TERRESTRIAL ARTHROPOD MONITORING PROGRAM METABARCODING REPORT – *rare* Charitable Research Reserve

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

Results

A total of 2,422 different BINs (Barcode Index Numbers; a proxy for species) were encountered at the Ojibway Prairie Complex. Over half the BINs captured were flies (Diptera), followed by bees, ants and wasps (Hymenoptera), moths and butterflies (Lepidoptera), and beetles (Coleoptera; Figure 1).

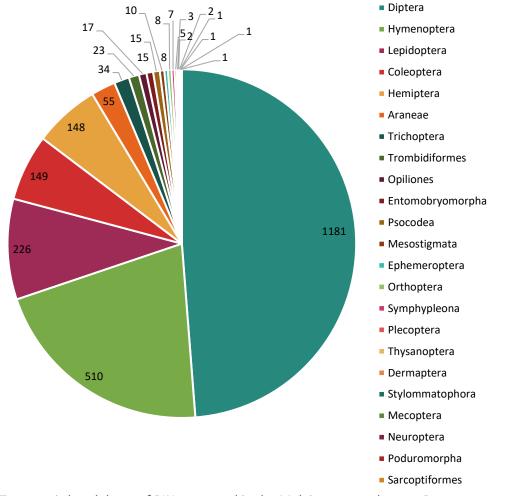


Figure 1. Taxonomic breakdown of BINs captured in the Malaise trap at the rare Reserve.

Species diversity and insect abundance varied throughout the collecting period; the period that captured the most BINs was also the largest sample collected (Figure 2). The peak of species diversity was obtained at the end of July.

In total, 744 species were named, representing 33% of the BINs. All but two BINs were assigned at least to family and 70% of the BINs were assigned to a genus. Specimens collected from this site represent 258 different families and 915 genera. A complete species list is attached separately.



Figure 2. Species diversity (measured by BINs) and approximate insect abundance (measured by wet weight of sample) captured at the trap over the 2021 collecting period.

In combination with the metabarcoding results collected in 2018, 2019, and 2020, a grand total of 4,731 BINs have been captured from *rare* Malaise trapping (Figure 3). There was an overlap of 415 BINs between all sampling years and the 2021 trap added 1,146 BINs to the total species pool (Figure 4).

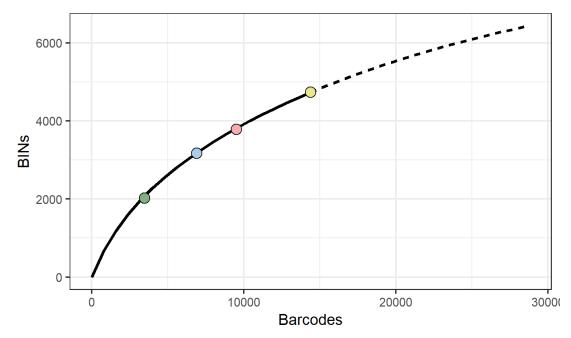


Figure 3. BIN accumulation curve over the four years of sampling at *rare* Charitable Research Reserve (green = 2018, blue = 2019, red = 2020, yellow = 2021)

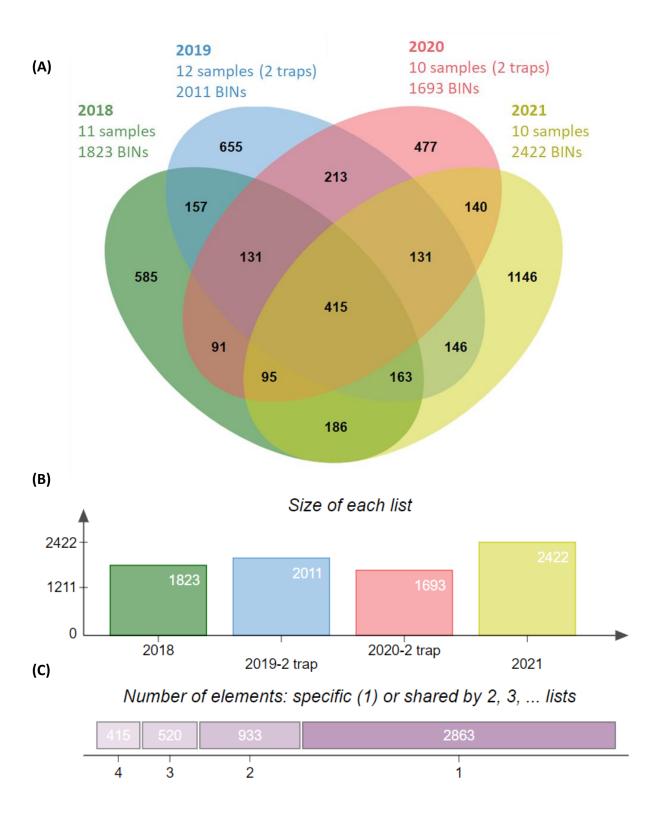


Figure 4. Diagram showing the species overlap (A), distinct BINs (B), and shared BINs (C) between the past four years of trapping. (Philippe Bardou, Jérôme Mariette, Frédéric Escudié, Christophe Djemiel and Christophe Klopp. jvenn: an interactive Venn diagram viewer. BMC Bioinformatics 2014, 15:293 doi:10.1186/1471-2105-15-293)