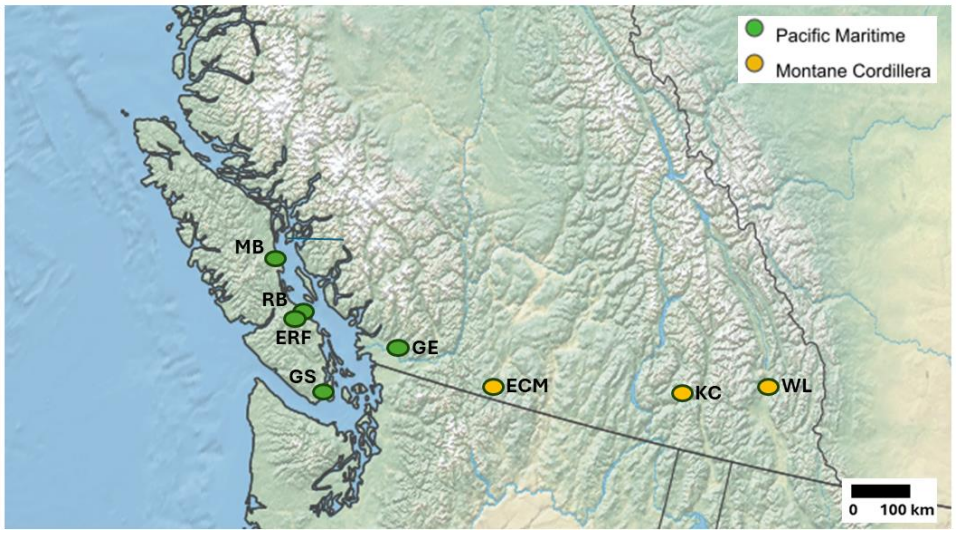


**Figure 1. Map of BC Parks trap sites.**

# Analysis

Samples were processed through the CBG's standard metabarcoding or "bulk analysis" protocol. In short, the bulk samples were assembled into batches of 30 for tissue lysis at the Canadian Centre for DNA barcoding (CCDB; http://ccdb.ca/). Three replicates of each sample lysate then underwent bulk DNA extraction. PCR amplification of the DNA barcode region was performed on the three replicates, followed by library preparation for high-throughput sequencing. Libraries were then submitted to The Centre for Applied Genomics (TCAG) in Toronto for sequencing on an Illumina NovaSeq platform.

This report outlines the metabarcoding results obtained from 115 samples; 1 sample was excluded from analysis as the sample was lost due to trap damage (GS-1|D). All sequencing results were uploaded to the online mBrave platform (http://mbrave.net/) into the project: "COI Metabarcoding with BF3-BR2 using Illumina NovSeq format. Library NSEQ-00044 LIMSID ZAK27583A1".

# Results

Approximately 230K specimens were analyzed, translating to approximately 2,000 specimens per sample. This resulted in a total of 22,850 occurrence records representing 6,481 distinct BINs (Barcode Index Numbers, a proxy for species), with 13% of the BINs being captured in both ecozones (Table 1; Figure 2; Supplementary Tab 3).

**Table 1. Breakdown of total BINs and BIN Occurrence Records for both ecozones.**

| Ecozones | Samples | Occurrence records | BINs |
|---|---|---|---|
| **Pacific Maritime** | 75 | 11,611 | 2,852 |
| **Montane Cordillera** | 40 | 11,239 | 4,452 |

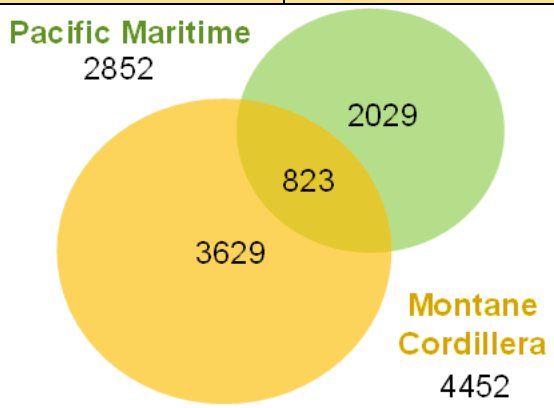


**Figure 2. Total BIN count from the 2023 collecting period showing overlap between the ecozones.**

A rarefraction analysis estimates 4,703 BINs for the Pacific Maritime and 7,313 BINS for the Montane Cordillera (Figure 3).

