The diet of *Myotis lucifugus* across Canada: assessing foraging quality and diet variability

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Running Head: Diet of little brown bats across Canada

Abstract

Variation in prey resources influences the diet and behaviour of predators. When prey become limiting, predators may travel farther to find preferred food or adjust to existing local resources. When predators are habitat limited, local resource abundance impacts foraging success. We analyzed the diet of *Myotis lucifugus* (little brown bats) from Nova Scotia (eastern Canada) to the Northwest Territories (north western Canada). This distribution includes extremes of season length and temperature and encompasses colonies on rural monoculture farms, and in urban and unmodified areas.

We ~~identified~~ recognized nearly 600 distinct species of prey, of which ≈30% could be identified using reference sequence libraries. We found a higher-than-expected use of lepidopterans, which comprised a range of dietary richness from ≈35% early in the summer to ≈55% by late summer. Diptera were the second largest prey group consumed, representing ≈45% of dietary diversity early in the summer. We observed extreme local dietary variability and variation among seasons and years. Based on the species of insects that ~~we recorded in the diet~~consumed, we suggest that two locations support prey species with extremely low pollution and acidification tolerances, suggesting that these are areas without environmental contamination. We conclude there is significant local population variability in little brown bat diet which is likely driven by seasonal changes in insect diversity and may be a good indicator of environment quality.

Introduction

Molecular techniques are increasingly used to identify species, particularly ~~morphology~~ morphologically cryptic taxa. This has generated databases of taxonomically validated reference sequences (e.g. BOLD, Ratnasingham & Hebert 2007) to quantify biodiversity (e.g. Hebert *et al.* 2003), detect food market substitutions (e.g. Wong & Hanner 2008; Hanner *et al.* 2011) and improperly labelled food (e.g. Cohen *et al.* 2009). Characterizing ecological connections is more complicated than indexing species' presence (McCann 2007) and the use of reference databases to document interactions (e.g. Smith *et al.* 2006, 2007) has expanded greatly. Molecular techniques provide a powerful means to unravel food webs (Symondson 2002; King *et al.* 2008; Pompanon *et al.* 2012) which cannot be observed. These techniques developed from monoclonal antibody methods (e.g. Symondson & Liddell 1993) to cloning (e.g. Zeale *et al.* 2011; Alberdi *et al.* 2012), and next generation sequencing (NGS) (Pompanon *et al.* 2012). NGS now dominates these analyses and has been applied to marine systems (Deagle *et al.* 2009, 2010), herbivores (Soininen *et al.* 2009; Valentini *et al.* 2009) and terrestrial insectivores (Bohmann *et al.* 2011; Brown *et al.* 2013). Next generation sequencing is particularly effective when applied to generalists.

One hypothesis to explain food web stability is that increased species richness is related to food-web complexity (the number of interactions). When richness is coupled with functional redundancy and behavioural flexibility, food webs become more stable (Solé & Montoya 2001; Kondoh 2003; Dunne *et al.* 2004). Generalism provides the opportunity for flexibility in prey choice and its importance is documented e.g. stabilizing both predator and prey population demography (Singer & Bernays 2003) or indirectly

controlling lower food web links (Rosenheim & Corbett 2003). The main prediction of this hypothesis is that, when resources become limited, flexible consumers become more general in resource use. Dietary flexibility can be driven by limited high quality food, and the necessity to diversify to achieve nutrition, to avoid toxins, to follow resources, or minimize foraging risks (Singer & Bernays 2003). Some generalists switch between specialized resources (e.g. omnivory, Clare *et al.* 2013) while others consume food in ratios based on abundance (Rosenheim & Corbett 2003; Bastille-Rousseau *et al.* 2011).

Bats are an ideal group to study dietary flexibility as they occupy multiple trophic levels (carnivores, sanguivores, frugivores, nectarivores, insectivores) and niches (e.g., active hunting, passive listening for prey, fishing, trawling). They are frequently top predators and may consume resources at different trophic levels (e.g. Clare *et al.* 2013). However, they consume resources cryptically (~~. They are~~ active at night, using high-frequency echolocation) and are thus difficult to observe. Molecular methods provide a solution and are particularly useful in insectivores where thorough mastication of prey limits traditional morphological analyses of faeces (guano) (Kunz & Whitaker 1983) or culled prey remains (e.g. *Nycteris grandis* Fenton *et al.* 1981, 1990). In both cases identification of prey is limited to order or family and small, soft bodied prey may be overlooked (Clare *et al.* 2009). Molecular analysis permits us to identify prey to species (Clare *et al.* 2009) particularly when coupled with reference libraries (Hebert *et al.* 2003; Ratnasingham & Hebert 2007) increasing precision.

Carter *et al.* (2006) showed a proof of the concept by amplifying chicken DNA from the faeces of white-winged vampire bats (*Diaemus youngi*). The first full molecular analysis of bat diet assessed predator-prey relationships between *Lasiurus borealis* and

Lepidoptera (Clare *et al.* 2009) by sequencing DNA directly from residual prey fragments. Cloning and prey-specific primers were developed (Zeale *et al.* 2011) and used to uncover a novel hunting strategy of *Barbastella barbastellus* (Goerlitz *et al.* 2010) and the diet of *Plecotus macrobullaris* (Alberdi *et al.* 2012). These methods have rapidly been replaced by NGS (Bohmann *et al.* 2011; Razgour *et al.* 2011; Clare, Symondson, *et al.* 2013; Emrich *et al.* 2013) which are faster and more cost effective.

Myotis lucifugus, the little brown bat, was one of the most common and widespread bats in North America, though populations are in decline due to white nose syndrome (Frick *et al.* 2010). They have a distribution from Alaska, through southern Northwest Territories, the prairies, Ontario, Quebec and the Maritime provinces in Canada, and south through the continental United States and northern Mexico (Fenton & Barclay 1980). Arthropod consumption by bats (including *Myotis lucifugus*) varies by species and season (tied to lack of many prey early and late in the year and reproductive cycle) (Kunz *et al.* 2011), and by age (Fraser & Fenton 2007). At peak metabolic demand during lactation, little brown bats may consume more than their body mass in prey each night (Kurta *et al.* 1989) and thus potentially provide a significant ecosystem service through insect consumption (Boyles *et al.* 2011). They are generalists consuming insects of low prey hardness (Freeman 1981) mostly emerging from aquatic systems e.g. Diptera and Trichoptera (Belwood & Fenton 1976; Freeman 1981; Ober & Hayes 2008), although adult females consume more Lepidoptera and Trichoptera (Belwood & Fenton 1976).

Myotis lucifugus' tendency to forage over water provides a means to assess foraging location quality. In this context, our reference to foraging habitat/location quality refers to both type of habitat (such as moving or still water) and also to the

potential acid and pollution content of the aquatic system. Benthic macro-invertebrates are frequently used as environmental indicators. Their pollution tolerance (e.g. organic pollutants, acidification) and habitat requirements have been documented (Hilsenhoff 1988). If we consider bats as a sampling mechanisms, species-level diet analysis provides data for assessing the quality of foraging areas without complicated, potentially invasive methods such as radio tracking bats to locate foraging followed by mass insect sampling. Thus, while bats may not be used as a method of general habitat assessment (their sampling is biased by perceptual characters and preferences etc.), their diet can provide us which information on specific areas they have visited.

Clare *et al.* (2011) performed the first molecular analysis of little brown bat diet in three locations in Southern Ontario. They identified 66 prey species and noted a shift from consumption of Diptera early in the summer to Ephemeroptera in mid and late summer. There was evidence of local diet variation which allowed inferences about foraging-location quality. There is evidence that diet diversity is a function of location; populations in northern Ontario have greater dietary variability than those in southern areas (Belwood & Fenton 1976). The range of little brown bats in Canada includes areas of high and low insect species richness. If prey themselves are a limited (and limiting) resource, as prey richness decreases, the null hypothesis is that predators should similarly consume a lower species richness; however, if abundance is high, diet may change little or predators may adopt a more general strategy and consume a wider variety of prey (higher values of Simpson's diversity index, Simpson 1949).

Our study had two objectives. First, we assessed variability of little brown bat diets across Canada, over the summer and between years, and tested the hypothesis that

they have high degree of dietary variability across location and time. Second, we used the identity of prey to make inferences about habitat, based on known habitat requirements and pollution tolerances of the prey. We tested four predictions about diet: 1) latitude has an effect on diet, 2) temporal patterns of prey exploitation across the summer are stable from year to year, 3) there is a significant shift from the consumption of species of Diptera to Ephemeroptera associated with phases of the reproductive cycle and 4) species-level analysis of prey provides criteria for assessing foraging location ~~area~~ quality and yields quantitatively different insights than ordinal level analysis.

Methods:

Sample Collection:

We collected guano under maternity roosts of *M. lucifugus* across Canada (Figure 1) during three periods, including pregnancy (early summer = May to mid-June), lactation (middle summer = mid-June to mid-July) and post lactation (late summer = mid-July to September). Collections in Ontario were performed in 2009 (at Clinton, the Pinery), 2009 and 2011 (Lake St. George) and in 2011 for all other locations. Sampling was performed weekly in Ontario throughout the summer (fine grained analysis), and during the three established periods in other locations (see Figure 1 for details). Additional material was collected at two locations in Quebec but due to sampling differences and difficulties with molecular analysis we include this only as a supplement (see details in Supplemental Files 1 and 2) for comparison. We adopted the definitions of seasons from Clare *et al.* (2011) (see Supplemental File 3 for collection dates and locations). We froze samples or preserved them in high-percentage ethanol (70-100%).

Because we collected samples from colonies rather than individuals, the volume of material was substantial (exceeding half a liter per week by volume in some cases) and reflected deposition by many individuals (potentially exceeding a thousand in some locations), we analyzed a random subset of the pellets from each collection (volume c.1.5ml of guano or c.50 pellets, hereafter a "sample").

DNA Extraction, Amplification and Sequencing:

We extracted DNA from homogenized samples using the QIAmp DNA Stool Mini Kit (Qiagen, UK) following manufacturer's instructions with modifications from Zeale *et al.* (2011), further modified as follows: 1) to encompass more individuals and thus greater prey diversity we used approximately 50x more starting material and 2) we extended the first centrifuge step (Zeal step 4) to 3 minutes to aid in pelleting the particulate material. Extracted DNA was stored at -20 °C prior to amplifications.

We tested DNA extractions success using the primers ZBJ-ARTF1c and ZBJ-ArtR2c (Zeale *et al.* 2011). We then amplified each sample using a modified fusion-primer version for the Roche FLX sequencer (Bohmann *et al.* 2011) consisting of a Lib-L adaptor, the key sequence, a unique 10 bp DNA sequence (MID) and the original primer sequence (ZBJ-ARTF1c or ZBJ-ArtR2c). In our design (Brown *et al.* 2013; Clare *et al.* 2013), MID sequences were used on both forward and reverse primers allowing fewer primers to be used to resolve the same number of samples (i.e. rather than 100 unique forward MID tagged primers for 100 samples, 10 unique forward and 10 unique reverse MIDsd can yield the same resolution power) while reducing primer costs. We assigned

each sample a unique primer combination so all sequences could be identified to original samples.

We performed PCR reactions as described by Bohmann *et al.* (2011) in a 20 µl reaction containing 1µl of template DNA using Qiagen multiplex PCR kits (Qiagen, UK) with the following modifications. We did not use Q solution (from the kit) or BSA (as suggested by Bohmann *et al.* 2011). We visualized PCR products on a 1.5% agarose gel and quantified them following Brown *et al.* (2013) and mixed approximately equal molar quantities of each sample. We size-selected ~~and samples~~products using a QIAquick Gel Extraction kit (Qiagen, UK) and quantified the final PCR mix using a Qubit dsDNA BR Assay Kit (low sensitivity with a Qubit Fluorometer, Invitrogen life technologies).

We concentrated the final product to 10µg/1µl in molecular grade water. Sequencing was conducted at the Liverpool Center for Genomic Research (University of Liverpool) using a ¼ plate, Lib-L chemistry on a Roche 454 GS FLX+ sequencing system (Roche Applied Sciences).

Sequence Analysis:

We analyzed sequences using Galaxy (https://main.g2.bx.psu.edu/root, Giardine *et al.* 2005; Blankenberg *et al.* 2010; Goecks *et al.* 2010). We screened all recovered sequences for those longer (>180 bp) or shorter (<100 bp) than expected, collapsed all sequences to unique haplotypes, split the file by forward and reverse MIDs, removed primers, MIDs and adaptors and excluded rare haplotypes (<2 copies).

We clustered the sequences into molecular operational taxonomic units (MOTU) in jMOTU (Jones *et al.* 2011) and tested thresholds from 1-10 bp. A graph of recovered

MOTU vs. threshold (not shown) suggests a 4 bp cut-off was most appropriate (Razgour *et al.* 2011).

We compared representative sequences for each MOTU to the BOLD database (www.barcodinglife.org) following criteria modified from Razgour *et al.* (2011): 1a=match to one species or several species in a genus (100% similarity), most conservative taxonomy kept; 1b=good match (>98% similarity), but could belong to a congener showing a higher sequence match; 2=match to more than one species (>98%), only one of which is present in the sampling range (that taxonomy kept); and 3=close match (as above) to several species from different genera, or to a reference sequence which lacks a full taxonomic record. In these cases, the most conservative taxonomy (normally family) was kept (note this is not an identification to higher level taxonomy, but a match meeting criteria 1b but retaining ambiguity in the assignment due to multiple similar matches or incomplete data in the reference collection).

