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Investigation of Potential Trapping Bias in Malaise Traps Due to Mesh Gauge, in Two Habitats

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Investigation of Potential Trapping Bias of Insects in Malaise Traps

Due to Mesh Gauge, in Two Habitats

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A thesis submitted to the faculty of
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ABSTRACT

Investigation of Potential Trapping Bias of Insects in Malaise Traps

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Malaise traps are a common tool for collecting insects used by many researchers. Although there have been variations in the models and materials used for Malaise traps, the potential for sampling bias due to mesh gauge has been explored inadequately. This study compared coarse and fine mesh Townes model Malaise traps in two habitats on the Grand Staircase-Escalante National Monument. The two habitats next to the Lick Wash trailhead were defined by dominant vegetation type – sagebrush and grasses or Piñon-Juniper. We collected from three sites per habitat type, over three consecutive days in June in both 2006 and 2007. A pair of Malaise traps consisting of one coarse mesh and one fine mesh trap was used at each site in order to compare differences in the diversity and in the average size of individuals collected by each type of Malaise trap. We measured diversity using both presence-absence data such as richness scores and Jaccard's Index of Similarity, and abundance-based measures of comparison, including Simpson's Index of Diversity and non-metric multidimensional scaling. We identified all individuals according to Order, and because of our interest in flies and their abundance, we further identified the Diptera to the Family level. Average insect size was determined by categorizing individuals according to one of 14 distinct size-classes. In sum, 71 samples totaling approximately 62,500 insects were identified and sized. Because we sampled from two adjacent habitats, we also discuss beta diversity across the sample sites. Although mesh-size appears to have a significant effect on the diversity of the catch according to some tests, not all of our analysis agrees. In addition, the gain in the amount of diversity collected by incorporating both mesh-sizes may not be worth the costs of that kind of sampling. Other means of collection may adequately make up that difference. Habitat on the other hand was a clear marker for difference in diversity. Size was not found to be significant overall, but there still may be reasons to examine the effect of mesh-size with respect to the Hymenoptera.

Keywords: Malaise traps, sampling bias, insects, Diptera (flies), Grand Staircase-Escalante National Monument, Utah, body-size, richness, abundance, similarity indices, Simpson's Index of Diversity, Jaccard's Index, beta diversity

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Introduction

Cataloging Biodiversity

Part of the work of Biology is to catalogue communities and their components (Wilson 1992; Magurran 2004). Whether your concern is with conservation and preservation, taxonomy and systematics, ecological and community relationships, or a single taxon or subset of taxa there remains the basic need of getting an estimate of community composition.

Insects are the most abundant taxon within the animal kingdom (Wilson 1987; Dial and Marzluff 1988; Wilson 1988; Wilson 1992) Insects play significant roles in their communities and with respect to humanity. There are familiar negative roles as pests to humans, crops, and livestock, or as vectors for disease. Insects also have positive characters as pollinators, decomposers, and as significant links in the food chain(Brown 2005). From a human standpoint, insects have also been used as bioindicators (Lenat 1988; Burgio and Sommaggio 2007), as models in genetics and evolution (Mitchell-Olds 2001; Celniker and Rubin 2003), and multiple other aspects of scientific research (Wigglesworth 1985; Papaj and Lewis 1992; Finlay, Thomas et al. 2006). Inadequate sampling due to sampling bias could very well result in a misunderstanding of not only the diversity and biogeography of insects, but perhaps humanity may overlook other potential explanatory patterns and models (Brown 2005; Fraser, Dytham et al. 2008).

Mitigating Sampling Bias for More Accurate Estimates of natural populations

As scientists, we also have to recognize the limitations of time and money with respect trying to maximize efficiency of collecting. Past research has shown that with insects, more than one method of trapping is needed in order to collect a high percentage of the available taxa

(Covell and Freytag 1979; Darling and Packer 1988; Brown 1995; Brown and Feener 1995; Faulds and Crabtree 1995; Campos, Pereira et al. 2000; Suh, Spurgeon et al. 2003; Bartholomew and Prowell 2005; Brown 2005; Holusa and Drapela 2006; Fraser, Dytham et al. 2008; Mazon and Bordera 2008; van Hennekeler 2008; Missa 2009). These and other studies recognize that there are limitations to each collection method, passive or active.

Regardless of the sampling method(s) used, efforts should always be made to reduce bias in order to obtain better estimates of diversity of natural populations. Even with highly successful trapping methods – success being measured strictly by the number of individuals captured – it should not be assumed that every available taxon is captured or that each taxon captured is captured proportionally to the natural population (Magurran 2004).

If a sampling bias is present, an understanding of this bias will help us to better mitigate these limitations and increase the economy of our sampling efforts (Darling and Packer 1988; Campos, Pereira et al. 2000).

Malaise Traps: a common method of collection

Current use

Our concern for this paper is the Malaise trap. The first model was developed by René Malaise, a Hymenopterist, in 1934 (Malaise 1937), and the trap was well adopted into use by at least the 1960s . By the mid 1970s, several trap designs and modifications had been made and experimented with and some consensus has been arrived in using the Townes model (Townes 1972; Matthews and Matthews 1983). The Townes model is the model we used in this study.

The Malaise trap is used in particular for Hymenopterans (Darling and Packer 1988; Noyes 1989; Saaksjarvi, Haataja et al. 2004; Bartholomew and Prowell 2005; Fraser, Dytham et

al. 2008; Mazon and Bordera 2008) and Dipterans (Cerretti, Whitmore et al. 2004; Brown 2005; Fritzler 2006; Marinoni, Marinoni et al. 2006; Ziegler 2006; Tschorsnig, Domingo-Quero et al. 2007; Wilson 2007; Ackland 2008). Several other orders have also been listed as taxa of interest in studies citing the use Malaise traps, including: Lepidoptera (Covell and Freytag 1979; Tangmitcharoen, Takaso et al. 2006; Liska and Modlinger 2007; Dapporto and Strumia 2008), Coleoptera (Cook ; Ulyshen, Hanula et al. ; Cunningham and Murray 2007; Noguera, Chemsak et al. 2007; Abdullah, Sina et al. 2008; Linzmeier and Ribeiro-Costa 2008), Psocoptera (Read ; Chan and Yang 2005); Hemiptera (Quednau ; Gonzon, Bartlett et al. 2006; Inoue, Goto et al. 2007), Thysanoptera (Olsen and Midtgaard 1996), and even some apparently stubborn Collembola (Riedel, Marinoni et al. 2008).

