TECHNIQUES & METHODOLOGY

Voegtlin-style suction traps measure insect diversity and community heterogeneity

COLIN FAVRET, VINCENT LESSARD, ALEXIS TRÉPANIER, TITOUAN EON-LE GUERN and THOMAS THÉRY   University of Montreal, Biodiversity Centre, Montreal, QC, Canada

Abstract. 1. Comparing ecologically relevant communities of insects in heterogeneous environments requires methods capable of sampling a sufficient number of individuals and diversity of species to measure β diversity.

2. A battery-operated computer fan powers a 1.5 m high Voegtlin suction trap. These traps are efficient at capturing small, weakly flying insects, and can be used to sample the α and β diversity of Microhymenoptera in discrete habitats within a temperate forest ecosystem.

3. During a preliminary study comparing Voegtlin-style suction and Townes-style Malaise traps, we found that the suction traps caught a greater number and a greater diversity of Hymenoptera than the Malaise traps, especially of those OTUs smaller than 1.5 mm.

4. Placed along a transect at 50 m intervals, the suction traps also yielded more heterogeneous samples than the Malaise traps, suggesting they may be particularly useful for quantifying β diversity at small spatial scales. The same analyses with brachyceran Diptera were more nuanced. Malaise traps outperformed suction traps in terms of measuring α diversity, but suction traps resolved a higher degree of brachyceran community heterogeneity using β diversity.

5. Insofar as Hymenoptera are amongst the most diverse of insect orders and the vast majority of species are specialist parasitoids of other insects, suction trapped Hymenoptera diversity may be a useful proxy for measuring α and β insect diversity in general.

Key words. Brachycera, Diptera, forest habitat, Hymenoptera, Malaise trap, Microhymenoptera, Parasitica, α diversity, β diversity.

Introduction

As efforts to characterise biodiversity evolve, cost-effective means to compare relevant communities of organisms often comes down to the choice of sampling strategy. Originally tackled by Fisher *et al.* (1943) and elaborated by Whittaker (1960, 1972) diversity indices α, β, and γ are widely used to evaluate insect diversity. Different sampling strategies resolve, over different temporal and spatial scales, what Tuomisto (2010) called discrete sampling units. In situations where the goal is to compare diversity amongst regions, α diversity, the within-sampling-unit species diversity (i.e., the effective number of species per compositional unit), and γ diversity, the total diversity of the dataset over all sampling units (i.e., the effective number of species in the dataset) together are used to evaluate β diversity, the relative diversity of the sampling units.

Correspondence: Colin Favret, University of Montreal, IRBV, 4101 East Sherbrooke Street, Montreal, QC H1X 2B2, Canada. E-mail: colinfavret@aphidnet.org

Biodiversity is frequently measured across broad geographic and habitat space. Whether comparing political geographic entities, islands, or habitat categories, or measuring latitude or elevation gradients, the reality is that there is always an arbitrary element in defining these regions or habitats (Tuomisto, 2010). Any ecosystem is a mosaic of habitats, these in turn mosaics of those yet smaller, and the complexity of interactions within these mosaics is increasingly of interest in understanding how to support and maximise ecosystem services (Mori *et al.*, 2018).

The heterogeneity of a terrestrial ecosystem is most often described in terms of vegetation (e.g., Table 1 in Mori *et al.*, 2018), for example a deciduous temperate forest being a patchwork of areas with larger or smaller trees and understory plants of different taxonomic or functional affinities. Ecosystem patchiness, or habitat heterogeneity, can be quantified using various β diversity indices (Mori *et al.*, 2018). Higher β diversity in turn has been shown to provide stability in ecosystem functioning in some heterogenous (or patchy) environments (Loreau *et al.*, 2003; Mokany *et al.*, 2013; Pasari *et al.*, 2013) and can be used to inform conservation (Socolar *et al.*, 2016). The scales over

Table 1. Number of specimens, OTUs, and unique OTUs (those collected by one trap but not the other at each site, or those collected at only one site) and the respective Shannon (*H'*) and Simpson (*E*) α diversity indices.

