

# TERRESTRIAL ARTHROPOD MONITORING PROGRAM

## METABARCODING REPORT – SÉPAQ

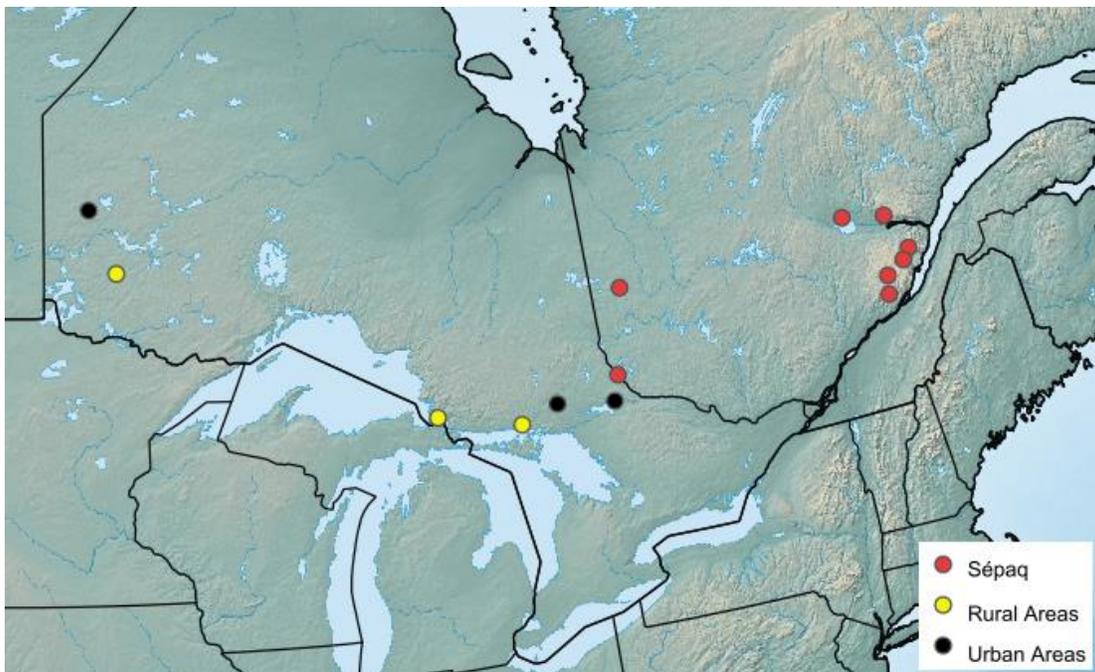
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### Overview

From May to October 2020, Malaise traps were deployed in seven National Parks across the Boreal Shield ecozone of Quebec to collect arthropod samples for metabarcoding (Figure 1). Samples were processed using the ‘bulk sample analysis protocol’ outlined in a previous project called Ontario Provincial Park Malaise (OPP) Program (<https://biodiversitygenomics.net/projects/oppmp/>).

In short, the bulk samples were assembled into batches of ten for tissue lysis at the Canadian Centre for DNA Barcoding (CCDB; <http://ccdb.ca/>). Eight replicates for each trap sample lysate then underwent bulk DNA extraction. PCR amplification of the DNA barcode region was performed on three pooled replicates, followed by library preparation for high-throughput sequencing. Libraries were then submitted to the Centre d’expertise et de services Génome Québec for sequencing on an Illumina NovaSeq platform.

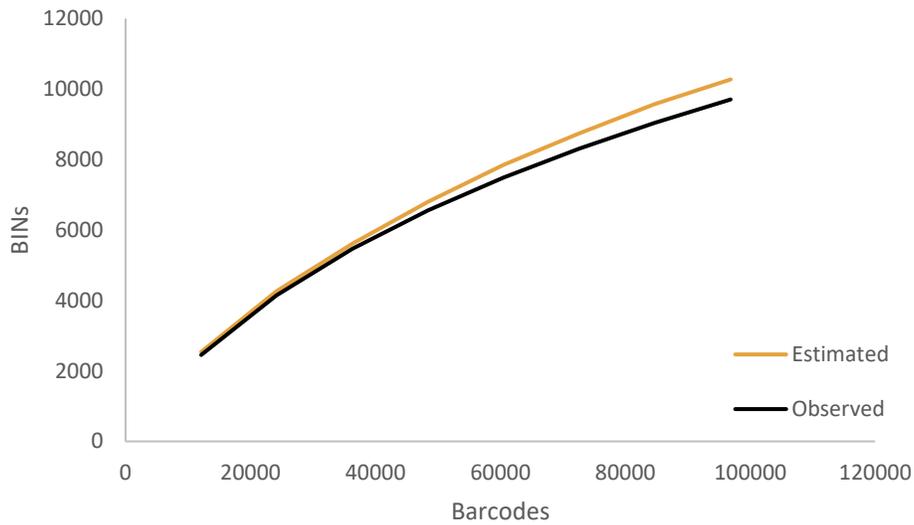
This report outlines the metabarcoding results obtained from the 74 samples collected from seven Quebec National Parks. For details on field sites and activities, please see November 2020 Field Report.