The Malaise trap finds preference because it is a passive form of collection with minimal maintenance (Matthews and Matthews 1971). Catches can be collected and traps refreshed easily after periods as long as one or two weeks. Malaise traps are also popular because of the large numbers of individuals it collects. (Brown and Feener 1995; Bartholomew and Prowell 2005)

Past research with respect to sampling bias

There has been some recognition that not all Malaise traps are equal with regards to what they collect. Some studies have focused on the shape or model of the trap (Platt, Caldwell et al. ; Roberts 1972; Townes 1972; Matthews and Matthews 1983), others have asked questions with regards to materials (Darling and Packer 1988), age of materials (Roberts 1975), color (Roberts 1970; Barbosa, Henriques et al. 2005), the addition of baits (Blume, Miller et al. ; Davis, Zwick et al. ; Roberts ; Schreck, Kline et al. 1993; Rohrig 2008), or placement (Noyes 1989; Schreck, Kline et al. 1993; Suh, Spurgeon et al. 2003; Grimbacher and Stork 2007; Irvine and Woods 2007; Vance, Smith et al. 2007; van Hennekeler 2008). Even with the variety of studies

comparing Malaise trap efficiency, the term Malaise trap is most frequently generalized in the literature regardless of the model or materials from which it is made, as evidenced by the sources cited in this paper and as noted by others (Campos, Pereira et al. 2000).

We have found just one study besides our own that attempts to address the possible bias due to the gauge of the mesh used to construct the trap (Darling and Packer 1988). This study does recognize the potential influence that mesh-size may have on the diversity of insects collected, and notes the possibility that body-size of the insects may be a part of the mechanism influencing that outcome. Unfortunately their experimental design was based on two traps that still differed in color. There are also other potential limitations due to the fact that Darling and Packer used only two individual traps.

Research Question

Influence of Mesh-size

Our research question is this: Are the kinds of insects collected in a Malaise trap different due to mesh-size? We examine this question via two means. First, is the diversity of insects collected different according to mesh-size? Second, are the sizes of insects different according to mesh-size? As with the Darling and Packer paper (1988), we are going to use insect body-size as a stand-in for potential influence of mesh-size. As to what aspect of behavior, perception or other factor is reflected by the size of insects collected per mesh-size we cannot say with this study.

We expected that the Malaise samples would show a difference due to habitat. We recognize that there are potential differences due to the year in which samples were collected, but we will only briefly discuss comparisons of year to help provide context to the two main

variables (mesh-size and habitat) that we are most interested in. Recognizing the possibility that some insects may be able to pass through the larger mesh-size, our expectation of a difference if we were to find one would favor more small individuals trapped with the fine mesh.

Diversity Across Habitats

We chose to sample in two habitats in order to provide greater strength to our comparisons of the influence of mesh-size. With the data we collected, we will also discuss some patterns we found with respect to beta diversity.

Materials and methods

Sampling Methods

Malaise traps

Our samples were collected with standard commercially available Townes' model Malaise traps, purchased from www.santetraps.com. Color, age, and dimension of all the traps were equal. The traps did differ according to the gauge of the holes in the mesh, which are listed as "coarse mesh" and "fine mesh" by the vendor. The holes in the coarse mesh are approximately 1.0mm in diameter (Fig. 1) while the holes in the fine mesh are between 0.3mm and 0.5mm (Fig. 2).
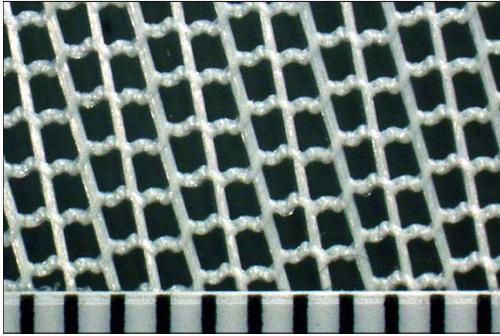
Fig. 1 - Coarse mesh (scale = 1mm)   **Fig. 2** - Fine mesh (scale = 1mm)
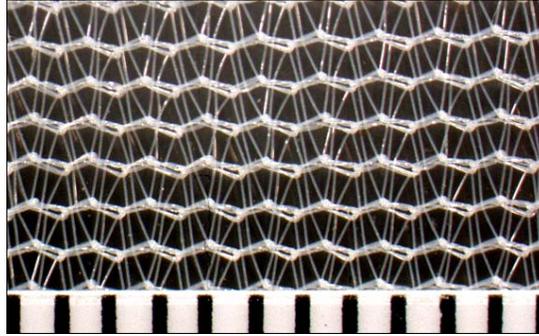
Sampling location

Our sampling location was in the Grand Staircase-Escalante National Monument near Kanab, Utah which is located in Southern Utah between the Zion, Bryce Canyon, and Capitol Reef National Parks and the Grand Canyon. We sampled from the sagebrush and grass dominant community (Flat) along Skutumpah Road at the head of Lick Wash, and within an adjacent plant community dominated by woody plants such as Piñon Pines, Utah Junipers, and various shrubs on the hillside (Hill) rising above the wash. Both habitats are open to grazing.

Habitat assessment

We completed vegetative surveys within 16 m^2 blocks adjacent to each of the sample sites. These surveys were done on a presence absence basis only. We were unable to identify all of the plants in each site. Nevertheless, comparing the number and kinds of woody species alone we were confident in the distinction between the two habitat sites. The grasses and forbs that were positively identified only strengthen this distinction. Overall, essentially all of the plants were indentified to the Family level, with many identified at the species level. The overwhelming majority of plants were identified to at least the level of Genus.