Site and trap	Hymenoptera					Brachycera				
	Specimens	OTUs	Unique	*H'*	*E*	Specimens	OTUs	Unique	*H'*	*E*
Site 1 suction	126	52	39	3.49	0.957	104	8	6	0.78	0.328
Site 1 Malaise	74	38	25	3.18	0.940	30	9	7	1.80	0.802
Site 1 subtotal	200	77	14	3.79	0.966	134	15	6	1.24	0.471
Site 2 suction	329	103	88	3.85	0.949	87	16	14	1.50	0.612
Site 2 Malaise	70	34	19	2.89	0.896	32	11	9	1.82	0.782
Site 2 subtotal	399	122	45	3.97	0.953	119	25	11	1.88	0.681
Site 3 suction	107	46	39	3.22	0.921	39	6	5	0.59	0.243
Site 3 Malaise	78	24	17	1.93	0.652	41	12	11	1.74	0.704
Site 3 subtotal	185	63	8	3.25	0.908	80	17	8	1.40	0.509
Site 4 suction	154	74	67	4.04	0.984	135	9	5	0.44	0.156
Site 4 Malaise	177	30	23	2.03	0.674	142	35	31	1.91	0.598
Site 4 subtotal	331	97	30	3.52	0.892	277	40	24	1.34	0.403
Suction subtotal	716	158	106	4.31	0.975	365	28	20	0.98	0.342
Malaise subtotal	399	92	40	2.96	0.790	245	48	40	2.22	0.682
Total	1115	198		4.21	0.954	610	68		1.67	0.495

which these patchy plant communities affect or are correlated with animal β diversity, and the nature and extent of these connections, have not been extensively studied, although some work has focused on correlating the diversity of plants and herbivorous insects (Novotny *et al.*, 2007; Kemp *et al.*, 2017). Logistical constraints to sampling a sufficient number of animals in a quantifiable manner restrict the possibilities: many animals move freely between habitat patches, leading to overlapping boundaries, and many collecting methods do not sample animals in numbers sufficient to make robust quantifiable comparisons.

Previous experience (Favret & Voegtlin, 2001) suggested suction traps may serve these purposes. Fan-driven suction traps were developed in Britain (Johnson, 1950) and are an integral part of the Rothamsted Insect Survey (Taylor 1979, 1986), including a network of suction traps covering the island of Great Britain. These traps, as well as those that have operated in the U.S. Pacific Northwest (Allison & Pike, 1988; Halbert *et al.*, 1990) and Midwest (Meehan *et al.*, 2011; Schmidt *et al.*, 2012), China (Miao *et al.*, 2011), and continental Europe (Taylor, 1979), are all of a similar design, about 10–12 m tall, placed singly, and connected directly to the power grid. Whereas these Johnson-style traps have largely been used to measure the aerial density of aphids and other economically important insects, it was to measure aphid habitat selection that David Voegtlin (Illinois Natural History Survey, Champaign, IL, USA) designed a smaller version. By placing paired traps in adjacent habitats, one could determine the numbers and species of aphids choosing one habitat over the other (Favret & Voegtlin, 2001, 2004). These Voegtlin-style suction traps (i) have a relatively restricted sphere of influence, favouring small, weak-flying insects, (ii) draw the same volume of air so as to yield comparable results, (iii) sample a large enough number of insects to yield quantifiable results, and (iv) are easy to maintain over the summer season and over multiple years.

To sample and compare the insect faunas of discrete forest habitat types, we deployed four of these Voegtlin-style suction traps along a 150 m transect and compared their relative catches of Hymenoptera and brachyceran Diptera. These two insect orders have been shown to be exceptionally diverse and under-documented in Canada (Hebert *et al.*, 2016; Bennett *et al.*, 2019; Savage *et al.*, 2019). To evaluate the adequacy of suction traps relative to the most commonly used comparable method (Matthews & Matthews, 1971; deWaard *et al.*, 2019), we also placed Townes-style Malaise traps (Townes, 1972) at each of the four sites.