In addition, we estimated the identity of all MOTU (including unidentified MOTU) using the methods of Emrich et al. (2013) and the programme MEGAN (Huson *et al.* 2011). See Emrich et al. (2013) for details of that procedure and a brief discussion.

Ecological Analysis:

We divided our collections into the three time periods. We conducted ecological analyses in PAST (Hammer *et al.* 2001) on species and order-level data with p-values estimated by permutation. We compared the Simpson's diversity indices for identified prey among locations (sequential Bonferroni correction) and among summer sampling periods, and estimated the magnitude of the effect (effective number of species), where

differences were statistically significant, following Jost (2006). We compared species richness from paired weekly samples from the high-density sampling sites at Clinton (rural monoculture farming area) and Lake St. George in 2009 (environmentally variable conservation area). We computed rarefaction curves for all data.

We compared the proportion of each order in the diet (proportion = frequency of occurrence of that order / total occurrences, where an occurrence is an identified MOTU in a sample) among locations and among sampling periods using a χ^2 frequency test with p-values computed using a Monte Carlo simulation with 2000 replicates in R 2.15.1 ("R Development Core Team: R: A language and environment for statistical computing" 2008).

We use the recovered species to evaluate the foraging ~~area~~ location of the populations using the Hilsenhoff Biotic Index for organic pollutants developed for the western Great Lakes (Hilsenhoff 1988) and the Fjellheim & Raddum (1990) index for acid tolerance.

Results

Sequence Processing:

We recovered 167,562 sequences. After filtering, these were resolved into 10,792 unique haplotypes that could be assigned to an original sample. We clustered these into molecular operational taxonomic units (MOTU) and examined a representative sequence from each cluster. We removed 6 MOTU as contaminants (nearest BLAST similarity was identified as a non-prey item e.g. bacteria). The remaining 566 MOTU were used in further analysis and represent a mean of ≈9 species per sample.

Diet of Little Brown Bats:

Through comparison to the reference library, we identified 211 MOTU to species using criteria 1a, 1b and 2 (Supplemental File 1), hereafter referred to as species. We also identified ~~of~~ an additional group of MOTU using criteria 3 but consider them as provisional identifications. Of the identified occurrences (defined above), ≈45% were Lepidoptera, ≈34% Diptera, ≈11% Ephemeroptera, ≈6% Trichoptera and ≈4% Coleoptera (Figure 2). An additional 9 species represented Araneae (four species), Hemiptera (one species), Hymenoptera (one species), Megaloptera (two species) and Neuroptera (one species). The most common prey were two species of Chironomids (Diptera): *Dicrotendipes tritomus* and *Paracladopelma winnelli* found in 29% and 22% of samples, respectively, and two species of Ephemeroptera: *Caenis youngi* and *Caenis amica* found in 28% and 22% of samples respectively (note that *Caenis* are difficult to separate morphologically or genetically and multiple cryptic species are suspected, thus the actual identity of species within this genus should be considered an estimate due to taxonomic limitations). A single species was identified as prey in all sampled locations, a moth, *Hydriomena* (Lepidoptera, Geometridae). However, *Hydriomena* contains species with overlapping DNA barcodes (shared haplotypes at COI), and thus this identification may correspond to more than one species. We recovered a similar analysis of prey diversity from MEGAN (Figure 8) which suggest that unidentified prey are relatively dispersed among the consumed insect groups.

Many of the prey consumed provide specific information on the type and quality of the aquatic system; the most sensitive taxa, including families Glososomatidae,

Ephemerellidae and Corydalidae and genera *Lemnephilus, Agrypnia* and *Phryganea*, were consumed in both the Northwest Territories and Lake St. George (for a site-by-site analysis see Table 1).

Spatial-Temporal Variation in Resource Use:

Considering species from the five main prey groups (Ephemeroptera, Coleoptera, Lepidoptera, Diptera and Trichoptera) with all data pooled, the proportion of consumption varied significantly among periods (χ^2 =26.89, p=0.0005, Figure 2). In early summer, the diet was dominated by Diptera (45% of occurrences) though ~~the bats'~~their presence decreased throughout the summer (30% in mid summer, 29% in late summer). In contrast, Lepidoptera increased from 35% of occurrences in early summer, to 46% in mid summer and 55% in late summer. The frequency of occurrence of Ephemeroptera, Coleoptera and Trichoptera remained stable. We did not observe a switch from consumption of Diptera to Ephemeroptera as previously reported (Clare *et al.* 2011).

Prey use varied significantly among locations (χ^2 =119.69, p=0.0005, Figure 3). In some locations (Northwest Territories, Lake St. George 2009), the main prey were Lepidoptera and Diptera, while in other locations (e.g. Lake St. George 2011) prey consumption was dominated by Lepidoptera. These differences do not appear to reflect sampling intensity; the three most heavily sampled locations (Clinton, Lake St. George 2009 and 2011) showed different patterns of prey use.

Despite difference in prey consumption, Simpson Index measures did not indicate a significant difference in dietary diversity among locations (Figure 4) except at Pinery Provincial Park ~~(Pinery)~~ in Ontario. When considered at the ordinal level, diversity of

prey at Pinery was particularly low. This pattern was different when considering species (MOTU) level resolution; diversity estimates were more even, and bats at Pinery had high diversity. Saturation of rarefaction curves (Figure 5) indicates sampling reached a plateau in ordinal level identifications, while species-level identifications were still increasing almost linearly (Figure 5c and 5d). Diversity estimates at ordinal and species level were not correlated (r=0.27, p=0.18). Latitude did not correlate with diversity at the ordinal (r=0.43, p=0.15) or species (r=-0.11, p=0.4) levels.

Diversity estimates varied significantly among seasons (early = 0.66, mid = 0.67, late = 0.60) with a nearly significant reduction in dietary diversity observed between early and late season (p=0.05) and a significant reduction between mid and late season (p=0.031) (Figure 6), reflecting reductions in the effective numbers of species of 14% and 20%, respectively.

We sampled the same colony at Lake St. George in 2009 and 2011. In 2009 we estimated that this colony consisted of several thousand individuals, although this number declined slightly in 2011 likely due to white nose syndrome (Frick *et al.* 2010). Sampling at this location was done during matched weeks between the two years, but we observed remarkable difference in the spatial-temporal pattern of prey use. In 2009, prey use mirrored that observed across all locations (Figure 2), while in 2011, Diptera represented a minority of prey, Lepidoptera dominated all seasons (91% in late season), and no Coleoptera or Trichoptera were consumed.

The most heavily sampled locations were Clinton (n=14 weeks) and Lake St. George in 2009 (n=18 weeks). Of these, 13 sampling weeks were common and could be directly compared (difference reflects differential colony establishment). Although not

significant, there is a trend towards higher species richness at Lake St. George in 2009; mean prey species richness was 20 species/sample compared to a mean of 17 in Clinton (Figure 7), although the number of species was higher in only 8 of 13 weeks.

Discussion

Our goal was to examine variation in resource use by bats across Canada and to use these data to infer foraging ~~area~~ location quality. Our analysis suggests that prey use by little brown bats at the most northern sampling location (NWT) consumed prey evenly between orders, although there was no consistent pattern of consumption among locations. Intensive sampling of populations in different locations in Ontario across two years indicated that there was spatial-temporal variation in prey use. We did not observe a seasonal shift between the consumption of Diptera and Ephemeroptera. Analyses at species level showed different patterns than at ordinal level, indicating that species-level resolution provides novel insights in dietary analysis.

Spatial Variation in Diet Across Canada

When we combined data from all locations, Diptera dominated the diet in the early season but was replaced by Lepidoptera in the mid and late seasons. This pattern was prominent at Lake St. George (2009) and the NWT, but variable at other locations. The reliance on Diptera in the early season agrees with previous morphological (Belwood & Fenton 1976; Freeman 1981; Ober & Hayes 2008) and molecular (Clare *et al.* 2011) analyses. Diptera are an important prey group in both species richness and dietary abundance. We found no evidence to support the reported heavy reliance on Trichoptera,

but found more species of Lepidoptera than expected. This may reflect the overabundance of Lepidoptera within the reference collection, biasing the number of taxonomic identities reported. It is possible that Trichoptera represent a large number of the "unknowns" within our sample however our estimations using MEGAN indicate that unknowns are relatively dispersed among taxonomic groups. ~~.~~

Traditional morphological analyses are based on estimating abundance of prey groups in any given sample. Lepidoptera are frequently identified from scales and small morphologically cryptic species may be lumped into a single unit or overlooked. One advantage of molecular analysis is the routine detection of rare prey (Clare *et al.* 2009). However, as molecular analyses cannot estimate abundance, biomass or volume (e.g. haplotype number ≠ abundance, MID tags, primers and adaptors influence sequencing, sequencing direction produces different results and biases in sequencing are not consistent between runs even using the same PCR products, ~~(~~Pompanon *et al.* 2012; Deagle *et al.* 2013; Piñol *et al.* 2013)~~)~~ within a sample, rare and common items are both "present". A large sample size may control for overrepresentation of rare prey (or underrepresentation of common prey) however there is a trade-off between increasing the volume of material analysed (the pooling method here) to increase our assessment of biodiversity and the potential for skew with presence and absence records, though it is not a correction that can be empirically assessed.

While we cannot estimate sample-based abundance, molecular analysis allows us to measure~~s~~ species richness and frequency across samples. While richness within an order can be related to abundance, there are important exceptions. Mass emerging prey like mayflies (Ephemeroptera) may be extraordinarily abundant but low in species

richness. In our analysis, Lepidoptera may appear as the most important food source because they are more speciose, while mayflies may be underrepresented. The abundance of Lepidoptera may also reflect previous observations that females consume more Lepidoptera than males (Belwood & Fenton 1976); all of the colonies we sampled were maternity groups dominated by females and their offspring. The results from Quebec based on males (Supplemental File 2) recovered more Diptera which may support this conclusion.

We observed significant spatial variation in diet. We use Simpson's Index which is less sensitive to rare events that frequently occur in species-level analysis (Bohmann *et al.* 2011; Razgour *et al.* 2011). Our estimates of diversity were not correlated with latitude and not related to sample size. The Saskatchewan and Pinery colonies had the lowest sample sizes (and could not be sampled in late season at all) but differ in patterns of prey use. Both were low in diversity at the ordinal level, but so was Lake St. George (2011) which had one of the largest sample sizes. Significant spatial variation in resource use is unsurprising across such a wide geographical area, however, it was also similarly variable within southern Ontario and between years. This matches previous observations (Clare *et al.* 2011) supporting the view that these bats responded to local variation in environment and prey. As such, predicted declines in the populations of little brown bats (Frick *et al.* 2010) may have locally-specific effects on insect populations.

The main assumption of the correspondence between insect diversity and diet is that resources themselves are limiting. Although little brown bat coloniess may ~~each~~ consume ~~hundreds or~~ thousands of insects in a night, it is not clear whether their populations are large enough to significantly reduce local populations of insects.

Temporal Variation in Diet

We observed a significant decrease in dietary diversity in late season when the effective reduction in species richness was 20%. This contrasts with a matching analysis of big brown bats (*Eptesicus fuscus*) (Clare *et al.* 2013) for which dietary diversity rose sharply in late season. These inverse patterns may reflect non-overlapping resource use by these predators. Big brown bats are a flexible hunter that appears to forage in most habitat types (Geggie & Fenton 1985; Furlonger *et al.* 1987) and consumess large numbers of beetles, moths, and flies (Clare *et al.* 2013). Insect diversity falls in late season just as both species must store fat for hibernation. While big brown bats may compensate by exploiting a wider variety of habitats (and thus prey), increasing their dietary diversity, little brown bats may simply consume a greater volume of more limited prey. Habitat selection by bats strongly influences insect availability and thus diet and may explain apparent resource partitioning among many species (Emrich *et al.* 2013). Current or historical competition for resources is also possible, but makes the assumption that resources are limiting. There is little direct evidence that competition drives patterns of resource use because this cannot be assessed without controlled removal experiments, which are exceedingly difficult with bats.

Clare *et al.* (2011) observed a significant shift from consumption of Diptera in early season to Ephemeroptera in middle and late season. The same pattern was not observed here in any location, including in the same samples originally analyzed by Clare *et al.* (2011). This likely reflects a difference in methodology. Clare *et al.* (2011) sequenced DNA directly from fragments of prey removed from guano under microscopic

dissection. The advantage of this technique is that the user can preferentially attempt to maximize the taxonomic richness of the sample but it is likely biased towards the detection of less-digestible prey (Razgour *et al.* 2011). Because Clare *et al.* (2011) took efforts to sample a large number of guano pellets, they also assumed that each fragment represented a different capture, and thus frequency was calculated directly from the recovered sequences. NGS provides an automated method to maximize the diversity of prey recovered, but does not allow for the same assumption of independence of each haplotype. The fragment and sampling method employed by Clare *et al.* (2011) is a hybrid between traditional morphological analysis and NGS and may be more similar to abundance-based methods. This is only likely to cause significant difference when the taxa are mass-emerging species found in high abundance but low species richness, such as Ephemeroptera. NGS may underestimate the importance of this prey group, while the fragment method may overestimate them if the assumption of independence between fragments is not met. In addition, our methods used short amplified regions (157 bp) compared to Clare *et al.* (2011) who used full DNA barcodes of ≈657 bp. Short primers may ~~provide lower~~limit taxonomic resolution in some cases but increases the likelihood that degraded DNA will be amplified. Different primers will always have different binding affinities and this may partially explain specific prey differences between these two analyses.