Trapping sites

The two habitats are separated by a graded dirt road, a distance of 500m and an elevation difference between the two habitats ranging from 20m to 40m. The Flat sites were all within two meters in elevation of each other, but the Hillside sites covered this range of twenty meters in order to have adequate spacing while staying within the same habitat type based on dominant plant composition.

Three replicate sites were selected per habitat with a 50m distance between each site and its nearest neighbor to ensure independence of sample sites while maintaining habitat similarity. Pairs of coarse and fine mesh Malaise traps (one trap of each mesh-size per site) were used in each of the two habitats for a total of six trapping locations and twelve traps.

All traps were placed with a north-south orientation for the long axis of the traps out of convenience (it is easy to find the north-south axis with even a simple compass) and for consistency over sampling seasons. Whether the coarse or fine net was on the north or south side of the center post was randomly selected at each site each year via coin toss. The location data for each site was recorded at the center post between the paired traps for each site. (Table 1)

Lick Wash Sample Sites

Site	Latitude	Longitude	Elevation (m)
Flat 1	37.36641	-112.18986	1903
Flat 2	37.36687	-112.18961	1904
Flat 3	37.36715	-112.19012	1905
Hill 1	37.36200	-112.18877	1925
Hill 2	37.36164	-112.18900	1934
Hill 3	37.36111	-112.18921	1945

Table 1 - GPS locations of sample sites.

Sampling schedule

Our samples were collected approximately every twenty-four hours in an attempt to encompass a complete diurnal cycle of activity for three consecutive days in June each year. The samples were collected on the 20th, 21st and 22nd in both 2006 and 2007. The traps were set up and collected from by the participants in the Utah Biodiversity Experiences of Students and Teachers (UBEST) program; by both the secondary science teachers enrolled in the program and the instructors and students from Brigham Young University in charge of directing the UBEST program.

Sample-bias Analysis

Taxonomic diversity

Our first means of comparing potential effects of mesh-size is to compare the diversity of the samples collected. Trap samples have been sorted down to the Order level, including the occasional non-insect arthropods. One trap sample is defined by the combination of day, location, and mesh-size – e.g. 20 Jun 2006, Flat habitat, coarse mesh. Because of the abundance of flies in the samples and our interest in this group, the Diptera were sorted to the Family level. Similarity will be measured using both presence-absence data and similarities based on abundance.

We used a simple richness score as our presence-absence measure per trap. To balance out against richness, we use Simpson's Index of Diversity ($1 - D$; $D = \frac{\sum_i^S n_i(n_i-1)}{N(N-1)}$) as one of our abundance measures. Richness by nature is strongly influenced by rare taxa, while Simpson's Index is less easily swayed by these taxa. Richness and Simpson's Index of Diversity were compared using mixed model analysis with the SAS statistical software.

Bray-Curtis estimates are another abundance-based diversity measure used to compare diversity between trap samples. *Primer 6* was used to calculate the majority of these indices and much of analyses of diversity. Within *Primer 6* we performed non-metric multi-dimensional scaling tests (NMDS), analysis of similarities (ANOSIM), and similarity percentages (SIMPER) to test for the similarity between mesh-size (Coarse vs. Fine), habitats (Flat vs. Hill), and years (2006 vs. 2007) in addition to trap site locations. We compared trap sites simply as a part of our discussion on beta diversity.

In addition, we will consider pair-wise comparisons of similarity using Jaccard's Index of similarity in order to examine the relationship between the flora and fauna of our sample sites, as well as to discuss the nature of presence-absence versus abundance measures when discussing diversity.

Insect size

To compare the potential for size-bias, individuals were sized using a template with circles of various diameters. (Fig. 3) The smallest circle has a diameter of 1mm and the largest circle has a diameter of 60mm. All individuals were placed into one of the 14 categories. Each individual was categorized according to the smallest diameter circle within which their entire body, including wings and legs, would fit. No individuals exceeded the largest circle. Because the size categories were neither in strict linear increments or followed a true logarithmic scale, our size estimates are based on the mid-point between categories.

Measurements in millimeters

1 2 3 4 5 6 7 8 9 10 15 20 30 60

Compare the circle to the insect you are measuring.
Category 1: up to 1 mm in body length
Category 2: greater than 1 mm up to 2 mm in body length.
Category 3: greater than 2 mm up to 3 mm in body length.
and so forth. . .
Category 60 includes all body lengths from greater than 30 to infinity
size measuring guide mm 200.cvx
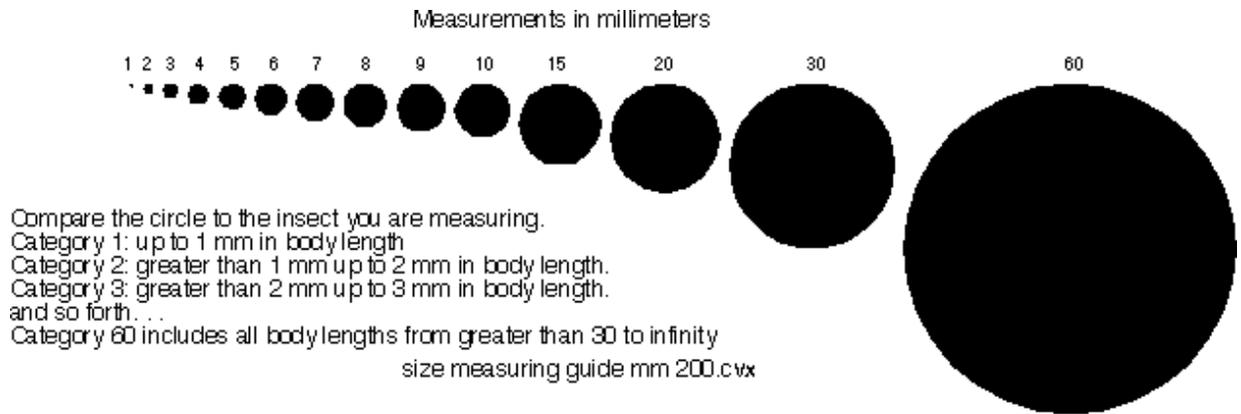
Fig. 3 – Sizing sheet used for categorizing individuals (not to scale).