Materials and methods

Voegtlin-style suction traps

The suction traps are vertical PVC pipes, 20 cm in diameter and 1.5 m in height (Fig. 1). A computer cooling fan located in the lower part of the pipe draws air in through the top, pulls it through a brass wire mesh funnel located above, and pushes it out the bottom. Insects that fly close enough to the top opening are caught by the suction, drawn into the pipe and down the funnel, and are collected into a preservative-containing receptacle. The brass mesh has grill openings of 178×178 μm, thus capturing the smallest of insects.

A flat plastic cap 40 cm in diameter and 5 cm above the trap opening prevents rainwater and other falling elements from entering. The trap opening is 2 m above the ground. Eight centimetres below the opening is the brass mesh cone that funnels down 22 cm and is soldered to a mason jar lid with the seal removed. Twenty-five centimetres below the jar lid is a 12 V, 10 cm diameter (120 mm × 120 mm) computer case cooling fan, an Xfan® model RDH1225B, spinning at 2400 rpm, and pulling 2.59 cubic meters of air per minute. A 12 V deep cycle battery sits on the ground in a weather-proof box. Ninety-five centimetres below the fan is the bottom opening of the pipe. The trap is held in place 50 cm above the ground by a fence
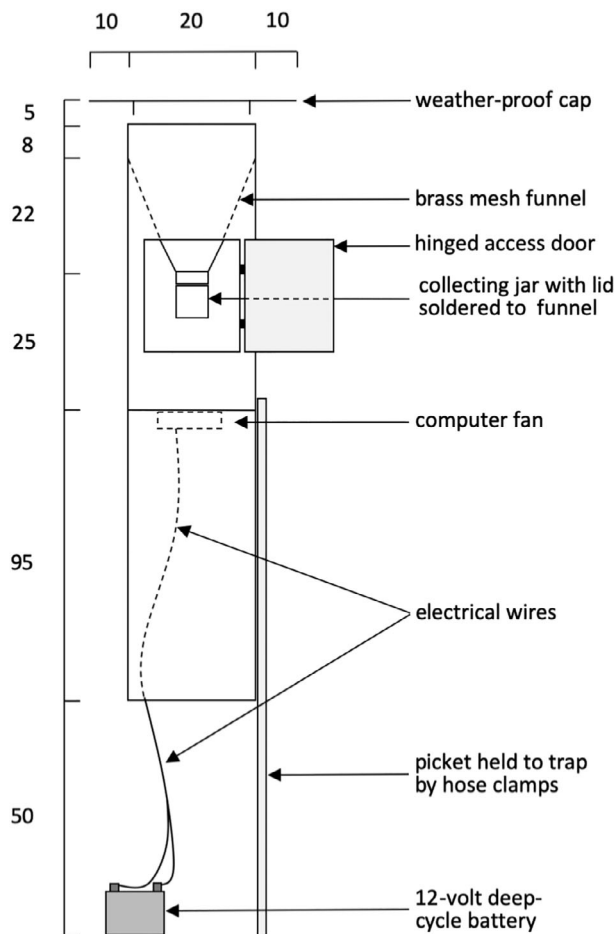
Fig. 1. Basic plan of suction trap. Measurements are in centimetres.

picket fastened to the PVC pipe by hose clamps. A hinged door is cut into the side of the trap for access to the collecting jar and the fan. The door and the fan assembly are ringed with foam seals to prevent air leakage and thus ensure a uniform air displacement.

