COLONIZATION OF RESTORED PEATLANDS BY INSECTS: DIPTERA ASSEMBLAGES IN MINED AND RESTORED BOGS IN EASTERN CANADA

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Canada

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PREFACE

This thesis is composed of three chapters; one of which is an original manuscript that will be submitted for publication in a refereed journal.

Chapter 1

This chapter is a general introduction and literature review.

Chapter 2

This chapter is a manuscript in preparation for submission to a refereed journal: Grégoire Taillefer, A. and Wheeler, T.A. Diptera assemblages in mined and restored bogs in eastern Canada

Chapter 3

This chapter is a general conclusion.

CONTRIBUTION OF AUTHORS

A. Grégoire-Taillefer designed the research and was responsible for field sampling, specimen preparation, identification of Diptera specimens, analyzing the data and writing the manuscript. T.A. Wheeler supervised the research, edited the manuscript, provided facilities and financial support for the equipment, the field season, the specimen preparation and conferences.

ABSTRACT

The impact of peatland restoration on Diptera assemblages was studied across multiple organizational levels (taxon, size class, trophic group) among abandoned-mined, restored and natural sites of three bogs and the environmental variables affecting those assemblages were determined. More than 22,000 individuals representing 716 species were collected using pan traps, sweeping and Malaise traps. Restored and abandoned sites were similar to each other and both distinct from natural sites as shown by small-size class, acalyptrate and trophic assemblages. However, abandoned sites showed much lower evenness and generally supported lower species richness than restored and natural sites, due to the dominance of one or two saprophagous species. The coverage of bare peat, *Sphagnum* mosses and ericaceous shrubs explained most of the variance in species composition. Those results suggest that restoration enhanced the recovery of high species diversity, although more than seven years are needed to recover a complete trophic structure or to enable species with low dispersal ability to recolonize to pre-disturbance levels.

RÉSUMÉ

L'impact de la restauration de tourbières sur les assemblages de diptères a été étudié sous différents niveaux d'organisation (taxon, groupe trophique et classe de taille) dans des sites abandonnés après extraction de la tourbe, restaurés et naturels de trois tourbières. De plus, les variables environnementales influençant la composition en espèces ont été déterminées. Plus de 22 000 individus représentant 716 espèces ont été récoltés à l'aide de pièges à cuvette, d'un filet et de pièges Malaise. Les sites restaurés et abandonnés étaient similaires entre eux et différents des sites naturels aux niveaux des assemblages des espèces de petite taille, des acalyptères et des groupes trophiques. Cependant, les sites abandonnés supportaient généralement une richesse en espèces plus basse que les sites restaurés et naturels dû à la dominance d'une ou deux espèces saprophages. Le couvert de tourbe à nue, de sphaignes et d'éricacées explique la majorité de la variance de la composition en espèces. Ces résultats suggèrent que la restauration a favorisée le recouvrement d'une diversité en espèces élevée, quoique plus de sept années soient nécessaires pour le rétablissement complet de la structure trophique ou la recolonisation des espèces à faible habilité de dispersion à un niveau de diversité semblable avant perturbation.

CHAPTER 1: GENERAL INTRODUCTION AND LITERATURE REVIEW

General introduction:

Anthropogenic disturbances are the primary causes of depletion of natural resources and loss of environmental integrity (Kim 1993). Site-specific biodiversity information is needed for conservation and management of natural and disturbed sites. This knowledge provides information on the effects of human activities on biodiversity and on the relationship between biodiversity and ecosystem properties. Biodiversity measurement is defined as the measure (genetic, taxonomic, population, interactions, etc.) of the variety of organisms inhabiting in a particular space and time (Hooper *et al.* 2005, Magurran 2005a). The most commonly measured components of biodiversity are species richness and abundance (Magurran 2004). Functional diversity, which is measured with the organismal traits that influence how an ecosystem operates or functions (Tilman 2001), is also a component of biodiversity. In assessing the effects of human disturbances, the entire biota is too complex to be completely quantified, even in small areas, because of high species richness and insufficient taxonomic knowledge (Niemelä *et al.* 2000, Kim and Byrne 2006). Therefore, diversity is usually measured at the community level, using a significant taxonomically or geographically delimited set of organisms (Magurran 2005b).

Terrestrial systems are frequently more complex and variable than aquatic systems, and abiotic factors tend to be more difficult to measure. This, combined with the lack of taxonomic resolution, available identification tools or available ecological knowledge partly explains why terrestrial arthropods are just beginning to be used in conservation studies (e.g. New 2006, New 2007, Samways 2007) even though arthropod species represent 65% of the world's biological diversity (Groombridge 1992) and have a significant impact on ecosystem processes.

Wetlands in Canada:

Approximately 25% (127 million hectares) of the world's wetlands are in Canada (Dahl and Zoltai 1997). A wetland is defined by the National Wetlands Working Group (1988) as: "*a land that is saturated with water long enough to promote wetland or aquatic processes as indicated by poorly drained soils, hydrophytic vegetation and various kinds of biological activity which are adapted to a wet environment*" . The Canadian Wetland Classification System separates wetlands into five classes based on the genetic origin and the nature of the wetland habitat (National Wetlands Working Group 1997). Inundated conditions over a long period of time can lead to the establishment of marsh vegetation (Kolka and Thompson 2006). Marsh vegetation is usually composed of aquatic macrophytes, rushes, reeds, grasses, sedges, shrubs, brown mosses, macroscopic algae and other herbaceous plants. Water sources include stream inflow, precipitation, groundwater discharges and tidal action. Marshes tend to be very alkaline due to the presence of dissolved minerals. Swamps are associated with rivers, lakes and waterways, they are dominated by trees or tall shrubs and dry periodically, which leads to forested systems. The dominant type of tree present defines the swamp type: shrub, coniferous or deciduous. Shallow water wetlands are transitional between saturated or seasonally wet (bog, fen, marsh and swamp) and aquatic ecosystems (lake, river and stream). Deposits can form when the water regime is stable, and provide a substrate for rooted, submerged and floating hydrophytic vegetation, as well as for algae and aquatic mosses (National Wetlands Working Group 1997). Peatlands are the most extensive type of wetlands (Chapman *et al.* 2003), representing 50-70% of the world's wetlands. In Quebec, peatlands cover between 7 to 9% of the province (Buteau 1988). Peatlands are typically divided into fens and bogs. A fen (minerotrophic peatland) typically develops through the process of paludification when an inundation occurs in low areas of mineral soils which leads to slower decomposition and organic matter deposition. A blanket of mosses eventually forms over the accumulation. In fens the dominant source of water comes from ground-water, which is generally associated with high pH and high levels of nutrients (Kolka and Thompson 2006). The vegetation is dominated by herbaceous plants, bryophytes (mostly brown mosses), shrubs and trees. *Sphagnum* mosses are rare or absent when the pH is high (Payette 2001). The term bog (ombrotrophic peatlands) refers to those peatlands that receive all water and nutrients from precipitation with no contribution from drainage water. They are characterized by their nutrient deficiency and their acidic pH (Payette 2001). Decomposition rate is slow due to the low oxygen availability as a consequence of waterlogging (Moore 2002). Over several millennia, the accumulations of *Sphagnum* and plant debris raise the mat above the water surface (terrestrialization) or the mineral soil (paludification) and create an inland peatland. (Vitt 1994, Quinty and Rochefort 2003). The water retention results in impacts on water and carbon cycling. A growing bog acts as a carbon sink in the dead and living tissue of the peat, due to the slow decomposition rather than the rapid productivity (Moore 2002). Peatland associated organisms have diversified and specialised to acclimatize with the harsh living conditions (Rochefort 2001). Wetland ecosystems share characteristics, flora and fauna with both terrestrial and aquatic habitats, but also exhibit microhabitats that are not found in either of these two latter habitats. They serve as breeding and feeding sites for waterfowl, wetland birds, amphibians and invertebrates. Therefore, wetlands are important for maintaining regional biodiversity by offering diverse and unique habitats.

Loss of Canadian peatlands:

The global loss of peatlands on Canada's landmass is estimated to be 20 million hectares since 1800 and degradation has affected millions of others. Peatlands have been lost, fragmented and drained for the benefits of peat mining, forestry, urbanization and agriculture activities (Government of Canada 1991). Most of the loss has taken place near urban areas, where access to peatland is easy. In contrast, pristine peatlands are usually located in the boreal region, where access is difficult and where exploitation would probably not be economically viable (Pellerin 2003, Chapman *et al.* 2003). Human disturbances have significantly altered the roles of peatlands in improving water quality, protecting shorelines, stabilizing water supplies, moderating the effects of floods, and recharging ground water aquifers (Keiper *et al.* 2002). The impact of human activities in the long and short term depends on the type of activities. Some of these activities are irreversible as they profoundly change the ecosystem properties, for example a peatland modified to agricultural land is drained and the organic deposit is extracted to expose the mineral soil necessary for cultivation. After the cessation of agriculture, the site cannot regenerate because bog characteristic plants are completely absent (Parent 2001, Pellerin 2003). The type and degree of disturbance and degradation are reasons why interest in conservation and restoration of peatlands has grown in recent years.

Disturbances by peat extraction:

In the St. Lawrence Lowland region of Canada, considerable attention and research has been focused on bog conservation. Horticultural peat extraction has disturbed more than 63% of this area (Pellerin 2003). *Sphagnum* peat is used in horticulture because its physical properties make it a good artificial growing environment. It has the advantage of good retention of water and air, high availability, a stable substrate and a low cost (Caron 2001). Two methods of extraction are used: manual and mechanical harvest. The manual method extracts the peat in blocks. The sites manually harvested are rapidly recolonized by vascular plants, but are poor in *Sphagnum*. Currently, with the improvement of mechanical activities and drainage techniques, the peat is harvested with vacuums that extract a fine layer each year. To facilitate access by heavy machinery the water table level must be lowered by drainage. In these sites, because of the lower water table, the hydrological fluctuations are more important and *Sphagnum* mosses are almost completely absent (Rochefort 2001). After disturbances, such as lowering of the water table by drainage and peat mining, bog-inhabiting plants have poor ability to re-establish on abandoned lands, which makes natural regeneration difficult and slow. This, in turn, has a major impact on biodiversity and species distribution (Maltby 1997, Price 2001). Restoration efforts are necessary for the renewal of peat accumulation and normal hydrology.

Bog restoration:

Restoration of a damaged bog should allow recovery of characteristics specific to ombrotrophic peatlands and should support a complete species spectrum (Rochefort 2000). The restoration techniques developed and currently used in Canada to re-establish a plant cover dominated by peatland species and a stable water table near the surface in a mined bog require several steps (Quinty and Rochefort 2003). Initially, the field must be prepared by reshaping fields that were previously profiled for drainage and peat extraction, by flattening them to avoid water runoff. Depending on the plant species already established on the site, some will be removed and others preserved (Rochefort 2000). Then plant materials (diaspores - considered here as any part of the plant capable of growing as a new plant: seeds, spores, leaves, stems, roots, etc.) (Quinty and Rochefort 2003) are collected from natural remnants or other peat bogs and spread over the restoration site (Gorham and Rochefort 2003). A large amount of those diaspores are *Sphagnum* spp. (Rochefort and Bastien 1998), but other mosses, *Eriophorum* (cotton grass) (Cyperaceae) and ericaceous shrubs (Ericaceae) are necessary for a successful restoration of the plant community (Quinty and Rochefort 2003). The plant diaspores are mulched with straw for optimal moisture conditions (Price *et al.* 1998) and drainage ditches are blocked to re-establish the water table at the site (Wheeler and Shaw 1995). Fertilization is the last step to increase the success of restoration (Ferland and Rochefort 1997). One of the goals of restoration is to re-establish a similar faunal organization (Gorham and Rochefort 2003); this means restoring a species or a trophic assemblage similar to the assemblage before human activities. Although, the physical characteristics and flora are actively restored in abandoned sites, no animals are actively reintroduced in the restoration process. The question is: if we facilitate colonization by plants by seeding them, will insects come back on their own without further facilitation? In North America, other than the study of Mazerolle *et al.* (2006) on the faunal recovery of aquatic arthropods in man-made bog pools in southeastern Canada, and studies on faunal recruitment of aquatic macroinvertebrates after restoration of wetlands (Keiper *et al.* 2002; Stanczak and Keiper 2004; Steinly 2004, Wrubleski 2005), the effects of restoration or disturbances on terrestrial arthropods colonizing the exposed substrate are largely unknown. Brady *et al.* (2002) investigated if inoculation and stocking of poorly dispersing taxa could facilitate the establishment in wetland restored areas. They found that in the short term assistance can facilitate the recruitment of some selected taxa that led to communities that approximate those of natural wetlands and differ from those of unassisted restored areas. Other studies (Howick *et al.* 1992, Ferrington *et al.* 1994, Brown *et al.* 1997) have attempted inoculation from natural ecosystems, although as in Brady *et al.* (2002), the results are ambiguous due to low replication, few target taxa, small area treated and short duration.

Insects in peatlands:

Bog insect inhabitants are adapted to specific conditions, can be obligatory associates or characteristic of bogs (Spitzer and Danks 2006) and a study in Alberta (Finnamore 1994) found that arthropods represent 77% of all species compare to 16% for plants and 6% for vertebrates. However the terrestrial insect fauna of peatlands has not yet been studied in detail and responses to anthropogenic disturbances are poorly understood. Insects play significant roles as recyclers, consumers, decomposers and prey for higher trophic levels. Insects have a high rate of population increase and have a short generation time, characteristics that imply rapid response to environmental disturbances (Kim 1993). Ecological studies of peatland restoration and monitoring in Quebec have focused on vegetation (Pellerin and Lavoie 1999, Pellerin and Lavoie 2003, Lachance and Lavoie 2004), birds (Calmé and Desrochers 2000, Calmé *et al.* 2002), aquatic arthropods (Mazerolle *et al.* 2006), amphibians (Mazerolle 2005) and microfauna (Andersen *et al.* 2006). Even though higher Diptera have important ecological roles, they have been excluded from most peatland conservation studies.

Species richness and abundance of higher Diptera can be high in wetlands (Keiper *et al.* 2002, Beaulieu and Wheeler 2002, Foote 2004). The families Empididae (Barták and Rohácek 1999), Dolichopodidae (Rampazzi 2002), Chironomidae (Wrubleski 1987), Sphaeroceridae (Marshall 1994), several acalyptrate families (Rohácek and Máca 1982, Rohácek *et al.* 1998) and biting flies (Lewis 1987) have been inventoried from a variety of peatlands around the world. Blades and Marshall (1994) surveyed the terrestrial arthropod fauna associated with substrate (pan trap collection) of Southern Ontario peatlands and found 50 families of Diptera, representing 522 species. The most species rich families of higher flies were, in decreasing order: Sphaeroceridae, Dolichopodidae, Tachinidae, Sarcophagidae, Empididae, Syrphidae, Chloropidae and Ephydridae. By using multiple families of Diptera representing different trophic and ecological groups, community responses are more likely to represent all possible responses to changes in environmental variables (Morris 2000; Woodcock *et al.* 2003).

Ecological diversity of peatland Diptera:

Habitat selection of higher Diptera (Brachycera) is, in part, determined by their wide diversity of feeding habits among phytophagous, saprophagous, predaceous and parasitic groups; thus groups might respond differently to disturbances or restoration. Higher Diptera are associated with a variety of peatland habitats that can be terrestrial, semi-aquatic or aquatic: mud shores, vascular plants, decaying organic matter, emergent vegetation, macrophytes, algal mats (Ferrar 1987, Keiper *et al.* 2002). The plant assemblages and hydrology of an ombrotrophic peatland are potentially heavily influenced by human activities, especially by drainage and peat mining.

Phytophagous flies are intimately tied to their host plant and the large majority feed internally as, for example, stem-borers, leaf-miners and/or flower consumers (Ferrar 1987). Changes in the plant community might have a strong effect on specialized phytophagous Brachycera by restricting their occurrence to habitats that support their host plants. Some species of Scathophagidae mine the stems of a variety of wetland-inhabiting graminoid genera such as *Carex, Scirpus, Juncus* and *Glyceria* (Wallace 1971, Keiper *et al.* 2002). Many Ephydridae are specialized for feeding on floating algal mats (Foote 1995) or are leaf miners on a variety of grasses and wetland monocots (Deonier 1971). Some species of Agromyzidae, Chloropidae, Anthomyiidae, etc. are monophagous, limiting their choice to a single host plant or to species in one genus to feed or to lay their eggs. Agromyzids attack a great variety of wetland monocots and dicots as stem miners, stem borers or seed predators (Spencer 1969). Chloropid larvae feed as stem borers in several *Carex* species (Rogers *et al.* 1991). On the other hand, polyphagous Diptera may be less affected in their distribution by changes in the vegetation cover. *Hydrellia griseola* (Fallén) (Ephydridae) has known hosts from 15 plant families (Deonier 1971).

Saprophagous flies feed on decaying plant or animal matter, therefore may influence the decomposition rate of habitat supporting them. As plant materials decompose, detritus consumers tend to increase on this material (Batzer and Wissinger 1996). Generalized scavengers such as species of sphaerocerids and ephydrids may not be affected in their spatial distribution by changes in vegetation composition. However, many species of sphaerocerids may be attracted by muddy areas appearing after drainage (Keiper *et al.* 2002). Saprophagous species such as clusiids and lauxaniids may be positively affected by the increased rate of decomposition due to compaction and oxidation of the peat in drained sites. The larvae of the genus *Fletcherimyia* Townsend and the species *Sarcophaga sarraceniae* Riley (Sarcophagidae) specialize on living in peatland-restricted pitcher plants where they breed and feed on insects trapped in the plant (Farkas and Brust 1986). Several species of Chloropidae are secondary invaders of plant tissue damaged by other phytophagous larvae (Valley *et al.* 1969).

Predacious Diptera are indirectly linked with substrate quality and plants as they prey on invertebrates living internally or externally. Larvae of many Syrphidae and Chamaemyiidae prey on Aphidoidea (Homoptera) that infest plants and thus act as biological control agents (Ferrar 1987). Predators such as species of Dolichopodidae that prey on invertebrates in muddy substrates along ponds (Brooks 2002) and empidids that feed on other Diptera larvae may be indirectly affected by changes in environmental variables. The abundance of snails or slugs may be affected by fluctuations in hydrology (Plum 2005), thus affecting the abundance of sciomyzids that prey on them (Ferrar 1987). Larvae of some chloropids are reported to be predators of Homoptera, caterpillars and spider egg cocoons (Ferrar 1987). A great diversity of Tabanidae is found in Canadian peatlands (Lewis 1987) and their larvae feed on soft-bodied insect larvae and earthworms in the substrate (Teskey 1990).

Parasites and parasitoids live in close association with their host from which they obtain food or breeding sites. A variety of arthropod families feeding on plants are parasitized by flies. Caterpillars of Lepidoptera are the favoured host of Tachinidae, but Coleoptera and Hemiptera are also widely attacked (Ferrar 1987). Certain sarcophagids are obligatory or facultative agents of myiasis or parasitoids of other insects and invertebrates (Ferrar 1987). Larvae of all pipunculid species known are endoparasites of leafhoppers and a variety of Homoptera; they may be indirectly affected by environmental changes because they are generally specific to a host family or subfamily (Ferrar 1987).

Identification to species level is necessary in community ecology studies that incorporate Diptera in their data set, so that accurate functional diversity (diversity of organismal traits that influence ecosystem processes) can be determined. Some families and even some genera are well represented in a variety of trophic groups, while other families are limited to one trophic group. For example, the species of the family Chloropidae are found in the phytophagous group as stem-borers (Rogers *et al.* 1991), in the saprophagous group as secondary invaders of damaged plant tissue (Teskey *et al.* 1976), in the parasitic group as parasites of Amphibia and in the predacious group as predators of other insects (Ferrar 1987). In contrast, all species in the family Tachinidae are parasitoids of insects and other arthropods (Stireman *et al.* 2006).

Peatland associated Diptera:

Some Diptera species are abundant and characteristic in peatlands, either because their larval or adult food resource or breeding media are restricted to or characteristic of peatlands.

Marshall (1994) identified 73 species of Sphaeroceridae in Canadian peatlands of which 15 were considered characteristic of peatlands. Six species in the genus *Spelobia* Spuler are associated with peatlands: *S. pappi* Rohácek, *S. acadiensis*

Marshall, *S. nana* (Rondani), *S. ibrida* Rohácek, *S. bispina* Marshall *and S. algida* Marshall. *Pteremis wirthi* Marshall and *Pseudocollinella abhorrens* Rohácek are the single bog-associated species found in these genera. Two species in the genus *Phthitia* Enderlein are associated with fens and bogs; *P. quadricercus* Marshall and *P. ovicercus* Marshall. Three species in the genus *Pullimosina* Rohácek live in close association with peatlands: *P. (Dahlimosina) dahli* (Duda), *P. geminata* Marshall and *P. (Dahlimosina) bladesi* Marshall. Two species from the genus *Ischiolepta* Lioy are considered as peatland associates: *I. barberi* Han and Marshall and *I. lama* Han and Marshall.