Average insect size per trap was compared in the same mixed model tests as richness and Simpson's Index of Diversity, using the SAS software. Because the traps were set up in pairs, coarse and flat nets are not truly independent. The mixed models analysis performed modified paired t-tests using the differences between the pairs of coarse and fine mesh traps, blocking the samples by day (six categories), and maintaining the variable for habitat (two categories).

Results

Overall diversity

71 of the possible 72 samples were sorted according to our protocol. One sample was lost before sorting was completed. A total of 62,497 individuals were identified and sized. The average number of individuals per trap was 880 insects, with a range from 239 individuals to 2,382 individuals. There are 13 orders, two of which were non-insect orders (Table 2 & Fig. 4).

As Brown (2005) noted with his citations, Malaise traps collect mostly flies. The Diptera clearly formed the overwhelming majority of the individuals collected (Fig. 4), with the Family Chloropidae alone constituting more than half of all individuals collected (Fig. 5). Even with such a high percentage of the total catch, chloropids have a range of 19 individuals to 2021 individuals per trap.

Arachnida

Araneae	22
Ixodida	53

Insecta

Coleoptera	316
Collembola	1
Diptera	50471
Hemiptera	744
Homoptera	2128
Hymenoptera	3687
Lepidoptera	4771
Neuroptera	177
Orthoptera	13
Psocoptera	8
Thysanoptera	106

Table 2 - Number of individuals per Order
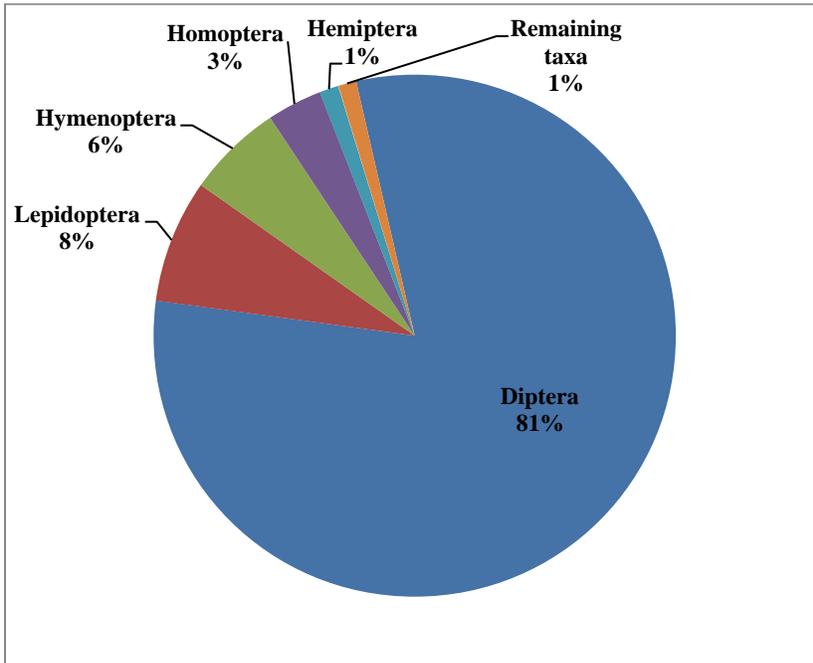
Fig. 4 - Relative abundance per Order

The total richness for the entire study included 55 taxa, once Diptera had been sorted to the Family level. The seven most abundant taxa have over 92 percent of the total number of individuals collected (Fig. 5). The remaining 48 taxa are individually less than 1% of the total number of individuals, and 23 of those are individually less than 0.1% of the total number of individuals collected. There were seven singletons represented by a single individual: one collembolan and six Diptera families. All other taxa were collected from two or more samples, with the seven most abundant taxa collected in every trap.
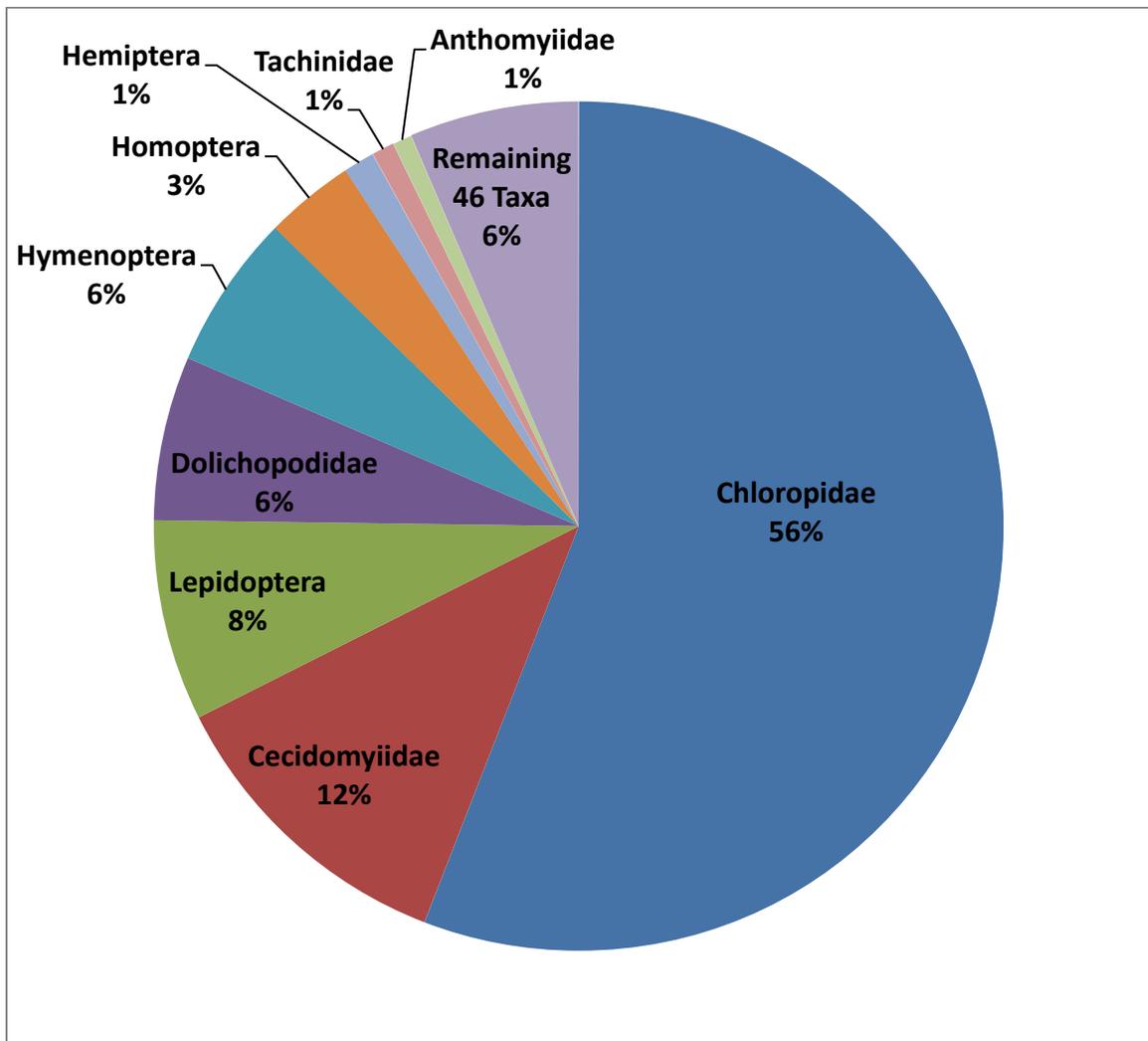
Fig. 5 - Relative abundance of Orders and Families