Field sites and sampling

The Laurentian Forest, located at the southern margin of the Canadian Shield and at a north-temperate latitude, is a mixed deciduous-conifer forest harbouring a diverse array of habitat types. Twenty forest habitat types have been classified just within the 16 km² territory of the University of Montreal's Laurentian Biology Research Station near Saint-Hippolyte, Quebec, Canada (Savage, 2001). The traps were placed in four of these discrete vegetation-based habitats along a straight transect, 50 m between adjacent traps. The first site (45.98990°, −74.00253°) was a relatively xeric location at the top of a hill and dominated by white pine (*Pinus strobus* Linnaeus) and red spruce (*Picea rubens* Sargent). Site 2 (45.99054°, −74.00267°) was a relatively humid location, with small pools of standing water after heavy rain, at the bottom of a small ravine, and with balsam fir (*Abies balsamea* (Linnaeus)

Miller) and white birch (*Betula papyrifera* Marshall). Site 3 (45.99107°, −74.00244°) was a mesic transition zone located on the other side of the ravine, with white birch (*B. papyrifera*) and red maple (*Acer rubrum* Linnaeus). Finally, site 4 (45.99141°, −74.00182°) was also a mesic transition zone with white birch (*B. papyrifera*) and trembling aspen (*Populus tremuloides* Michaux). In terms of general hygric conditions and vegetation community, sites 3 and 4 were the most similar whereas sites 1 and 2 were the most different. For the purposes of this preliminary study, we did not attempt to fully quantify the vegetation community. A high-resolution panoramic image was captured of each of the four sites and can be examined at www.gigapan.org/gigapans/ 202827, www.gigapan.org/gigapans/202828, www.gigapan.org/ gigapans/202829, and www.gigapan.org/gigapans/202830.

To compare the efficiency of the Voegtlin suction trap with a more frequently used method to capture flying insects, we placed a Townes-style BugDorm BT1002 'ez-Malaise trap' (MegaView Science Co., Ltd., Taiwan) approximately 5 m from each of the suction traps. The netting of the Malaise traps has a variable mesh size with spaces measuring up to, but no larger and mostly smaller than 430 μm. In both kinds of traps, insects were collected into recreational vehicle or marine antifreeze, that is, mostly propylene glycol (Höfer *et al.*, 2015). The eight traps were in place for 7 weeks in July and August 2015, with collection jars changed weekly. Resources have thus far allowed us to examine only 1 week's worth of material, namely between 23 and 30 July 2015.

The eight sample jars were recovered at the end of the sampling period, the samples transferred to 70% ethanol, and the insect specimens rough-sorted to order. Diptera and Hymenoptera overwhelmingly dominated both suction and Malaise trap samples and were therefore chosen as the focus of the study. Hymenoptera were sorted to superfamily and brachyceran Diptera to family, and then both groups were further sorted to morphospecies (operational taxonomic units, OTUs). We omitted Nematocera entirely and classed all Phoridae as a single OTU, despite their abundance, because we had little confidence that our OTUs could adequately reflect real species diversity. Care was taken to evaluate OTUs across all eight traps so that the different catches would be comparable. A variety of subjectively chosen characteristics were used to sort OTUs: antennomere count and body length were of particular focus in sorting Hymenoptera, whereas wing patterning and venation was important in sorting Diptera. A representative specimen of each OTU was photographed and its overall body length measured. The insect samples are deposited in the University of Montreal's Ouellet-Robert Entomological Collection (QMOR) and will be determined in greater taxonomic detail as resources allow.

Diversity analyses

The number of individuals of each OTU from each trap was compiled. α diversity was calculated using the Shannon (1948) and Simpson (1949) indices, H' and E, respectively. The former permits us to compare the diversity of each trap, taking into account the number of species as well as the number of individuals of each species. The latter calculates the likelihood that any

two specimens from a given trap are of different species. To compare the similarity of the different traps, we calculated β diversity with the Morisita (1959) and Chord (Orlóci, 1967) indices (Horn, 1966; Legendre & Gallagher, 2001) using the *beta. div*, and *beta.div.comp* functions in the R package 'adespatial' (Legendre & De Cáceres, 2013). These indices were chosen because they are relatively insensitive to rare species or incomplete samples (Barwell *et al.*, 2015), as in our case having examined only 1 week, and yield comparable results (Legendre & De Cáceres, 2013). In each case, the higher the index value, the more dissimilar is the diversity of the compared samples. To graphically represent the relative similarity and dissimilarity between the various habitats and trapping methods, we plotted the β diversity results with UPGMA dendrograms (http://genomes.urv.cat/UPGMA/; Garcia-Vallve *et al.*, 1999).