Smaller numbers of species in other families are also known to be associated with peatlands. Two species of Sarcophagidae found in Canada, *Fletcheromyia fletcheri* (Aldrich) and *Sarcophaga sarraceniae* Riley, are indicators of the presence of the peatland-restricted pitcher plant *Sarracenia purpurea* Linné (Farkas and Brust 1986). In the family Tabanidae (Teskey 1969, Teskey and Burger 1976), the genus *Hybomitra* Enderlein has a number of species that are considered characteristic of bogs: *H. minuscula* (Hine), *H. hinei* (Johnson), *H. sodalis* (Williston), *H. trepida* (Mcdunnough), *H. typhus* (Whitney) and *H. pechumani* Teskey and Thomas. The genus *Atylotus* Osten Sacken contains three species whose larvae are found in *Sphagnum* bogs or fens: *A. sphagnicolus* Teskey, *A. sublunaticornis* (Zetterstedt) and *A. thoracicus* (Hine). The genus *Tabanus* Linnaeus has several species associated with peatlands: *T. fulvicallus* Philip, *T. nigripes* Wiedemann and *T. novaescotiae* Macquart. In the family Lauxaniidae, Miller (1977) considered *Homoneura sheldoni* (Coquillett) a usual inhabitant of bogs. In the family Empididae, many species of the genus *Rhamphomyia* Meigen appear to be characteristic of peatlands (Barták and Rohácek

1999), although in Canada there is still a large number of undiscribed species and there is a lack of identification tools for the described species. In addition to the above known Diptera species, there is probably a large number of peatland associates still to discover and the status of a large number of species is unknown because of insufficient ecological knowledge.

Objectives:

Diptera are abundant and diverse in peatlands, occupy a wide range of ecological roles (including a number of bog specialists), have a large range of body sizes and may exhibit different colonization and dispersal abilities depending on size, flight ability and ecological traits; all these qualities make them suitable target organisms for a study of effects of human activities and habitat restoration. The principal objectives of this study were to: 1) determine the effects of peatland restoration on species diversity, functional diversity and community structure of Brachycera in comparing three treatments (sites restored in 1999-2000, natural sites and abandoned mined sites) of three bogs in southeastern Quebec; and 2) establish the relationship between Diptera diversity and environmental variables (vegetation cover, pH, field moisture and peat chemistry) within the three treatments.

Hypotheses and Predictions

Hypothesis 1:

Species/functional composition and diversity of the restored sites should be intermediate to that in natural sites (positive control) and abandoned sites (negative control). Disturbances can alter fly community composition (King and Brazner 1999) and cause densities of certain taxa to increase or decrease. The natural bog area should have the higher species richness, because species diversity of terrestrial arthropod communities has been usually found to be positively correlated with habitat complexity (Siemann *et al.* 1998; Siemann 1998). Habitats with higher species richness should also have a greater functional diversity, because a large number of species exhibit a large number of traits. Anthropogenic disturbances in the abandoned sites should have significantly reduced species richness, decreased evenness, diminished functional diversity and allowed establishment of a different Brachycera assemblage compared to the natural site. Peatland's abiotic characteristics and flora should have recover to a certain point since seven years after the restoration process, so Diptera species associated with these environmental conditions should re-colonize from the surrounding area. The natural area probably acts as a source of colonists in the restored site. Phytophages, predators, saprophages, parasites and omnivores react differently to changes in the environment in a manner related to their feeding habits. So, it is reasonable to predict that Diptera assemblages should be influenced by the modification of their habitat.

Hypothesis 2:

Vegetation cover and/or abiotic site characteristics (pH, soil moisture and peat chemistry) will explain the differences in Diptera species and functional diversity among restored, natural and abandoned bog sites. The environmental variables outlined above are the most susceptible to differ among sites because of disturbances by peat extraction and the restoration processes. The differences in species and/or functional diversity will be explained by different variables among the three treatments because of differences in the habitat's physical properties. The spatial distribution of some Diptera taxa is restricted to particular plant species, plant density and substrate type (Keiper *et al.* 2002). Rochefort *et al.* (2003) estimated that a significant number of characteristic bog plant species can be established in 3-5 years following the period of restoration. Therefore, we can predict that the environmental conditions will be more similar between the restored and the natural sites, so the species associated with natural peatlands will be able to become established in the restored sites. The presence of nearby natural peatland areas may facilitate the recovery of a characteristic fauna in the restored areas, by providing a source of colonists (Keesing and Wratten 1998).

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CONNECTING STATEMENT

The impact of peatland restoration on insect assemblages is poorly known in Canada. Most studies have determined the restoration status based on flora, birds, aquatic arthropods, amphibians and microfauna. As described in Chapter 1, Brachycera (Diptera) are abundant and diverse in peatlands, play major ecological roles, include a number of bog specialists, display a large range of body sizes, dispersal ability and ecological tolerance. All these qualities make them suitable target organisms for a study of restoration ecology. The comparative study discussed in Chapter 2 is a contribution to the knowledge of peatland faunal recovery following restoration of mined sites. These data may be combined with data on other taxa to assess the success of the restoration technique used in Canada and the time needed for recovery of a fully functioning peatland ecosystem.

CHAPTER 2: DIPTERA ASSEMBLAGES IN MINED AND RESTORED BOGS IN EASTERN CANADA

ABSTRACT

Peatlands have been fragmented, drained and lost as a result of peat mining in southeastern Quebec. Natural regeneration of mined bogs is slow and difficult to achieve, this is why restoration of abandoned mined sites is an important tool for the re-establishment of ecosystem properties that existed prior to disturbance. Because renewal and reorganization of fauna cannot be taken for granted after the restoration process, the success of restoration was determined by assessing colonization of restored areas by Brachycera (Diptera) seven years after restoration of mined bogs. Species assemblages in restored sites were compared to those in nearby natural and abandoned-mined areas in three bogs, and environmental variables influencing community composition were identified. More than 22,000 specimens, representing 716 species, were collected from pan traps, sweeping and Malaise traps. The three treatment types were not significantly different in overall species composition of Brachycera, suggesting high resilience to disturbance. However, abandoned-mined areas generally supported lower species richness and evenness than restored and natural areas, which shown similar species abundance distribution; indicating that restoration enhanced the recovery of high species diversity and community structure. Analysing species by ecological traits (trophic groups and body size-classes) provided a different insight into the status of restored sites. The trophic and small size-class (<5 mm) composition in restored sites were similar to those in abandoned-mined sites. However, there was successful recolonization of predators and saprophages in restored sites, as shown by high species richness estimates. Species and trophic

composition were strongly linked to vegetation type and substrate quality. Species assemblages were mostly affected by the coverage of bare peat, *Sphagnum* mosses and ericaceous shrubs, while trophic assemblages were affected by variables directly linked to their feeding habits. Our results suggest that active restoration efforts are necessary for the renewal of high species and trophic diversity, although it is clear from observation of the environmental conditions, trophic structure and body size distribution that the restored sites are not fully functioning peatland ecosystems after seven years; however as the sites age they will probably tend toward a natural peatland.

INTRODUCTION

Canada has approximately 170 million ha of peatlands, and in the southern part of the country bogs are the dominant peatland type (Gorham 1990). These southern bogs are under considerable anthropogenic pressure through horticultural peat extraction, particularly prevalent in the St. Lawrence Lowland region of Quebec (Pellerin 2003). Peat mining leads to major ecosystem changes: the water table is lowered to dry the peat and to allow the bog surface to support tractors and vacuum extractors, living vegetation is eliminated, and a fine layer of peat is extracted each year by aspiration (Gorham and Rochefort 2003). Sites abandoned after multiple years of extraction have altered substrate stability (erosion and compaction) and quality (decomposition and nutrient availability) (Shouwenaars 1993, Campbell *et al.* 2002, Holden *et al.* 2004).

Because natural regeneration of mined bogs is slow and difficult to achieve, restoration of abandoned-mined sites is becoming an important tool for the re-establishment of ecosystem properties and functions that existed prior to disturbance; these properties include normal hydrology, biotic composition and biogeochemical cycling (Rochefort *et al.* 2003). The restoration approach used in Canada was developed to assist in the recovery of abiotic and biotic characteristics, re-establish a stable water table and a plant cover dominated by native peatland species. Drainage ditches are blocked to raise and stabilize the water table near the surface, fields are re-profiled by flattening the peat surface to avoid water runoff and fertilizers are applied to facilitate growth of plants. The plant community is actively re-introduced by spreading fragments of *Sphagnum* L. species, other mosses, *Eriophorum* L. (cotton grass) (Cyperaceae) and ericaceous shrubs; which were previously harvested from natural remnants or other peat bogs. The growing environment is improved by mulching with straw to protect plant fragments from desiccation (Quinty and Rochefort 2003).

Because plants are actively re-introduced; emphasis has often been placed on monitoring the success of vegetation establishment in peatland restoration (Pellerin and Lavoie 1999, Campeau *et al.* 2004, Chirino *et al.* 2006). Although animals have not been actively introduced in the course of these restoration projects, the colonization of birds (Desrochers *et al.* 1998), aquatic arthropods (Mazerolle *et al.* 2006), amphibians (Mazerolle 2005) has been monitored. Microbial establishment has also been assessed (Andersen *et al.* 2006). The key question is if we facilitate colonization by plants by seeding them, will the fauna re-establish without further facilitation? There is little knowledge on how terrestrial arthropod assemblages react to the reintroduction of peatland associated plant communities and normal ecosystem properties, even though arthropod species represent 65% of the world's biological diversity (Groombridge 1992) and have a significant impact on ecosystem processes. The focus of this study is on higher Diptera (Brachycera), because this is an important group in peatland biodiversity and ecosystem function. Brachycera species exhibit a great diversity of functional groups, include a number of bog specialists, are species rich and abundant, and thus may display a broad array of responses to environmental changes (Cameron 1972, Blades and Marshall 1994, Marshall 1994, Keiper *et al.* 2002, Spitzer and Danks 2006).

Recovery from disturbance was defined as the reestablishment of community structure and functions to pre-disturbance level (Wallace 1990). Recovery of disturbed and restored sites may be slow and unpredictable, mainly if the source of colonists is distant and isolated. Disturbances can alter community composition (King and Brazner 1999) and cause abundance of certain taxa to increase or decrease. Most theoretical and experimental studies suggest that a more diverse environment should support a greater number of species (e.g., Rosenzweig 1995, Siemann 1998, Perner *et al.* 2003). Therefore, a higher number of microhabitats, usually associated with high plant diversity, high plant structural heterogeneity and/or different substrate types, should sustain a higher diversity of species with different ecological requirements.

Taxonomic analyses should be coupled to functional analyses, because pooling taxonomically different species into similar functional groups can reveal different effects of human activities and environmental conditions (Boström *et al.* 2006, Petchey and Gaston 2006). Changes in plant quality and quantity are likely to influence phytophagous insect diversity and this should cascade up to higher trophic levels, by indirectly or directly affecting the diversity and distribution of parasites and predators (Hunter and Price 1992, Siemann *et al.* 1998, Brose 2003). Saprophages are dependant on decaying plant or organic matter, and thus may be influenced by the rate of decomposition and soil characteristics of the habitat that support them (Rotheray *et al.* 2001, Keiper *et al.* 2002).

It is important to determine if similar species communities and/or similar trophic assemblages can be recovered following peatland restoration. Because establishment of species in restored sites depends on biotic and abiotic habitat constraints, the main objectives of this study are to determine (1) the effects of peatland restoration on species diversity, functional diversity and species composition of Brachycera in natural bogs, restored bogs, and abandoned-mined bogs in southeastern Canada; and

(2) the extent to which Brachycera diversity is associated with environmental variables (abiotic and biotic) within the three treatments.

MATERIALS AND METHODS

Study area and sampling sites:

The study was conducted in three bogs that have been, or are still being mined using the vacuum technique (Rochefort 2001), in the lowlands of the St. Lawrence River estuary, Quebec (Figure 2.1). These sites were chosen because they each contain a section that was abandoned after vacuum peat extraction, a section that was restored in 1999-2000 by the Peatland Ecology Research Group (PERG) and a natural section that has not been subject to obvious disturbances.

Bois-des-Bel bog (BB) (47°57' N, 69°25' W) has an area of 187 ha. From 1972 to 1980, a 11.5 ha section was mined. One section (8 ha) consisting of eight peat fields of 30 x 240 m was restored in 1999-2000, and an abandoned-mined area of 3 ha (two peat fields of 30 x 240 m) was kept as a control zone (*public communications*).

Chemin-du-Lac bog (CL) (47°45' N, 69°31' W) is part of the Rivière-du-Loup peatland, the largest bog in this region. Several sectors are still mined, but a 12.78 ha area was abandoned in 2000 and used in this study. Eight sections were restored from 1997 to 2004, although only those restored in 1999 (3 ha) and 2000 (4 ha) were used as restored sites in this study.

St-Charles bog (SC) (46°45' N, 70°59' W) has an area of 1306 ha with sections still mined. Four sections were abandoned in 1983, 1986, 1990 and 2000-2001 and one peat field (30 x 220 m) was restored in 1999. The section abandoned in 1986 was used in this study, because the others were re-opened for extraction in 2006.

Insect sampling and processing:

The bogs were sampled from 01 June to 29 July 2006. Each sample plot was 30 x 220 m in size. In each of the nine sampling sites, two sweeping transects and five yellow pan traps were installed. Each transect was sampled for Diptera using 60 sweeps of a sweep net. Sweep samples were collected every 7-8 days. The five pan traps were placed 20 m apart on a 80 m transect in the center of the sites and emptied every 7-8 days. Traps consisted of yellow plastic bowls placed in the soil with their upper rim flush with the ground surface and filled with salt water, propylene glycol and a drop of liquid detergent as a wetting agent. One Malaise trap was also installed in each site for three days consecutively during the second, fifth and eighth weeks.

Insects were preserved in 70% ethanol. Small flies were dried using hexamethyldisilazane; while larger flies were transferred into ethyl acetate, then pinned and air-dried. Specimens were deposited in the Lyman Entomological Museum (McGill University, Ste-Anne-de-Bellevue, QC.). All specimens of Brachycera, except the families Phoridae and Anthomyiidae, were identified to named species, if published taxonomic keys or taxonomic expertise was available, or to numbered morphospecies.

Species were classified into ecological groups according to body size and trophic group, to assess functional diversity; defined here as a component of biodiversity that is measured with organismal traits that influence ecosystem processes (Tilman 2001, Petchey and Gaston 2006). Diptera species were divided into three size classes: small (<5 mm), medium (5–10 mm) and large (>10 mm). The trophic group was determined at the larval stage for each species, since that stage is the dominant feeding part of the life cycle. Species were placed in one of six trophic groups and 14 subgroups (Appendix 2.1) (based on Beaulieu and Wheeler 2001) according to information given in Ferrar (1987) and other available literature. Given that Brachycera exploit a wide range of breeding media, the trophic group classification was based on families most likely to be encountered in peatlands (Rohácek and Máca 1982, Ferrar 1987, Blades and Marshall 1994, Marshall 1994, Rohácek *et al.* 1998, Barták and Rohácek 1999). Species not assigned to a trophic subgroup, either because they were reared from a variety of media or because their precise food resource was unknown, were pooled together in their main trophic group. Species for which the trophic group is unknown were excluded from analyses.

Habitat and vegetation variables:

Vegetation cover was quantified using the Braun-Blanquet scale (Goldsmith *et al.* 1986): 0 (less than 1%); 1 (1-5%); 2 (6-25%); 3 (26-50%); 4 (51-75%); 5 (76-100%) to estimate the percent cover of each of the following strata: *Sphagnum* mosses, other mosses, lichens, herbs, ericaceous shrubs, grasses and sedges, horsetails, bare peat and open water. Overlap in layers was included; this means that total cover for all strata may exceed 100%. Soil moisture was described qualitatively using the following scale: 0 (very dry, soil cracking); 1 (dry); 2 (moist); 3 (water table at surface); 4 (water table above surface).

Total N, P, K, Ca, Mg, Fe, Mn, Na concentrations and pH were measured from one peat sample (25 cm x 25 cm and 3 cm deep) collected in the center of each site. A subsample of 250 ml was separated for pH analysis and the fresh homogenized material was immediately frozen. For N as NO_3 and N as NH_4 concentrations, a KCl extraction was performed on wet samples and analysed by colorimetry. For total concentrations of P, K, Ca, Mg, Fe, Mn, Na, defrosted samples were dried at 65°C in an air oven for 2-3 days. For pH analysis, the subsamples at air temperature were saturated with deionised water and measured with a pH-meter directly from the saturated samples. Soil analyses were conducted at the Soil Science Laboratory, McGill University.

STATISTICAL ANALYSES

Because pan traps were occasionally disturbed by animals or wind, analyses were based on four pan trap replicates per treatment per week instead of five. For weeks in which five pan trap samples were available, one trap per treatment was randomly omitted from the analyses. Species abundance data from each trap type in each sampling week were pooled for each treatment per site. The species composition in each trap type (Malaise trap, pan trap and sweeping) is different and complementary to each other (Fast 2003), which support the use of a variety of methods to sample an accurate portion of the biodiversity. Intra-site comparison was done to compare diversity, dominance and composition in the three treatments, to account for regional variation in species composition.

Sampling efficiency for Brachycera species was examined using rarefaction curves (Gotelli and Colwell 2001). If the curves reach an asymptote, it can be assumed that most species present in the site have been collected (Magurran 2004). Overall species richness and species richness of the dominant trophic groups of each treatment per site were calculated using rarefaction estimates standardised to the lowest number of individuals collected in any of the three treatments in each study site. Individual-based rarefaction was used because the number of individuals collected may differ among study areas (Gotelli and Colwell 2001). Rarefaction curves also function as a diversity index because both species richness and abundance are incorporated (Olszewski 2004). Rarefaction curves based on 1000 permutations with species richness as a diversity index were generated using ECOSIM version 7.0 (Gotelli and Entsminger 2001). Simpson's diversity index (Simpson 1949) was also calculated for Brachycera species for a measure of dominance by treatment type using EstimateS version 7.5 (Colwell 2005).

In addition to rarefaction curves, the total estimated species richness was calculated in each treatment per site using a non-parametric estimator, the abundance based coverage estimator (ACE). Non-parametric estimators are preferred to parametric estimators because they are not based on a fitted species abundance model, but on the underlying distribution (Magurran 2004). ACE extrapolates to estimate how many species would be found in a larger set of samples from the same assemblage based on the rare species (=10 individuals in total). Compared to other indices that consider the number of singletons and doubletons, ACE is considered to provide a conservative estimate of species richness (Colwell 2005). ACE was calculated using EstimateS version 7.5.

Species abundance data of each site were plotted as a rank/abundance graph from most to least abundant and abundances displayed in a Log_{10} format. To examine community structure of the three treatments, Brachycera species abundance data were fitted to a truncated log normal distribution with the truncation point at 0.5 (May 1975), a log series distribution (Fisher 1943) and a geometric series distribution using the Kolmogorov-Smirnov (Sokal and Rohlf 1995) goodness of fit test for $P = 0.05$. Although those three models are only a subset of the models that can be applied, they are the most commonly used (Tokeshi 1993, Magurran 2004). For the log series and truncated log normal models, abundance data are assigned to abundance classes (Log_2 and Log_{10} respectively) and the goodness of fit test is used to evaluate the relationship between the observed and expected frequencies of species in each abundance class (Magurran 2004). To test the geometric series fit, the expected number of individuals for each species was compared to the observed number using the goodness of fit test. Pair-wise comparison of rank/abundance plots of treatments in each site was done with the kolmogorov-Smirnov two-sample test (Sokal and Rohlf 1995) for $P = 0.05$.

Community composition was analysed on multiple taxonomic and ecological groups based on log-transformed relative abundance of species represented by three or more individuals. Community composition was first analysed for all Brachycera species, and analyses were repeated for three subordinate groups of Brachycera (Lower Brachycera + Aschiza, Acalyptratae and Calyptratae). The species composition of subordinate taxa was considered separately because phylogenetically close taxa often have similar life-history and resource bases (Tokeshi 1993). Community composition was also analysed for each size class and each trophic group. Community composition among the three treatments was compared using non-metric multidimensional scaling

(NMDS) and multi response permutation procedures (MRPP). For NMDS, an initial 6-dimensional analysis was done stepping down in dimensionality until the number of ordination axes was sufficient to achieve low stress values. For the final ordination, the *n*-dimensional Sorenson ordination with 500 iterations was used as the starting configuration. A Monte Carlo test with 100 runs was performed to determine the validity of the final configurations. A Sorenson distance metric was applied to each MRPP, in a similar fashion to the NMDS ordination to test for pair-wise differences in species composition between treatment types. These analyses were performed using the program PC-ORD version 4.36 (McCune and Mefford 2005).

To determine the associations of particular Brachycera species or trophic groups with treatment type, indicator species analysis (Dufrêne and Legendre 1997) was performed on log-transformed abundance of species with 3 or more individuals using PC-ORD version 4.36. Only species/trophic groups with more than 10 individuals, a significant p-value (=0.05) assessed using a Monte Carlo randomization test based on 1000 permutations and an indicator value (IndVal) greater than 50 were considered as indicators for a treatment.