Richness

Richness

	Arthropods	Plants
Overall Richness	55	44
Mesh-size		
Coarse	49	--
Fine	52	--
Habitat		
Flat	50	18
Hill	52	38
Year		
2006	50	--
2007	50	--

Table 3 - Richness for arthropod and plant taxa

	Plants
Site	**Richness**
Flat 1	16
Flat 2	18
Flat 3	15
Hill 1	38
Hill 2	28
Hill 3	20

Table 4 - Plant taxa richness per site

Similarity comparisons

Jaccard's Indices of Similarity

Flat Vs. Hill (Arthropods)	0.85	Flat Vs. Hill (Plants)	0.18
Coarse Vs. Fine	0.84		
2006 Vs. 2007	0.82		

Table 5 – Pair-wise similarity comparisons using Jaccard's Index of Similarity

NMDS plots
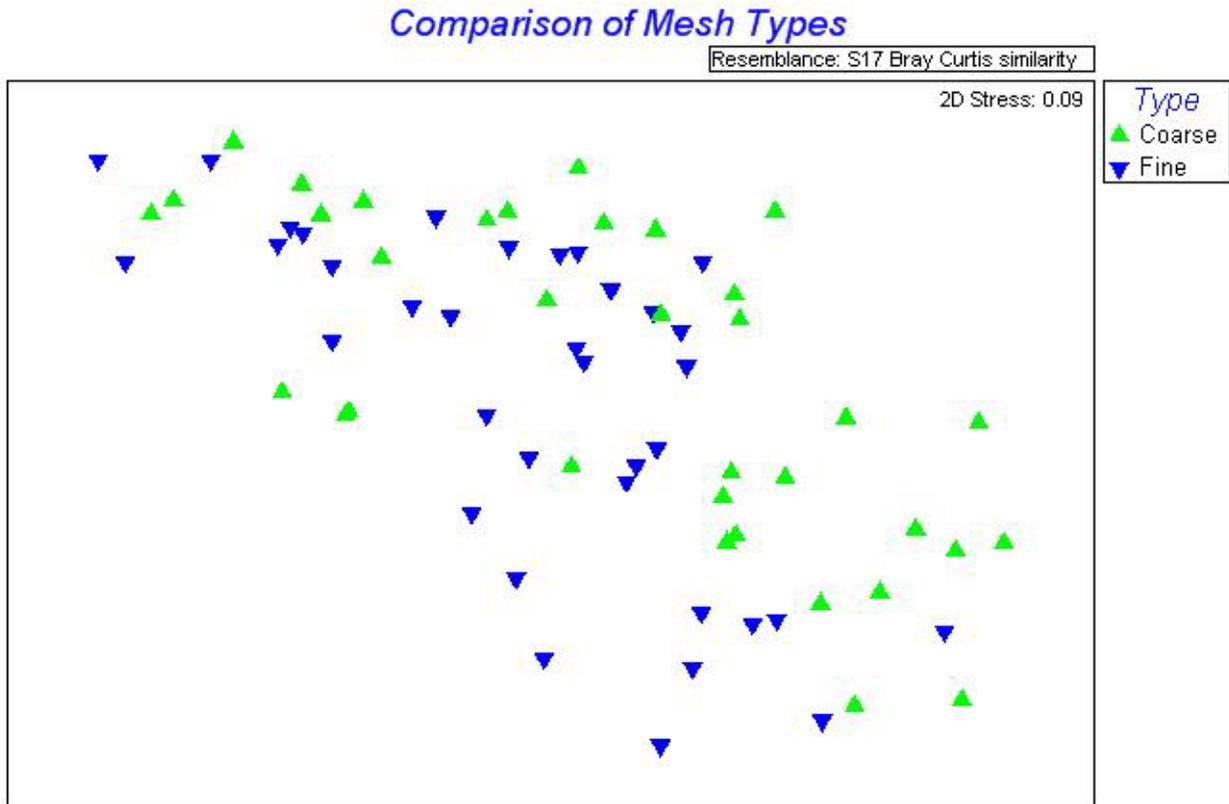
Fig. 6 - Similarity comparison of mesh-size (Coarse vs. Fine)

Fig. 7 - Similarity comparison of Year (2006 vs. 2007)