Results

In all, 1115 and 610 specimens of Hymenoptera and brachyceran Diptera were collected and sorted into 198 and 68 OTUs, respectively (Table 1). Hymenoptera were consistently captured in higher specimen numbers and in higher OTU numbers in suction traps than in Malaise traps. However, controlling for sample size, the ratio of OTUs to specimens was greater in Malaise traps at two sites (1 and 2). Brachycera were, overall, collected in greater numbers but in lower OTU diversity in suction traps than in Malaise traps. At only one site (2) was the number of OTUs higher in the suction trap, but in all cases the ratio of OTUs to specimens was higher in Malaise traps. At lower taxonomic levels, Braconidae, Ceraphronoidea, Chalcidoidea, and Platygastroidea were collected in larger specimen and OTU numbers in the suction traps, whereas Cynipoidea and Diaprioidea were more numerous and diverse in the Malaise traps (Table 2). Ichneumonidae were more numerous in Malaise traps but equally diverse in both kinds of traps. The vast majority of Brachycera were of the family Phoridae (80% and 56% of the suction and Malaise trap samples, respectively). Suction traps caught larger numbers of smaller

Hymenoptera than did Malaise traps, the former capturing 86% of all specimens and 69% of all OTUs smaller than 1.5 mm in length (Fig. 2). Conversely, suction traps captured fewer specimens and OTUs longer than 1.5 mm, 31% and 55%, respectively.

α diversity

Hymenoptera exhibited a higher α diversity, as measured with Shannon and Simpson indices, in the suction traps than in the
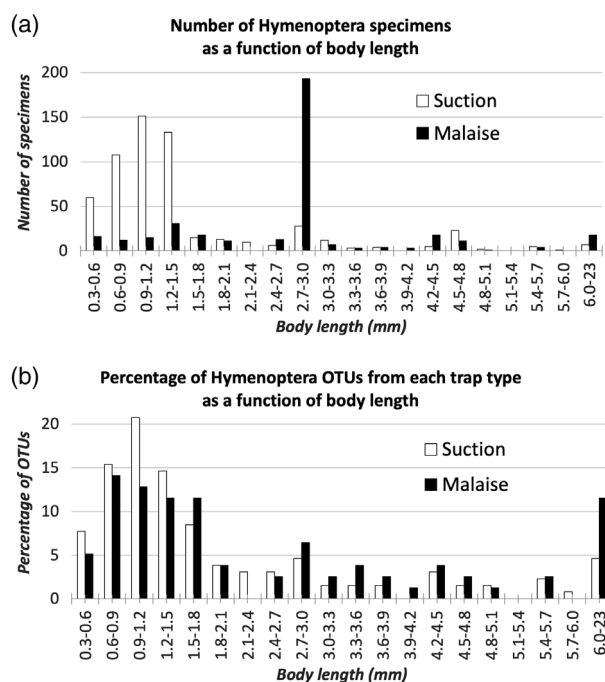

Fig. 2. Absolute number of Hymenoptera specimens (a) and percentage of Hymenoptera OTUs from each trap type (b) captured in suction and Malaise traps, as a function of size.

Table 2. Number of specimens and OTUs of abundant taxa. Numbers in parentheses are the numbers of OTUs found uniquely in one kind of trap.

	Specimens			OTUs		
Taxon	Suction traps	Malaise traps	Both traps	Suction traps	Malaise traps	Both traps
Braconidae	73	20	93	20 (15)	6 (1)	21
Ceraphronoidea	206	16	222	35 (26)	10 (1)	36
Chalcidoidea	240	44	284	43 (33)	16 (6)	49
Cynipoidea	5	16	21	4 (1)	5 (2)	6
Diaprioidea	37	205	242	8 (2)	10 (4)	12
Ichneumonidae	30	52	82	19 (12)	19 (12)	31
Platygastroidea	108	22	130	20 (10)	13 (3)	23
All other Hymenoptera	17	24	41	9 (7)	13 (11)	20
Hymenoptera subtotal	**716**	**399**	**1115**	**158 (106)**	**92 (40)**	**198**
Phoridae*	295	137	432	1 (0)*	1 (0)*	1*
All other Brachycera	70	108	178	27 (20)	47 (40)	67
Total	**1081**	**644**	**1725**	**186 (126)**	**140 (80)**	**266**

*Phoridae were not sorted to individual OTUs.