To reduce the number of environmental variables, two principal component analyses (PCA) were performed with PC-ORD to condense the peat chemistry and vegetation cover variables. To produce a standardized PCA, cross-products matrix containing Pearson correlation coefficients were used. From each PCA, the first three axis scores explaining most of the variance were used as independent variables in the subsequent multivariate analysis.

The log-transformed relative abundance of species represented by three or more individuals and the log-transformed abundance of the 18 trophic subgroups were analysed in relation to eight variables (Peat1, Peat2, Peat3, Vege1, Vege2, Vege3, pH and field moisture). When abundant species were plotted against environmental variables, a tendency for unimodal distribution was observed, supporting the choice of Canonical Correspondence Analysis (CCA). Axis scores were centered and standardized to unit variance. A Monte Carlo test based on 200 runs was used to assess the significance of the axis eigenvalues. The null hypothesis was that there is no relationship between the environment and species matrices. The multivariate analyses were performed with the program PC-ORD version 4.36.

RESULTS

Diptera species:

Pooled taxa — A total of 22,226 Brachycera individuals in the target families was collected, of which 20,653 individuals representing 711 named species and morphospecies were used in the analyses (Appendix 2.1). Many of those species were collected in low numbers; between 39 and 50% were represented by only one specimen in each treatment. The rarefaction curves for all treatments per site did not reach an asymptote (Figure 2.2 A, B, C); and ACE suggested that between 15 and 41% of the species present in the treatments remain to be collected. The most species rich families were Dolichopodidae (85 species), Muscidae (75 species), Empididae (64 species), Chloropidae (61 species), Tachinidae (61 species) and Syrphidae (53 species).

The greatest number of specimens was collected in the abandoned-mined treatments in each site, the restored treatments were intermediate and the natural treatments were the lowest in relative abundance (Table 2.1). Simpson's diversity index, a measure of dominance, was lower in each of the abandoned-mined treatments indicating that the high number of specimens was due to one or two species constituting a large proportion of the total abundance. In BB, the diversity (rarefaction estimate) of the restored treatment was not significantly different than that in the natural treatment, but was significantly higher than that in the abandoned-mined treatment. In CL, the diversity of the restored treatment was significantly lower than that in the natural and abandoned-mined treatments, which were not significantly different from one another in diversity. In SC, the restored treatment had the highest diversity, followed by the natural, then the abandoned-mined treatments (Table 2.1). Indicator species analysis revealed that two species were significantly associated with natural sites and four species with abandoned-mined sites; none were associated with restored sites (Table 2.2).

All the data sets did not fit any of the three abundance distribution models tested (truncated log normal, log series and geometric series). The Kolmogorov-Smirnov two-sample test shown that the restored and natural treatments exhibited similar species abundance distribution in all sites (BB: $D=1906.4$, $D_{0.05}=5053.8$; CL: $D=2124.0$, $D_{0.05}=3425.3$; SC: $D=1762.7$, $D_{0.05}=6743.8$). The restored and abandoned-mined treatments were significantly different in species distribution pattern in all sites (BB: $D=9801.1$, $D_{0.05}=6254.1$; CL: $D=7859.4$, $D_{0.05}=5954.0$; SC: $D=18812.2$, $D_{0.05}=7036.0$). The natural and abandoned-mined treatments showed significant differences in species abundance distribution in BB ($D=9284.5$, $D_{0.05}=5580.3$) and SC

($D=13750.5$, $D_{0.05}=5511.2$) and no significant differences in CL ($D=4972.8$, $D_{0.05}=6049.2$). As shown by the rank/abundance curve (Figure 2.3), the abandoned-mined treatments had one or two very dominant species in all sites.

The species assemblages of the three treatments clearly clustered together in each site as shown by NMDS ordination (Figure 2.4) and this was supported by the non significant p-values obtained with MRPP comparisons (Table 2.3). However, the overall regional assemblage of species was significantly different between the three peatlands ($P = 0.0018$).

Subordinate taxa of Brachycera — In separate analyses of the three subordinate groups of Brachycera, only the acalyptrates showed a different pattern of distribution among the three treatments. The restored and the abandoned-mined treatments were characterized by similar assemblages of acalyptrate species as indicated by MRPP comparisons. In contrast, the natural sites showed significant differences in acalyptrate assemblages with both restored and abandoned-mined sites (Table 2.3). In the acalyptrate taxa, 93% of the species were in the small size-class.

Ecological groups:

Size classes — Within each treatment, the small size-class had the most individuals, followed by the medium size-class and the large size-class (Figure 2.5). The relative abundance of the small size-class decreased from the abandoned-mined, to restored to natural treatments. With the size class comparisons, significant differences in species composition were detected from the small sized species among natural and abandoned-mined treatments and differences were marginally significant between natural and restored treatments. Therefore, the composition of the small size class of the restored treatments was similar to that in the abandoned-mined treatments (Table 2.3). The species richness of the small size-class in the restored treatments was either intermediate to that in the natural and abandoned-mined treatments or higher than the natural treatments. The higher number of specimens in the abandoned-mined treatments was due to *Scatella stagnalis* (Fallén) and *Chrysotus* spp. which made up a large proportion of the total Brachycera assemblage in those sites (Appendix 2.1).

Trophic Groups — The trophic group and subgroup for each species are given in Appendix 2.1. Local assemblages in each treatment were dominated by predators and saprophages, followed by phytophages. There were relatively few parasites or omnivores. The relative abundances of saprophages and predators decreased from the abandoned-mined, to the restored to the natural treatments (Figure 2.6). The species diversity in the restored treatments for the predator group was either not significantly different from the other two treatments (BB), intermediate between the abandoned-mined (highest diversity) and the natural (lowest diversity) sites (CL) or significantly higher than the natural and abandoned-mined sites which were not significantly different (SC). Even though the saprophages were more abundant in the abandoned-mined treatments, the species richness was lower than in the restored and natural treatments, particularly so in SC (Table 2.4). The lower evenness in the abandoned-mined treatments were due to two saprophagous species, *Scatella stagnalis* (CL, SC) and *Paramyia nitens* (Loew) (BB), which accounted for a high proportion of individuals. Only the substrate saprophages (SAsu) showed discrimination among the three treatments; they were a good indicator of the abandoned-mined treatments (Table 2.2). The trophic assemblages in the restored and abandoned-mined treatments were not significantly different from one another, as shown by MRPP comparisons, but both were significantly different from the natural treatments (Table 2.3).

Community composition and ecosystem properties:

The NMDS ordination (Figure 2.7) showed that the three treatment types significantly differed in the environmental variables measured (Appendix 2.2, 2.3) and this was supported by the MRPP comparison ($P = 0.001$). The environmental conditions in the restored treatments were intermediate to that in the natural and abandoned-mined treatments.

In the first PCA on peat chemical data, the first three axes explained a total of 80% of the variance in the data. In the second PCA on the vegetation cover data, the first three axes explained 82% of the variance. Thus, little of the information contained in the environmental variables was lost with the three axes extracted from the PCA reduction. Those six PCA-axes scores along with the peat pH and the field moisture were used as independent variables in the CCA to determine the combination of variables that best explain the species and trophic distribution among the treatments. The variables with the highest eigenvector values for each axis are indicated on the CCA graphs.

The CCA explained 56.1% of the variance in Brachycera species composition (Figure 2.8). The graph of the CCA ordination depicts the first two axes explaining the largest amount of variation. The proportion of variance explained for each ordination axis was 24% for axis 1, 18.3% for axis 2 and 13.7% for axis 3. Axis 1 mostly separated the sites by Peat3 and Vege3 gradient, axis 2 separated them by Peat1 and Vege1 gradient, while axis 3 separated them by pH. Most of the Brachycera assemblages in the restored and abandoned-mined treatments were negatively related to axis 2, indicating a preference for a high coverage of bare peat where phosphorus, potassium and zinc were in lower concentrations. The assemblages in the natural treatments were associated with a high coverage of *Sphagnum* mosses and ericaceous shrubs.

The CCA explained 78% of the variation in trophic composition (Figure 2.9). Data are plotted on axis 1 and 3 to show the primary environmental gradient driving the separation of trophic assemblages. The proportion of variance explained for each ordination axis was 41.1% for axis 1, 21.3% for axis 2 and 15.6% for axis 3. Axis 1 was positively related with Peat3 gradient, axis 2 was negatively related with Vege3 gradient, while axis 3 was positively related to Vege1 gradient and negatively to pH. The distribution of predacious flies in dung (PRco) was mostly affected by peat chemical properties (Peat3). The mollusc predators (PRmo) and the substrate saprophages (SAsu) were mostly affected in their distribution by the coverage of bare peat (Vege1) and peat pH. The saprophages in leaf litter (SAlf) were positively associated and the necrophagous saprophages (SAne) were negatively associated with herbs and trees (Vege3). The fungivores (SAfu) were mostly affected by the peat chemical properties (Peat 3) and the type of vegetation (Vege3). The abundance patterns of stem-borers (PHsb) and flower consumers (PHfl) were mostly predicted by the coverage of other mosses, lichens and horsetails. The distribution of the other trophic groups was more evenly affected by a set of environmental variables, because they were plotted very close to the centre of the biplot.

DISCUSSION

The success of restoration has been identified in a variety of studies. Ecosystems are spatially and temporally heterogeneous (Bakler 2000) and incorporate a variety of organisms that respond differently to restoration, which makes clear demonstration of success not always straightforward. However, studies looking at one site per treatment are common in the field of restoration ecology (e.g., Williams 1993, Armitage *et al.* 2006) and higher-taxon level identification is often used in invertebrate studies. Results found in one site can only be appropriately applied to that site, and this limits the ability to make predictions of the important patterns and mechanisms governing successful habitat restoration at a broader scale (West *et al.* 2000). A preferred approach, as was used in this study, is to use true replicates, true controls and species level identification. By using true replication in multiple sites, the observed results are more unlikely to be due to an unusual set of circumstances or idiosyncracies of a particular site (Bisson *et al.* 2003). Comparison of restored sites should be based on more than one reference site (Ruiz-Jaen and Aide 2005) ranging from those with highest levels of functioning to those that are highly disturbed (Brinson and Rheinhardt 1996) and, when possible, on comparison with multiple other restored sites in the same habitat to capture the degree of spatial and temporal variation that exists. Comparing restored sites to disturbed sites and not only to natural sites, provides the advantage of giving a notion of the resilience of the community under study following perturbation; and when complete recovery is not achieved, it indicates the status of the restored site.

In our investigation, restoration of abandoned-mined sites enhanced the recovery of Brachycera fauna in Canadian eastern peatlands. Abandoned sites tended to have lower species richness, much lower evenness and lower species richness of saprophages when compared to natural and restored sites. Restored and natural sites were characterized by similar community structure. However, the recovery is not complete after seven years in terms of species and trophic composition. Small-size class, acalyptrate and trophic assemblages are still similar in restored and abandoned-mined sites, which were both distinct from natural sites. The environmental conditions clearly affected species and trophic composition, suggesting that the distinctiveness of the composition of restored sites compared to natural sites may be a consequence of the intermediate status of the environmental conditions. Nonetheless, the ongoing recovery of peatland characteristic plant species, peat chemical properties and substrate quality promote recolonization of restored sites by sustaining more species.

Effects of peat mining and restoration:

The species pool contained a range of species with a variety of environmental requirements and a range of tolerance to changing environmental conditions. The environmental changes favour some species and disfavour others, which causes compensatory shifts in abundance of species at the site (Brown *et al.* 2001). The abandoned-mined treatments were characterized by lower evenness and in two of the bogs (BB, SC) the species richness was lower than the natural and restored treatments. In SC, the much lower species richness in the abandoned-mined site may be due to the strong dominance of *Scatella stagnalis*, which thrives on bare peat (Foote 1995). The presence of that species probably also changed the occurrence and colonization patterns of other species (Drake 1991, Shurin and Allen 2001), especially small, saprophagous acalyptrates that might compete with S*catella stagnalis* for detritus and algae. The low species richness of saprophages in the abandoned-mined areas was compensated by high numbers of individuals of a few species within that group. This was supported by the indicator species analysis where *Scatella stagnalis* was an indicator of the environmental conditions found in the abandoned-mined areas and this species made up the highest proportion of individuals found in the SAsu indicator group. The species favoured by disturbance were already present in natural sites and they may have immigrated after disturbance from natural sites and became established earlier than other species, which may explain their dominance. The new conditions caused by peat mining are probably a subset of the pre-existing conditions found in the natural sites, so species that are not dominant in the natural sites are maintained at high levels of abundance by the new conditions in the abandoned-mined sites.

Restoration of native characteristics in areas previously altered by peat mining can result in the reestablishment of diverse Brachycera assemblages and normal community structure. Although it was not possible to fit an abundance model to any of the data sets, it appears that the species abundance distributions are similar in natural and restored sites and that restored sites have distinctive species distribution patterns to abandoned-mined sites. This mirrors the response of the Simpson's diversity measures, similar indices being found in natural and restored sites. Species richness also tended to be higher in those sites than in abandoned-mined sites. It is hypothesized that perturbation resets the successional stage of a community and similar patterns should emerge in increasingly stable environments (Death 1996). As found in other studies of restored systems, an increase in arthropod diversity was observed with time after the restoration efforts (Jansen 1997, Waltz and Covington 2004, Summerville *et al.* 2007).

Restored areas had altered guild structure, because the composition by trophic group was still similar to an abandoned-mined area. Among all trophic groups, spatial dissimilarities in the saprophage group and the predator group were the most pronounced. The species in those groups were very abundant in the abandoned-mined treatments and this was also seen at an intermediate level in the restored treatments. However, there was successful recolonization of saprophagous and predacious species in the restored areas, as suggested by the species richness estimates. A high number of species per functional group is more likely to ensure community functioning and sustainability over time of ecosystems (Peterson *et al.* 1998, Tscharntke *et al.* 2005). Comparing trophic composition, Williams (1993) found similar results after restoration of riparian woodlands; some functional groups were responding to restoration as quickly as within three years, while other groups were indicating potential problems. Thus, it can be expected that as the restored sites age and progress toward a natural peatland, the Diptera fauna will come to resemble that of nearby natural sites.

Restoration efforts have often assumed that providing the proper habitat will lead to the natural re-colonization of small organisms such as invertebrates, fungi and micro-organisms, without further facilitation (e.g., Moynahan 2002, Andersen *et al.* 2006, Mazerolle *et al.* 2006). In our study, all the indicator species were small sized acalyptrate species. The disturbance had the greatest effect on the distribution of small sized Brachycera species and the acalyptrate taxa (most of which are small, and which made up the great majority of the small size class); many of these species may have limited dispersal abilities, because adults of several acalyptrate species do not appear to fly readily or cannot disperse over long distances (T.A. Wheeler, *personal* *observations*). Because those species experience the landscape on a small spatial scale, they may be more susceptible to changes in resource availability. In a study conducted on soil micro-arthropods of post-mining rehabilitating sites, Kumssa *et al.* (2004) found that rehabilitation could enhance the recovery of assemblages, although it would take a long time. In the above study, as in the present study, colonization potential is a limiting factor for the rapid recovery of species assemblages.

Data collected seven years after the restoration of abandoned-mined peatlands demonstrated few differences in overall Brachycera species composition among the three treatments. This could be attributed to the resilience (capacity to reorganize after disturbance) (Holling 1973) of Brachycera in a mosaic of well connected different habitat types. The natural areas probably act as a source of colonists, because the three site types are within one kilometre of each other. In addition, as shown by the non-significant MRPP differences, the species with high dispersal abilities were able to recover from constructive and destructive human activities (Schowalter 2006). However, dispersal-limited species were not able to recover quickly following restoration. For disturbed sites to regenerate after a perturbation, natural bog habitats should be maintained in the same area (or nearby) to allow bog associated species to colonize the sites; so that the composition of species is not affected by the degree of connectivity between populations (Tscharntke *et al.* 2005) and the surrounding non-bog landscape. Those natural areas would be best directly connected to restoration sites without physical barriers to dispersal (Scott *et al.* 2001). In BB and CL, the restored and natural sites were adjacent to each other, but were separated by an edge of dense trees and drainage ditches. When restoration sites are isolated from a natural source of colonists, facilitation (inoculation or stocking) could be a useful method to maximize the development of normal communities. Some studies have investigated if inoculation (indirect addition of eggs, larvae or adults through addition of a soil sample taken from a natural site) and/or stocking (direct addition of adult specimens) of poorly dispersing invertebrate taxa could facilitate the establishment in restored habitats (Brown *et al.* 1997, Brady *et al.* 2002). They found that, in the short term, assistance facilitated the recruitment of some selected taxa, mainly Gastropoda, Hemiptera, Coleoptera, Odonata, Ephemeroptera and Diptera; that led to communities that approximate those of natural reference areas and differ from those of unassisted restored areas where applicable.

Rare species are more susceptible to disturbance (Gaston 1994), although little conclusion can be drawn from the high number of rare species in this study, because the lack of ecological knowledge and the few Diptera inventories done in peatlands do not allow differentiation between species whose rarity is caused by human activities and species whose rarity is caused by their natural life history (Tscharntke *et al.* 2002).

Effects of environmental conditions:

At the site scale, vegetation composition and substrate quality significantly influenced the distribution of species and trophic groups among the three treatment types. The distribution of saprophages was mostly affected by substrate quality. The muddy surfaces in the abandoned-mined areas correlated with the higher success of the ephydrid fauna (indicator species) and SAsu indicator group. The ephydrid species *Scatella stagnalis* and *Discocerina obscurella* are considered deposit feeders and consumers of algae (Foote 1995), thus the exposed damp mud surfaces are a more suitable habitat than the compact and difficult to access substrate in the natural areas. The composition of the litter changes radically after drainage; from *Sphagnum* mosses, sedges and shrubs it becomes essentially composed of bare peat (Laiho *et al.* 2003). The improvement of aeration within the upper peat layer (Silins and Rothwell 1999) exposes the organic matter to substantial aerobic microbial activities (Vasander and Laiho 1995), increasing the amount of material available for saprophagous species. A study conducted in Finland (Silvan *et al.* 2000; Laiho *et al.* 2001) also found changes in abundance and composition of soil animals following drainage. The number of invertebrates was clearly positively correlated with the lower water table. As in our study, it suggests that conditions in the abandoned-mined areas were more suitable for litter and nutrient recycling organisms and this was supported by the SAsu indicator group.

A correlation between a given environmental variable and a given species or trophic group can either indicate a direct (use by the species) or an indirect (use by the prey) relationship (du Bus de Warnaffe and Dufrêne 2004). Consequently, the mollusc predators and the predators in dung were present where their prey was most likely to be found. Therefore, as the restored areas had not undergone full transformation into a natural peatland, as shown by the multivariate ordination, the environmental conditions suitable to maintain a high abundance of saprophages and predator's prey, especially the higher pH and the presence of bare peat, are still present in a high proportion. In the natural sites, the two indicator species are both associated with vegetation and indicate the presence of particular plant species. *Paroxyna albiceps* (Loew) (Tephritidae) attacks the flower heads of multiple species of *Aster* L. (Asteraceae) (Novak and Foote 1968). This species was absent or rare (one individual in CD) in the restored sites indicating that these plants have not recolonized. *Minettia lupulina* Fabricius (Lauxaniidae) mines decaying Sugar Maple (*Acer saccharum* Marshall), Wild Cherry (*Prunus serotina* Ehrhart) and Black Spruce (*Picea mariana* (Miller)) leaves (Miller 1977). Here it is probably feeding on Black Spruce leaves, because this is one of the tree species dominating the forest cover in peatlands of the St-Lawrence Lowland region (Pellerin and Lavoie 1999, Lachance and Lavoie 2004).

A feedback exists between species/trophic composition and ecosystem processes, and after restoration these processes will recover over different time scales (Palmer *et al.* 1997). It is estimated that characteristic bog plant species can be established in 3-5 years following restoration, normal hydrology in approximately 10 years and the peat accumulation system in 30 years (Rochefort *et al.* 2003). From this study, it can be assumed that when looking at the entire Brachycera community, seven years were sufficient to recover a species community and a level of diversity (in two of the bogs) that characterised a natural bog, although this time period did not allow the trophic composition and the small size species to recover fully. More data are needed to assess the period of time needed to achieve complete recovery of invertebrate species assemblages in restored wetlands; because currently it ranges from four years (Stanczack and Keiper 2004) to more than 17 years (Streever *et al.* 1996).

Conservation implications:

When assessing the success of restoration, it is important to determine the desired endpoint of restoration; recovery of a species community similar to that before the disturbance or recovery of a trophic structure without regard to the species that compose it. Several studies have been done on a variety of scales and organisms in

Quebec's peatlands, although there is a lack of knowledge of which faunal species or trophic groups really matter to natural peatland functioning, and if the presence of particular species accelerates or slows down the recovery in the restoration process. Biotic interactions may induce variability between diversity and ecosystem functioning (Peterson *et al.* 1998) and the sequence of species following restoration may have an important influence on ecosystem performance (Elmqvist *et al.* 2003). Passive restoration projects are still in need of information on the distribution, demography, dispersion and dispersal of many species (Scott *et al.* 2001). Many insect species may occur only in bogs or are characteristic of bogs, although in North America the lack of taxonomic resolution, knowledge of ecological roles of species, and species-level inventories do not allow those species to be distinguished (Spitzer and Danks 2006). Given the decline of natural peatlands, details of the role of the fauna appear to be central in achieving sustainability for conservation and restoration purposes.