Methodological Advances and Species vs Ordinal Level Data

We used two specific methodological advances in our analysis. To separate samples after sequencing, NGS uses incorporated tags in primers. These tags are often

called MIDs or 'barcodes' (although we do not use this term to avoid confusion with DNA barcodes as per Hebert *et al.* (2003)). Using MIDs on forward primers, each sample can be amplified with a unique forward primer and subsequently separated. However, for very large sample sizes, this becomes costly. As introduced (Brown *et al.* 2013), we incorporated MIDs in both forward and reverse primers so that each sample can be assigned a unique combination of MIDs (e.g. 10 forwards and 10 reverses = 100 unique combinations). This technique significantly reduces primer costs without impacting sequencing performance. Second, rather than extracting DNA from a single guano pellet (or even half a pellet as in some publications) we extracted DNA from a pool of pellets totalling 1-1.5 ml by volume. This roughly translated into 20-50 pellets per sample (depending on size). Previous analyses have estimated a mean of 5 taxa per pellet (Bohmann *et al.* 2011) while we recovered a mean of 9 per sample. In this study, each "sample" is, in effect, an assay of diet in what is likely dozens of individuals. The disadvantage of this method is that larger volume extractions lead to more PCR inhibitors that may complicate reactions. However, this also provides two specific advantages. In general it leads to greater taxonomic richness in the resulting sequencing run. More specifically, insectivorous bats have a very fast gut transit time with prey passing as fast as 35 minutes after ingestion (Buchler 1975). As such, any single pellet may be low in prey richness. Morphological analyses normally examine many dozens of pellets to estimate diet and we have incorporated this method. As discussed earlier, large sample sizes may control for the potential for overrepresentation of rare prey though this may explain our lower than expected measures of Ephemeroptera.

Molecular methods allow us to go beyond traditional ordinal-level assessments, available from morphological analysis, to establish species-level taxonomic assignments of prey. It is particularly interesting that when we remove these data, some dramatic changes (e.g. estimates of diversity in Pinery) can be observed. This is largely due to saturation of ordinal level collections, while species-level data have not reached a plateau.

Environmental Indicators and Foraging Assessment

Benthic macro-invertebrates are frequently used as environmental indicators of the quality of a water system (Hilsenhoff 1988; Fjellheim & Raddum 1990; Lenat 1993). The analysis of diet from bats foraging over these ~~areas~~ locations provides a direct (non-invasive) method to infer the quality of their foraging ~~areas~~location. This method is more specific than a general insect survey as it assesses where the bat has been rather than where it may have been. Insect tolerance estimates vary by season and area (see a comparison of Wisconsin and North Carolina, Lenat (1993)), but we can make a number of observations from our data using the Hilsenhoff Biotic Index for organic pollutants developed for the western Great Lakes (Hilsenhoff 1988) and the Fjellheim & Raddum (1990) index for acid tolerance (extrapolating from related species) and inferences about other Canadian regions (Table 1).

Among the Trichoptera, Hydropsychidae, Leptoceridae and Phryganeidae have moderate pollution tolerances of 4 while Helicopsychidae have a tolerance of 3 and Glossosomatidae a tolerance of 0. Glossosomatidae also have a low tolerance for acidification. Leptoceridae and Phryganeidae were eaten by bats in the Northwest

Territories, Nova Scotia, Long Point and Lake St. George (2009), while Helicopsychidae occurred in the diet at -Clinton. The pollution intolerant gGlososomatides ae -were eaten in the Northwest Territories and Lake St George (2009). Diptera in the family Tipulidae have a tolerance of 3 and were also found at Clinton. The Ephemeroptera family Ephemerellidae has a pollution tolerance of 1. These were detected in the Northwest Territories and Lake St. George (2011); the Megaloptera family Corydalidae has a pollution tolerance of 0 and was detected in Lake St. George (2009). Species of *Molanna* may be acid intolerant and were detected in Nova Scotia.

While habitat specificity of many macro-invertebrate species declines (or becomes more variable) at higher latitudes (Lenat 1993), these observations suggest that bats at Clinton forage in good quality habitat (Helicopsychidae and Tipulidae both have tolerance =3). However, there is convincing evidence that the sites in the Northwest Territories and Lake St. George have an excellent quality habitat with little apparent organic pollution (species with tolerance of 0 and 1 detected frequently) or acidification. This might be expected for the remote Northwest Territories locations (which are far from major human modification), but is less expected for Lake St. George, which lies on the edge of the greater Toronto area. The continued presence of prey with low pollution tolerances at Lake St. George in 2011 demonstrates the stability of this site and may be an indication of the effectiveness of small-scale conservation efforts even in areas near intensive urban modification.

Some macro-invertebrates are relatively good indicators of habitat type. Species in the Trichoptera genera *Agrypnia* and *Traenoides* were identified in Northwest Territories, Long Point and Lake St. George. They are associated with pond or lake-like

habitats in northern parts of their range. We have previously confirmed that the Lake St. George bats hunt in the vicinity of Lake St. George (a very small water body) less than 300 m from the roost site. It is likely that the Long Point bats are hunting along the shores of Lake Erie, and the Northwest Territories population may be using any of hundreds of variously sized water bodies.

Summary

In response to resource fluctuations, species may move to track prey or adapt to match local variability. The little brown bat, *M. lucifugus*, occupies a broad niche, foraging over aquatic systems. Species-level identifications of benthic macro-invertebrate prey serve as environmental indicators and allow us to use information about diet to directly measure the quality of the foraging habitat. In total, we recorded nearly 600 species of prey consumed by this predator and present one of the largest and most geographically diverse molecular dietary analyses to date. With these data, we demonstrate seasonal, regional and inter-annual variation in little brown bat diets across Canada which is independent of latitude. We identify two locations where the prey consumed are particularly intolerant to organic pollution or acidification and thus locations where foraging ~~area~~ habitat is of high quality, even when in the vicinity of high-density urban development.

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References

Alberdi A, Garin I, Aizpurua O, Aihartza J (2012) The foraging ecology of the mountain long-eared bat *Plecotus macrobullaris* revealed with DNA mini-barcodes. *PLoS ONE*, **7**, e35692.

Bastille-Rousseau G, Fortin D, Dussault C, Courtois R, Ouellet J-P (2011) Foraging strategies by omnivores: are black bears actively searching for ungulate neonates or are they simply opportunistic predators? *Ecography*, **34**, 588–596.

Belwood JJ, Fenton MB (1976) Variation in the diet of *Myotis lucifugus* (Chiroptera-Vespertilionidae). *Canadian Journal of Zoology*, **54**, 1674–1678.

Blankenberg D, Von Kuster G, Coraor N *et al.* (2010) Galaxy: a web-based genome analysis tool for experimentalists. *Current protocols in molecular biology*, **Supplement**, 19.10.1–19.10.21.

Bohmann K, Monadjem A, Lehmkuhl Noer C *et al.* (2011) Molecular diet analysis of two african free-tailed bats (molossidae) using high throughput sequencing. *PloS ONE*, **6**, e21441.

Boyles JG, Cryan PM, McCracken GF, Kunz TH (2011) Economic importance of bats in agriculture. *Science*, **332**, 41–42.

Brown DS, Symondson WOC, Burger R *et al.* (~~2013~~THIS ISSUE) Dietary competition between the alien Asian Musk Shrew (*Suncus murinus*) and a reintroduced population of Telfair's Skink (*Leiolopisma telfairii*). *Molecular Ecology*, **(XXX-XXX)**~~**In press**~~.

Buchler ER (1975) Food transit time in *Myotis lucifugus* Chiroptera: Vespertilionidae. *Journal of Mammalogy*, **56**, 252–255.

Carter GG, Coen CE, Stenzler LM, Lovette IJ (2006) Avian host DNA isolated from the feces of white-winged vampire bats (Diaemus youngi). *Acta Chiropterologica*, **8**, 255–274.

Clare EL, Barber BR, Sweeney BW, Hebert PDN, Fenton MB (2011) Eating local: influences of habitat on the diet of little brown bats (*Myotis lucifugus*). *Molecular Ecology*, **20**, 1772–1780.

Clare EL, Fraser EE, Braid HE, Fenton MB, Hebert PDN (2009) Species on the menu of a generalist predator, the eastern red bat (*Lasiurus borealis*): using a molecular approach to detect arthropod prey. *Molecular Ecology*, **18**, 2532–2542.

Clare EL, Goerlitz HR, Drapeau VA *et al.* (2013) Trophic niche flexibility in *Glossophaga soricina*: how a nectar seeker sneaks an insect snack. *Functional Ecology*, **In press**.

Clare E, Symondson WOC, Fenton MB (~~2013~~THIS ISSUE) An inordinate fondness for beetles? Variation in seasonal dietary preferences of night roosting big brown bats (Eptesicus fuscus). *Molecular Ecology*, ~~**In review**~~**(XXX-XXX)**.

Cohen NJ, Deeds JR, Wong ES *et al.* (2009) Public health response to puffer fish (Tetrodotoxin) poisoning from mislabeled product. *Journal of Food Protectionrot*, **72**, 810–817.

Deagle BE, Chiaradia A, McInnes J, Jarman SN (2010) Pyrosequencing faecal DNA to determine diet of little penguins: is what goes in what comes out? *Conservation Genetics*, **11**, 2039–2048.

Deagle BE, Kirkwood R, Jarman SN (2009) Analysis of Australian fur seal diet by pyrosequencing prey DNA in faeces. *Molecular Ecology*, **18**, 2022–2038.

Deagle BE, Thomas AC, Shaffer AK, Trites AW, Jarman SN (2013) Quantifying sequence proportions in a DNA-based diet study using Ion Torrent amplicon sequencing: which counts count? *Molecular Ecology Resources*, **13**, 620–633.

Dunne JA, Williams RJ, Martinez ND (2004) Network structure and robustness of marine food webs. *Marine Ecology Progress Series*, **273**, 291–302.

Emrich MA, Clare EL, Symondson WOC, Koenig SE, Fenton MB (~~2013~~THIS ISSUE) Resource partitioning by insectivorous bats. *Molecular Ecology*, **(XXX-XXX)** ~~**In review**~~.

Fenton MB, Barclay RMR (1980) *Myotis lucifugus*. *Mammal Species*, **142**, 1–8.

Fenton MB, Swanepoel CM, Brigham RM, Cebek J, Hickey MBC (1990) Foraging behaviour and prey selection by large slit-faced bats (*Nycteris grandis*; Chiroptera: Nycteridae). *Biotropica*, **22**, 2–8.

Fenton MB, Thomas DW, Sasseen R (1981) *Nycteris grandis* (Nycteridae): an African carnivorous bat. *Journal of Zoology (London)*, **194**, 461–465.

Fjellheim A, Raddum G. (1990) Acid precipitation: biological monitoring of streams and lakes. *Science of the Total Environment*, **96**, 57–66.

Fraser EE, Fenton MB (2007) Age and food hardness affect food handling by insectivorous bats. *Canadian Journal of Zoology*, **85**, 985–993.

Freeman PW (1981) Correspondence of food habits and morphology in insectivorous bats. *Mammalogy Papers: Univeristy of Nebraska State Museum*, **62**, 166–173.

Frick WF, Pollock JF, Hicks AC *et al.* (2010) An emerging disease causes regional population collapse of a common North American bat species. *Science*, **329**, 679–682.

Furlonger CL, Dewar HJ, Fenton MB (1987) Habitat use by foraging insectivorous bats. *Canadian Journal of Zoology*, **65**, 284–288.

Geggie JF, Fenton MB (1985) A comparison of foraging by *Eptesicus fuscus* (Chiroptera: Vespertilionidae) in urban and rural environments. *Canadian Journal of Zoology*, **63**, 263–267.

Giardine B, Riemer C, Hardison RC *et al.* (2005) Galaxy: a platform for interactive large-scale genome analysis. *Genome Research*, **15**, 1451–1455.

Goecks J, Nekrutenko A, Taylor J (2010) Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. *Genome biology*, **11**, R86.

Goerlitz HR, Ter Hofstede HM, Zeale MRK, Jones G, Holderied MW (2010) An aerial-hawking bat uses stealth echolocation to counter moth hearing. *Current Biology*, **20**, 1568–1572.

Hammer Ø, Harper DAT, Ryan PD (2001) PAST: paleotological statistics software package for education and data anaysis. *Palaeontologia Electronica*, **4**, 1–9.

646 Hanner R, Becker S, Ivanova N V, Steinke D (2011) FISH-BOL and seafood
647 identification: geographically dispersed case studies reveal systemic market
648 substitution across Canada. *Mitochondrial DNA*, **22**, 106–122.

649 Hebert PDN, Cywinska A, Ball SL, DeWaard JR (2003) Biological identifications
650 through DNA barcodes. *Proceedings of the Royal Society B-Biological Sciences*,
651 **270**, 313–321.

652 Hilsenhoff WL (1988) Rapid field assessment of organic pollution with a family-level
653 biotic index. *Journal of the North American Benthological Society*, **7**, 65–68.