Malaise traps at all four sites (Table 1). The average Shannon index was 45% higher in the suction traps (3.65 vs. 2.51), and the index for the four suction traps combined was 46% higher (4.31 vs. 2.96). The average Simpson index was 20% higher in the suction traps (0.953 vs. 0.791), and the index for the four suctions traps combined was 23% higher (0.975 vs. 0.790). The relatively xeric and humid sites (sites 1 and 2, respectively) were more diverse than the mesic ones (3 and 4), as measured by both indices. Additionally, the α diversity of suction and Malaise traps was more divergent at the two mesic sites than at the xeric and humid sites: at the mesic sites, the differences in Shannon and Simpson indices were, respectively, 40–50% and 29–32%
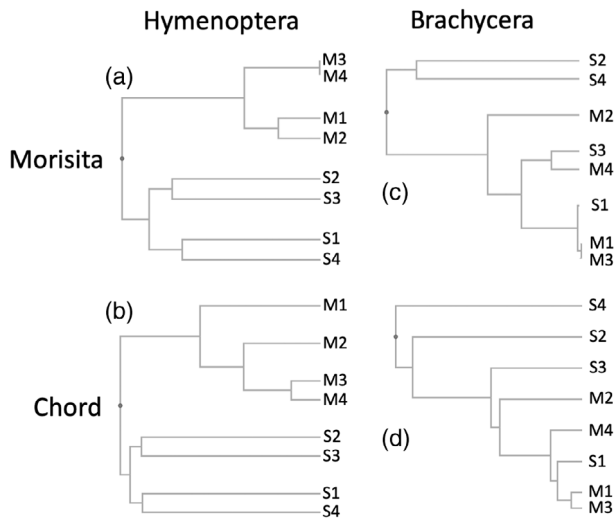

Fig. 3. UPGMA dendrograms of Hymenoptera (a, b) and Brachycera (c, d) β diversity as measured by Morisita (a, c) and Chord (b, d) indices. Suction and Malaise traps at sites 1, 2, 3, and 4 are labelled S1 through M4.

between suction and Malaise traps, whereas at the xeric and humid sites, they were 9–25% and 2–6% divergent.

The brachyceran Diptera exhibited the opposite trends of the Hymenoptera, being more diverse in the Malaise traps than in the suction traps at all four sites and as measured by both α diversity indices; the differences were also more pronounced than with the Hymenoptera (Table 1). The average Shannon index was twice as high in the Malaise traps (0.83 vs. 1.68), and the index for the four Malaise traps combined was 125% higher (0.98 vs. 2.22). The average Simpson index was over twice as high in the Malaise traps (0.335 vs. 0.722), and the index for the four Malaise traps combined was also twice as high (0.342 vs. 0.682). The Diptera followed the same trend as the Hymenoptera at the habitat level, however, being more diverse in the xeric and humid sites (1 and 2) than in the mesic sites (3 and 4). Also as with the Hymenoptera, the α diversity of suction and Malaise traps was more divergent at the two mesic sites than at the xeric and humid sites: at the mesic sites, the differences in Shannon and Simpson indices were, respectively, 66–67% and 65–74% between suction and Malaise traps, whereas at the xeric and humid sites, they were 18–57% and 22–59% divergent.