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Table 2.1: Raw species richness (S_{obs}), number of individuals (N), rarefaction estimates of species richness (S_{est}) (species ± SD, standardized at 1100 (BB), 1300 (CL) and 1400 (SC) individuals) and Simpson's diversity indices of total Brachycera in natural (N), restored (R) and abandoned-mined (A) treatments in the three study sites.

Site	S_{obs}	N	S_{est}	Simpson
BB-N	177	1198	169.94 ± 2.42	19.78
BB-R	207	1629	171.31 ± 4.87	17.38
BB-A	235	2486	159.34 ± 5.73	8.39
CL-N	180	1389	174.20 ± 2.3	12.14
CL-R	176	1531	162,15 ± 3.3	15.62
CL-A	255	2559	182.82 ± 6.18	9.03
SC-N	197	1514	190.57 ± 2.3	15.94
SC-R	271	2719	205.79 ± 5.76	16.08
SC-A	209	5628	112.85 ± 5.88	3.53

Table 2.2: Indicator species analysis of Brachycera species and trophic groups for natural, restored and abandoned-mined treatments in the three study sites. Only species/trophic groups with an indicator value (IndVal) greater than 50.0 and a significant ($P = 0.05$) indicator value are shown.

Species/ Trophic group	Number of individuals	Significant Association	IndVal	p-value	Trophic group
Paroxyna albiceps (Tephritidae)	22	Natural	100	0.040	PHfl
Minettia lupulina (Lauxaniidae)	66	Natural	51	0.040	SAlf
Cerodontha dorsalis (Agromyzidae)	12	Abandoned	85	0.036	PHlm
Oscinella sp.A (Chloropidae)	60	Abandoned	63	0.011	PH
Discocerina obscurella (Ephydridae)	25	Abandoned	100	0.036	SAsu
Scatella stagnalis (Ephydridae)	3503	Abandoned	85	0.036	SAsu
SAsu	3640	Abandoned	97	0.023	

Table 2.3: p-values for MRPP pairwise comparisons among treatments for each site, where Diptera are separated by taxa, size classes and trophic habits. Significant differences ($P = 0.05$) in species composition between treatments are in bold.

Treatments	**p (N-R)**	**p (R-A)**	**p (N-A)**
All Brachycera	0.30	0.70	0.085
Acalyptratae	**0.026**	0.42	**0.025**
Calyptratae	0.25	0.68	0.09
Lower Brachycera + Aschiza	0.77	0.83	0.58
Small size	0.055	0.64	**0.035**
Medium size	0.71	0.68	0.43
Large size	0.86	0.81	0.82
Trophic habits	**0.023**	0.45	**0.036**

Table 2.4: Rarefaction estimates of species richness (species ± SD) for predator (standardised at 330 (BB), 480 (CL) and 685 (SC) individuals) and saprophage (standardised at 350 (BB), 300 (CL) and 300 (SC) individuals) trophic groups in natural (N), restored (R) and abandoned-mined (A) treatments in the three study sites.

Site	Predator	Saprophage
BB-A	58.04 ± 4.05	43.54 ± 3.23
BB-R	52.91 ± 3.64	55.77 ± 1.45
BB-N	55.62 ± 3.09	49.14 ± 1.73
CL-A	67.99 ± 4.19	37.22 ± 3.29
CL-R	61.0 ± 2.53	47.26 ± 2.77
CL-N	53.8 ± 3.29	45.76 ± 1.35
SC-A	73.66 ± 3.65	17.86 ± 2.59
SC-R	93.57 ± 3.69	49.38 ± 3.38
SC-N	77.91 ± 3.08	48.32 ± 0.8

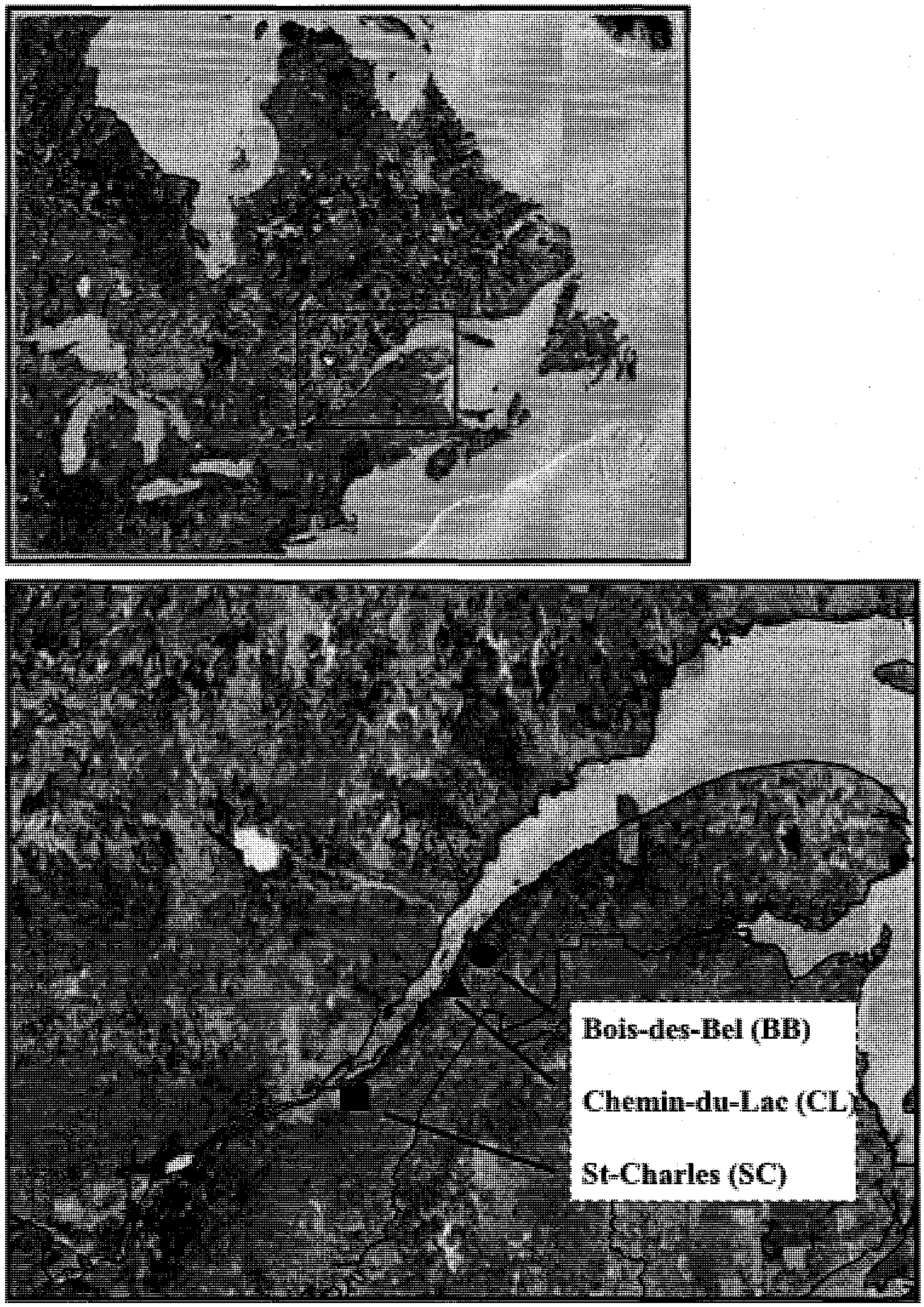

Figure 2.1: Location of study sites, southeastern Quebec, Canada

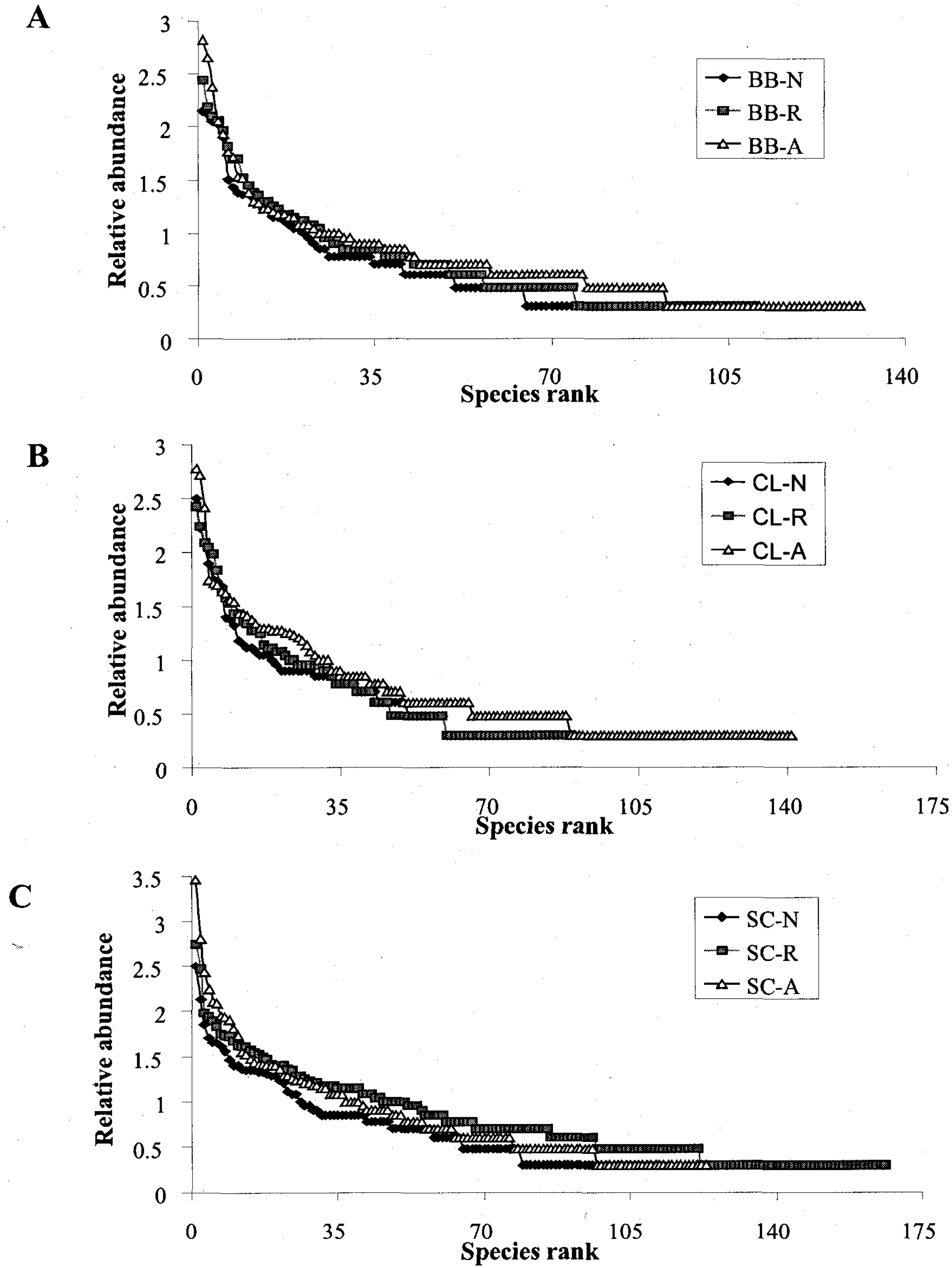

Figure 2.2: Rank/abundance curves illustrating the species abundance distribution. The y axis shows the relative abundance of species plotted using a Log_{10} scale, while the x axis ranks each species in order from most to least abundant. The three lines show the abundance of Brachycera in natural (N), restored (R) and abandoned-mined (A) treatments of A) Bois-des-Bel bog, B) Chemin-du-Lac bog and C) St-Charles bog.

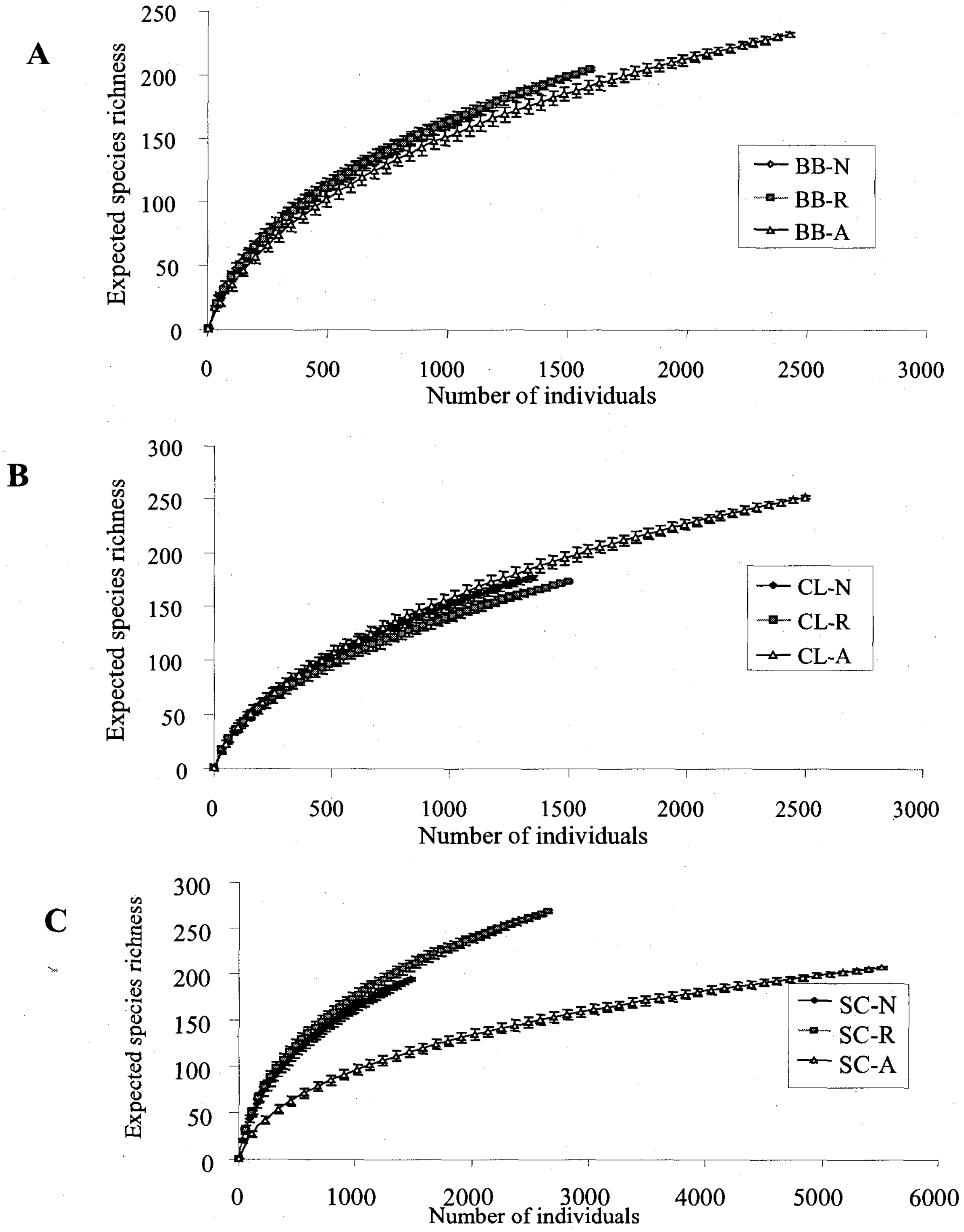

Figure 2.3: Rarefaction estimates of expected species richness (±1 SD) of Brachycera plotted against number of individuals for natural (N), restored (R) and abandoned-mined (A) treatments in A) Bois-des-Bel bog, B) Chemin-du-Lac bog and C) St-Charles bog.

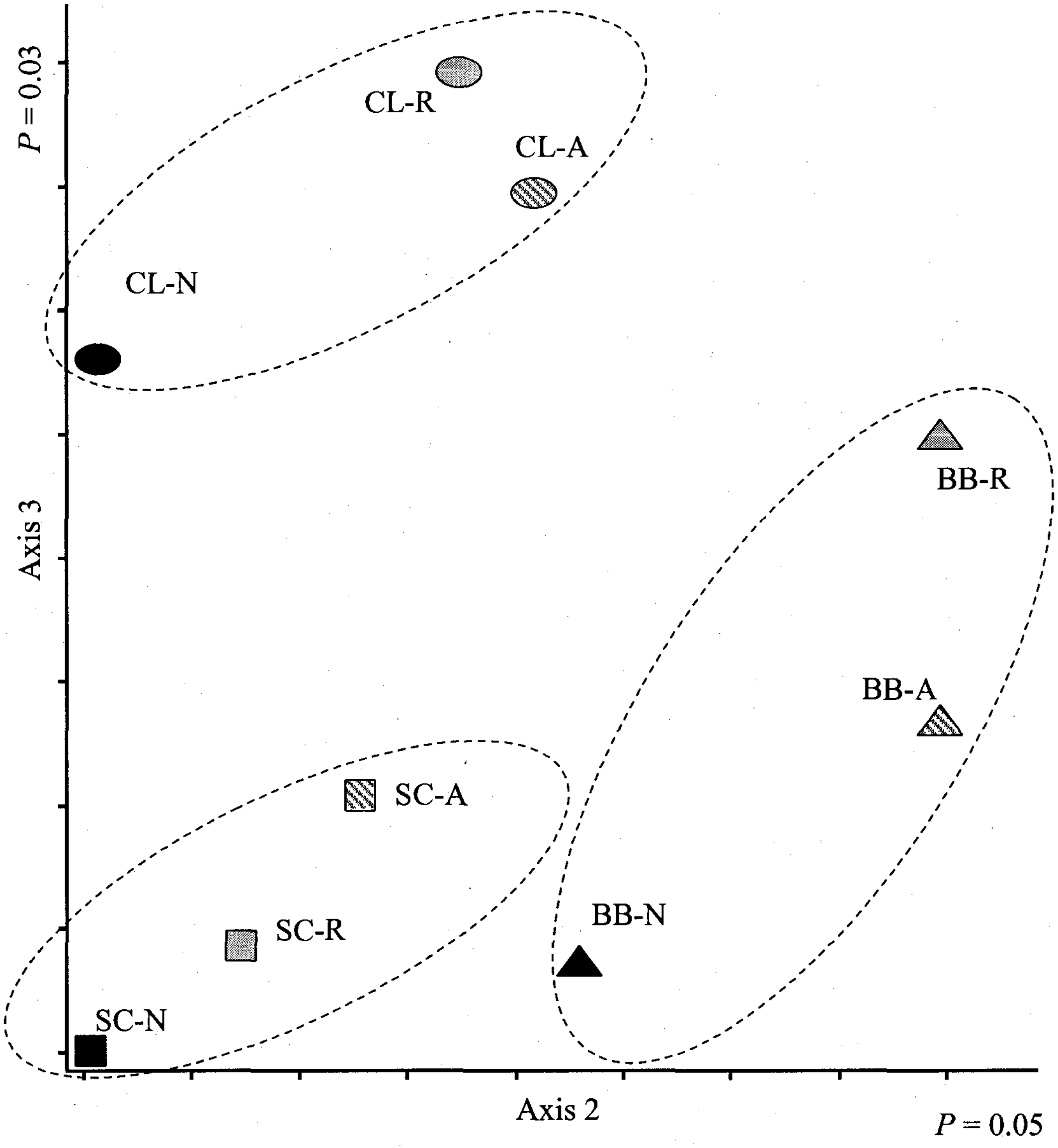

Figure 2.4: Non-metric multidimensional scaling ordination based on log-transformed relative abundance of Brachycera. Axes 2 and 3 with significant p-value at $P < 0.05$ for stress in randomized data (Monte-Carlo test, 100 permutations) of a three dimensional solution are plotted. Symbols represent assemblages in natural (N), restored (R) and abandoned-mined (A) treatments in the three study sites.