Fig. 8 - Similarity comparison of Habitat (Flat vs. Hill)
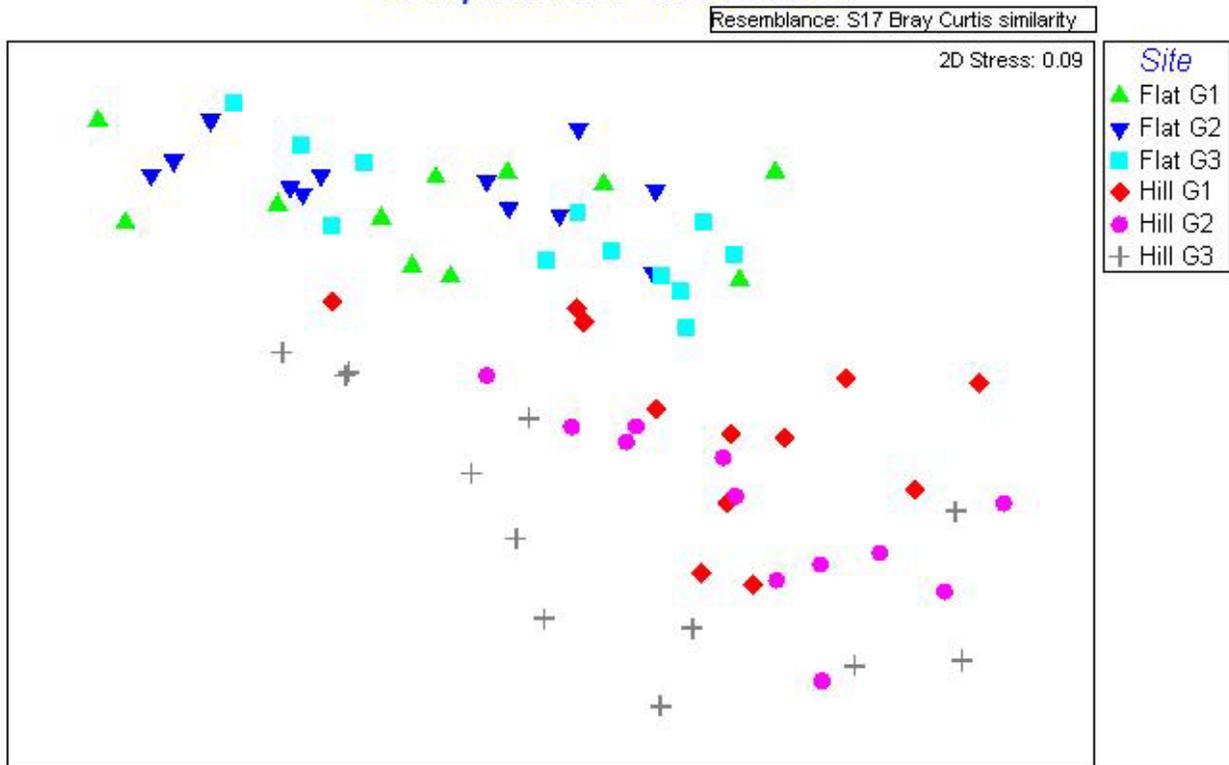
Fig. 9 - Similarity comparison of trap sites

ANOSIM
p-values

Factor	p-value
Mesh-size	0.029
Year	0.004
Habitat	0.001
Trap Site	0.001

Table 6 - Corresponding p-values to the NMDS plots

SIMPER

SIMPER lists the taxa most responsible for the characterization of the trap samples, and we

compared results across each of the four factors represented in the NMDS plots (Figs. 6, 7, 8 &

9). The results of all comparisons largely followed the relative abundance of all 55 taxa (Fig. 5).

Chloropidae was nearly always the taxa responsible for the largest percentage of similarity. In

order to reach the 90% level of characterization using SIMPER, there was only moderate

variation away from the overall abundance levels.

Insect Size
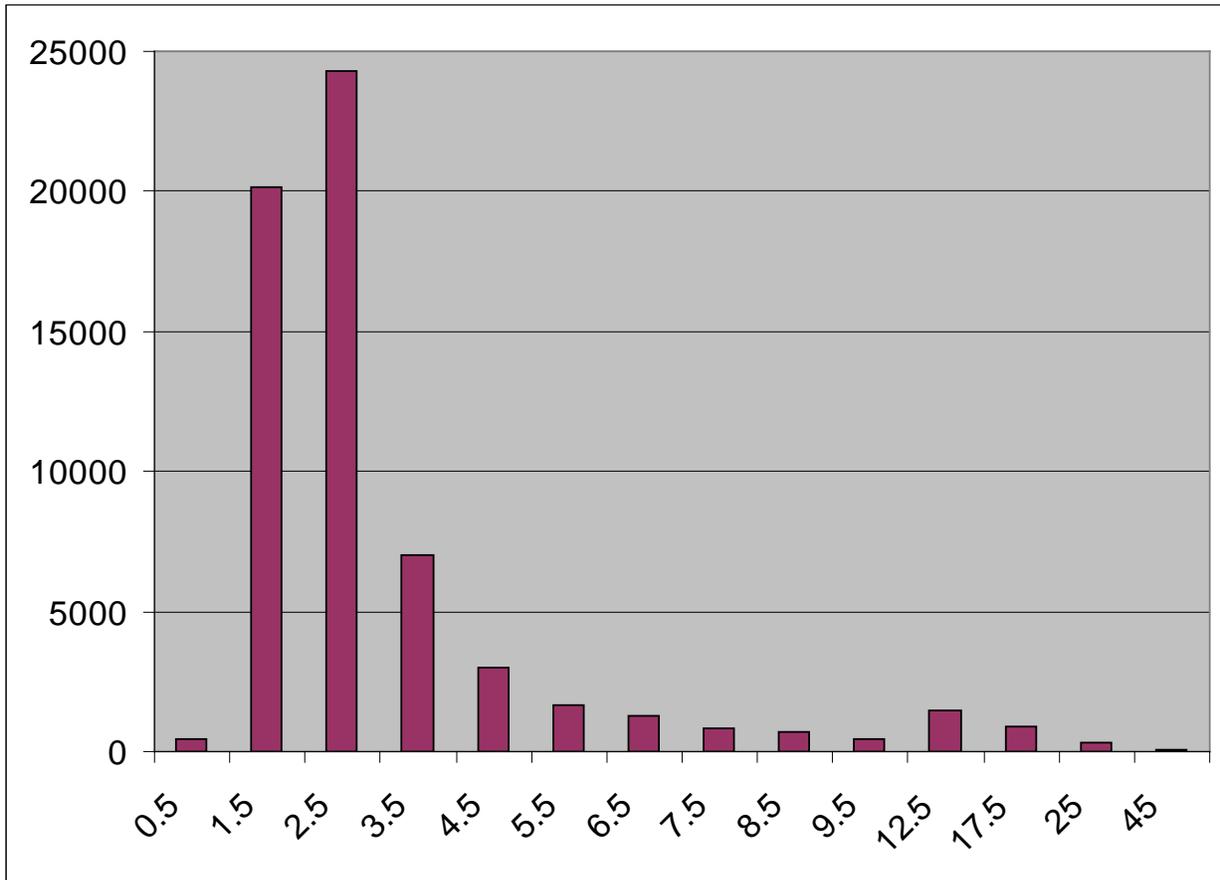
Fig. 10 - Insect abundance per size category. (Size in mm).

