

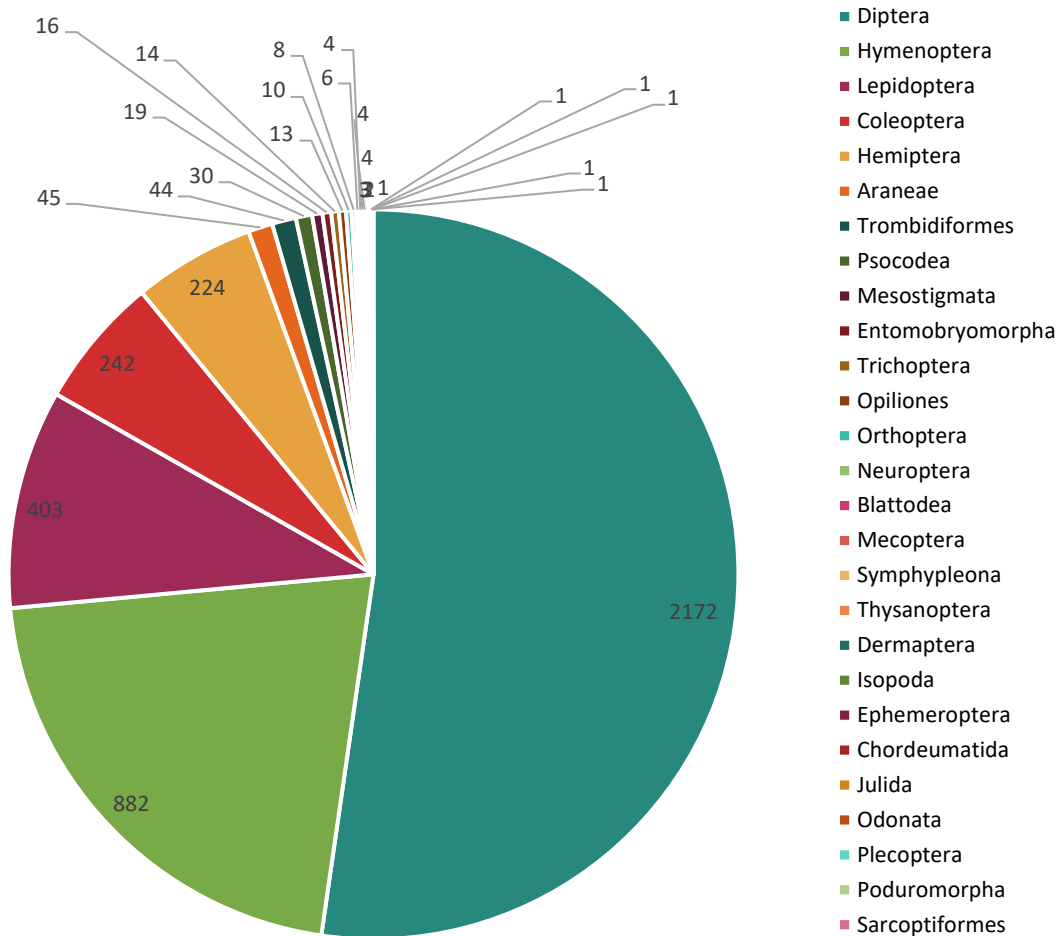
# TERRESTRIAL ARTHROPOD MONITORING PROGRAM