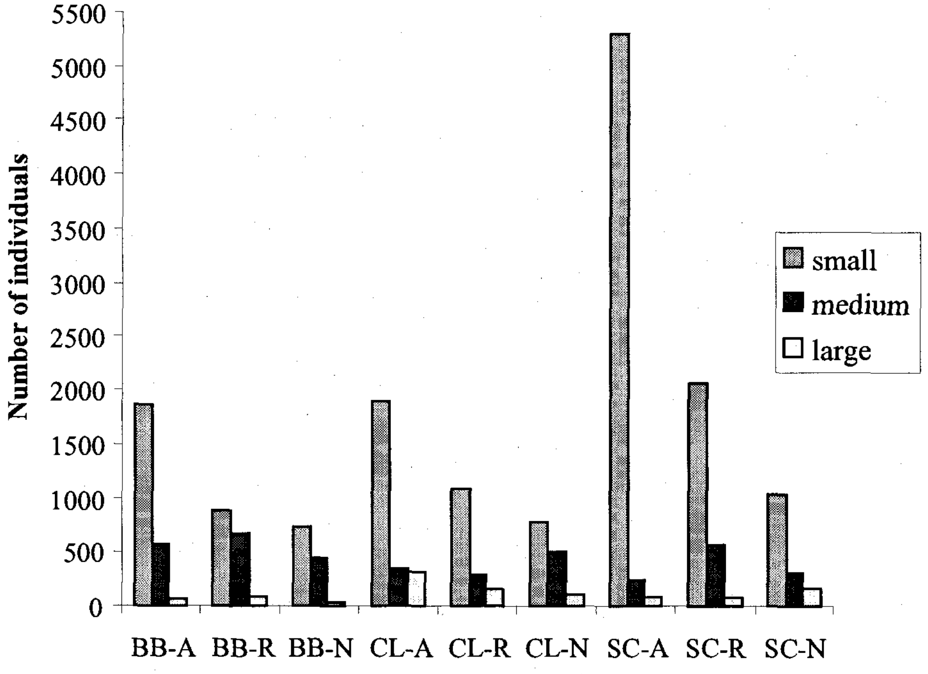

Figure 2.5: Relative abundance by size-classes collected from each treatment in the three study sites.

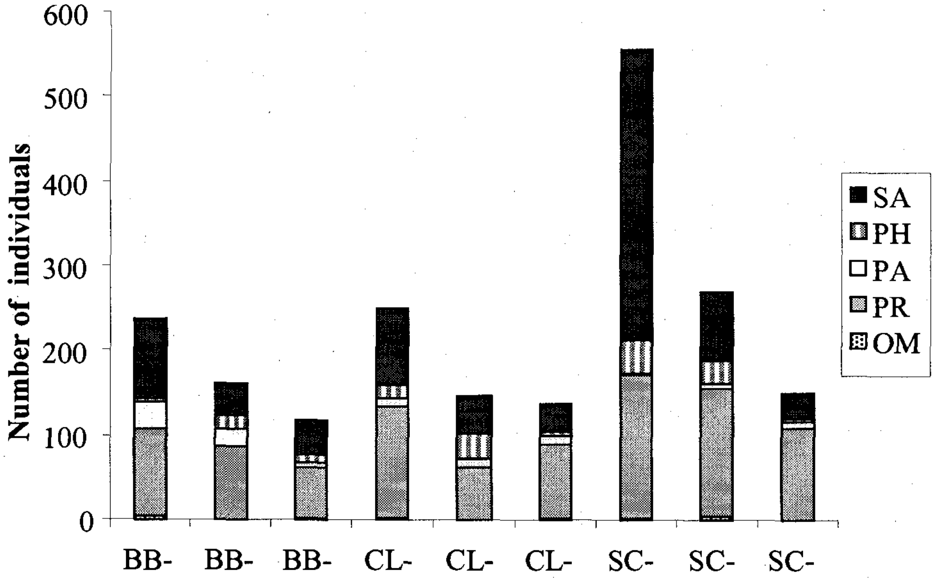

Figure 2.6: Relative abundance of the five trophic groups for Brachycera in each treatment in the three study sites.

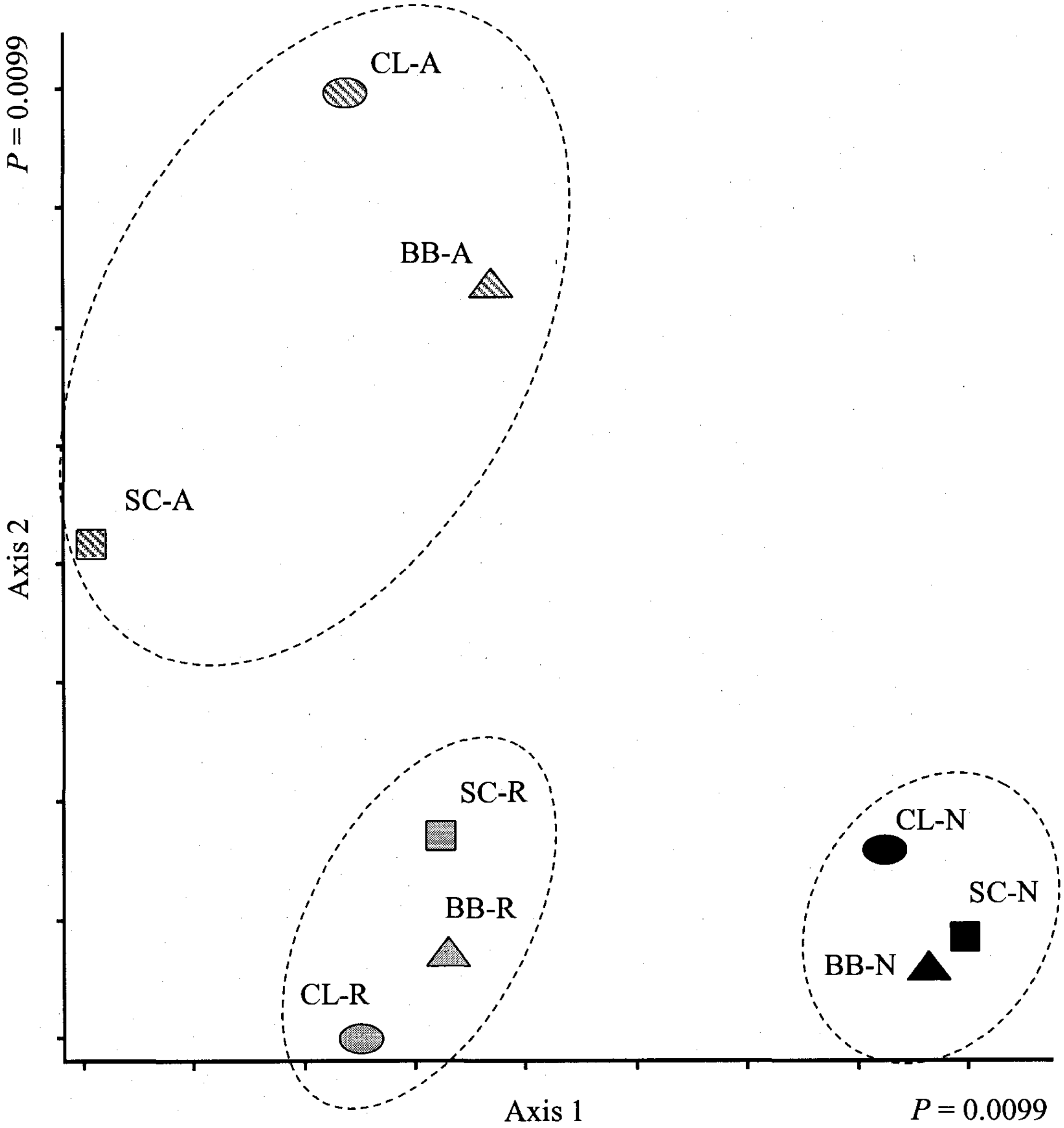

Figure 2.7: Non-metric multidimensional scaling ordination of environmental variables based on vegetation cover, peat chemistry, pH and soil moisture in the three treatments. The two axes of a two-dimensional solution are plotted. Symbols represent variables in natural (N), restored (R) and abandoned (A) treatments in the three study sites. Ordination differs from randomly derived matrices at $P < 0.05$ (Monte-Carlo test, 100 permutations).

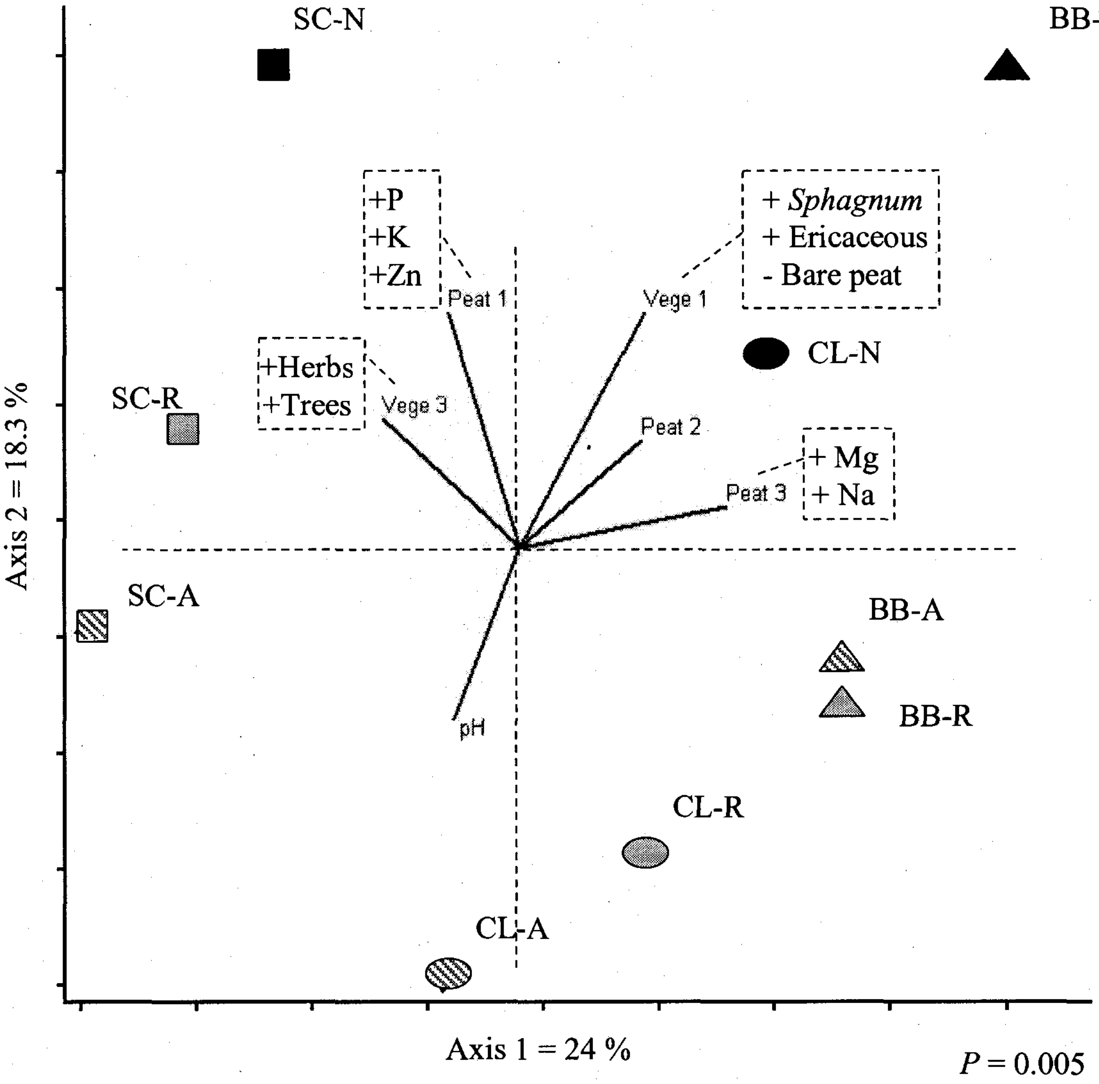

Figure 2.8: Canonical correspondence analysis of Brachycera assemblages showing the two main axes. Environmental vectors are inserted as plain lines. For clarity, individual species are not shown. Variables with highest eigenvector values for PCA reduction are indicated in the dotted boxes beside the vectors, + indicates a positive correlation with the vector and – indicates a negative correlation with the vector. Percent variance and stress values are shown by the axes.

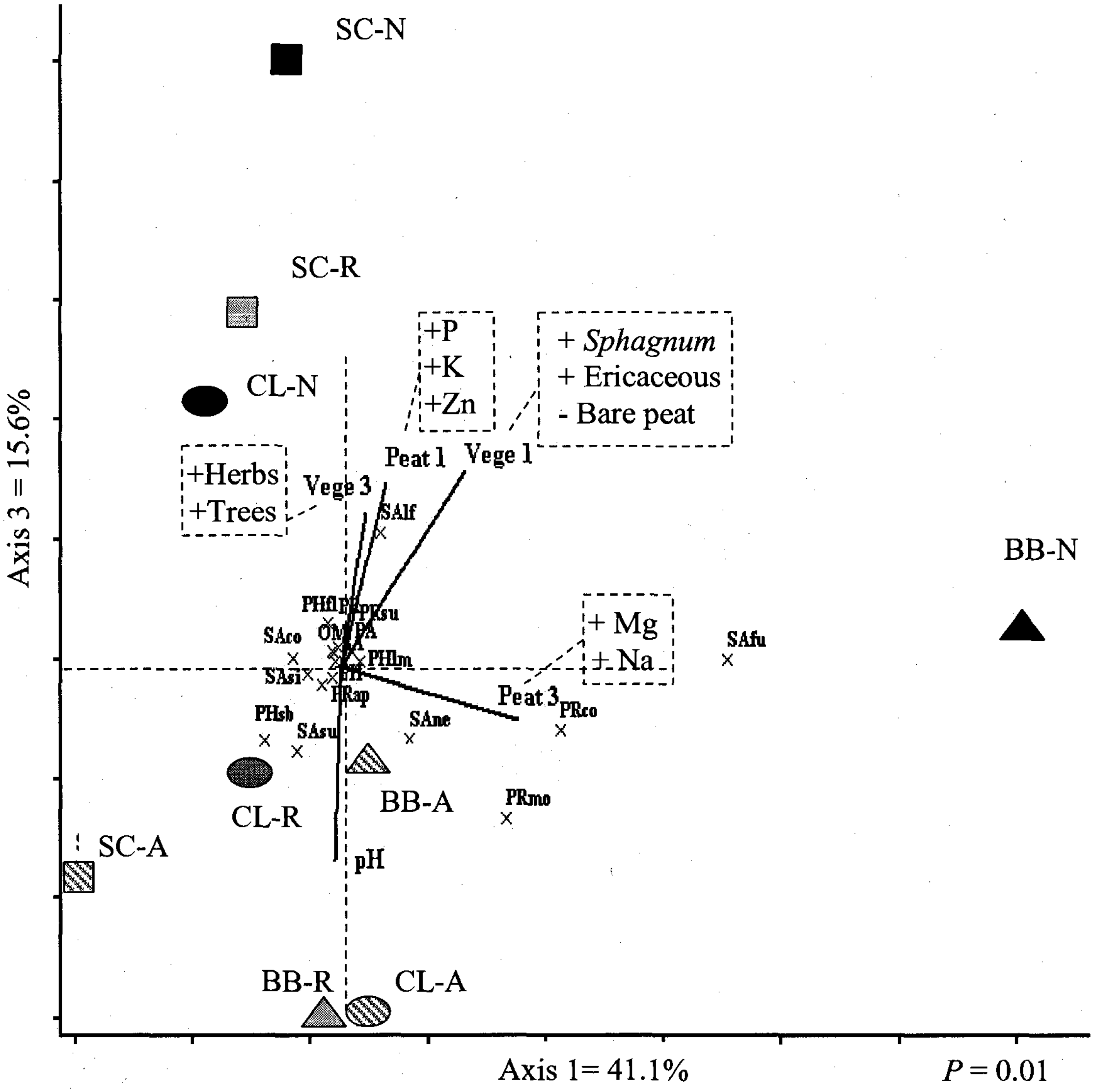

Figure 2.9: Canonical correspondence analysis of trophic assemblages showing axes 1 and 3. Environmental vectors are inserted as plain lines. Variables with highest eigenvector values for PCA reduction are indicated in the dotted boxes beside the vectors, + indicates a positive correlation with the vector and – indicates a negative correlation with the vector. Percent variance and stress values are shown by the axes.

Appendix 2.1: Brachycera species and morphospecies collected from each treatment per site. Taxon names are followed by the size-class, the trophic group and the number of specimens collected in each treatment. Abbreviations of trophic groups and subgroups:
PR: Predator, ap: predator of Aphidoidea, mo: predator of molluscs, in: predator of insects
SA: Saprophage, fu: fungivore or saprophagous in rotting wood, co: coprophagous, ne: necrophagous, su: saprophagous in the substrate, lf: feeding on leaf litter, si: secondary invader
PH: Phytophage, fl: flower consumer, fr: fruit consumer, lm: leaf-miner, sb: stem-borer, al: algivore,
PA: Parasite or parasitoid
OM: Omnivore
?: Unknown

Families	**Species**	**Size class**	**Trophic group**	**BB-A**	**BB-R**	**BB-N**	**CL-A**	**CL-R**	**CL-N**	**SC-A**	**SC-R**	**SC-N**
Lower Brachycera												
Xylophagidae	*Xylophagus (Archimyia) reflectens* Walker	3	PR	1	0	0	0	0	0	0	0	0
Stratiomyidae	*Allognosta fuscitarsis* Say	2	SAsu	0	1	0	1	0	0	0	0	0
	Allognosta obscuriventris Loew	2	SAsu	1	2	2	0	0	0	0	0	0
	Microchrysa polita Linnaeus	2	SAsu	0	0	0	0	1	0	1	0	0
	Odontomyia pubescens Day	2	SAsu	8	9	1	0	1	0	1	0	0
	Odontomyia sp.	2	SAsu	0	0	0	1	0	0	0	0	0
	Sargus cuprarius (Linnaeus)	2	SAsu	1	0	0	0	0	0	0	1	0
	Stratiomys normula Loew	3	SAsu	3	1	0	0	0	1	0	0	0
Rhagionidae	*Chrysopilus proximus* (Walker)	2	SAsu	1	0	0	2	0	0	0	0	0
	Symphoromyia fulvipes group	2	SAsu	0	0	0	1	2	6	0	0	0
	Rhagio gracilis (Johnson)	2	SAsu	0	0	0	0	0	0	0	1	0
	Rhagio mystaceus (Macquart)	2	SAsu	8	0	0	4	0	5	1	2	2
Tabanidae	*Atylotus ?duplex/hyalicosta*	2	PRsu	2	0	0	0	1	0	0	1	3
	Atylotus thoracicus (Hine)	2	PRsu	0	3	1	0	0	0	0	0	3
	Chrysops ater Macquart	2	PRsu	2	5	4	12	11	12	3	53	17
	Chrysops calvus Pechuman & Teskey	2	PRsu	0	0	0	0	0	0	3	10	8
	Chrysops carbonarius Walker	2	PRsu	0	0	0	0	0	0	3	10	3