Mixed Model Procedures in SAS

Although all 71 samples were used with the analysis with the analysis using *Primer 6,* the

sample without a corresponding pair (Flat 1, Fine, 21 Jun 2007) was left out of the analysis using

SAS.

Richness

Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	F Value	Pr > F
Habitat	1	10	0.53	0.4814

Least Squares Means

Effect	Habitat	Estimate	Standard Error	DF	t Value	Pr > |t|
Habitat	Flat	0.4118	0.8942	10	0.46	0.655
Habitat	Hill	-0.5	0.8691	10	-0.58	0.5778

Table 7 - Analysis of the effect of mesh-size on richness

Simpson's

Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	F Value	Pr > F
Habitat	1	10	0.18	0.6783

Least Squares Means

Effect	Habitat	Estimate	Standard Error	DF	t Value	Pr > |t|
Habitat	Flat	0.009488	0.04462	10	0.21	0.8359
Habitat	Hill	-0.01709	0.04336	10	-0.39	0.7018

Table 8 - Analysis of the effect of mesh-size on Simpson's Index of Diversity

Average Size

Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	F Value	Pr > F
Habitat	1	10	2	0.1876

Least Squares Means

Standard Effect	Habitat	Estimate	Error	DF	t Value	Pr > |t|
Habitat	Flat	0.3922	0.3386	10	1.16	0.2736
Habitat	Hill	1.066	0.3351	10	3.18	0.0098

Table 9 - Analysis of the effect of mesh-size on Average body-size per trap

Hymenoptera

Total individuals (Hymenoptera) per mesh type
            Coarse   757   Fine   2119

Individuals (Hymenoptera) per trap

| | | | | | 95.0% | 95.0% |
| | | | Standard | Standard | LCL | UCL |
Variable	Count	Mean	Deviation	Error	of Mean	of Mean
Individuals Coarse	35	21.62857	10.20405	1.7248	18.12336	25.13379
Individuals Fine	36	58.86111	29.71787	4.952978	48.80603	68.91619

Table 10 - Number of individual Hymenoptera per trap

Average Size (mm) per trap - Hymenoptera

| | | | | | 95.0% | 95.0% |
| | | | Standard | Standard | LCL | UCL |
Variable	Count	Mean	Deviation	Error	of Mean	of Mean
AvgSize_Coarse	35	6.791719	2.308826	0.390263	5.99861	7.584829
AvgSize_Fine	36	4.051429	1.392027	0.232004	3.580435	4.522423

Table 11 - Average size (mm) of Hymenoptera per trap

Discussion

Differences in Diversity

Presence-Absence Estimates

The Jaccard's Index of Similarity of 0.18 for the two plant communities (Table 5) and the difference in richness scores across habitats (Table 3) support our initial visual assessment of distinct habitat types. In comparison, the corresponding indices for the arthropod communities are much more similar.

Arthropod richness is essentially equal both within and between the three variables we listed: mesh-size, habitat, and year (Table 3). It is no surprise that the mixed model analysis gave no evidence of a difference in richness due to mesh-size; p-value = 0.48 (Table 7). The Jaccard's Indices for these same variables also show a high degree of similarity, with all three

indices between 0.82 and 0.85 (Table 5). From a presence-absence standpoint, the arthropod communities across each variable are highly similar.

Abundance-based estimates

When we examine abundance on an per trap basis, the mixed model analysis of Simpson's Index of Similarity gives no evidence that there is a difference due to mesh-size; p-value = 0.68 (Table 8). With both the Simpson's Index and with richness, these scores are calculated with no reference to the other samples or groups of samples. Two samples could have equal richness scores or Simpson's Indices, while being comprised of entirely different taxa. In order to compare abundance-based diversity relative to other samples we used the tools in *Primer 6*.

The Stress value of 0.09 for the NMDS plots (Figs. 6, 7, 8 & 9) gives evidence that much of the diversity of the insects we collected is well represented by the two-dimensional plots. The ANOSIM p-values of all the variables displayed with the NMDS plots are significant (Table 6). Including abundance levels that have relationships across samples has modified our view of what is similar. There is a statistically discernable difference due to these variables.

Body-size

The average size of insects

On a purely individual basis, insects are small (Fig. 10). Overall more taxa were at the smaller end of the size scale on average and the most abundant taxa were prominently categorized in these lower size-classes.

One size-class pattern that may not be easily apparent due to the scale of the graph is a second concentration of individuals around the size class of 12.5mm. The most abundant Orders

besides Diptera (Lepidoptera and Hymenoptera) (Fig. 4) had many individuals in these upper size-classes. In addition, several fly families, but especially the calypterate flies which had some of the more abundant taxa (Tachinidae, Anthomyiidae, Muscidae, etc.) (Fig. 5) also had size distributions that more closely centered near the 12.5mm size class. While most of the insects we sampled are small, there appears to be a second mode of size distribution close to 12.5mm.

Differences Due to Mesh-size

The mixed model analysis in SAS was our only means of comparing the effect of mesh-size on the diversity of body-size. Although the individual t-tests give some support that body-size is influenced by mesh-size, overall we do not have enough evidence (p-value = 0.19) to conclude that mesh-size affects the average size of insect collected per trap (Table 9).