## METABARCODING REPORT – Ojibway Prairie Complex

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

### Results

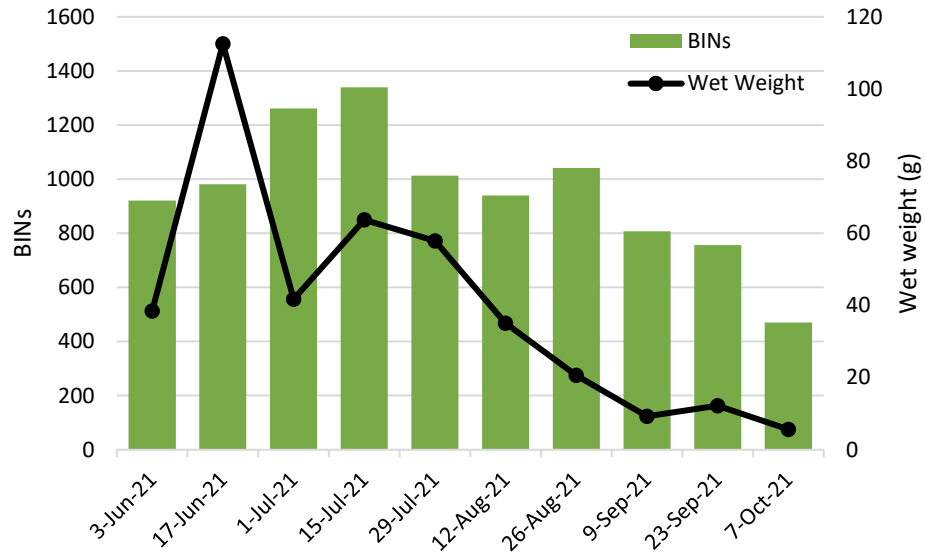
A total of 4,154 different BINs (Barcode Index Numbers; a proxy for species) were encountered at the Ojibway Prairie Complex. Over half the BINs captured were flies (Diptera), followed by bees, ants and wasps (Hymenoptera), moths and butterflies (Lepidoptera), and beetles (Coleoptera; Figure 1).



**Figure 1.** Taxonomic breakdown of BINs captured in the Malaise trap at Ojibway Prairie Complex.

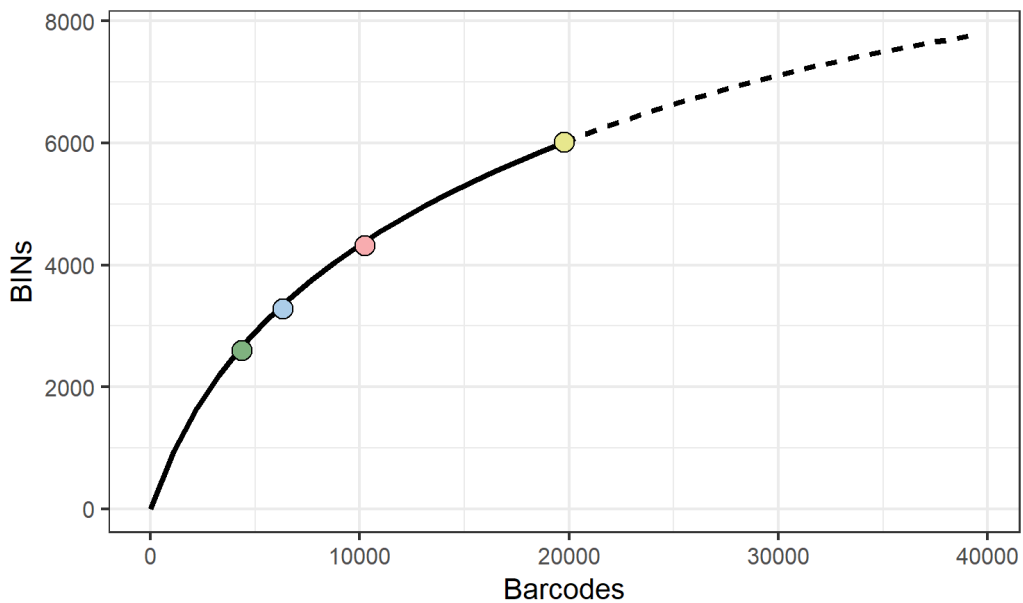
Species diversity and insect abundance varied throughout the collecting period; the period that captured the most BINs was not the largest sample collected (Figure 2). The peak of species diversity was obtained in mid-July.

In total, 1081 species were named, representing 28% of the BINs. All but five BINs were assigned at least to family and 62% of the BINs were assigned to a genus. Specimens collected from this site represent 308 different families and 1239 genera. A complete species list is attached separately.