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Chrysops cuclux Whitney	2	PRsu	0	0	0	8	27	48	0	11	9
	Chrysops excitans Walker	3	PRsu	0	0	0	2	2	2	23	26	71
	Chrysops frigidus Osten Sacken	2	PRsu	2	3	6	2	1	15	0	3	1
	Chrysops furcatus Walker	2	PRsu	17	156	79	0	0	0	0	0	0
	Chrysops mitis Osten Sacken	2	PRsu	1	3	0	19	45	25	2	12	4
	Chrysops niger Macquart	2	PRsu	0	2	1	3	1	4	1	0	7
	Chrysops vittatus Wiedemann	2	PRsu	0	0	0	0	0	0	0	1	0
	Chrysops zinzalus Philip	2	PRsu	0	0	0	0	0	0	0	2	1
	Hybomitra ?arpadi (Szilady)	3	PRsu	0	0	0	0	1	0	0	0	0
	Hybomitra ?trepida (McDunnough)	3	PRsu	0	0	0	0	0	0	0	0	2
	Hybomitra affinis (Kirby)	3	PRsu	1	2	0	4	2	1	0	0	0
	Hybomitra epistates Osten Sacken	3	PRsu	0	0	0	1	0	1	0	0	0
	Hybomitra frontalis (Walker)	3	PRsu	8	23	11	0	0	0	0	0	5
	Hybomitra frosti Pechuman	3	PRsu	0	0	0	0	0	0	0	0	1
	Hybomitra illota (Osten Sacken)	3	PRsu	0	0	0	1	0	0	1	0	0
	Hybomitra lasiophthalma (Macquart)	3	PRsu	2	15	1	259	124	54	5	5	16
	Hybomitra liorhina (Philip)	3	PRsu	0	2	0	0	0	0	0	0	0
	Hybomitra longiglossa Philip	3	PRsu	0	0	0	0	0	0	6	2	6
	Hybomitra lurida (Fallén)	3	PRsu	1	0	0	0	0	0	0	4	2
	Hybomitra minuscula (Hine)	2	PRsu	0	0	0	0	0	0	10	1	25
	Hybomitra nitidifrons ssp. nuda (McDunnough)	3	PRsu	0	3	0	1	1	0	4	12	6
	Hybomitra pechumani Teskey & Thomas	3	PRsu	1	0	0	1	2	6	8	9	36
	Hybomitra sodalis (Williston)	3	PRsu	0	0	0	0	0	0	1	1	0
	Hybomitra typhus (Whitney)	3	PRsu	0	0	0	0	0	0	1	1	9
	Hybomitra zonalis (Kirby)	3	PRsu	0	0	0	1	2	1	1	5	4
	Tabanus marginalis Fabricius	3	PRsu	1	0	0	1	0	1	5	1	1
	Tabanus novaescotiae Macquart	3	PRsu	0	0	0	0	0	0	8	6	0
	Tabanus similis Macquart	3	PRsu	0	1	0	16	3	7	5	3	2
	Tabanus sp. 1	3	PRsu	0	0	0	0	0	0	2	0	1
	Tabanus sp. 2	3	PRsu	0	0	0	2	1	2	0	0	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
Acroceridae	*Ogcodes (Ogcodes) borealis* Cole	2	PA	1	0	0	0	0	0	0	0	0
Bombyliidae	*Anthrax* sp.	2	PA	0	0	0	0	0	0	0	1	0
	Hemipenthes sp.	2	PA	0	1	0	0	0	0	0	0	0
	Villa ?squamigera Coquillett	2	PA	2	2	1	0	0	0	0	3	7
Therevidae	*Spiriverpa* sp.	2	PR	0	0	2	0	0	0	0	0	0
	Thereva sp.	3	PR	0	0	2	0	0	0	0	0	0
Asilidae	*Cyrtopogon marginalis* Loew	3	PR	0	0	0	1	0	2	0	0	0
	Dioctria (Dioctria) baumhaueri Meigen	2	PR	0	0	0	0	0	0	0	3	0
	Laphria ?aktis McAtee	3	PR	0	1	1	0	0	0	0	0	0
	Laphria sadales Walker	3	PR	1	2	0	0	0	0	0	0	0
	Leptogaster (Leptogaster) flavipes Loew	3	PR	0	0	0	0	0	0	0	3	0
Empididae	*Anthalia bulbosa* (Melander)	1	PRsu	2	0	0	2	0	1	0	0	0
	Anthalia sp. 1	1	PRsu	0	0	0	1	0	1	0	0	0
	Baeodromia pleuritica (Melander)	1	PRsu	0	0	0	0	0	0	0	1	0
	Bicellaria sp.	1	PRsu	15	0	4	0	0	169	0	3	0
	Brachystoma sp.	1	PRsu	0	0	0	1	0	0	0	0	0
	Drapetis (Crossopalpus) sp. 1	1	PRsu	0	2	0	2	0	0	0	1	0
	Drapetis (Crossopalpus) sp. 2	1	PRsu	112	12	0	51	2	0	4	5	0
	Drapetis (Crossopalpus) sp. 3	1	PRsu	1	0	0	0	0	0	0	2	0
	Euhybus sp. 1	1	PRsu	10	16	23	0	0	1	7	6	4
	Euhybus sp. 2	1	PRsu	10	6	9	18	10	1	0	4	5
	Euhybus sp. 3	1	PRsu	0	0	0	0	0	0	3	0	0
	Euhybus sp. 4	1	PRsu	2	0	7	0	0	2	0	0	0
	Euhybus sp. 5	1	PRsu	0	0	1	0	0	0	0	0	0
	Euthyneura sp.	1	PRsu	1	0	3	1	0	0	1	0	0
	Hilara sp. 1	1	PRsu	0	0	0	0	0	0	26	7	23
	Hilara sp. 2	1	PRsu	0	0	0	1	0	0	0	0	0
	Hilara sp. 3	1	PRsu	5	4	0	1	2	0	0	0	0
	Hilara sp. 4	1	PRsu	1	0	0	0	0	0	0	0	0
	Hilara sp. 5	1	PRsu	0	0	0	0	0	0	0	0	2

Families	**Species**	**Size class**	**Trophic group**	**BB-A**	**BB-R**	**BB-N**	**CL-A**	**CL-R**	**CL-N**	**SC-A**	**SC-R**	**SC-N**
	Hilara sp. 6	1	PRsu	0	0	0	0	0	0	1	0	0
	Hilara sp. 7	1	PRsu	0	0	0	0	0	0	1	0	0
	Hilara sp. 8	1	PRsu	0	0	0	0	0	0	1	0	6
	Hilara sp. 9	1	PRsu	0	0	0	0	0	0	2	3	45
	Leptopeza sp.	1	PRsu	3	1	0	0	0	1	0	0	0
	Oedalea sp.	1	PRsu	1	0	0	1	0	0	0	0	0
	Platypalpus holosericus Melander	1	PRsu	4	2	1	3	3	1	0	1	0
	Platypalpus nr. albiseta Panzer	1	PRsu	1	0	0	1	0	0	3	7	0
	Platypalpus trivialis Loew	1	PRsu	0	0	0	1	2	1	0	1	0
	Platypalpus sp. 1	1	PRsu	0	0	0	1	0	0	0	0	0
	Platypalpus sp. 2	1	PRsu	1	0	0	0	0	0	0	0	0
	Rhamphomyia sp. 1	2	PRsu	0	0	0	0	0	11	0	2	0
	Rhamphomyia sp. 2	1	PRsu	10	4	0	0	1	0	4	0	3
	Rhamphomyia sp. 3	2	PRsu	4	0	0	3	0	0	0	3	0
	Rhamphomyia sp. 4	2	PRsu	4	2	0	0	0	0	5	6	5
	Rhamphomyia sp. 5	2	PRsu	1	0	0	3	0	1	19	42	7
	Rhamphomyia sp. 6	2	PRsu	0	1	0	1	0	1	1	1	0
	Rhamphomyia sp. 7	1	PRsu	0	0	0	0	0	0	0	1	0
	Rhamphomyia sp. 8	1	PRsu	6	0	1	3	1	0	1	0	1
	Rhamphomyia sp. 9	1	PRsu	2	0	1	0	0	0	0	0	0
	Rhamphomyia sp. 10	1	PRsu	5	4	1	0	0	0	0	0	0
	Rhamphomyia sp. 11	2	PRsu	0	0	0	0	0	0	3	0	0
	Rhamphomyia sp. 12	1	PRsu	1	0	0	0	0	0	1	5	0
	Rhamphomyia sp. 13	1	PRsu	3	1	0	0	0	1	0	0	0
	Rhamphomyia sp. 14	1	PRsu	1	0	0	1	0	0	0	2	0
	Rhamphomyia sp. 15	2	PRsu	2	0	2	2	0	0	1	0	1
	Rhamphomyia sp. 16	1	PRsu	8	0	1	0	0	0	0	0	0
	Rhamphomyia sp. 17	1	PRsu	1	2	6	0	0	0	0	0	0
	Rhamphomyia sp. 18	1	PRsu	3	3	0	0	0	0	0	0	0
	Rhamphomyia sp. 19	2	PRsu	0	0	0	0	0	0	0	2	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Rhamphomyia sp. 20	1	PRsu	0	0	0	0	0	0	0	1	0
	Rhamphomyia sp. 21	1	PRsu	1	0	0	0	0	0	0	0	0
	Rhamphomyia sp. 22	1	PRsu	0	1	0	0	0	0	0	0	0
	Rhamphomyia sp. 23	1	PRsu	0	0	0	1	0	0	0	0	0
	Rhamphomyia sp. 24	1	PRsu	0	0	0	1	0	0	0	0	0
	Stilpon curvipes Melander	1	PRsu	1	0	0	2	0	0	1	4	0
	Stilpon curvipes/varipes ? ?	1	PRsu	0	0	0	3	0	0	15	9	0
	Stilpon varipes Loew	1	PRsu	0	0	0	3	2	0	2	5	0
	Stilpon vockerothi Cumming	1	PRsu	0	0	0	0	0	0	0	1	1
	Syndyas polita Loew	1	PRsu	0	0	0	3	1	1	25	16	23
	Syneches pusillus Loew	1	PRsu	0	0	0	0	0	0	0	0	1
	Syneches simplex Walker	1	PRsu	0	0	0	0	0	0	0	0	1
	Tachydromia sp.	1	PRsu	1	0	0	0	0	0	0	0	0
	Tachypeza sp.	1	PRsu	0	0	0	0	0	0	1	0	0
	Trichina sp.	1	PRsu	0	0	1	0	0	1	0	0	0
Dolichopodidae	*Argyra albicans* Loew	2	PRsu	0	8	2	22	10	0	10	2	1
	Argyra robusta Johnson	2	PRsu	2	1	0	0	0	0	0	0	0
	Campsicnemus nr. montanus Harmston & Knowlton	1	PRsu	0	0	0	4	1	1	0	0	0
	Campsicnemus vanduzeei Curran	1	PRsu	0	0	0	35	2	0	0	0	0
	Campsicnemus wheeleri Van Duzee	1	PRsu	0	0	1	0	0	0	0	0	0
	Chrysotimus delicatus Loew	1	PRsu	0	0	0	1	0	0	0	0	0
	Chrysotus spp.	1	PRsu	548	288	132	555	191	317	696	597	147
	Condylostylus caudatus (Wiedemann)	1	PRsu	0	0	0	0	0	0	3	2	1
	Condylostylus connectans (Curran)	1	PRsu	1	0	0	0	0	0	0	0	0
	Condylostylus flavipes (Aldrich)	1	PRsu	0	0	0	0	0	0	0	1	0
	Condylostylus inermis (Loew)	1	PRsu	0	0	0	0	0	0	20	21	23
	Condylostylus nigrofemoratus (Walker)	1	PRsu	48	1	0	2	0	0	15	4	0
	Condylostylus patibulatus (Say)	1	PRsu	0	0	0	0	0	0	0	2	0
	Condylostylus spp. *? ?*	N/A	PRsu	31	1	0	1	0	1	59	36	14
	Diaphorus sp. 1	1	PRsu	3	0	2	1	3	5	2	0	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Diaphorus sp. 2	1	PRsu	0	0	0	0	0	2	2	1	0
	Diaphorus sp. 3	1	PRsu	0	0	0	0	0	0	2	0	0
	Diaphorus sp. 4	1	PRsu	0	0	0	1	0	0	1	1	0
	Diaphorus sp. 5	1	PRsu	3	18	2	15	5	1	89	7	3
	Dolichopus ?amphicerus Melander & Brues	2	PRsu	0	0	0	1	0	0	0	0	0
	Dolichopus ?coloradensis Aldrich	2	PRsu	2	0	0	2	1	0	0	0	0
	Dolichopus ?dakotensis Aldrich	2	PRsu	0	0	0	0	1	0	0	0	0
	Dolichopus ?setosus Loew	2	PRsu	0	0	0	0	0	0	1	0	0
	Dolichopus affinis Walker	2	PRsu	0	0	0	0	1	0	3	0	1
	Dolichopus agronomus Melander & Brues	1	PRsu	5	0	0	2	1	0	180	41	19
	Dolichopus alacer/aequalis	2	PRsu	0	0	0	2	0	0	0	0	0
	Dolichopus albiciliatus Loew	2	PRsu	0	0	0	2	1	0	0	0	0
	Dolichopus brevimanus Loew	2	PRsu	0	0	0	3	0	4	2	0	2
	Dolichopus calcaratus Aldrich	2	PRsu	0	3	1	0	0	0	8	5	0
	Dolichopus celeripes Van Duzee	1	PRsu	3	0	0	0	0	0	0	0	0
	Dolichopus coecens Walker	2	PRsu	1	0	0	1	7	7	0	0	0
	Dolichopus cuprinus Weidemann	2	PRsu	3	3	3	8	1	2	3	2	2
	Dolichopus demissus Van Duzee	1	PRsu	0	0	0	0	0	0	141	15	21
	Dolichopus finitus Walker	2	PRsu	0	0	0	22	2	2	8	2	1
	Dolichopus flagellitenens Wheeler	1	PRsu	0	2	0	4	0	0	0	0	0
	Dolichopus flavilacertus Van Duzee	2	PRsu	0	0	0	0	0	0	7	10	2
	Dolichopus footei Harmston	2	PRsu	0	0	0	0	0	0	10	0	1
	Dolichopus fulvipes Loew	2	PRsu	0	1	0	2	1	0	1	3	0
	Dolichopus genualis Van Duzee	1	PRsu	3	7	1	11	3	1	13	15	7
	Dolichopus gladius Van Duzee	1	PRsu	0	1	0	8	1	1	0	1	0
	Dolichopus johnsoni Aldrich	1	PRsu	0	0	0	0	0	0	2	2	2
	Dolichopus lobatus Loew	2	PRsu	0	1	0	1	0	0	0	0	0
	Dolichopus melanocerus Loew	1	PRsu	1	1	0	8	0	1	5	6	0
	Dolichopus nigricornis Meigen	2	PRsu	1	0	4	5	1	1	5	0	0
	Dolichopus nr. *lundbecki* Curran	2	PRsu	0	0	0	0	0	0	1	0	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Dolichopus nr. *virga* Coquillett	1	PRsu	0	0	0	0	0	0	91	1	41
	Dolichopus obsoletus Van Duzee	1	PRsu	0	0	0	26	1	0	4	17	0
	Dolichopus ornatipennis Van Duzee	2	PRsu	0	0	0	0	0	0	11	5	6
	Dolichopus packardi Van Duzee	2	PRsu	0	0	0	0	0	0	0	0	2
	Dolichopus plumipes Scopoli	1	PRsu	6	7	6	0	0	1	0	0	0
	Dolichopus setifer Loew	1	PRsu	0	0	0	4	1	0	1	2	2
	Dolichopus sincerus Melander	2	PRsu	4	4	3	20	2	3	26	33	6
	Dolichopus spp. (*virga* group)	N/A	PRsu	1	7	4	47	16	3	213	34	50
	Dolichopus spp. ? ?	N/A	PRsu	1	2	0	10	2	1	3	3	2
	Dolichopus stenhammeri Zetterstedt	2	PRsu	0	2	3	5	0	0	0	0	2
	Dolichopus trisetosus Van Duzee	1	PRsu	3	1	0	0	0	0	2	5	1
	Dolichopus variabilis Loew	2	PRsu	0	0	0	0	0	0	4	5	0
	Dolichopus virga Coquillett	1	PRsu	1	1	0	1	6	1	59	15	5
	Dolichopus wheeleri Melander & Brues	2	PRsu	4	9	1	2	4	1	38	12	2
	Dolichopus sp. 1	1	PRsu	0	0	0	2	0	0	0	0	0
	Dolichopus sp. 2	2	PRsu	0	0	0	1	0	0	0	0	0
	Dolichopus sp. 3	2	PRsu	0	0	0	2	0	0	0	0	0
	Dolichopus sp. 4	2	PRsu	0	0	0	1	0	0	0	0	0
	Gymnopternus ?opacus Loew	1	PRsu	0	0	0	0	0	0	0	1	0
	Gymnopternus constrictus Robinson	1	PRsu	0	0	0	0	0	3	0	1	0
	Gymnopternus cuneicornis Robinson	1	PRsu	0	0	0	0	0	1	0	11	0
	Gymnopternus exilis Loew	1	PRsu	0	0	0	0	0	0	1	10	0
	Gymnopternus frequens Loew	1	PRsu	0	0	0	0	0	2	0	10	0
	Gymnopternus humilus Loew	1	PRsu	1	1	0	2	3	0	9	11	0
	Gymnopternus nigribarbus Loew	1	PRsu	53	7	3	4	13	7	15	26	26
	Gymnopternus nigricomus Robinson	1	PRsu	0	0	0	1	0	0	0	0	0
	Gymnopternus obtusicauda Van Duzee	1	PRsu	1	0	0	4	1	4	15	53	0
	Gymnopternus scotias Loew	1	PRsu	12	0	0	2	0	0	0	0	0
	Gymnopternus sp. 1	1	PRsu	1	0	0	0	0	0	0	0	1
	Gymnopternus sp. 2	1	PRsu	0	0	0	0	0	0	1	0	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Gymnopternus spectabilis Loew	1	PRsu	0	0	0	0	0	0	0	6	0
	Gymnopternus subulatus Loew	1	PRsu	1	0	4	2	0	0	0	3	1
	Hydrophorus chrysologus (Walker)	1	PRsu	0	0	0	0	0	0	27	0	0
	Medetera sp. 1	1	?	1	0	0	0	0	0	0	0	0
	Medetera sp. 2	1	?	0	0	1	0	0	0	0	0	0
	Medetera veles Loew	1	?	2	0	3	2	0	0	1	2	2
	Medetera vockerothi Bickel	1	?	0	0	0	0	0	0	0	3	0
	Pelastoneurus vagans Loew	1	PRsu	0	0	0	0	0	0	1	0	0
	Sympycnus ?lineatus Loew	1	PRsu	0	0	0	0	0	0	0	0	1
	Tachytrechus laticrus Van Duzee	2	PRsu	0	0	0	0	0	0	0	0	3
	Thrypticus sp.	1	PHpt	0	0	0	0	0	0	1	0	0
Aschiza												
Lonchopteridae	*Lonchoptera furcata* (Fallén)	1	SAsu	0	0	0	0	2	0	0	1	0
Syrphidae	*Cheilosia ?sialia* Shannon	2	PHfu	0	1	0	0	0	0	0	0	0
	Chrysotoxum flavifrons Macquart	3	PR	1	0	0	0	0	0	0	0	0
	Chrysotoxum sp.	3	PR	0	0	0	0	1	0	0	0	0
	Epistrophe (Epistrophe) nitidicollis Meigen	2	PRap	1	0	0	0	0	0	1	0	0
	Eristalis anthophorina Fallén	2	SAsu	0	0	0	0	0	0	0	0	1
	Eristalis arbustorum (Linnaeus)	2	SAsu	8	6	1	2	1	1	3	5	1
	Eristalis barda Say	3	SAsu	4	0	0	0	0	0	0	1	0
	Eristalis dimidiata Wiedemann	3	SAsu	0	2	0	1	1	0	0	0	0
	Eristalis nemorum (Linnaeus)	2	SAsu	0	3	0	0	0	0	0	0	0
	Eristalis obscura Loew	3	SAsu	0	1	0	2	0	0	0	0	0
	Eristalis sp.	3	SAsu	0	0	0	0	0	1	0	0	0
	Eupeodes (Eupeodes) sp. 1	2	PRap	0	1	0	0	0	0	0	0	0
	Eupeodes (Eupeodes) sp. 2	2	PRap	2	0	0	0	0	0	0	0	0
	Eupeodes (Eupeodes) spp.	2	PRap	0	0	0	2	1	0	1	2	1
	Eupeodes (Lapposyrphus) lapponicus (Zetterstedt)	2	PRap	0	0	0	1	0	0	0	0	0
	Helophilus borealis Staeger	3	SA	0	1	0	0	0	0	0	0	0
	Helophilus fasciatus Walker	3	SA	4	0	0	1	1	0	2	0	1