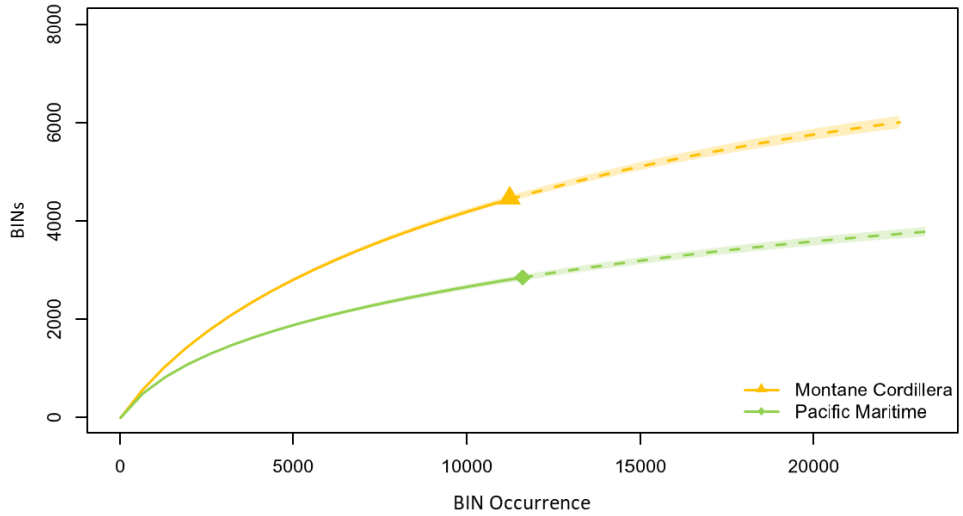


**Figure 3. BIN accumulation curve of both ecozones based on BIN occurrence records.**

ERF-1 had the lowest total BIN count of all sites with 336 BINs, while ECM-1 showed the highest total BIN count of 1,651. The average number of BINs captured per trap throughout the whole season was 766 BINs (Figure 4; Supplementary File Tab 4). In total, 45.8% of BINs were only captured in one trap, on average 165 BINs per trap. ECM-1 had the highest number of such unique BINs (N=542).

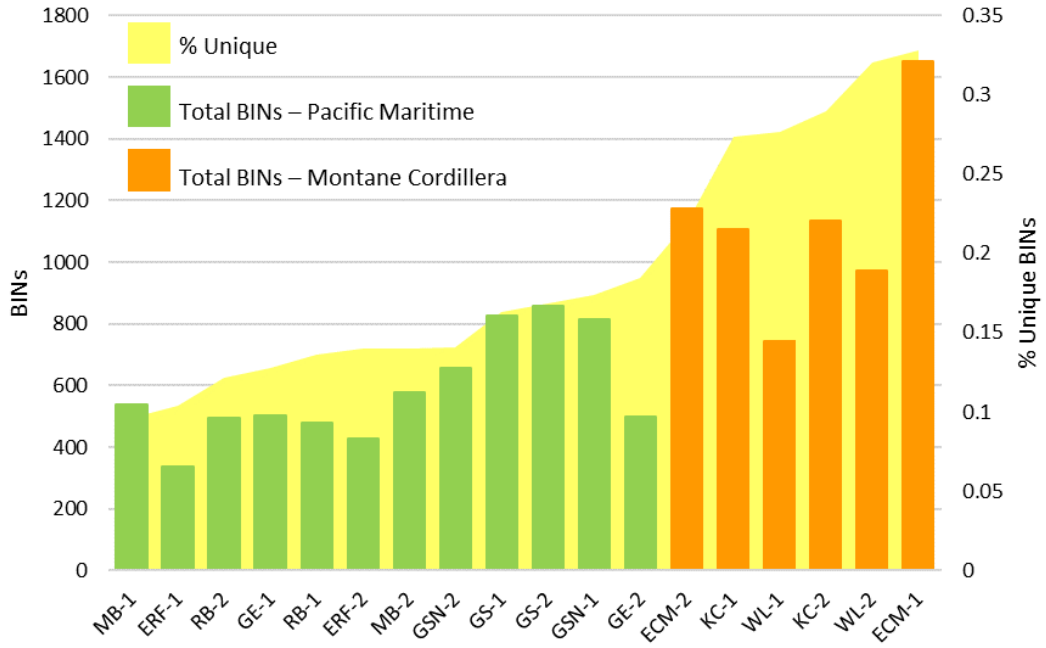


**Figure 4. Total BINs of all sites and proportion of BINs unique to each site.**

Biomass ranged from a low of 1.75g (RB-2|F) to a high of 81.23g (ECM-1|D; Figure 5).