**Figure 1.** Map of 14 sampling sites across the Boreal Shield ecozone of Ontario and Quebec.

# Results

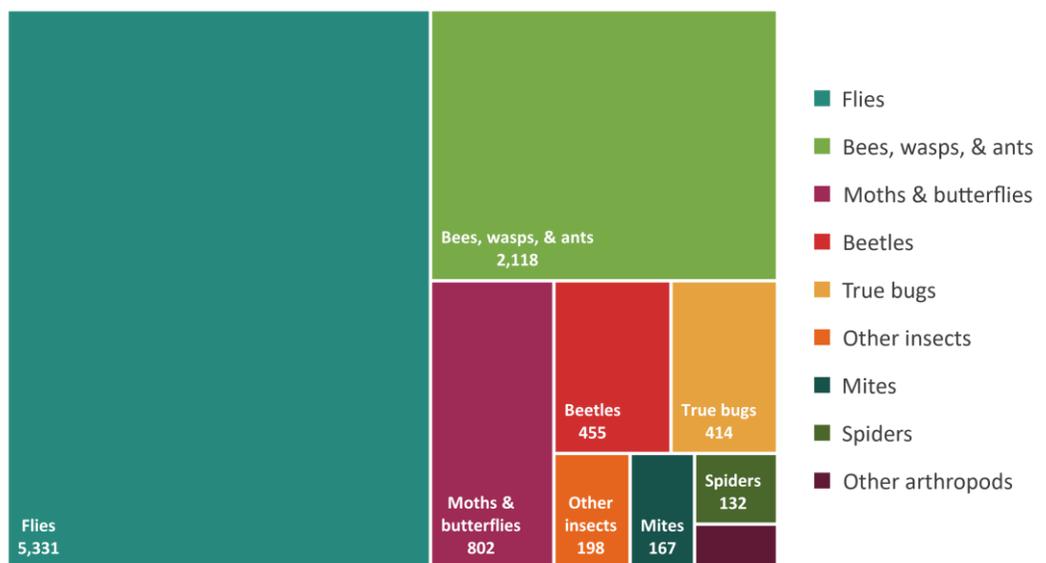
A pooled total of 9,703 different BINs (Barcode Index Numbers; a proxy for species) were encountered at the eight Quebec National Park sites. The Chao species estimate suggests that approximately 10,271 BINs are present in these sites and could be collected with this method if sampling effort was extended (Chao et al., 2005; Figure 2). Just over half the BINs captured were flies (Diptera), followed by bees, ants and wasps (Hymenoptera), moths and butterflies (Lepidoptera), and beetles (Coleoptera; Figure 3).



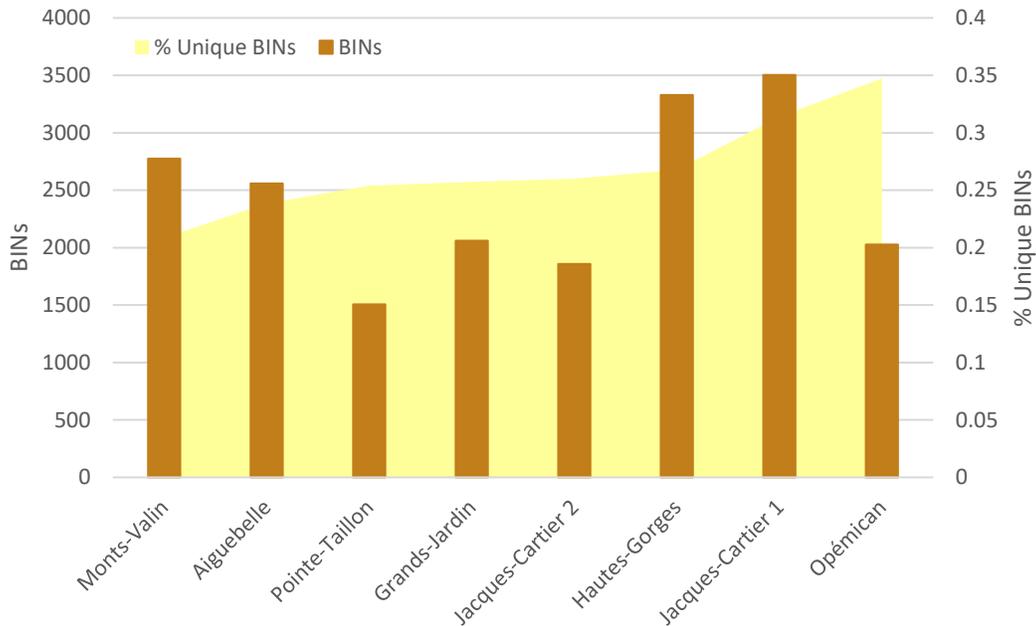
**Figure 2.** BIN accumulation curve of samples from Quebec National Parks in 2020.

In total, 4,094 species were named; 99.9% of BINs were assigned at least to family and 67% of the BINs were assigned to a genus. Specimens collected from this project represent 401 different families and 2,184 genera.

**Figure 3.** Taxonomic breakdown of BINs captured in Malaise traps in Quebec National Parks.



The number of BINs detected from a single site ranged from a low of 1,505 at Pointe-Taillon NP to a high of 3,503 at Site 1 Jacques-Cartier NP (Figure 4). Approximately 54.4% of BINs were only found in a single site while 69 BINs were found at all eight sites. The proportion of BINs that were only collected at a single site (i.e. unique BINs) also varied with Monts-Valin NP having less than 21% unique BINs while Opémican NP had 34.7% of its BINs only detected at that site.



**Figure 4.** Total BINs generated and proportion of unique BINs detected at each sampling site. Numbers and park codes correspond to Table 1.

## Acknowledgements

CBG would like to thank the various staff of Sépaq (Head of Conservation and Education Department, Deputy Director, field technicians) for their support in this project – including logistical consultation and facilitating maintenance and service of traps throughout the field season.

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