654 Huson DH, Mitra S, Ruscheweyh H-J, Weber N, Schuster SC (2011) Integrative analysis
655 of environmental sequences using MEGAN4. *Genome Research*, **21**, 1552–1560.

656 Jones M, Ghoorah A, Blaxter M (2011) jMOTU and Taxonerator: turning DNA barcode
657 sequences into annotated operational taxonomic units. *PloS ONE*, **6**, e19259.

658 Jost L (2006) Entropy and diversity. *Oikos*, **113**, 363–375.

659 King RA, Read DS, Traugott M, Symondson WOC (2008) Molecular analysis of
660 predation: a review of best practice for DNA-based approaches. *Molecular Ecology*,
661 **17**, 947–963.

662 Kondoh M (2003) Foraging adaptation and the relationship between food-web
663 complexity and stability. *Science*, **299**, 1388–1391.

664 Kunz TH, Braun de Torrez E, Bauer D, Lobova T, Fleming TH (2011) Ecosystem
665 services provided by bats. *Annals of the New York Academy of Sciences*, **1223**, 1–38.

666 Kunz TH, Whitaker JO (1983) An evaluation of fecal analysis for determining food
667 habits of insectivorous bats. *Canadian Journal of Zoology*, **61**, 1317–1321.

668 Kurta A, Bell GP, Nagy KA, Kunz TH (1989) Energetics of pregnancy and lactation in
669 freeranging little brown bats (*Myotis lucifugus*). *Physiologiacl Zoology*, **62**, 804–
670 818.

671 Lenat DR (1993) A biotic index for the doutheastern United States: derivation and list of
672 tolerance values, with criteria for assigning water-quality ratings. *Journal of the*
673 *North American Benthological Society*, **12**, 279–290.

674 McCann K (2007) Protecting biostructure. *Nature*, **446**, 29.

675 Ober HK, Hayes JP (2008) Prey selection by bats in forests of western oregon. *Journal of*
676 *Mammalogy*, **89**, 1191–1200.

677 Piñol J, San Andrés V, Clare EL, Mir G, Symondson WOC (2013) A pragmatic approach
678 to the analysis of diets of generalist predators: the use of next-generation sequencing
679 with no blocking probes. *Molecular ecology resources*.

680 Pompanon F, Deagle BE, Symondson WOC *et al.* (2012) Who is eating what: diet
681 assessment using next generation sequencing. *Molecular Ecology*, **21**, 1931–1950.

682 R Development Core Team: R: A language and environment for statistical computing
683 (2008)

684 Ratnasingham S, Hebert PDN (2007) BOLD: the barcode of life data system
685 (www.barcodinglife.org). *Molecular Ecology Notes*, **7**, 355–364.

686 Razgour O, Clare EL, Zeale MRK *et al.* (2011) High-throughput sequencing offers
687 insight into mechanisms of resource partitioning in cryptic bat species. *Ecology and*
688 *Evolution*, **1**, 556–570.

689 Rosenheim J, Corbett A (2003) Omnivory and the indeterminacy of predator function:
690 can a knowledge of foraging behaviour help? *Ecology*, **84**, 2538–2548.

691 Simpson EH (1949) Measurement of Diversity. *Nature*, **163**, 688–688.

692 Singer M, Bernays E (2003) Understanding omnivory needs a behavioural perspective.
693 *Ecology*, **84**, 2532–2537.

694 Smith MA, Wood DM, Janzen DH, Hallwachs W, Hebert PDN (2007) DNA barcodes
695 affirm that 16 species of apparently generalist tropical parasitoid flies (Diptera,
696 Tachinidae) are not all generalists. *Proceedings of the National Academy of Sciences*
697 *of the United States of America*, **104**, 4967–4972.

698 Smith MA, Woodley NE, Janzen DH, Hallwachs W, Hebert PDN (2006) DNA barcodes
699 reveal cryptic host-specificity within the presumed polyphagous members of a genus
700 of parasitoid flies (Diptera: Tachinidae). *Proceedings of the National Academy of*
701 *Sciences of the United States of America*, **103**, 3657–3662.

702 Soininen EM, Valentini A, Coissac E *et al.* (2009) Analysing diet of small herbivores: the
703 efficiency of DNA barcoding coupled with high-throughput pyrosequencing for
704 deciphering the composition of complex plant mixtures. *Frontiers in Zoology*, **6**, 16.

705 Solé R V, Montoya JM (2001) Complexity and fragility in ecological networks.
706 *Proceedings of the Royal Society B-Biological Sciences*, **268**, 2039–2045.

707 Symondson WOC (2002) Molecular identification of prey in predator diets. *Molecular*
708 *Ecology*, **11**, 627–641.

Symondson WOC, Liddell JE (1993) A monoclonal antibody for the detection of arionid slug remains in carabid predators. *Biological Control*, **3**, 207–214.

Valentini A, Miquel C, Nawaz MA *et al.* (2009) New perspectives in diet analysis based on DNA barcoding and parallel pyrosequencing: the trnL approach. *Molecular Ecology Resources*, **9**, 51–60.

Wong EH-K, Hanner RH (2008) DNA barcoding detects market substitution in North American seafood. *Food Research International*, **41**, 828–837.

Zeale MRK, Butlin RK, Barker GLA, Lees DC, Jones G (2011) Taxon-specific PCR for DNA barcoding arthropod prey in bat faeces. *Molecular Ecology Resources*, **11**, 236–244.

Data Accessibility:

All DNA sequencing reads and an explanatory "read me" file along with BLAST scores for figure 8 have been placed in Dryad:
http://datadryad.org/submit?journalID=MolEcol&manu=MEC-13-0701

Author's contributions: ELC, HB, FF, EF, AM, AB, RH, CW, FM, AM, KN, MB, JP, JR, RMRB, JPR designed and conducted field research. ELC conducted the molecular analysis. WOCS contributed to molecular protocols. All authors contributed to manuscript production.

Figure Legends:

Figure 1: Distribution of sampling sites across Canada. Samples in Northwest Territories (n=5) were collected at sites in Kakisa (1) and Salt River (2) (considered as one unit in statistical analysis). Samples in the prairies (n=3) were collected between Medicine Hat (Alberta) and Swift Current (Saskatchewan) (3). Samples in Ontario were collected in Clinton (4) (n=14), Long Point (5) (n=7), Lake St. George (6) (2009 n=18, 2011 n=7) and Pinery Provincial Park (7) (n=4). Samples in Nova Scotia (n=8) were collected at sites in Martock (8) and Tatamagouche (9) (considered as one unit in statistical analysis). Samples in Quebec were collected at Jacques-Cartier and Aiguebelle National Parks (10) and Montmorency Forest Station (11).
(Map Modified from: Canada Outline Map. St. Catharines, Ontario: Brock University Map Library. Available: Brock University Map Library Controlled Access http://www.brocku.ca/maplibrary/maps/outline/North_America/canadaNONAMES.pdf (Accessed April 2, 2013).)

Figure 2: Seasonal diversity in prey consumed by *M. lucifugus*. The proportion of each prey group in the diet varied significantly across seasons. Diptera dominated the early season diet while Lepidoptera become more important in the middle and late seasons. Proportion = frequency of occurrence of that order / total occurrences, where an occurrence is an identified MOTU in a sample.

Figure 3: Seasonal diversity in prey consumed by *M. lucifugus* at 8 locations across Canada. The proportion of each prey group composing the diet varied significantly across seasons and with location. Proportion = frequency of occurrence of that order / total occurrences, where an occurrence is an identified MOTU in a sample.

Figure 4: Estimates of *M. lucifugus'* dietary diversity with 95% confidence intervals, based on the Simpson diversity index on data restricted to ordinal-level taxonomy (A) and using MOTU as a proxy for species (B).

Figure 5: A comparison of rarefaction curves for operational taxonomic units at the order (A, B) and species (C, D) level. Lines are mean estimates (A, B, C) or mean with 95% confidence levels (D) based on permutations.

Figure 6: Estimates of *M. lucifugus'* dietary diversity with 95% confidence intervals based on the Simpson diversity index from three seasons. Early season=females are pregnant, middle season=females are lactating, late season=young are independent.

Figure 7: Weekly species richness in the diet of *M. lucifugus* for the two most heavily sampled sites, at Clinton and Lake St. George in 2009, showing a trend of higher mean species richness with 95% confidence intervals in bats at Lake St. George, which is also an area where prey have a lower pollution tolerance suggesting higher quality habitat.

Figure 8: A schematic of prey species consumed including all MOTU (including those that could not be identified using a reference database). Identifications have been made by BLAST score and are limited to hypothesis at the order level. Values at nodes or tips represent the number of MOTU assigned. Node size is scaled to the number of assignments. See Emrich et al. (2013) for additional details.

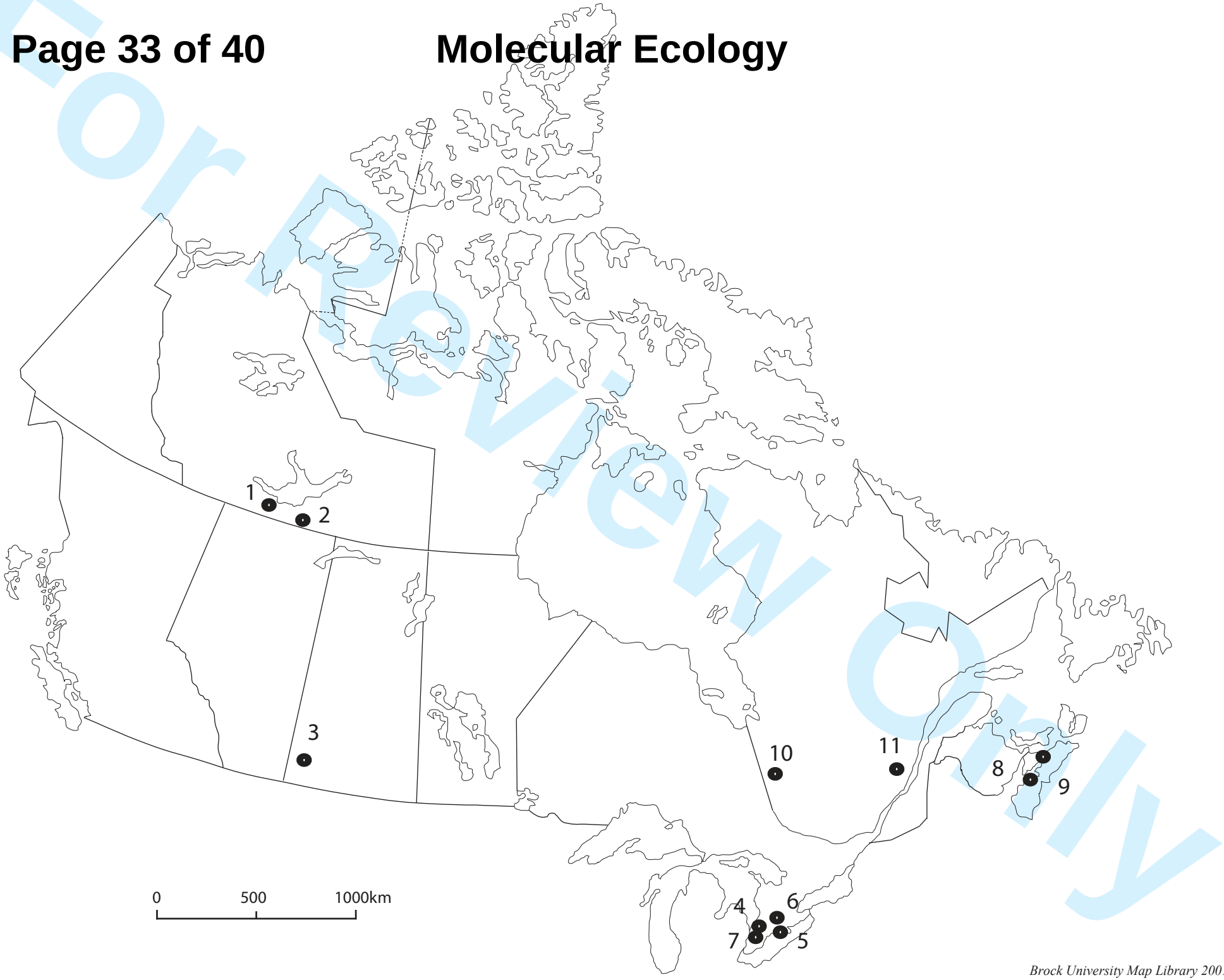
780 Table 1: Approximate habitat assessments based on the lowest scoring (lease tolerant to pollution or
781 acidification) taxa identified in the diet of bats at each location.