β diversity

The Hymenoptera diversity captured in suction traps was distinct from that captured in Malaise traps, and vice-versa: suction trap samples clustered together and Malaise trap samples clustered together in both β diversity analyses (Fig. 3). Additionally, the Hymenoptera diversity of the suction traps was more heterogeneous than that of the Malaise traps: the Morisita and Chord β diversity indices were consistently higher between suction traps (average of 0.666 and 1.169 for Morisita and Chord indices, respectively) than they were between Malaise traps (0.247 and 0.581) (Table 3). The greater heterogeneity of the suction trap

Table 3. β diversity indices for Hymenoptera (above the diagonal) and Brachycera (below the diagonal) as measured with Morisita and Chord indices. Suction and Malaise traps at sites 1, 2, 3, and 4 are labelled as S1 through M4.

Index	Trap	S1	S2	S3	S4	M1	M2	M3	M4
Morisita	S1		0.680	0.800	0.571	0.630	0.781	0.870	0.838
	S2	0.241		0.611	0.616	0.555	0.585	0.920	0.909
	S3	0.062	0.184		0.717	0.906	0.886	0.961	0.965
	S4	0.253	0.178	0.198		0.672	0.754	0.867	0.865
	M1	0.002	0.270	0.082	0.273		0.187	0.446	0.436
	M2	0.095	0.101	0.063	0.134	0.112		0.209	0.198
	M3	0.008	0.294	0.101	0.297	0.000	0.135		0.004
	M4	0.035	0.135	0.033	0.145	0.046	0.102	0.065	
Chord	S1		1.193	1.278	1.118	1.171	1.257	1.273	1.274
	S2	0.552		1.124	1.124	1.100	1.090	1.330	1.319
	S3	0.274	0.628		1.180	1.355	1.340	1.381	1.384
	S4	0.596	0.731	0.655		1.176	1.194	1.208	1.210
	M1	0.113	0.561	0.293	0.594		0.744	0.773	0.772
	M2	0.307	0.571	0.422	0.620	0.296		0.498	0.493
	M3	0.095	0.559	0.290	0.592	0.060	0.291		0.204
	M4	0.146	0.530	0.305	0.557	0.123	0.259	0.110	

samples is also visible in the relatively longer branches in the UPGMA dendrograms (Fig. 3).

The brachyceran Diptera β diversity analyses did not exhibit distinctive clustering, neither based on trap type, as seen in the Hymenoptera, nor based on site (Fig. 3). However, as seen with the Hymenoptera, the suction trap samples were more heterogeneous than the Malaise trap samples, with longer branches and higher β diversity indices. The average Morisita and Chord indices between suction traps were 0.186 and 0.573, respectively, whereas between Malaise traps they were 0.077 and 0.190 (Table 3).

Discussion

In terms of brachyceran Diptera α diversity, the Malaise traps clearly outperformed the suction traps: they captured more individuals of more OTUs yielding higher Shannon and Simpson α diversity indices. However, β diversity analyses indicated that the suction traps yielded more heterogenous catches between sites than did the Malaise traps. In contrast with the Hymenoptera, our Diptera results were surely affected by the fewer number of individuals and OTUs: we only considered 178 non-phorid Brachycera and 68 OTUs, in comparison with 1115 Hymenoptera and 198 OTUs (Table 2). Perhaps our Diptera results would have been different had we included the Nematocera and multiple Phoridae OTUs.

In contrast, with respect to Hymenoptera diversity, the Voegtlin suction traps outperformed the Townes Malaise traps at all levels: they captured more individuals of more OTUs, and therefore a greater α diversity, and their catches more adequately reflected the heterogeneity of Hymenoptera diversity between sites (β diversity). The white caps on the suction traps may have had an attractive effect, as some insects are known to be attracted to bright colours, including white (Joshi *et al.*, 2015). However, the roof netting of the Malaise traps also was white and it therefore seems unlikely that the colouring would bias our results towards one trap over the other. Some insects are attracted to the tops of prominent structures such as fence posts (Sullivan, 1981) and hence perhaps to suction traps, although this effect is best documented in Nematocera (Gibson, 1945; Downes, 1955), excluded from this study.