Beta Diversity

Both the data comparing plant communities (Tables 3, 4 & 5) and the data comparing arthropod communities (Figs. 8 & 9) show how easily beta diversity can change over a short distance. As noted earlier, our habitats were 500m apart and immediately adjacent.

While our intent was to sample from two distinct habitats, the NMDS plot based on sample site location (Fig. 9) provides strong evidence that the Hill habitat was not homogenous. The groupings of the samples from the Flat sites in this figure are indistinguishable, while the proximity of the sites in the Hill habitat to the Flat habitat is reflected by the groupings in the NMDS plot. Differences in elevation correlate with this same plot. The lowest sample sites from an effectively equal elevation group together. The remaining samples sites fall in line in the plot according to increasing elevation.

The data with respect to the plant community also reflects this pattern of proximity to the Flat habitat. The richness scores of each sample site should be noted (Table 4). The plant richness scores from the Flat sites show a strong sense of equality, while the highest richness score of the Hill sites is found in the site nearest the Flat habitat and the remaining scores decrease with the corresponding increase in distance from the Flat habitat. We suggest that some of this heterogeneity of the Hill habitat is due to an intermediate zone between the plants at the lowest elevation of our study and the highest elevation. For example, the presence of sagebrush (*Artemesia tridentata*) decreased according to elevation. Site Hill 1 was placed within the first grouping of Piñons and Junipers where much sagebrush was still present, while site Hill 3 was entirely devoid of sagebrush and Hill 2 was at some intermediate level. We do not have specific abundance data for the plants, but perhaps the high richness score of site Hill 1 is due to the overlapping of two plant communities.

Conclusion

Influence of Mesh-size on Diversity

The main purpose of this study was to determine the influence of mesh-size on sampling bias, because of the potential influence on experimental design. We found evidence that mesh-size influences the diversity of the overall sample of insects collected, although not all forms of our analysis agreed (Tables 3 & 4 as compared to Figs. 6, 7 & 8). The corresponding ANOSIM p-value to the NMDS plot comparing mesh-size (Fig. 6) gives evidence that the insect diversity collected by the two mesh types are not the same. The large overlap with respect to diversity as present in the NMDS plot is perhaps evidence enough that although the differences in diversity are statistically significant, these differences may not be biologically significant. It should be

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recognized that our sampling periods were limited to three days each summer and that we sampled a total of six sites. Accounting for the differences we found in future sampling efforts may be too labor intensive for the small gains that would be achieved with a detailed experimental design with respect to mesh-size. The same may be said with respect to the differences due to year. The differences we found in the diversity of our samples might be overcome at a lower cost with more traps, the combination of other trapping methods, an extended trapping season, or any combination of those or other variables.

Influence of Mesh-size on Average Body-size

We found no evidence to support the hypothesis that mesh-size influences the average body-size of insects collected overall. The results from the mixed model analysis give evidence that perhaps we might find a true difference if we could increase the power of our test (Table 9), but again that kind of study is most likely not worth the effort to find a difference that might not be biologically significant. The estimated average differences in body-size were 1.1mm for the Hill habitat and 0.39mm for the Flat habitat. For insects as a whole, the meaning of those differences still needs to be explored.

Hymenoptera May Be an Exception

There is one caveat to these assessments of the influence of mesh-size – the Hymenoptera. Hymenoptera are the one Order of insects that is probably of interest to those who use Malaise traps as often as or more often than the Diptera. Our analysis was with regard to overall diversity and average body-size across all taxa collected; Diptera being the largest portion. Knowing that Hymenopterists would be the next most likely group interested in this study, we compared the sampling patterns of the Hymenoptera alone.

The data collected do not meet the requirements of a t-test, but the descriptive statistics we include in Tables 10 and 11 do provide some evidence that further examination of our data may be warranted. First of all, the fine mesh Malaise traps collected a total of 2119 individuals (excluding the Formicidae); while the coarse mesh Malaise traps collected only 757 individuals (excluding the Formicidae). The means and their confidence intervals for the number of individuals captured per trap (Table 10), and the average body-size per trap (Table 11) do not overlap. The fine mesh Malaise traps not only collected more individuals of all categories, but collected insects belonging to higher size categories that were not collected by the coarse mesh Malaise traps. These results agree with the results from Darling and Packer that the fine mesh may be more effective than the coarse mesh at collecting the smaller Hymenoptera (1988).

Again, this data has not been properly analyzed, but we think that there is sufficient evidence for those interested in this taxon to take a closer look. Likewise, for those interested in collecting small taxa, e.g. parasitic wasps, or for those who are trying to reduce their work load by excluding smaller taxa, there may be undiscovered valid reasons to consider the mesh-size of the Malaise traps you use.

Patterns of Beta Diversity

As biologists, we want to find what is different. Differences within the context of overarching relationships and similarities are the keys to discovery of pattern and process. To continue the advancement of our biological understanding, being able to predict where differences are found would improve the way we study Biology. We could better diversify and standardize our sampling. We would more closely understand where to look for the next unknown species, population, community, etc.

In this study we see a change in diversity at some level across all variables. With only 500m between sites, we do not have to go far to find different plant communities. In an even shorter distance within the Hill habitat, we can see further evidence of changes in beta diversity when we use the abundance data for the arthropods. Even our limited scope in time of three days per year displays how differences can be found (Fig. 7).

In addition, this same design and locality was used in the summer of 2005, but that data was not included in this analysis because several samples were lost in the intervening time between collection and identification. In 2005 sampling was done during the first week, rather than the third week of June. With preliminary identification, community composition already appeared to be different from the 2006 and 2007 data. In 2006 and 2007, we did not catch a single individual from the family Tipulidae. With our incomplete sorting of the 2005 data, we have found nearly ten tipulids per sample. Time also appears to provide a broad opportunity for collecting new levels of diversity.

As researchers we should recognize that when concerned with plants or insects, we may not have to go far geographically in order to find different communities. We should also consider that to discover the composition of a community, our sampling seasons should match the natural community cycles. Our brief sampling does not define the boundaries of these seasons, but does support how much can change over a short period of time.

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