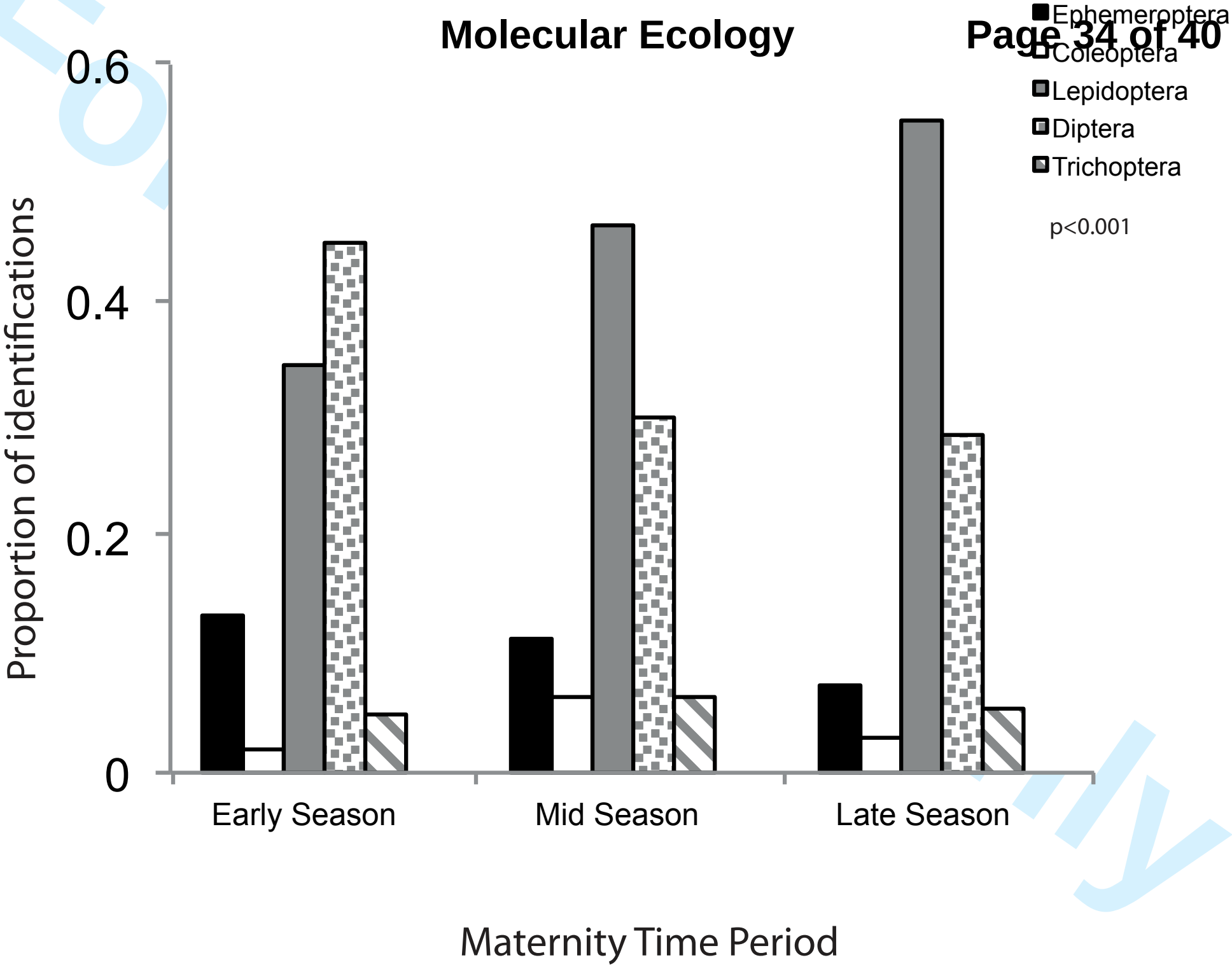
Location	Example Taxa	Pollution Tolerance	Acid Tolerance	Maximum Quality
NWT	Glososomatidae	0	low	
	Ephemerellidae	1		Low organic pollution
	Heptagenia sp		Low-med	No acidification
Lake St. George	Glososomatidae	0	low	
(Ontario)	Ephemerellidae	1	high	Low organic pollution
	Corydalidae	0		No acidification
Clinton	Helicopsychidae	3		
(Ontario)	Tipulidae	3		Trace organic
	Isonychia	3		pollution
Long Point	Leptoceridae	4		Some organic
(Ontario)	Phryganeidae	4		pollution
Nova Scotia	Leptoceridae	4		
	Phryganeidae	4	high	Some organic
	Stenacron	4		pollution
	Molanna sp.		low	No Acidification
Pinery	Chironomidae	6		Some organic
(Ontario)	Psychodidae	10		pollution
	Phryganeidae	4	high	Possibly acidified
Saskatchewan	Chironomidae	6		Likely organic pollution*

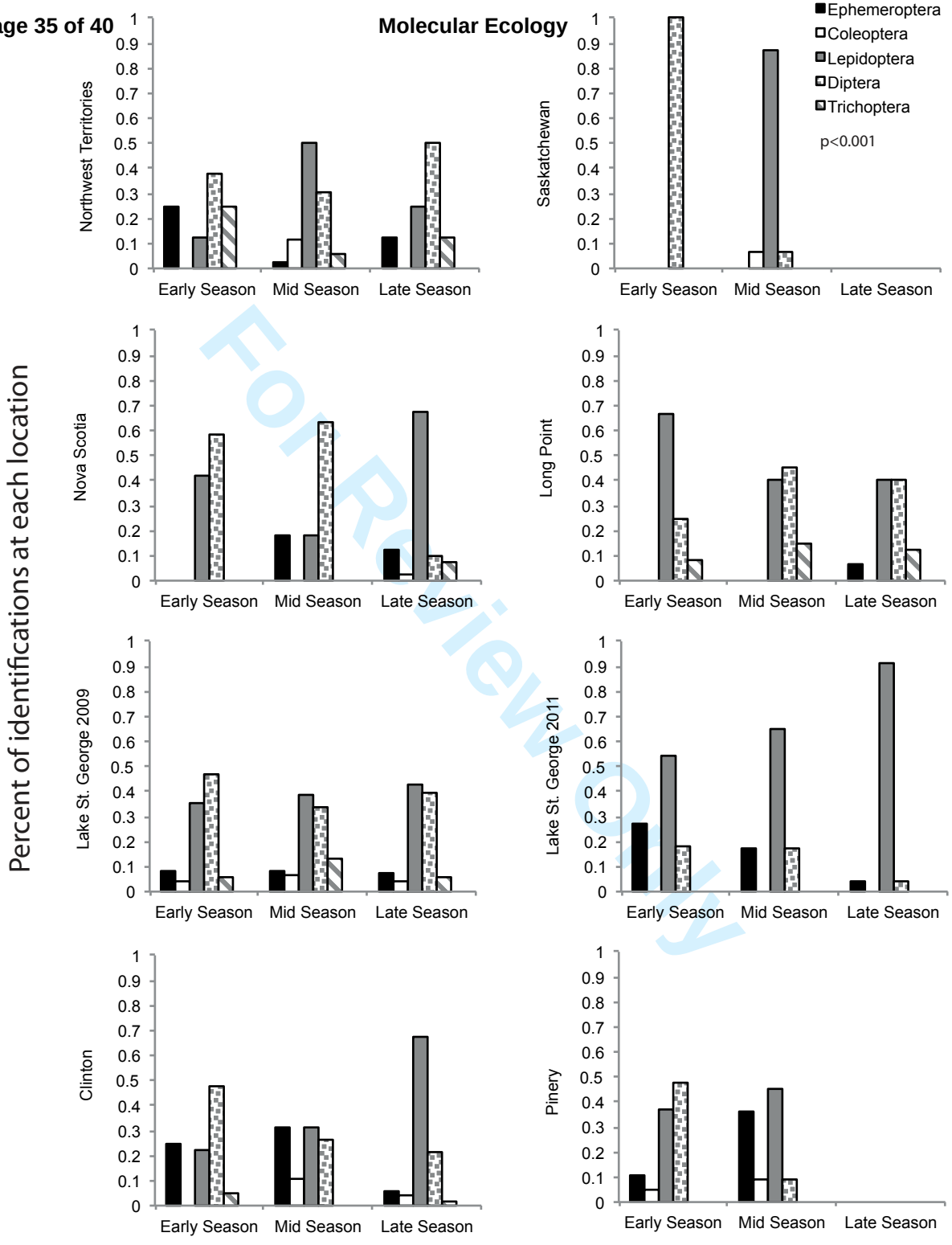
782 * Little Data Available

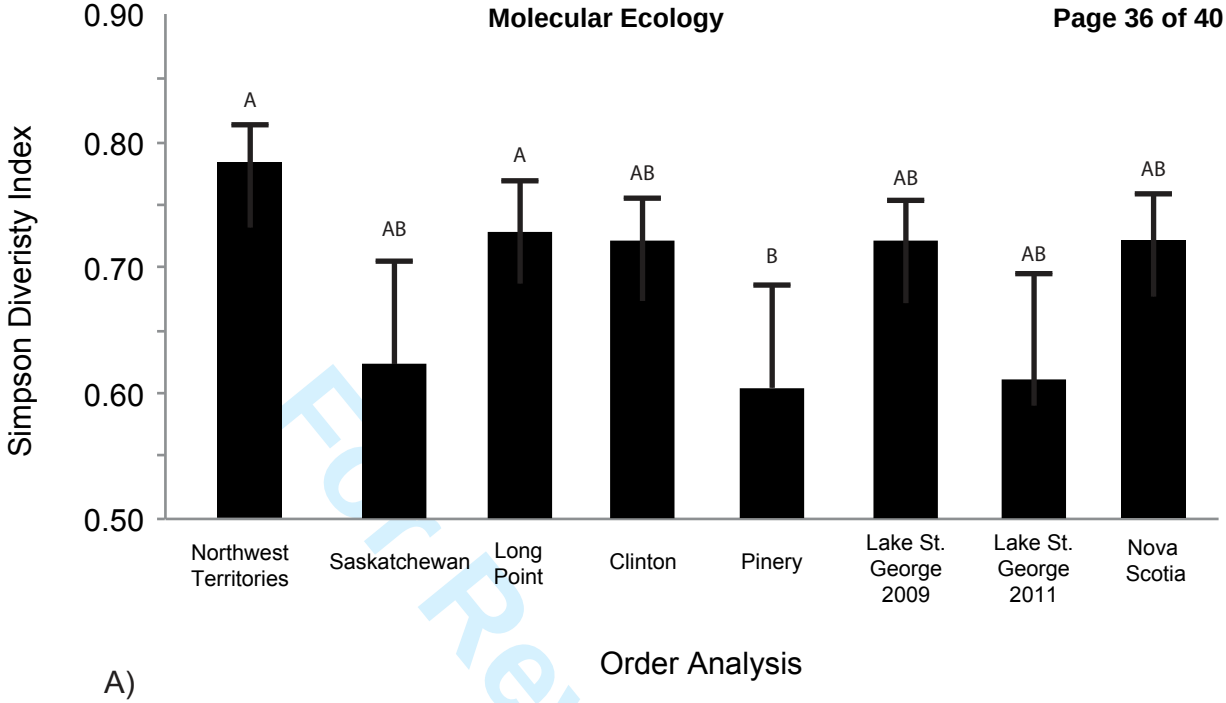
783 Hilsenhoff index goes from 1(low) to 10 (high) tolerance

784




Ephemeroptera
Coleoptera
Lepidoptera
Diptera
Trichoptera
p<0.001
0.6
0.4
0.2
0
Proportion of identifications
Early Season
Mid Season
Late Season
Maternity Time Period





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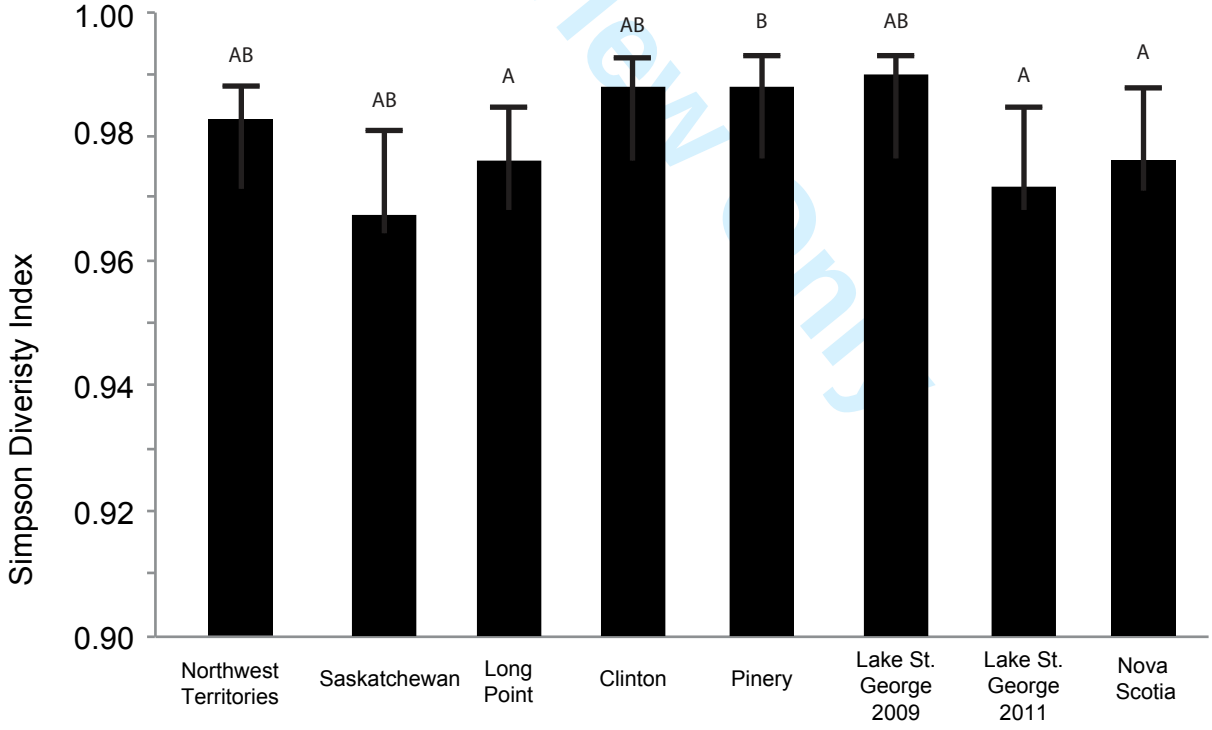