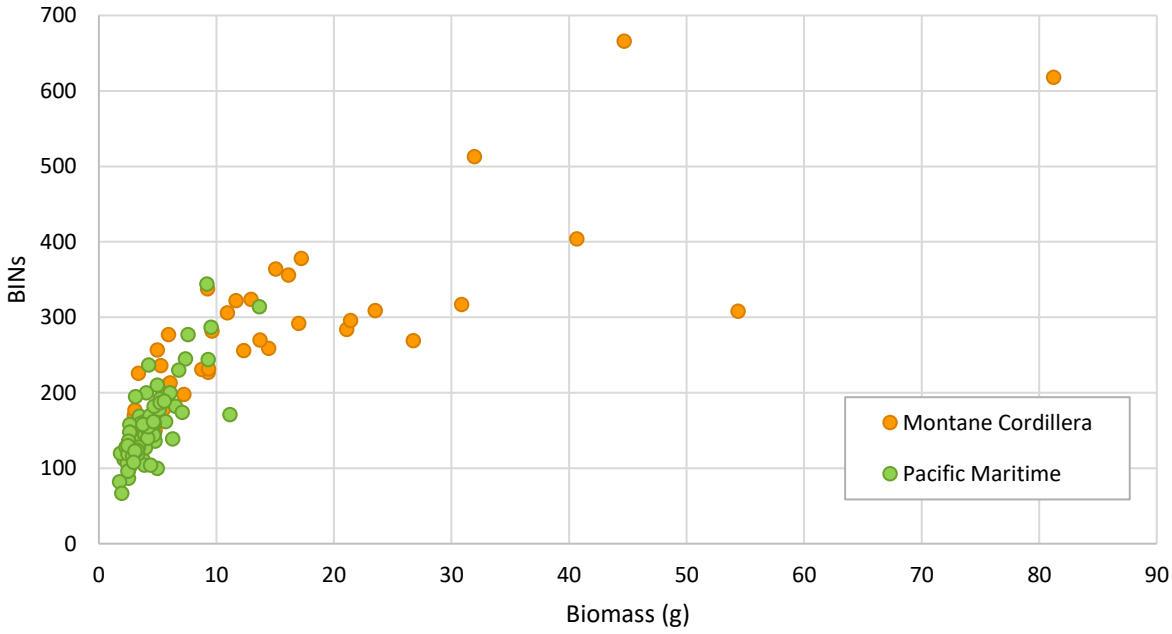


**Figure 5. BIN count per sample by biomass (wet weight, g).**

BIN counts per collecting cycle ranged from a low of 67 to a high of 666, with a mean of 199. The sample with the highest BIN count were GS-1|A|19-Jun-2023 (N=344) in the Pacific Maritime ecozone and ECM-1|E|16-Aug-2023 (N=666) in the Montane Cordillera ecozone. Under half of the BINs collected were Diptera (39.8%), followed by Hymenoptera (16.2%), Lepidoptera (9.7%), Hemiptera (5.2%), and Coleoptera (4.4%, Figure 6). A taxonomic reference for all BINs captured is provided in Supplementary File Tab 5 and a species inventory can be found in Tab 6.