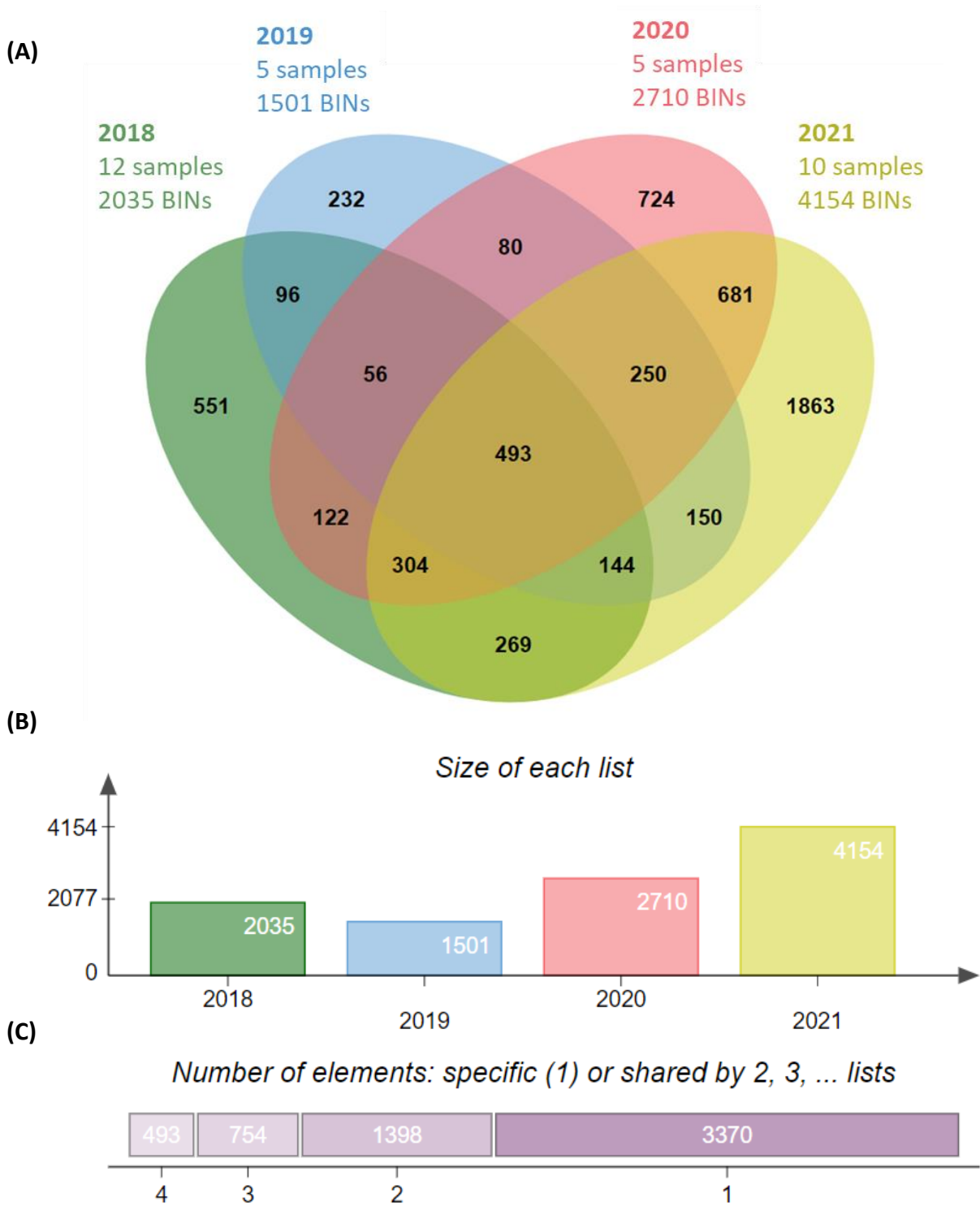


**Figure 2.** Species diversity (measured by BINs) and approximate insect abundance (measured by wet weight of sample) captured at the trap over the 2021 collecting period.

In combination with the metabarcoding results from 2018, 2019, and 2020, a grand total of 6,015 BINs have been captured from Ojibway (Figure 3). There was an overlap of 493 BINs between all sampling years and the 2021 trap added 1,863 BINs to the total species pool (Figure 4).



**Figure 3.** BIN accumulation curve over the four years of sampling at Ojibway Prairie Complex (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 Escudie, Christophe Djemiel and Christophe Klopp. jvenn: an interactive Venn diagram viewer. BMC Bioinformatics 2014, 15:293 doi:10.1186/1471-2105-15-293)