A major component of the Hymenoptera diversity stems from the small size of the insects captured: the suction traps were more effective than the Malaise traps at capturing Hymenoptera 1.5 mm or smaller, although relative OTU richness was greatest for small insects for both trap types (Fig. 2). It appears that low-powered suction traps simply favour small insects not strong enough to escape the suction. We speculate that larger insects, capable of escaping the effect of suction traps, are also more likely to fly longer distances and thus have a homogenising effect across habitat space, as seen in the lower β diversity of the Malaise trap samples.

That said, insect diversity and abundance are highly stochastic at small spatial and geographic scales. For example, Microhymenoptera are known to form swarms (van Achterberg, 1977; Quimio & Walter, 2000; Eberhard, 2007) and capturing one would spontaneously and greatly affect the results from a single sample, as made evident in our data by the overabundance of a single (Diapriidae) OTU, 2.8 mm in length (Fig. 2a). Although we had four spatial replicates, they were all within 150 m of each other and we analysed only a single week's worth of data. As such, and especially considering that a large number of OTUs were captured in only one or the other trap type (Tables 1 and 2) and that Hymenoptera β diversity clustered based on trap type (Fig. 3), our preliminary study suggests the two trap are complementary, rather than one being definitively better than the other. Indeed, multiple other studies have underlined the fact that any single collecting method is insufficient for collecting the full diversity of Microhymenoptera, with certain methods favouring some taxa over others (Darling & Packer, 1988; Noyes, 1988; Mazón & Bordera, 2008; Larsen *et al.*, 2014).

Our suction traps document that there is significant insect community heterogeneity in the Laurentian forest ecosystem at a scale of 50 m. The suction trap samples are capable in particular of resolving this patchiness for Microhymenoptera. A relative lack of habitat heterogeneity, that is, an increase in homogeneity, has been shown to have detrimental effects on forest productivity and ecosystem services (van der Plas *et al.*, 2016; Felipe-Lucia *et al.*, 2018). Being able to measure and monitor that heterogeneity with especially diverse and sensitive taxa (Sánchez-Bayo & Wyckhuys, 2019) is therefore of great value with respect to biological conservation efforts (Olden, 2006; Socolar *et al.*, 2016).

The four sampling sites in this present study were each ecologically distinct, however. With no habitat replicates, it is not possible to distinguish whether insect and vegetation patchiness are specifically correlated, or if suction traps might yield equally heterogeneous insect samples within specific habitat types. Our future work will seek to compare the insect β diversity across similar versus different habitats to assess the scale of patchiness of insect communities.

In the absence of performing exhaustive but logistically prohibitive surveys, insofar as most Hymenoptera are parasitoids of other insects and likely represent the most speciose of all insect orders (Forbes *et al.*, 2018), they may serve as a proxy for insect diversity generally. Based on our results, for the purposes of measuring general forest insect diversity, suction-trapped Hymenoptera seem to be ideal.

The use of OTUs in biodiversity sampling

Given the large amount of cryptic diversity amongst Hymenoptera (Stahlhut *et al.*, 2013) and a documented identification error rate amongst parataxonomists (Krell, 2004; Derraik *et al.*, 2010), we are certain to have inadvertently lumped and split specimens within and amongst our OTUs. However, given the vast numbers of undescribed Hymenoptera in Canada (Stahlhut *et al.*, 2013; Hebert *et al.*, 2016; Bennett *et al.*, 2019) and the relative paucity of professional taxonomists available for such a task (Giangrande, 2003; Council of Canadian Academies & Expert Panel on Biodiversity Science, 2010; Pearson *et al.*, 2011; Sluys, 2013), traditional morphological identification to the species level would not be feasible. DNA barcoding and subsequent assignation to molecular OTUs (Morinière *et al.*, 2016; Wang *et al.*, 2018; deWaard *et al.*, 2019) is a workable solution

that we will seek to incorporate in future work. That being said, however imperfect, the use of OTUs has been validated and used in a number of modern studies (Obrist & Duelli, 2010; Hackman *et al.*, 2017). We believe it adequate for the present project, documenting the efficacy of the Voegtlin suction trap for measuring and comparing the diversity of insect communities, especially those of Microhymenoptera.

Acknowledgements

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