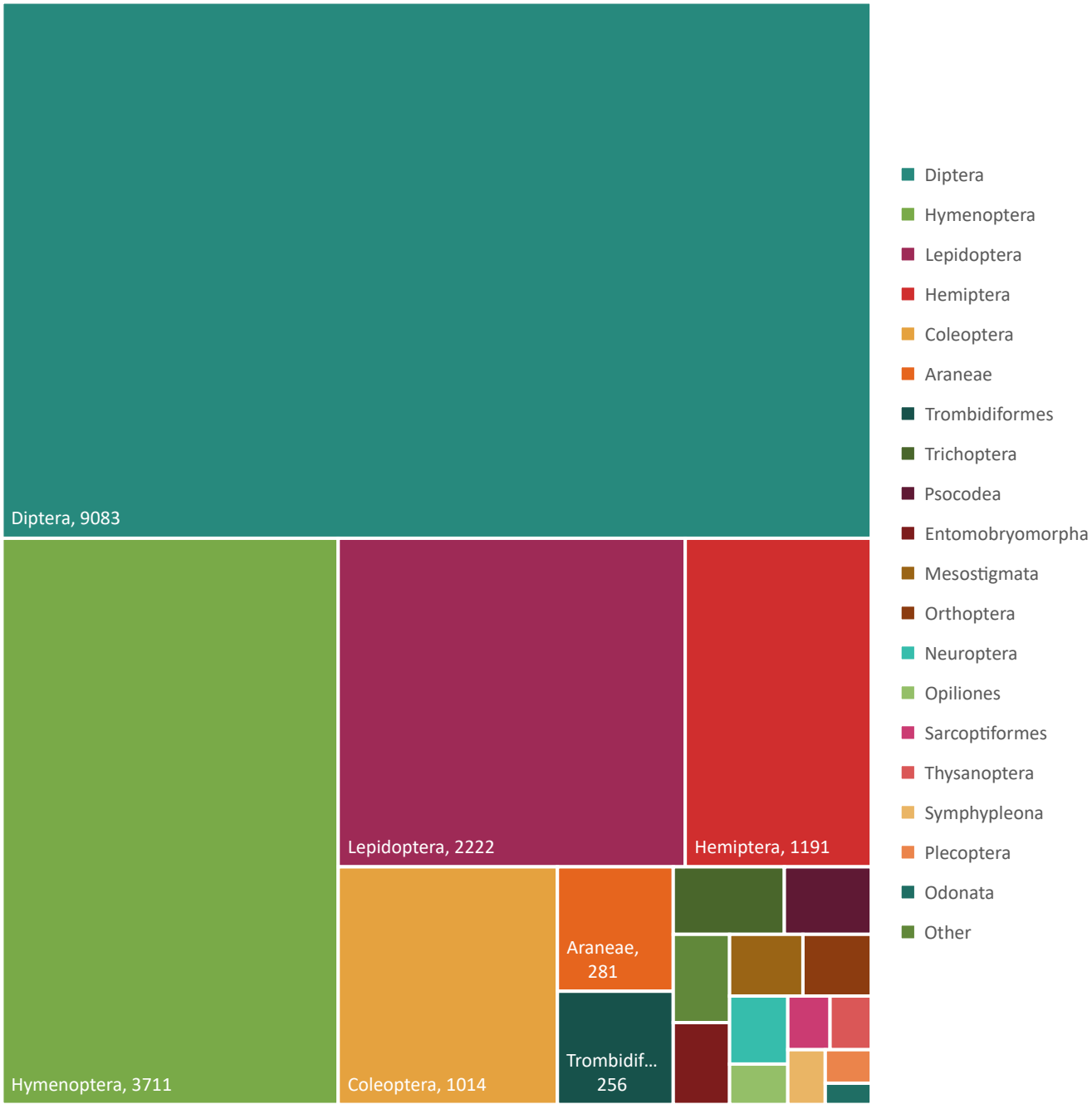


**Figure 6. Taxonomic breakdown of BINs collected from all 18 traps.**

# Supplementary File

**Tab 1.** Trap site details including locality, habitat, and GPS coordinates
**Tab 2.** Complete sample summary including collection dates and weight of analyzed sampled
**Tab 3.** BIN Occurrence Records per Sample (Trap, Sample, BINs)
**Tab 4.** Trap-Cycle summary (BINs per sample, total BINs and min, mean, max BINs per cycle)
**Tab 5.** BIN Taxonomy Reference
**Tab 6.** Taxonomy Report


## Acknowledgements

CBG would like to thank the various staff of BC Parks; Tse-Lynn Loh, Rory Moorhead and the Discover Parks Ambassadors (BC Parks Foundation); René and Owain McKibbin (Environment and Climate Change Canada); Ike Boston (Stswecem'c Xget'tem First Nation); Jason Jones (EcoLogic Consultants Ltd.); Jenny Heron (BC Ministry of Environment); Joanne Siderius (Kokanee Creek Nature Centre Society); Jo Hughes (Manning Park Resort); Karen Drysdale (Citizen Scientist); and Kate Lansley, Matt Lemay and Rute Carvalho (Hakai Institute) for their support in this project – including logistical consultation and/or field work management.


### LAND ACKNOWLEDGEMENT

All of Canada resides on traditional and current unceded and treaty lands of First Nations, Inuit, and Métis. We recognize that all our research occurs on Indigenous land. We are grateful to the Indigenous peoples for their care for and teachings about our earth and wish to honour their ongoing legacy.

The CBG and University of Guelph are grateful to operate on the treaty lands and territory of the Mississaugas of the Credit. We respectfully acknowledge that the sampling work for this project was conducted on the unceded traditional territory of many Indigenous communities including but not limited to: the Cayuse, Colville, Umatilla, and Walla Walla tribes; and the Heiltsuk, Homalco, Hul'qumi'num, Katzie, Klahoose, K'ómoks, Ktunaxa, Kwantlen, Malahat, Nlaka'pamux, Sc'ianew (Beecher Bay), Secwépemc, Semiahmoo, Sinixt, Snaw-Naw-As (Nanoose), Snuneymuxw, Songhees, Stoney Nakoda, Stswecem'c Xget'tem, Syilx Okanagan, Stó:lō, Tla'amin, Wei Wai Kum, We Wai Kai, W̱SÁNEĆ, and Wuikinuxv (Oweekeno) Nations.

Our acknowledgement of the land is our declaration of our collective responsibility to this place and its peoples' history, rights, and presence. It is important to understand the longstanding history that has brought us to and across Turtle Island, and to seek to understand our place within that history.

## Contact Information


Centre for Biodiversity Genomics

Jayme Sones, BSc
Manager
Collections
jsones@uoguelph.ca

Kristen McCabe, BSc
Senior Field Operations Technician
Collections
kmccabe@uoguelph.ca

Kate Perez, MSc
Field Operations Lead
Collections
kperez@uoguelph.ca



Funding provided by:

UNIVERSITY of GUELPH

Ontario Genomics