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Lejops (Anasimyia) anausis (Walker)	2	SAsu	8	3	4	1	0	0	0	0	0
	Lejops (Anasimyia) relictus Curran & Fluke	2	SAsu	1	1	0	1	0	0	2	0	0
	Lejops (Polydontomyia) curvipes Wiedemann	3	SAsu	14	7	0	0	0	0	0	0	0
	Melanostoma mellinum (Linnaeus)	2	PRap	0	5	5	0	0	2	0	0	0
	Ocyptamus fascipennis Wiedemann	3	PR	0	0	1	0	1	0	0	0	0
	Orthonevra ?anniae Sedman	2	?	0	0	0	0	0	0	0	1	1
	Orthonevra pulchella Williston	2	?	13	1	5	3	0	2	0	0	2
	Orthonevra sp.	2	?	3	1	0	0	0	0	0	0	0
	Paragus (Paragus) angustifrons Loew	1	PRap	0	3	0	1	0	0	0	1	0
	Parhelophilus porcus (Walker)	2	PRap	0	0	0	0	0	0	0	0	1
	Platycheirus ?granditarsis (Forster)	2	PRap	0	0	0	0	1	0	0	0	0
	Platycheirus hyperboreus (Staeger)	2	PRap	0	0	0	0	0	2	0	0	0
	Platycheirus jaerensis Nielson	2	PRap	1	0	0	0	0	0	0	0	0
	Platycheirus nearcticus Vockeroth	2	PRap	5	0	0	0	0	0	0	0	0
	Platycheirus rosarum Fabricius	2	PRap	10	6	4	0	2	11	0	2	1
	Platycheirus scambus (Staeger)	2	PRap	0	0	0	0	0	2	1	0	0
	Platypcheirus spp. ? ?	2	PRap	1	2	0	3	1	2	3	2	0
	Sericomyia militaris Walker	3	SA	0	1	0	0	0	0	0	0	0
	Sericomyia transversa Osburn	3	SA	0	0	3	0	0	1	0	0	0
	Sphaerophoria ? ?philanthus/asymmetrica	2	PRap	3	1	0	4	1	1	1	4	0
	Sphaerophoria asymmetrica Knutson	2	PRap	0	0	0	1	0	0	0	0	0
	Sphaerophoria contigua Macquart	2	PRap	0	0	0	0	0	0	1	0	1
	Sphaerophoria philanthus (Meigen)	2	PRap	3	1	0	1	0	0	0	3	0
	Syrphus ribesii (Linnaeus)	2	Prap	0	1	0	0	0	0	0	0	0
	Temnostoma alternans Loew	3	SAsu	0	0	0	0	0	0	0	0	1
	Toxomerus ?politus (Say)	2	PH	0	0	0	1	0	0	0	0	0
	Toxomerus geminatus (Say)	2	PRap	0	0	0	0	0	6	1	15	1
	Toxomerus marginatus (Say)	1	PRap	1	17	2	7	12	4	14	10	4
	Trichopsomyia ?modesta (Loew)	2	?	1	0	0	0	0	1	0	0	1
	Trichopsomyia ?pulchella (Williston)	2	?	0	0	0	1	0	1	0	2	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Tropidia quadrata (Say)	3	SA	4	2	0	10	3	1	1	0	1
	Volucella sp.	3	SA	0	0	0	0	0	0	0	0	1
	Xylota ?ouelleti Curran	3	SA	0	2	1	0	0	0	1	0	0
	Xylota annulifera Bigot	2	SA	5	5	1	3	0	0	2	0	1
	Xylota segnis Linnaeus	3	SA	1	0	0	1	0	0	0	0	0
	Xylota subfasciata Loew	3	SA	2	0	0	0	0	1	0	0	0
Pipunculidae	*Cephalops varius* (Cresson)	1	PA	0	1	0	0	0	0	0	0	0
	Cephalosphaera appendiculatus (Cresson)	1	PA	0	0	1	0	0	0	0	0	0
	Cephalosphaera brevis (Cresson)	1	PA	0	0	0	0	5	1	0	1	1
	Cephalosphaera n. sp.	1	PA	0	0	0	0	0	0	0	1	0
	Chalarus sp.	1	PA	1	1	1	0	0	0	0	0	1
	Dorylomorpha occidens (Hardy)	1	PA	0	1	2	0	2	0	0	0	0
	Dorylomorpha subdavata Albrecht	1	PA	0	0	4	0	0	0	0	0	2
	Elmohardyia atlantica (Hough)	1	PA	0	1	1	1	0	1	0	0	0
	Jassidophaga pilosa (Zetterstedt)	1	PA	0	0	1	0	0	0	0	0	1
	Pipunculus (Eudorylas) sp. 1	1	PA	0	1	0	0	0	0	0	0	0
	Pipunculus (Eudorylas) sp. 2	1	PA	0	0	2	0	0	0	0	0	0
	Pipunculus (Eudorylas) sp. 3	1	PA	0	0	0	0	0	0	0	2	0
	Pipunculus (Eudorylas) sp. 4	1	PA	0	0	0	0	0	1	0	0	0
	Pipunculus (Eudorylas) sp. 5	1	PA	0	0	0	0	0	1	0	0	0
	Pipunculus (Eudorylas) sp. 6	1	PA	0	0	0	0	0	0	0	0	1
	Pipunculus (Eudorylas) sp. 7	1	PA	0	0	0	0	0	0	0	0	2
	Pipunculus (Eudorylas) sp. 8	1	PA	0	0	0	0	0	0	0	0	1
	Pipunculus (Eudorylas) sp. 9	1	PA	0	0	0	0	0	0	0	1	0
	Pipunculus hertzogi (Rapp)	1	PA	0	3	2	0	0	1	0	0	3
	Pipunculus sp.	1	PA	0	0	0	0	0	0	0	0	1
	Pipunculus torus Skevington	1	PA	0	1	1	0	0	0	0	0	2
	Tomosvaryella sp. 1	1	PA	0	0	0	0	0	1	0	0	0
	Tomosvaryella sp. 2	1	PA	0	2	0	0	0	1	0	0	0
	Tomosvaryella sp. 3	1	PA	0	0	0	1	1	2	0	0	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Tomosvaryella sylvatica (Meigen)	1	PA	4	15	0	2	8	2	0	1	0
	Verrallia aucta (Fallén)	1	PA	1	0	0	0	0	0	0	0	0
Acalyptratae												
Micropezidae	*Compsobata univitta* (Walker)	2	SAsu	1	0	0	11	2	0	0	1	0
Psilidae	*Loxocera (Loxocera) cylindrica* Say	2	PHsb	0	1	0	0	0	1	0	1	0
	Psila sp.	1	PH	0	0	0	1	0	0	0	0	0
Conopidae	*Myopa* sp.	2	PA	0	0	0	0	0	0	0	0	1
	Physocephala sp.	3	PA	0	0	0	0	0	0	0	1	1
	Thecophora sp. 1	1	PA	3	0	0	5	1	0	0	0	0
	Thecophora sp. 2	1	PA	1	0	0	1	1	1	0	0	0
	Zodion fulvifrons Say	2	PA	0	0	0	0	0	1	0	0	0
	Zodion sp. 1	1	PA	0	0	0	6	0	3	0	5	0
Lonchaeidae	*Lonchea* sp. 1	1	?	1	0	1	0	0	0	0	0	0
	Lonchea sp. 2	1	?	0	0	1	0	0	0	0	0	0
	Lonchea sp. 3	1	?	0	0	1	0	0	0	0	0	0
Otitidae	*Chaetopsis massyla* (Walker)	2	SAsi	0	0	0	0	0	0	4	19	0
	Chaetopsis sp.	1	SA	0	0	0	0	0	0	0	1	0
	Melieria ochricornis (Loew)	2	?	0	0	0	5	0	0	0	0	0
	Melieria similis (Loew)	2	?	0	0	0	50	0	0	6	7	0
	Pseudotephritis vau (Say)	2	SAfu	0	0	0	1	0	0	0	1	0
	Seioptera vibrans (Linnaeus)	2	SA	1	0	0	1	0	0	0	0	0
Tephritidae	*Orellia ruficauda* (Fabricius)	1	PHfl	0	1	0	0	0	0	0	0	0
	Paroxyna albiceps (Loew)	1	PHfl	0	0	4	0	1	14	0	0	4
	Urophora quadrifasciata quadrifasciata (Meigen)	1	PHfl	0	0	0	0	0	0	0	0	1
	Urophora stylata (Fabricius)	1	PHfl	0	0	0	0	0	0	0	1	0
Lauxaniidae	*Homoneura (Tarsohomoneura) americana* (Wiedemann)	1	SAlf	0	0	0	0	0	0	0	2	0
	Homoneura (Tarsohomoneura) houghii (Coquillett)	1	SA	0	0	0	0	0	0	0	2	51
	Homoneura (Tarsohomoneura) johnsoni (Coquillett)	1	SA	0	0	0	0	0	0	0	2	0
	Homoneura sheldoni (Coquillett)	1	SAlf	0	1	0	0	0	0	0	7	7

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Lauxania shewelli Pérusse & Wheeler	1	SAlf	0	0	11	1	0	6	3	33	6
	Minettia cana Melander	1	SA	1	0	1	0	0	2	1	0	12
	Minettia glauca (Coquillett)	1	SA	0	0	2	0	0	0	0	0	0
	Minettia lupulina Fabricius	1	SAlf	10	2	23	7	1	22	3	15	27
	Poecilolycia browni Curran	1	SA	0	1	0	1	0	0	0	0	0
Chamaemyiidae	*Leucopis (Leucopis)* sp. 1	1	?	0	1	0	0	0	1	0	0	1
	Leucopis (Leucopis) sp. 2	1	?	0	0	0	0	0	1	0	0	0
	Leucopis (Leucopis) sp. 3	1	?	0	0	1	0	0	0	0	0	0
	Pseudodinia (varipes group*) ?melanitida* Barber	1	?	1	0	0	0	18	0	0	0	0
Coelopidae	*Coelopa gravis* Haliday	1	PHal	2	0	0	0	0	0	0	0	0
Sciomyzidae	*Anticheta melanosoma* Melander	1	PRmo	0	0	0	0	1	0	0	0	0
	Dictya sp.	1	PRmo	0	0	0	0	1	0	0	0	0
	Limnia sparsa (Loew)	1	PRmo	0	0	1	0	0	0	0	0	0
	Tetanocera clara Loew	2	PRmo	0	0	2	0	0	0	0	0	0
	Tetanocera melanostigma Steyskal	2	PRmo	1	0	0	0	0	0	0	0	0
	Tetanocera plebeja Loew	2	PRmo	1	6	0	2	1	0	1	1	0
	Tetanocera sp.	2	PRmo	0	0	0	0	0	0	1	0	1
	Tetanocera valida Loew	2	PRmo	4	1	15	2	0	0	0	0	0
Sepsidae	*Enicita annulipes* (Meigen)	1	SAco	1	0	0	0	1	0	1	3	0
	Enicomira minor (Haliday)	1	SAco	1	2	0	7	1	0	88	19	2
	Saltella sp.	1	SAco	0	0	0	0	0	0	0	1	0
	Saltella sphondylii (Schrank)	1	SAco	0	0	0	0	0	0	2	0	0
	Sepsis biflexuosa Strobl	1	SAco	1	2	0	0	3	0	0	2	0
	Sepsis punctum Fabricius	1	SAco	0	2	0	0	2	1	0	7	0
Agromyzidae	*Agromyza ?sulfuriceps* Strobl	1	PHlm	0	0	0	1	0	1	0	0	0
	Agromyza sp. 1	1	PHlm	0	0	0	1	0	0	0	0	0
	Agromyza sp. 2	1	PHlm	0	1	0	0	0	0	0	0	0
	Amauromyza karli (Hendel)	1	PH	0	0	0	0	1	0	4	1	0
	Calycomyza novascotiensis Spencer	1	PHlm	0	0	0	2	0	0	7	11	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Cerodontha (Cerodontha) dorsalis (Loew)	1	PHlm	6	2	0	3	0	0	3	1	0
	Cerodontha (Icteromyza) longipennis(Loew)	1	PHlm	0	0	0	0	0	0	1	0	0
	Cerodontha (Poemyza) ?muscina/calamagrostidis ?	1	PHlm	1	2	0	0	0	0	0	1	0
	Cerodontha (Poemyza) incisa (Meigen)	1	PHlm	0	0	0	0	0	0	0	2	2
	Cerodontha (Poemyza) inconspicua (Malloch)	1	PHlm	0	0	1	0	0	0	0	0	0
	Chromatomyia fuscula (Zetterstedt)	1	PHlm	0	0	0	0	0	0	0	0	1
	Japanagromyza viridula (Coquillett)	1	PHlm	0	0	0	0	0	0	0	1	0
	Liriomyza fricki Spencer	1	PHlm	2	0	0	0	1	0	1	1	1
	Liriomyza sp. 1	1	PHlm	5	1	2	0	0	0	1	0	0
	Liriomyza sp. 2	1	PHlm	0	0	0	0	0	0	1	0	0
	Napomyza plumea Spencer	1	PHlm	0	0	0	0	0	0	1	0	0
	Ophiomyia ?duodecima Spencer	1	PH	0	1	0	0	0	0	0	0	0
	Ophiomyia ?maura/kingmerensis ?	1	PH	0	1	0	1	0	0	0	0	0
	Ophiomyia asterovora Spencer	1	PHlm	0	0	0	1	0	0	0	0	0
	Ophiomyia labiatarum Hering	1	PHsb	0	0	0	0	0	0	0	1	0
	Ophiomyia nasuta (Melander)	1	PH	1	1	0	0	0	1	0	1	0
	Ophiomyia quinta Spencer	1	PH	0	1	0	0	0	0	0	1	0
	Ophiomyia sp. 1	1	PH	1	0	0	0	0	0	0	1	0
	Ophiomyia sp. 2 *?*	1	PH	0	0	0	1	0	0	0	0	0
	Phytobia sp.	1	PHsb	0	1	0	0	1	0	0	0	0
	Phytoliriomyza artica (Lundbeck)	1	PHsb	0	0	0	0	0	0	4	0	0
	Phytoliriomyza pacifica (Melander)	1	PHsb	0	1	0	0	0	0	0	0	0
	Phytomyza ilicicola Loew	1	PHlm	0	1	5	0	1	0	0	0	1
	Phytomyza sp.	1	PH	0	0	0	1	0	0	0	0	0
	Pseudonapomyza europaea Spencer	1	PHlm	0	0	0	0	0	0	0	1	1
Opomyzidae	*Geomyza apicalis* (Meigen)	1	PHsb	0	0	0	1	2	0	1	1	0
Anthomyzidae	*Anthomyza* sp. 1	1	?	0	0	0	0	0	1	0	0	0
	Anthomyza sp. 2	1	?	0	0	0	0	1	0	0	0	0
	Anthomyza sp. 3	1	?	0	0	0	1	0	0	0	0	0
	Anthomyza sp. 4	1	?	0	0	0	0	0	0	0	0	2

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
Periscelididae	*Cyamops* sp.	1	?	1	0	0	0	0	0	0	0	0
	Stenomicra angustata Coquillett	1	?	0	0	0	0	0	0	0	1	0
Milichiidae	*Desmometopa sordida* (Fallén)	1	SAco	0	1	0	0	0	0	0	0	0
	Eusiphona mira Coquillett	1	SA	1	1	0	19	1	0	0	0	0
	Leptometopa latipes (Meigen)	1	SAco	0	2	0	0	1	0	0	0	0
	Neophyllomyza quadricornis Melander	1	SA	1	0	0	2	0	1	0	1	0
	Neophyllomyza sp.	1	SA	1	0	2	0	0	0	0	0	0
	Paramyia nitens (Loew)	1	SA	707	28	8	42	119	25	27	337	22
	Phyllomyza securicornis Fallén	1	SA	5	1	0	0	0	0	0	1	0
Chloropidae	*Apallates neocoxendix* (Sabrosky)	1	SA	5	0	1	0	1	8	0	0	0
	Aphanotrigonum scabrum (Aldrich)	1	SA	0	0	0	0	2	0	0	0	0
	Aphanotrigonum sp. A	1	SA	1	0	0	0	0	0	0	0	0
	Aphanotrigonum trilineatum (Meigen)	1	SAsi	4	3	0	24	19	1	2	6	0
	Biorbitella virgata (Coquillett)	1	SA	0	0	0	0	1	0	0	0	0
	Calamoncosis n.sp. A	1	PH	0	1	0	0	0	0	0	7	0
	Cetema elongatum (Meigen)	1	PH	0	0	0	4	2	0	0	0	0
	Chlorops sp. A	1	PHsb	0	2	0	2	0	0	8	1	0
	Chlorops sp. B	1	PHsb	0	0	0	4	0	0	0	1	0
	Chlorops sp. C	1	PHsb	0	0	0	0	0	0	3	0	0
	Chlorops sp. D	1	PHsb	0	1	0	0	0	0	0	0	0
	Chlorops sp. E	1	PHsb	0	0	0	1	0	0	0	0	0
	Chlorops sp. F	1	PHsb	0	0	0	1	0	0	0	0	0
	Chlorops sp. G	1	PHsb	0	0	0	0	0	0	1	0	0
	Conioscinella sp. A	1	SA	0	0	0	0	0	0	2	14	0
	Conioscinella sp. B	1	SA	1	0	0	0	0	0	0	0	0
	Conioscinella flavescens (Tucker)	1	SA	0	0	0	0	1	0	1	2	0
	Conioscinella zetterstedti Andersson	1	SAsi	0	0	0	0	0	0	0	3	0
	Dasyopa sp.	1	SA	20	1	114	0	6	7	2	14	12
	Diplotoxa versicolor (Loew)	1	PHsb	0	0	0	55	0	0	35	0	0
	Elachiptera ?nigriceps (Loew)	1	SAsi	0	0	0	2	0	0	1	1	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Elachiptera costata Loew	1	SAsi	3	1	0	0	3	0	0	0	2
	Elachiptera flaviceps Sabrosky	1	SAsi	0	1	0	0	0	0	0	0	0
	Elachiptera pechumani Sabrosky	1	SAsi	0	0	0	2	1	0	3	3	0
	Elachiptera sp. A	1	SAsi	0	0	0	0	4	0	0	0	0
	Elachiptera vittata Sabrosky	1	SAsi	1	0	0	1	0	0	0	1	0
	Elliponeura diplotoxoides Becker	1	PH	0	0	0	0	0	0	1	0	0
	Eribolus longulus (Loew)	1	SAsi	0	0	0	0	0	0	2	5	0
	Hippelates plebejus Loew	1	SA	0	0	0	0	0	0	1	1	3
	Incertella bispina (Malloch)	1	SAsi	0	0	0	1	0	0	10	25	1
	Incertella incerta (Becker)	1	SAsi	0	1	0	0	1	1	0	1	0
	Incertella minor (Adams)	1	SAsi	10	13	1	20	96	1	19	55	1
	Lasiosina canadensis Aldrich	1	SAsi	0	0	0	0	1	0	1	0	0
	Liohippelates bishoppi Sabroski	1	SA	4	0	0	2	0	0	0	1	0
	Malloewia nigripalpis (Malloch)	1	SA	0	0	0	0	0	0	0	0	1
	Meromyza sp. 1	1	PH	0	0	0	0	0	0	0	2	0
	Meromyza sp. 2	1	PH	0	1	0	0	0	0	0	2	0
	Olcella sp. 1	1	PH	17	11	24	0	0	0	0	0	0
	Olcella sp. 2	1	PH	0	0	0	2	0	2	0	1	0
	Olcella sp. 3	1	PH	0	0	0	0	0	1	0	0	0
	Oscinella sp. B	1	PH	1	1	0	4	1	0	6	68	7
	Oscinella sp. A	1	PH	8	2	1	44	7	4	10	5	0
	Oscinella sp. C	1	PH	0	0	0	2	0	0	0	0	0
	Oscinella sp. D	1	PH	0	0	0	0	0	0	0	0	1
	Oscinella sp. E	1	PH	0	0	0	0	0	0	2	0	0
	Parectecephala eucera (Loew)	1	PHsb	0	0	1	0	0	0	0	3	0
	Pseudopachychaeta approximatonervis (Zetterstedt)	1	PHfl	0	1	0	17	6	0	278	87	0
	Pseudopachychaeta ruficeps (Zetterstedt)	1	PH	1	125	2	3	263	0	1	0	0
	Rhopalopterum ?painteri (Sabrosky)	1	SAsi	0	0	1	1	9	1	1	2	0
	*Rhopalopterum ?*sp.A/*painteri*	1	SAsi	0	1	0	1	9	1	0	4	1
	Rhopalopterum atriceps (Loew)	1	SAsi	0	0	0	0	0	0	0	3	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Rhopalopterum carbonarium (Loew)	1	SAsi	0	1	0	4	0	0	134	37	1
	Rhopalopterum soror (Macquart)	1	SAsi	3	20	0	38	1	0	17	1	0
	Rhopalopterum sp. A	1	SAsi	1	0	1	0	1	8	0	3	2
	Rhopalopterum umbrosum (Loew)	1	SAsi	5	7	1	6	72	2	2	4	5
	Thaumatomyia annulata (Walker)	1	PR	1	0	0	0	0	0	0	0	0
	Thaumatomyia glabra (Meigen)	1	PRap	85	93	0	27	23	1	12	4	6
	Thaumatomyia grata (Loew)	1	PR	6	50	1	27	38	1	4	5	1
	Thaumatomyia pulla (Adams)	1	PR	0	0	22	1	0	0	1	22	21
	Tricimba melancholica group	1	SAsi	5	1	6	3	4	2	0	43	10
	Tricimba trisulcata (Adams)	1	SAsi	0	0	2	0	0	0	0	2	0
Heleomyzidae	*Allophyla laevis* Loew	2	SAfu	0	0	7	2	0	0	1	0	0
	Suilla apicalis (Loew)	1	SAfu	0	0	2	0	0	0	0	0	0
	Suilla loewi (Garrett)	2	SAfu	0	0	117	0	0	0	0	0	0
Sphaeroceridae	*Coproica ?ferruginata* (Stenhammar)	1	SA	0	0	0	8	2	2	4	0	0
	Coproica acutangula (Zetterstedt)	1	SA	0	0	0	0	0	0	0	1	0
	Coproica sp. 1	1	SA	0	0	0	0	0	1	0	1	0
	Copromyza sp.	1	SAco	0	0	0	0	4	0	0	0	0
	Crumomyia sp.	1	SA	0	0	0	1	0	0	0	0	0
	Dahlimosina dahli (Duda)	1	SA	0	0	2	0	0	0	0	0	6
	Ischiolepta sp.	1	SA	0	0	1	0	0	0	0	0	0
	Leptocera spp.	1	SA	8	3	3	2	1	0	26	17	4
	Limosininae sp. A	1	SA	0	0	5	0	0	1	0	0	0
	Lotophila sp.	1	SAco	0	1	0	1	0	0	0	1	2
	Minilimosina ?parvula (Rohacak)	1	SA	0	0	1	1	0	1	0	2	0
	Minilimosina parva (Malloch)	1	SA	0	0	0	0	0	1	0	0	0
	Minilimosina sp.	1	SA	0	0	0	0	0	0	0	1	0
	Nearcticorpus sp.	1	SA	0	0	2	0	0	0	0	0	0
	Opalimosina liliputana (Rondani)	1	SA	0	0	1	0	0	0	0	0	0
	Opalimosina mirabilis (Collin)	1	SA	2	3	2	8	0	0	73	1	1
	Phthitia ovicercus Marshall	1	SA	0	0	0	0	3	0	1	0	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Pullimosina pullula (Zetterstedt)	1	SA	0	0	0	1	0	0	0	1	0
	Pullimosina sp. A	1	SA	0	0	0	0	0	0	1	0	0
	Rachispoda limosa (Fallén)	1	SAsu	0	0	0	0	0	0	3	0	0
	Spelobia ?frustrilabris Marshall	1	SA	0	0	0	0	0	0	0	2	0
	Spelobia bifrons (Stenhammar)	1	SA	0	0	0	0	0	0	1	0	3
	Spelobia brevipteryx Marshall	1	SA	0	0	0	0	0	1	0	0	0
	Spelobia clunipes (Meigen)	1	SA	1	0	0	0	0	0	0	1	2
	Spelobia maculipennis (Spuler)	1	SA	0	0	0	1	1	0	0	0	1
	Spelobia ochripes (Meigen)	1	SA	11	5	3	0	1	1	37	67	5
	Spelobia pappi Rohacak	1	SA	0	0	0	2	9	0	1	4	0
	Spelobia spp.	1	SA	0	0	2	0	0	0	1	0	3
	Sphaerocera sp.	1	SA	0	0	0	0	0	0	0	1	0
	Terrilimosina pexa Marshall	1	SA	0	0	1	0	0	0	0	0	0
Drosophilidae	*Drosophila* sp. 1	1	?	0	0	0	1	0	0	0	0	0
	Drosophila sp. 2	1	?	0	0	0	0	0	0	1	4	0
	Drosophila sp. 3	1	?	0	0	1	0	0	0	0	2	2
	Scaptomyza ?borealis Wheeler	1	?	2	0	0	0	0	0	0	0	0
	Scaptomyza adusta (Loew)	1	?	0	0	0	0	0	1	0	0	0
	Scaptomyza pallida (Zetterstedt)	1	PHfl	4	2	28	1	2	6	1	35	7
	Scaptomyza sp. 1	1	?	1	0	0	0	0	0	0	0	0
	Scaptomyza sp. 2	1	?	0	0	0	0	0	0	0	1	0
Diastatidae	*Diastata* sp. 1	1	?	0	0	7	0	7	0	0	1	0
	Diastata sp. 2	1	?	0	0	4	0	1	0	0	1	0
	Diastata sp. 3	1	?	0	0	1	0	0	0	0	0	0
	Diastata sp. 4	1	?	0	0	3	0	0	1	0	0	0
	Diastata sp. 5	1	?	0	0	0	2	0	0	1	0	0
	Diastata sp. 6	1	?	0	0	0	1	0	0	0	0	0
Ephydridae	*Allotrichoma simplex* (Loew)	1	SA	2	0	0	0	0	0	2	0	0
	Allotrichoma sp.	1	SA	7	7	1	4	1	1	2	0	0
	Callinapaea laurentiana Wirth	1	?	0	0	0	3	0	0	0	0	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Discocerina obscurella (Fallén)	1	SAsu	2	0	0	20	0	0	4	0	0
	Hyadina binotata Cresson	1	SAsu	0	2	0	0	0	0	0	0	0
	Hydrellia americana Cresson	1	PH	0	0	1	0	0	0	1	0	0
	Hydrellia griseola (Fallén)	1	PHlm	1	1	2	2	2	0	6	2	3
	Hydrellia sp. 1	1	PH	0	0	0	0	0	0	1	0	1
	Hydrellia sp. 2	1	PH	0	0	0	2	0	0	0	1	0
	Hydrellia sp. 3	1	PH	0	0	0	1	0	0	1	0	1
	Limnellia lecocercus Mathis	1	?	0	0	0	1	0	0	0	0	0
	Limnellia stenhammari (Zetterstedt)	1	SAsu	3	0	0	1	0	0	0	0	0
	Nostima picta (Fallén)	1	?	0	0	0	0	0	0	0	1	0
	Notophila (caudata group) sp. 1	1	SAsu	0	0	0	0	0	0	5	0	0
	Notophila (caudata group) sp. 2	1	SAsu	1	0	0	0	0	0	2	0	0
	Notophila (Dichaeta) olivacea Cresson	1	SAsu	1	0	0	0	0	0	0	0	0
	Notophila (Dichaeta) sp.	1	SAsu	0	0	0	1	0	0	0	0	0
	Notophila (Notophila) phaeopsis Mathis	1	SAsu	0	0	0	0	0	0	1	0	0
	Ochthera borealis Clausen	1	PRin	0	0	0	0	0	0	1	0	0
	Parydra (Parydra) abbreviata Loew	1	PHal	1	0	0	1	0	0	0	0	0
	Philygria debilis (Loew)	1	?	18	8	3	2	34	11	18	7	2
	Philygria nigrescens Cresson	1	?	2	0	0	1	0	0	0	0	0
	Philygria opposita (Loew)	1	?	5	0	0	0	0	0	0	0	0
	Polytrichophora orbitalis (Loew)	1	SAsu	0	0	0	1	0	0	0	0	0
	Psilopa compta (Meigen)	1	?	58	0	0	0	0	0	0	0	0
	Scatella (Scatella) favillacea Loew	1	SAsu	0	0	0	1	0	0	2	0	0
	Scatella (Scatella) stagnalis (Fallén)	1	SAsu	14	3	1	598	1	1	2907	6	1
Calyptratae												
Scathophagidae	*Cordilura (Achaetella)* sp.	2	PHsb	0	0	0	0	0	0	0	1	0
	Cordilura (Achaetella) varipes (Walker)	2	PHsb	0	0	0	0	0	0	3	0	0
	Cordilura (Cordilura) carbonaria Walker	2	PHsb	0	0	0	1	0	0	0	1	0
	Cordilura (Cordilura) gagatina Loew	2	PHsb	0	0	1	3	0	9	2	19	0
	Cordilura (Cordilura) variabilis Loew	2	PHsb	0	0	0	2	0	0	0	0	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Cordilura (Cordilurina) pleuritica Loew	2	PHsb	0	1	0	2	0	0	0	0	0
	Nanna sp.	2	PH	0	0	1	0	0	0	0	0	0
	Neochirosa sp.	2	PH	0	1	5	0	0	0	0	0	0
	Parallelomma vittatum (Meigen)	2	PHlm	0	0	1	0	0	1	0	0	1
	Scathophaga furcata Say	2	SAco	1	0	1	0	1	2	0	0	0
	Scathophaga stercoraria Linnaeus	3	SAco	2	0	0	1	0	0	0	0	2
	Scathophaga suilla Fallén	2	SAco	0	1	0	0	0	0	0	0	0
Fanniidae	*Fannia abrupta* Malloch	1	SA	1	0	0	0	0	0	0	0	0
	Fannia canicularis (Linnaeus)	1	SA	6	0	0	1	3	0	0	2	0
	Fannia fuscula (Fallén)	2	SA	0	0	3	1	1	5	0	0	2
	Fannia immaculata Malloch	1	SA	0	0	0	0	0	1	0	0	0
	Fannia spathiophora Malloch	1	SA	0	0	12	0	0	1	0	0	1
	Fannia sociella (Zetterstedt)	1	SA	0	0	0	0	0	0	0	2	0
	Fannia sp. 1	1	SA	1	0	0	0	0	0	0	0	0
	Fannia sp. 2	1	SA	0	0	0	0	0	2	0	0	0
	Fannia sp. 3	1	SA	0	0	0	0	0	0	1	0	0
	Fannia sp. 4	1	SA	0	0	0	0	0	0	0	0	1
	Fannia sp. 5	1	SA	0	1	0	0	0	0	0	0	0
	Fannia sp. 6	1	SA	0	2	7	0	0	1	0	2	2
	Fannia sp. 7	1	SA	0	0	2	0	0	0	0	0	0
	Fannia sp. 8	1	SA	0	0	0	1	0	0	0	0	0
	Fannia sp. 9	1	SA	0	0	0	0	1	0	0	0	0
	Fannia sp. 10	1	SA	0	0	1	0	0	0	0	0	0
	Piezura graminicola (Zetterstedt)	2	SAfu	0	0	0	1	2	0	1	2	0
Muscidae	*Azelia* sp.	1	OM	0	2	0	0	0	0	0	0	0
	Caricea erythrocera Rob.-Desv.	1	PR	4	5	2	1	19	2	4	3	1
	Caricea tinctinervis Malloch	1	PR	0	0	0	0	0	1	0	0	0
	Ceonosia (Oplogaster) ?flavidipalpis Huckett	1	PR	0	1	0	0	0	0	0	0	0
	Coenosia (Coenosia) tigrina Fabricius	2	PR	0	3	0	4	1	0	6	6	0
	Coenosia (Limosia) ?bonita Huckett	1	PR	0	0	0	0	0	0	2	3	1