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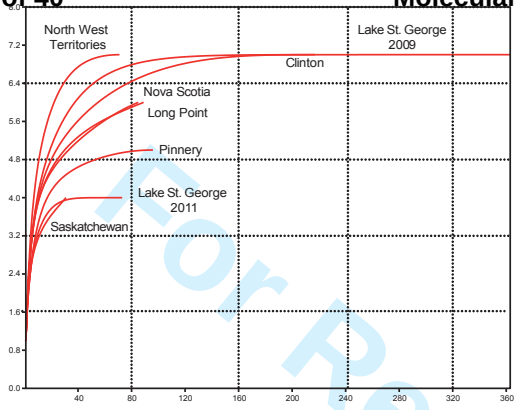

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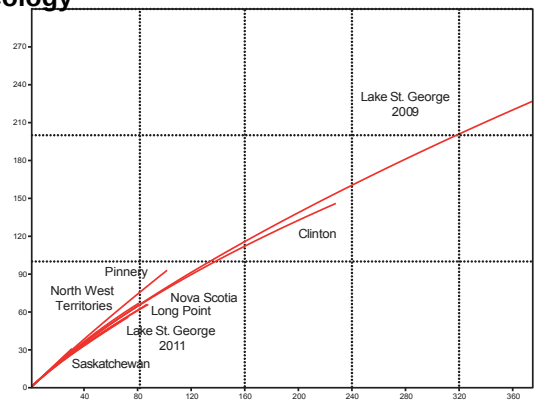
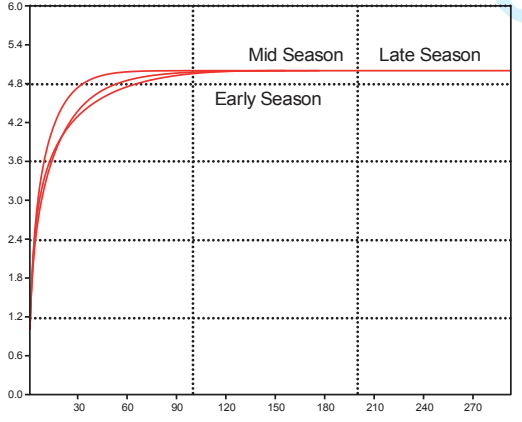


C)

Taxa (95% confidence)



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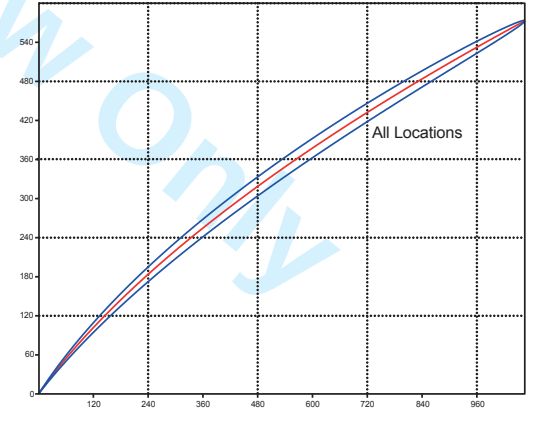
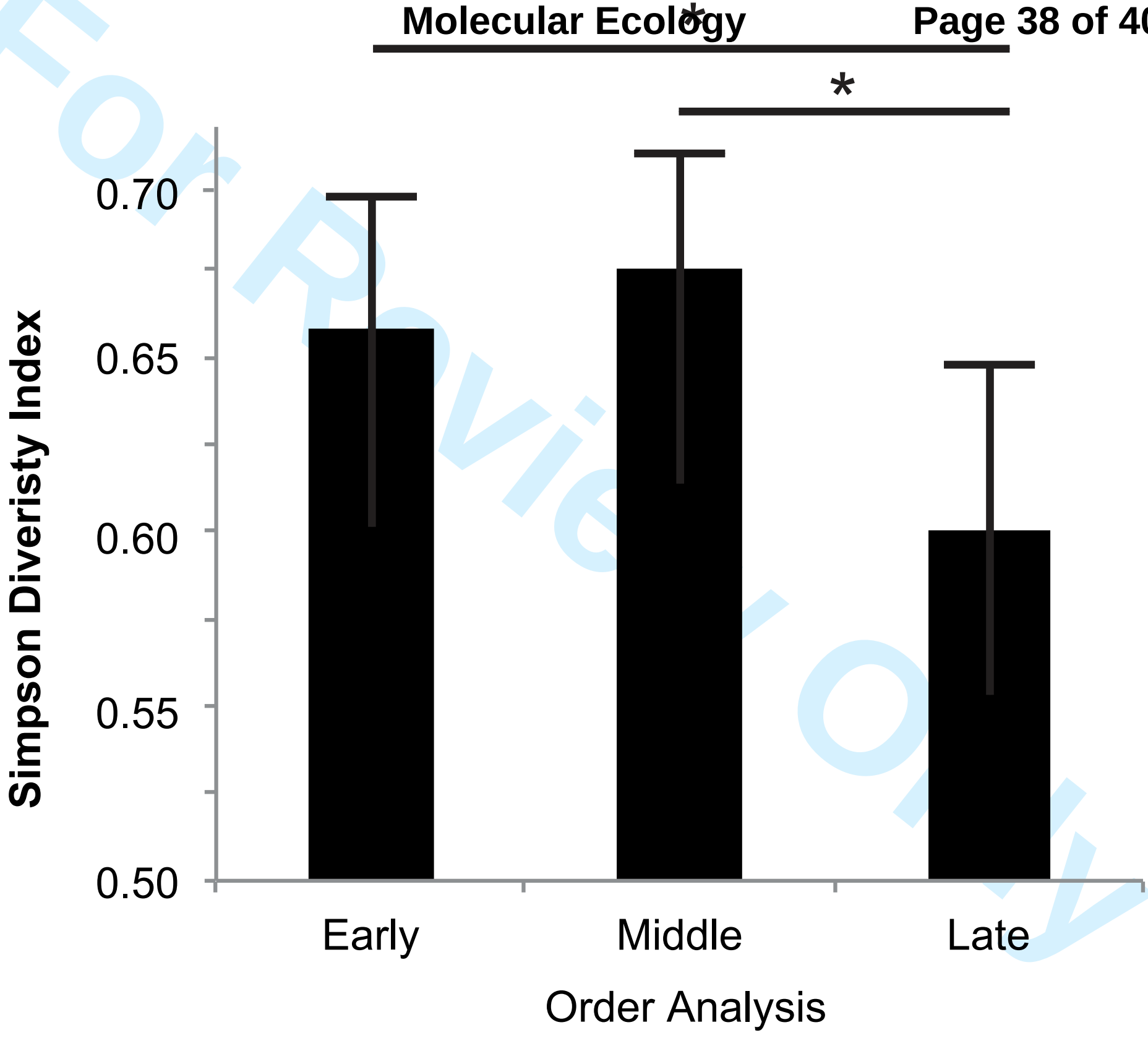
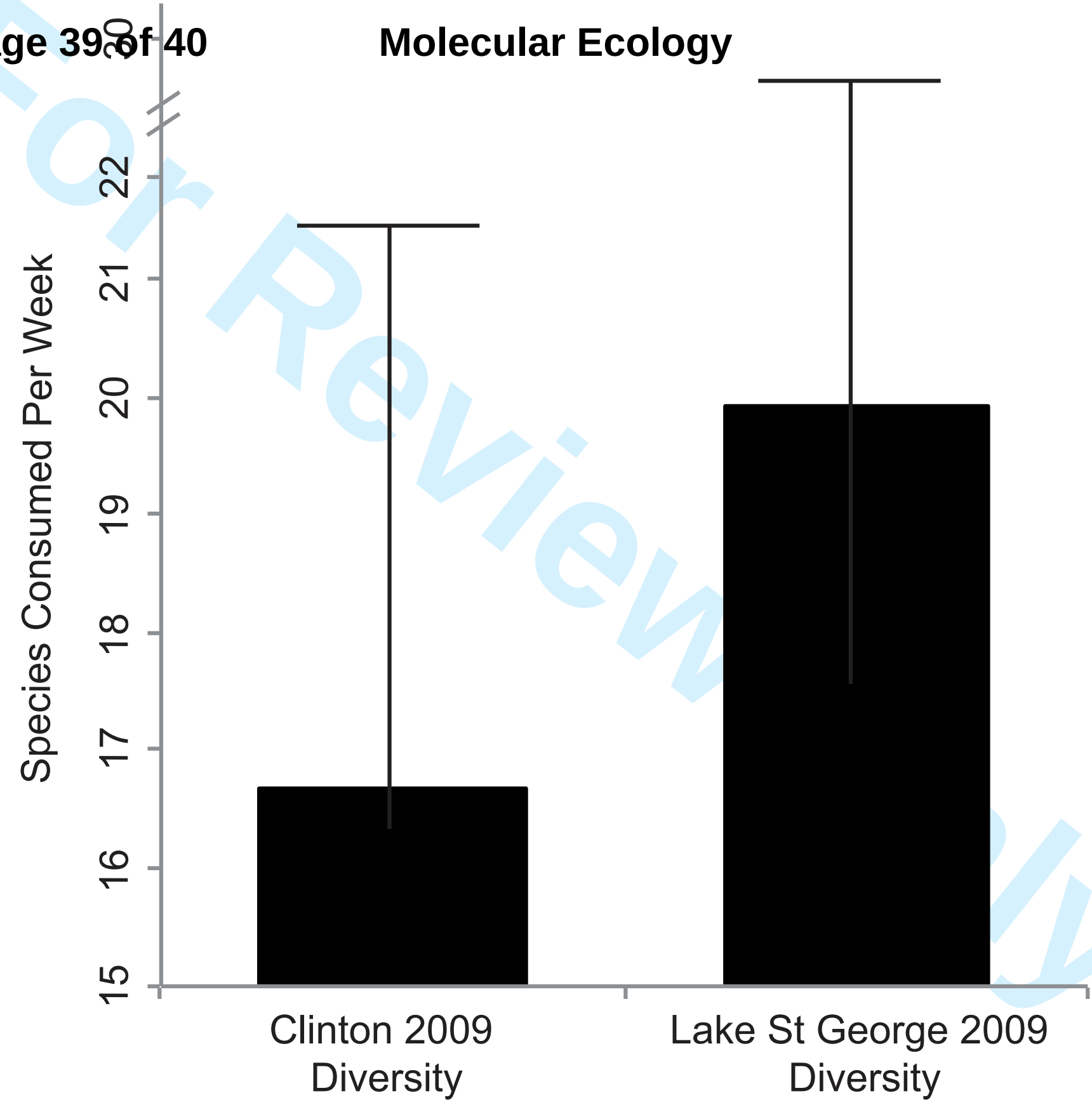
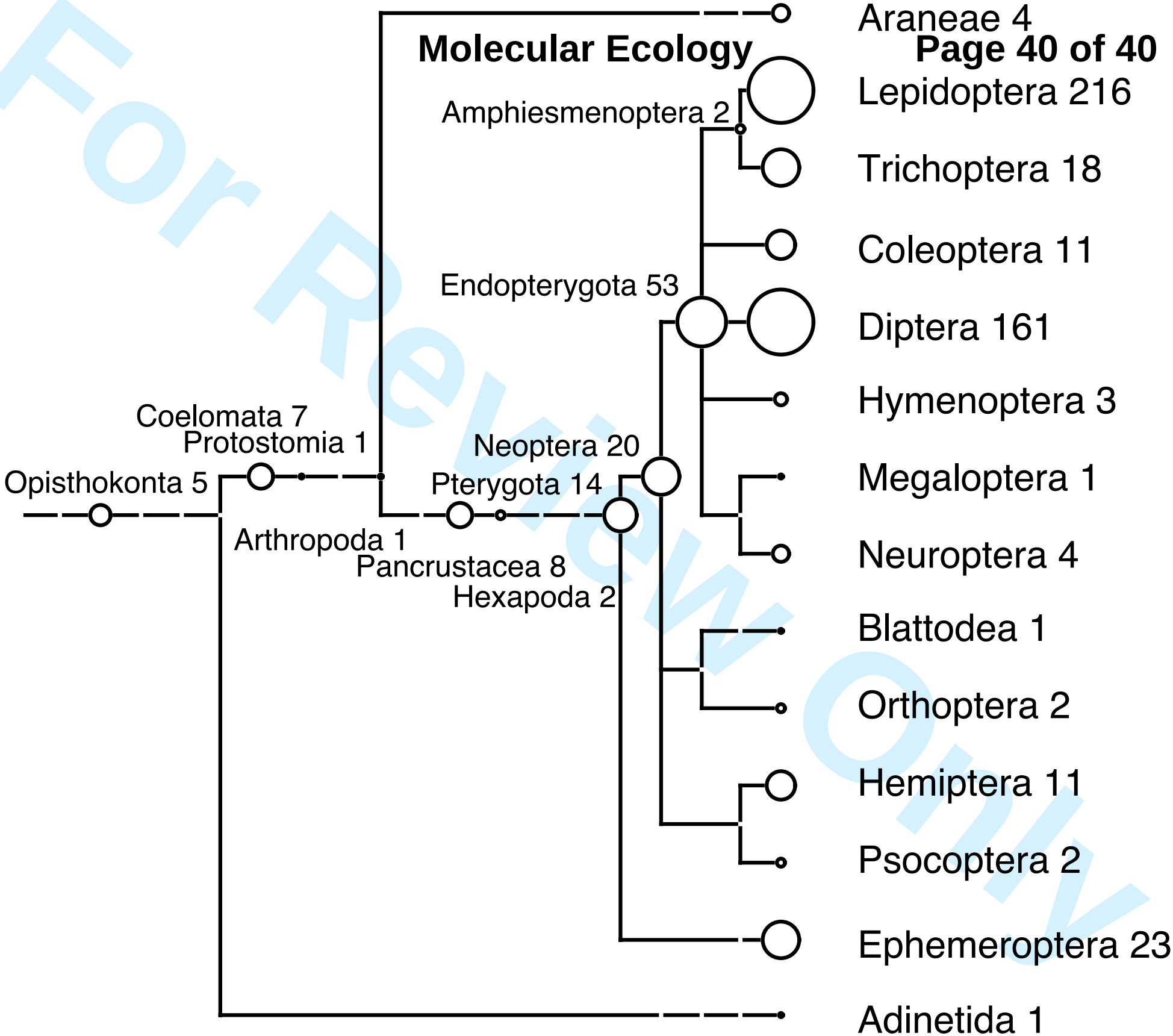


D)







All taxonomic matches are 1 or 1a unless indicated with a *=level 2

Frequency	Class	Order	Family	*Species*	NWT	Saskatchewan	Nova Scotia	Pinnery	Long Point	Lake St. George 2011	Clinton	Lake St. George 2009
1	Arachnida	Araneae	Araneidae	*Anyphaena pectorosa*					1			
1	Arachnida	Araneae	Araneidae	*Larinioides cornutus*							1	
2	Arachnida	Araneae	Araneidae	*Larinioides patagiatus*	2							
1	Arachnida	Araneae	Araneidae	*Larinioides sclopetarius*								1
2	Insecta	Coleoptera	Carabidae	*Dromius piceus*							2	
1	Insecta	Coleoptera	Carabidae	*Notiobia terminata*								1
1	Insecta	Coleoptera	Carabidae	*Selenophorus sp.*		1						
1	Insecta	Coleoptera	Carabidae	*Stenolophus ochropezus*				1				
1	Insecta	Coleoptera	Cleridae	*Cymatodera bicolor*							1	
1	Insecta	Coleoptera	Curculionidae	*Hypera sp.*							1	
2	Insecta	Coleoptera	Curculionidae	*Polydrusus sericeus*								2
1	Insecta	Coleoptera	Dytiscidae	*Ilybius sp.*	1							
1	Insecta	Coleoptera	Elateridae	*Denticollis denticornis*							1	
1	Insecta	Coleoptera	Leiodidae	*Catops luridipennis*	1							
1	Insecta	Coleoptera	Scarabaeidae	*Onthophagus sp.*								1
7	Insecta	Coleoptera	Scirtidae	*Cyphon sp.*			1	1				5
1	Insecta	Diptera	Asilidae	*Dioctria sp.*							1	
3	Insecta	Diptera	Chironomidae	*Ablabesmyia americana*								3
1	Insecta	Diptera	Chironomidae	*Axarus sp.*				1				
3	Insecta	Diptera	Chironomidae	*Chironomus acidophilus*				1	1			1
1	Insecta	Diptera	Chironomidae	*Chironomus sp.*		1						
1	Insecta	Diptera	Chironomidae	*Chironomus sp.*	1							
1	Insecta	Diptera	Chironomidae	*Cryptochironomus psittacinus*							1	
7	Insecta	Diptera	Chironomidae	*Cladopelma sp.*								7
2	Insecta	Diptera	Chironomidae	*Cladopelma sp.*								2
2	Insecta	Diptera	Chironomidae	*Cricotopus bicinctus*				1			1	
1	Insecta	Diptera	Chironomidae	*Diamesa sp.*								1
18	Insecta	Diptera	Chironomidae	*Dicrotendipes tritomus*			1	1				16
1	Insecta	Diptera	Chironomidae	*Microtendipes pedellus*								1
6	Insecta	Diptera	Chironomidae	*Parachironomus tenuicaudatus*								6
12	Insecta	Diptera	Chironomidae	*Paracladopelma winnelli*				2			10	
1	Insecta	Diptera	Chironomidae	*Procladius sp.*								1
1	Insecta	Diptera	Chironomidae	*Psectrotanypus sp.*		1						
1	Insecta	Diptera	Chironomidae	*Rheopelopia ornata*							1	
7	Insecta	Diptera	Chironomidae	*Tanytarsus mendax*				1				6
1	Insecta	Diptera	Chironomidae	*Unknown*		1						
2	Insecta	Diptera	Culicidae	*Aedes implicatus*	2							

1	Insecta	Diptera	Culicidae	*Aedes sp.*	1							
1	Insecta	Diptera	Culicidae	*Aedes stimulans*						1*		
11	Insecta	Diptera	Culicidae	*Aedes vexans*	3				1	1	2	4
1	Insecta	Diptera	Culicidae	*Anopheles sp.*								1
1	Insecta	Diptera	Culicidae	*Anopheles sp.*	1							
3	Insecta	Diptera	Culicidae	*Coquillettidia perturbans*	2							1
6	Insecta	Diptera	Culicidae	*Culex sp.*					6			
1	Insecta	Diptera	Culicidae	*Culex sp.*	1							
1	Insecta	Diptera	Culicidae	*Culiseta inornata*	1							
1	Insecta	Diptera	Culicidae	*Culiseta minnesotae*					1			
1	Insecta	Diptera	Culicidae	*Culiseta sp.*	1							
2	Insecta	Diptera	Culicidae	*Ochlerotatus sp.*	1							1
4	Insecta	Diptera	Empididae	*Trichoclinocera pectinifemur*							4	
1	Insecta	Diptera	Limoniidae	*Elephantomyia westwoodi*			1					
4	Insecta	Diptera	Limoniidae	*Erioptera septemtrionis*			4					
2	Insecta	Diptera	Limoniidae	*Euphylidorea platyphallus*	2							
1	Insecta	Diptera	Limoniidae	*Helius flavipes*			1					
1	Insecta	Diptera	Limoniidae	*Idiocera blanda*					1			
9	Insecta	Diptera	Limoniidae	*Ormosia affinis*			7	1				1
1	Insecta	Diptera	Limoniidae	*Symplecta sp.*							1	
1	Insecta	Diptera	Muscidae	*Musca autumnalis*							1	
1	Insecta	Diptera	Muscidae	*Spilogona sp.*	1							
2	Insecta	Diptera	Pediciidae	*Pedicia inconstans*							2	
4	Insecta	Diptera	Psychodidae	*Phychodid sp.*				2			1	1
1	Insecta	Diptera	Sepsidae	*Sepsis punctum*							1	
1	Insecta	Diptera	Tabanidae	*Hybomitra lurida*	1							
1	Insecta	Diptera	Tachinidae	*Cryptomeigenia sp.*				1				
1	Insecta	Diptera	Tachinidae	*Medina sp.*							1*	
1	Insecta	Diptera	Tachinidae	*Unnkown*		1						
1	Insecta	Diptera	Tipulidae	*Tipula caloptera*							1	
1	Insecta	Diptera	Tipulidae	*Tipula oleracea*								1
10	Insecta	Ephemeroptera	Caenidae	*Caenis amica sp.?*	1			4	1	4		
4	Insecta	Ephemeroptera	Caenidae	*Caenis latipennis ?*							3	1
1	Insecta	Ephemeroptera	Caenidae	*Caenis sp.*				1				
1	Insecta	Ephemeroptera	Caenidae	*Caenis sp.*				1				
1	Insecta	Ephemeroptera	Caenidae	*Caenis sp.*				1				
2	Insecta	Ephemeroptera	Caenidae	*Caenis sp.*			2					
6	Insecta	Ephemeroptera	Caenidae	*Caenis sp.*							6	
18	Insecta	Ephemeroptera	Caenidae	*Caenis youngi sp.?*					1		2	15
1	Insecta	Ephemeroptera	Ephemerellidae	*Ephemerella sp.*	1							

5	Insecta	Ephemeroptera	Ephemerellidae	*Eurylophella temporalis*						3			2
4	Insecta	Ephemeroptera	Ephemeridae	*Hexagenia sp.*			4						
2	Insecta	Ephemeroptera	Heptageniidae	*Heptagenia sp.*	2								
6	Insecta	Ephemeroptera	Heptageniidae	*Maccaffertium mediopunctatum*							6		
1	Insecta	Ephemeroptera	Heptageniidae	*Maccaffertium vicarium*							1		
1	Insecta	Ephemeroptera	Heptageniidae	*Stenacron interpunctatum*			1						
2	Insecta	Ephemeroptera	Isonychiidae	*Isonychia bicolor*							2		
4	Insecta	Hemiptera	Notonectidae	*Notonecta kirbyi*									4
1	Insecta	Hymenoptera	Vespidae	*Polistes sp.*									1
1	Insecta	Lepidoptera	Amphisbatidae	*Machimia tentoriferella*						1*			
3	Insecta	Lepidoptera	Amphisbatidae	*Psilocorsis reflexella*			3						
1	Insecta	Lepidoptera	Argyresthiidae	*Argyresthia alternatella*				1					
1	Insecta	Lepidoptera	Argyresthiidae	*Argyresthia aureoargentella*									1
1	Insecta	Lepidoptera	Argyresthiidae	*Argyresthia canadensis*									1
1	Insecta	Lepidoptera	Argyresthiidae	*Argyresthia thuiella*									1
2	Insecta	Lepidoptera	Batrachedridae	*Batrachedra praeangusta*	1								1
1	Insecta	Lepidoptera	Blastobasidae	*Asaphocrita busckiella*									1
1	Insecta	Lepidoptera	Blastobasidae	*Blastobasis floridella*							1		
2	Insecta	Lepidoptera	Blastobasidae	*Holcocera chalcofrontella*						1			1
1	Insecta	Lepidoptera	Blastobasidae	*Holcocera crassicornella**		1							
1	Insecta	Lepidoptera	Carmbidae	*Herpetogramma sp.*									1
1	Insecta	Lepidoptera	Carmbidae	*Ostrinia obumbratalis*						1			
1	Insecta	Lepidoptera	Coleophoridae	*Coleophora limosipennella*						1			
2	Insecta	Lepidoptera	Coleophoridae	*Coleophora pruniella*			1						1
1	Insecta	Lepidoptera	Coleophoridae	*Coleophora sp.*									1
1	Insecta	Lepidoptera	Cosmopterigidae	*Limnaecia phragmitella*									1
1	Insecta	Lepidoptera	Crambidae	*Acentria ephemerella*							1		
1	Insecta	Lepidoptera	Crambidae	*Ostrinia penitalis*					1				
1	Insecta	Lepidoptera	Crambidae	*Thopeutis forbesellus*					1				
12	Insecta	Lepidoptera	Elachistidae	*Agonopterix robiniella*		1			1*		3		7
2	Insecta	Lepidoptera	Elachistidae	*Semioscopis packardella*							1		1
1	Insecta	Lepidoptera	Erebidae	*Ctenucha virginica*									1
1	Insecta	Lepidoptera	Erebidae	*Idia sp.*	1								
2	Insecta	Lepidoptera	Erebidae	*Unknown***				1					1
2	Insecta	Lepidoptera	Erebidae	*Unknown***									2
3	Insecta	Lepidoptera	Erebidae	*Unknown***	1				1	1			
2	Insecta	Lepidoptera	Erebidae	*Unknown***					1		1		
1	Insecta	Lepidoptera	Erebidae	*Unknown***							1		
1	Insecta	Lepidoptera	Gelechiidae	*Carpatolechia sp.*			1						
1	Insecta	Lepidoptera	Gelechiidae	*Caryocolum cassella*		1							

1	Insecta	Lepidoptera	Gelechiidae	*Chionodes fuscomaculella*				1						
1	Insecta	Lepidoptera	Gelechiidae	*Chionodes mediofuscella*									1	
3	Insecta	Lepidoptera	Gelechiidae	*Coleotechnites sp.*				1						2
2	Insecta	Lepidoptera	Gelechiidae	*Coleotechnites sp.*				2						
1	Insecta	Lepidoptera	Gelechiidae	*Coleotechnites thujaella*										1
1	Insecta	Lepidoptera	Gelechiidae	*Filatima sp.*						1				
1	Insecta	Lepidoptera	Gelechiidae	*Gelechia sp.*	1									
2	Insecta	Lepidoptera	Gelechiidae	*Metzneria lappella*							1			1
1	Insecta	Lepidoptera	Gelechiidae	*Pseudotelphusa quercinigracella*					1					
1	Insecta	Lepidoptera	Gelechiidae	*Pseudotelphusa querciphaga*					1					
1	Insecta	Lepidoptera	Gelechiidae	*Xenolechia sp.*					1					
2	Insecta	Lepidoptera	Gelechiidae	*Xenolechia ontariensis*					1	1				
1	Insecta	Lepidoptera	Geometridae	*Blastobasis glandulella*					1*					
10	Insecta	Lepidoptera	Geometridae	*Hydriomena sp.**	1	1		1	2		3		1	1
1	Insecta	Lepidoptera	Geometridae	*Lycia ursaria*										1
1	Insecta	Lepidoptera	Geometridae	*Operophtera bruceata*										1
1	Insecta	Lepidoptera	Geometridae	*Perizoma alchemillata*				1						
1	Insecta	Lepidoptera	Gracillariidae	*Caloptilia negundella*										1
1	Insecta	Lepidoptera	Gracillariidae	*Cameraria caryaefoliella*									1	
5	Insecta	Lepidoptera	Lasiocampidae	*Malacosoma americana*									4	1
1	Insecta	Lepidoptera	Lasiocampidae	*Malacosoma disstria*									1	
3	Insecta	Lepidoptera	Leptoceridae	*Nectopsyche albida*							1		2	
1	Insecta	Lepidoptera	Leptoceridae	*Oecetis cinerascens*										1
1	Insecta	Lepidoptera	Limacodidae	*Lithacodes fasciola*				1						
1	Insecta	Lepidoptera	Momphidae	*Mompha epilobiella*							1			
1	Insecta	Lepidoptera	Momphidae	*Mompha brevivittella*										1
1	Insecta	Lepidoptera	Noctuidae	*Anicla sp.*									1	
1	Insecta	Lepidoptera	Noctuidae	*Apamea devastator*		1								
2	Insecta	Lepidoptera	Noctuidae	*Apamea sp.*										2
2	Insecta	Lepidoptera	Noctuidae	*Condica sp.*									1	1
1	Insecta	Lepidoptera	Noctuidae	*Feltia jaculifera*		1*								
1	Insecta	Lepidoptera	Noctuidae	*Mythimna unipuncta*										1
2	Insecta	Lepidoptera	Noctuidae	*Spodoptera sp.*									1	1
2	Insecta	Lepidoptera	Noctuidae	*Spodoptera sp.*		1							1	
1	Insecta	Lepidoptera	Noctuidae	*Unknown***		1								
1	Insecta	Lepidoptera	Notonectidae	*Notonecta kirbyi*							1			
3	Insecta	Lepidoptera	Pterophoridae	*Geina sheppardi*							1		2	
7	Insecta	Lepidoptera	Pterophoridae	*Geina sp.*									1	6
1	Insecta	Lepidoptera	Pterophoridae	*Hellinsia lacteodactylus*									1	
1	Insecta	Lepidoptera	Pyralidae	*Scotomera gielisi*					1					

1	Insecta	Lepidoptera	Sphingidae	*Amorpha juglandis*							1		
1	Insecta	Lepidoptera	Sphingidae	*Deidamia inscriptum*						1			
2	Insecta	Lepidoptera	Tineidae	*Acrolophus heppneri**	1								1
1	Insecta	Lepidoptera	Tineidae	*Homosetia fasciella*									1
2	Insecta	Lepidoptera	Tortricidae	*Acleris chalybeana*						1	1		
3	Insecta	Lepidoptera	Tortricidae	*Acleris forsskaleana*						1	1		1
1	Insecta	Lepidoptera	Tortricidae	*Acleris negundana*						1			
1	Insecta	Lepidoptera	Tortricidae	*Adoxophyes negundana*						1*			
1	Insecta	Lepidoptera	Tortricidae	*Aethes sp.*							1		
1	Insecta	Lepidoptera	Tortricidae	*Ancylis divisana*						1			
1	Insecta	Lepidoptera	Tortricidae	*Argyrotaenia quercifoliana*			1						
1	Insecta	Lepidoptera	Tortricidae	*Argyrotaenia sp.*		1							
1	Insecta	Lepidoptera	Tortricidae	*Catastega aceriella*									1
1	Insecta	Lepidoptera	Tortricidae	*Choristoneura fumiferana*						1			
1	Insecta	Lepidoptera	Tortricidae	*Choristoneura sp.*	1								
1	Insecta	Lepidoptera	Tortricidae	*Clepsis virescana*	1								
4	Insecta	Lepidoptera	Tortricidae	*Cnephasia sp.*		1					3		
1	Insecta	Lepidoptera	Tortricidae	*Epinotia transmissana*				1					
2	Insecta	Lepidoptera	Tortricidae	*Eucosma sp.*				1					1
1	Insecta	Lepidoptera	Tortricidae	*Grapholita eclipsana*						1			
3	Insecta	Lepidoptera	Tortricidae	*Gretchena sp.*						1	2		
1	Insecta	Lepidoptera	Tortricidae	*Oecetis cinerascens*						1			
1	Insecta	Lepidoptera	Tortricidae	*Olethreutes glaciana*	1								
1	Insecta	Lepidoptera	Tortricidae	*Olethreutes sp.*									1
2	Insecta	Lepidoptera	Tortricidae	*Pandemis lamprosana*				2					
1	Insecta	Lepidoptera	Tortricidae	*Pandemis sp.*	1								
1	Insecta	Lepidoptera	Tortricidae	*Phtheochroa sp.*									1
1	Insecta	Lepidoptera	Tortricidae	*Platynota idaeusalis*	1								
1	Insecta	Lepidoptera	Tortricidae	*Platynota sp.*						1			
1	Insecta	Lepidoptera	Tortricidae	*Platynota sp.*				1					
4	Insecta	Lepidoptera	Tortricidae	*Proteoteras crescentana*						1	1		2
4	Insecta	Lepidoptera	Tortricidae	*Pseudexentera sp.*									4
3	Insecta	Lepidoptera	Tortricidae	*Pseudexentera sp.*						2	1		
1	Insecta	Lepidoptera	Tortricidae	*Pseudexentera sp.*						1			
1	Insecta	Lepidoptera	Tortricidae	*Pseudexentera sp.*							1		
7	Insecta	Lepidoptera	Tortricidae	*Sparganothis pettitana*				2		1	4		
1	Insecta	Lepidoptera	Tortricidae	*Zeiraphera sp.*		1							
1	Insecta	Megaloptera	Corydalidae	*Chauliodes sp.*									1
1	Insecta	Megaloptera	Sialidae	*Sialis sp.*							1		
3	Insecta	Neuroptera	Hemerobiidae	*Hemerobius sp.*							1		2

3	Insecta	Tricoptera	Glossosomatidae	*Glossosoma intermedium*	2									1
2	Insecta	Tricoptera	Helicopsychidae	*Helicopsyche borealis*								2		
1	Insecta	Tricoptera	Hydropsychidae	*Arctopsyche ladogensis*	1									
1	Insecta	Tricoptera	Hydropsychidae	*Cheumatopsyche sp.*								1		
2	Insecta	Tricoptera	Limnephilidae	*Limnephilus sp.*										2
3	Insecta	Tricoptera	Leptoceridae	*Triaenodes injustus*										3
1	Insecta	Tricoptera	Leptoceridae	*Triaenodes nox*										1
5	Insecta	Tricoptera	Leptoceridae	*Triaenodes sp.*					5					
1	Insecta	Tricoptera	Leptoceridae	*Triaenodes sp.*					1					
2	Insecta	Tricoptera	Molannidae	*Molanna sp.*			2							
8	Insecta	Tricoptera	Nectopsyche	*Nectopsyche albida*										8
2	Insecta	Tricoptera	Phryganeidae	*Agrypnia colorata*	2									
1	Insecta	Tricoptera	Phryganeidae	*Agrypnia deflata*	1									
3	Insecta	Tricoptera	Phryganeidae	*Phryganea cinerea*			1		1					1
		Additional unidentiifed prey (includes level 3 identifications)			33		18	42	64	42		27	88	158

Procedures for Quebec samples:

Samples from Quebec were not included in regular statistical analyses for three reasons. First, they were collected from individuals rather than from under roosts in large "community" samples. Second, for reasons that are not clear, the DNA was difficult to amplify and so additional steps were taken to recover the data. We include these data then as a supplement to the full analysis. Third, the sample includes males rather than all females and young (as expected in maternity roosts).

Collection procedures: The sampling in Quebec was performed from 15th of June to 5th of August in 2011 (Jacques-Cartier National Park and Montmorency Research Forest) and 2012 (Aiguebelle National Park). A total of 2-5 pellets were collected directly from males.

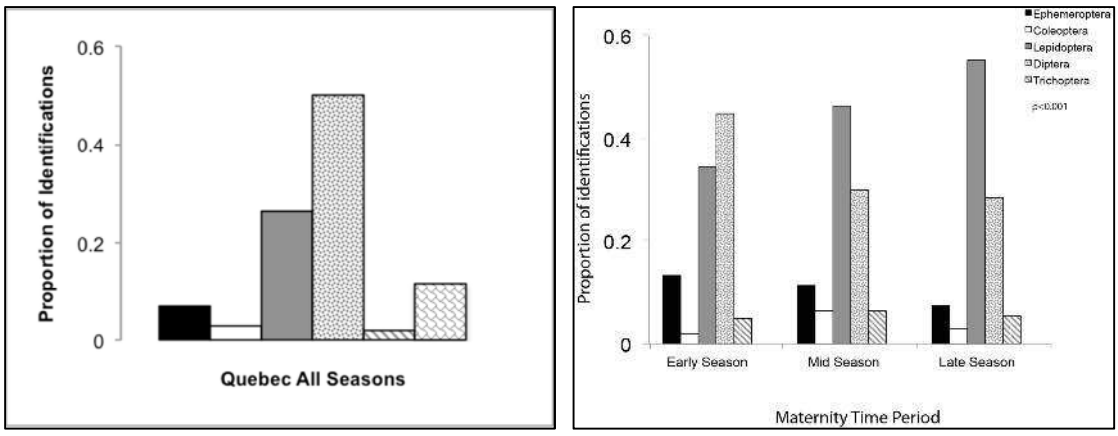
Sample preparation: We extracted DNA as described in the main manuscript. We encountered a high rate of PCR failure for these samples. Thus we treated all as "recalcitrant" and the PCR was conducted using Q-solution (provided by the Qiagen, UK multi-plex PCR kit) and modified hot start PCR programme.

PCR mixture: 12µl reactions contains 5µl of Master Mix, 1µl of Q solution, 0.5µl of each primer, 3µl H2O and 2µl template DNA.

Thermocycler protocols: An initial denaturation period of 15 min at 95°C followed by 35 cycles of 94°C for 30s, 53°C for 90s and 72°C for 90s, with a final extension period of 10min at 72°C. Using this protocol >90% of samples provided a band on an agarose gel.

Sequencing: To maximize sequencing potential and recovery, the reverse primers were modified for the Ion Torrent platform (Clare et al. 2014) and sequencing and informatics was carried out as described in that same publication.

Results: We recovered sequences from all samples (Supplemental File 1, worksheet 2)



Supplemental Figure: A comparison of the overall diet of little brown bats at locations in Quebec (across all seasons) with the overall results from Figure 2.

Location	Collection Date
Long Point	June 27, 2011
Long Point	July 5, 2011
Long Point	July 18, 2011
Long Point	August 1, 2011
Long Point	August 17, 2011
Long Point	June 6, 2011
Long Point	June 13, 2011
Clinton	May 20, 2009
Clinton	May 27, 2009
Clinton	June 3, 2009
Clinton	June 11, 2009
Clinton	June 17, 2009
Clinton	July 8, 2009
Clinton	July 15, 2009
Clinton	July 22, 2009
Clinton	July 29, 2009
Clinton	August 5, 2009
Clinton	August 12, 2009
Clinton	August 19, 2009
Clinton	August 26, 2009
Clinton	September 9, 2009
Lake St George	June 8, 2011
Lake St George	June 21, 2011
Lake St George	July 5, 2011
Lake St George	July 12, 2011
Lake St George	July 18, 2011
Lake St George	Aug 1, 2011
Lake St George	Aug 15, 2011
Lake St George	May 21, 2009
Lake St George	May 27, 2009
Lake St George	May 29, 2009
Lake St George	June 3, 2009
Lake St George	June 10, 2009
Lake St George	June 16, 2009
Lake St George	June 26, 2009
Lake St George	July 2, 2009
Lake St George	July 8, 2009
Lake St George	July 15, 2009
Lake St George	July 22, 2009
Lake St George	July 29, 2009
Lake St George	August 5, 2009
Lake St George	August 12, 2009
Lake St George	August 19, 2009
Lake St George	August 26, 2009

Lake St George	September 2, 2009
Lake St George	September 9, 2009
Praries	June 22, 2011
Praries	July 18, 2011
Praries	August 15, 2011
Pinery Provincial Park	June 14, 2009
Pinery Provincial Park	Exact Date Not Know
Pinery Provincial Park	Exact Date Not Know
Pinery Provincial Park	July 13, 2008
Kakisa NWT	June 28, 2011
Salt river NWT	June 23, 2011
Kakisa NWT	July 27, 2011
Salt river NWT	July 20, 2011
Salt river NWT	Sept 1, 2011
Martock, Nova Scotia	June 16, 2011
Martock, Nova Scotia	July 10, 2011
Martock, Nova Scotia	July 24, 2011
Martock, Nova Scotia	August 29, 2011
Tatamagouche Nova Scotia	May 31, 2011
Tatamagouche Nova Scotia	July 5, 2011
Tatamagouche Nova Scotia	July 1, 2011
Tatamagouche Nova Scotia	August 1, 2011