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Coenosia (Limosia) ?errans Malloch	1	PR	0	0	0	0	1	0	0	0	0
	Coenosia (Limosia) nigrescens Stein	1	PR	4	4	1	20	12	2	2	0	0
	Coenosia (Limosia) pedella (Fallén)	1	PR	0	1	0	0	1	0	0	0	0
	Coenosia (Limosia) triseta Stein	1	PR	0	0	0	3	0	1	8	1	7
	Coenosia (Oplogaster) ?intacta (Walker)	1	PR	0	0	1	0	0	0	0	2	0
	Coenosia (Oplogaster) laeta Huckett	1	PR	12	1	142	1	1	82	1	80	340
	Coenosia (Oplogaster) nigritarsis Stein	1	PR	0	0	0	0	0	0	0	25	13
	Coenosia (Oplogaster) octopunctata (Zetterstedt)	1	PR	0	0	8	0	0	0	0	0	7
	Eudasyphora cyanicolor setosa Loew	2	SAco	0	0	2	0	0	0	0	0	1
	Graphomya americana Rob.-Desv.	2	PRsu	1	0	0	0	0	0	1	0	0
	Graphomya transitionis Arntfield	2	PRsu	0	1	0	0	0	0	0	1	0
	Haematobosca alcis (Snow)	1	SAco	0	0	0	0	0	0	1	0	0
	Helina aldrichi Snyder	2	PR	2	1	4	1	0	0	1	1	4
	Helina duplicata (Meigen)	2	PR	0	0	0	1	0	0	0	1	0
	Helina troene (Walker)	2	PR	1	0	0	0	0	0	2	0	0
	Helina sp. 1	2	PR	0	0	1	0	0	0	0	0	0
	Helina sp. 2	2	PR	0	0	1	0	0	0	0	0	0
	Helina sp. 3	2	PR	0	1	0	0	0	0	0	0	0
	Helina sp. 4	2	PR	0	1	0	0	0	0	0	0	0
	Hydrotaea militaris (Meigen)	2	PR	0	0	0	0	1	2	0	2	1
	Hydrotaea pilitibia Stein	2	PR	1	0	0	0	0	0	0	0	0
	Hydrotaea scambus (Zetterstedt)	2	PR	1	0	14	2	1	8	0	0	0
	Hydrotaea unispinosa Stein	2	PR	0	0	0	0	0	1	0	2	0
	Limnophora discreta Stein	1	PR	1	0	0	0	0	0	0	0	0
	Lispe albitarsis Stein	2	PR	0	0	0	2	0	0	0	0	1
	Lispe cotidiana Snyder	2	PR	0	0	0	0	0	0	1	0	0
	Lispe nasoni Stein	2	PR	0	0	0	1	0	0	0	0	0
	Macrorchis ausoba (Walker)	2	?	5	2	0	0	0	0	1	0	0
	Morellia sp. 1	2	SAco	0	0	1	0	0	0	0	1	0
	Morellia sp. 2	2	SAco	0	0	1	0	0	0	0	0	2

Families	**Species**	**Size class**	**Trophic group**	**BB-A**	**BB-R**	**BB-N**	**CL-A**	**CL-R**	**CL-N**	**SC-A**	**SC-R**	**SC-N**
	Musca autumnalis DeGeer	2	SAco	2	0	0	3	4	2	0	1	0
	Muscina assimilis (Fallén)	2	OM	44	4	11	13	9	10	21	38	5
	Muscina pascuorum (Meigen)	2	OM	1	2	0	0	0	0	1	0	0
	Muscina stabulans (Fallén)	2	OM	1	0	0	3	0	0	1	0	0
	Mydaea ?impedita Stein	2	PRco	1	0	0	1	0	0	0	0	0
	Mydaea ?nubila Stein	2	PRco	0	1	1	1	0	0	0	0	0
	Mydaea obscurella Malloch	2	PRco	0	1	0	0	1	1	0	0	0
	Mydaea occidentalis Malloch	2	PRco	0	1	1	1	0	0	0	0	0
	Mydaea urbana (Meigen)	2	PRco	0	0	4	0	0	0	0	0	0
	Myospila meditabunda (Fabricius)	2	PRco	1	0	0	1	0	0	0	0	2
	?Neomyia cornicina (Fabricius)	1	SAco	0	1	0	0	0	0	0	0	0
	Phaonia ?consobrina Zetterstedt	2	PR	1	0	0	0	0	0	0	0	0
	Phaonia apicata Johannsen	2	PR	0	0	0	0	0	0	0	4	0
	Phaonia bysia (Walker)	2	PR	0	0	0	1	0	1	0	0	0
	Phaonia serva Fallén	2	PR	7	8	6	1	1	0	0	1	0
	Phaonia solitaria Stein	2	PR	0	0	0	1	0	0	0	0	0
	Phaonia sp. 1	2	PR	1	1	1	0	0	0	0	108	0
	Phaonia sp. 2	2	PR	1	0	0	0	0	0	0	0	0
	Phaonia sp. 3	2	PR	1	0	1	1	0	0	0	0	0
	Phaonia sp. 4	2	PR	0	0	1	0	0	0	0	0	0
	Phaonia sp. 5	2	PR	0	0	0	0	1	0	0	1	1
	Potamia querceti (Bouché)	2	OM	0	0	0	0	0	1	0	0	0
	Schoenomyza chrysostoma Loew	1	?	2	1	0	2	3	0	16	1	0
	Schoenomyza dorsalis Loew	1	?	1	1	0	0	0	0	12	0	0
	Spilogona ?rufitibia Stein	1	PR	2	0	0	0	0	0	0	0	0
	Spilogona ?semiglobosa Ringdahl	1	PR	0	1	2	0	0	0	0	0	0
	Spilogona fatima Huckett	1	PR	0	3	2	0	0	0	0	0	1
	Spilogona narina Walker	1	PR	7	9	13	0	3	4	0	0	0
	Spilogona suspecta Malloch	1	PR	1	0	2	2	0	0	0	0	2
	Spilogona sp. 1	2	PR	2	2	17	0	0	8	0	0	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Spilogona sp. 2	1	PR	0	0	2	0	0	0	0	1	1
	Spilogona sp. 3	1	PR	0	0	5	0	1	0	0	0	0
	Spilogona sp. 4	1	PR	0	0	0	1	0	0	0	0	0
	Spilogona sp. 5	1	PR	0	1	1	0	0	0	0	0	0
	Spilogona sp. 6	1	PR	0	0	1	0	0	0	0	0	0
	Spilogona sp. 7	1	PR	0	0	1	0	0	0	0	0	0
	Stomoxys calcitrans (Linnaeus)	2	SAco	0	0	0	1	1	0	1	1	0
	Thricops innocuus (Zetterstedt)	2	PR	2	2	1	0	0	0	0	0	0
	Thricops spiniger (Stein)	2	PR	0	2	1	0	0	0	0	0	0
Calliphoridae	*Calliphora vomitoria* (Linnaeus)	3	?	0	1	0	0	0	0	0	0	0
	Cynomya cadaverina Rob.-Desv.	3	SAne	2	4	2	3	1	4	0	0	1
	Lucilia illustris (Meigen)	2	SA	2	0	1	2	0	3	0	1	0
	Opsodexia sp.	2	?	0	0	3	0	0	0	0	1	0
	Phaenicia sp.	2	?	1	0	0	0	0	0	0	0	0
	Phormia regina (Meigen)	2	SAne	4	0	0	0	0	0	0	0	0
	Pollenia pediculata Macquart	2	PA	3	0	0	1	0	0	0	2	0
	Pollenia rudis (Fallén)	2	PA	273	67	4	20	16	13	0	2	0
	Protocalliphora sp.	2	PA	0	0	0	1	0	0	0	0	0
Sarcophagidae	*Agria housei* Shewell	2	PA	0	0	0	0	0	2	0	0	0
	Blaesoxipha (Acridiophaga) kyrtonidion Pape	2	PA	16	14	0	5	6	15	0	0	0
	Blaesoxipha (Acridiophaga) reversa Aldrich	2	PA	29	5	0	4	6	9	0	0	0
	Blaesoxipha (Servaisia) falciformis Aldrich	2	PA	0	0	0	1	0	1	0	4	0
	Blaesoxipha (Tephromyia) hunteri Hough	2	PA	0	0	0	2	2	5	0	0	0
	Boettcheria cimbicis (Townsend)	2	SA	28	43	35	9	27	62	8	27	36
	Boettcheria latisterna Parker	2	SA	20	14	22	1	14	131	5	27	17
	Brachicoma devia Fallén	2	PA	2	8	2	3	12	8	0	3	11
	Fletcherimyia fletcheri (Aldrich)	2	SA	9	137	4	0	32	6	8	2	58
	Helicobia rapax (Walker)	1	SA	0	0	0	0	1	0	0	0	0
	Metopia sp.	1	PA	0	0	0	1	0	1	0	1	1
	Ravinia acerba Walker	2	SAco	2	2	0	1	0	0	0	4	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Ravinia anxia Walker	2	SAco	3	2	0	0	0	0	4	2	0
	Ravinia querula Walker	3	SAco	1	0	0	0	2	3	3	1	0
	Ravinia stimulans Walker	2	SAco	0	2	0	0	4	8	0	5	2
	Sarcophaga (Bercaeopsis) sarraceniae Riley	2	SA	6	60	0	1	11	4	2	9	23
	Sarcophaga (Helicophagella) melanura Meigen	2	PR	2	1	0	1	4	1	0	1	0
	Sarcophaga (Liosarcophaga) shermani Parker	2	OM	3	1	0	0	0	2	0	0	0
	Sarcophaga (Robineauella) nearctica (Parker)	3	SAne	1	0	1	0	0	2	0	0	0
	Sarcophaga (Sarcotachinella) sinuata Meigen	2	PA	8	25	2	3	22	8	4	5	3
	Sarcophaga aldrichi Parker	3	PA	5	4	1	3	1	8	1	0	1
	Sarcophaginae spp. *? ?*	N/A	?	2	2	1	0	1	0	0	0	3
	Senotainia trilineata (Wulp)	1	PA	2	0	0	10	0	0	0	0	0
	Taxigramma hilarella Zetterstedt	1	PA	0	0	0	0	0	0	0	1	0
Tachinidae	*Admontia* sp.	2	PA	5	0	0	2	0	0	0	1	0
	Archytas apicifer (Walker)	3	PA	0	0	0	0	2	3	0	0	0
	Archytas aterrimus (Rob.-Desv.)	3	PA	0	2	1	1	0	3	0	2	5
	Athrycia cinerea (Coquillett)	2	PA	0	0	0	0	0	1	0	0	0
	Blepharomyia sp.	2	PA	0	0	0	0	0	1	0	0	0
	Blondelia sp.	2	PA	0	0	0	0	0	0	0	0	1
	Campylochaeta orbitalis Webber	2	PA	0	1	0	0	0	2	0	0	0
	Campylochaeta semiothisae (Brooks)	2	PA	0	0	0	0	0	1	0	3	3
	Campylochaeta sp. 1	1	PA	0	0	0	0	1	0	0	0	1
	Campylochaeta sp. 2	1	PA	0	0	0	0	0	0	0	0	1
	Carcelia sp.	2	PA	0	0	0	0	0	0	0	0	1
	Catharosia sp.	1	PA	0	0	0	0	0	0	0	15	0
	Chrysotachina slossonae (Coquillett)	2	PA	0	0	0	2	0	0	0	0	0
	Cryptomeigenia sp.	2	PA	0	0	0	0	1	0	0	0	0
	Cylindromyia interrupta (Meigen)	2	PA	0	0	0	2	0	1	0	1	0
	Cylindromyia sp. 1	2	PA	0	0	0	0	0	0	0	0	1
	Cylindromyia sp. 2	2	PA	0	0	0	0	0	0	1	0	0
	Cyrtophleba sp.	2	PA	4	2	0	0	3	0	0	0	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	?Dichocera sp.	3	PA	1	0	0	0	0	0	0	0	0
	Distichona sp.	2	PA	0	0	0	0	0	1	0	0	0
	Eribella sp.	2	PA	2	0	0	0	0	0	0	0	0
	Eulasiona sp.	2	PA	0	0	0	0	0	0	0	1	0
	Gonia contumax Brooks	3	PA	2	0	0	0	0	0	0	0	0
	Gonia sp. 1	3	PA	1	0	0	0	0	0	0	0	0
	Gonia sp. 2	3	PA	0	1	0	0	1	0	0	0	0
	Graphogaster sp.	1	PA	0	0	0	0	0	0	0	1	0
	Gymnocheta ?rufipalpis Brooks	2	PA	0	0	0	1	0	0	0	1	0
	Gymnosoma sp.	2	PA	0	0	0	0	1	0	0	0	0
	Hemyda aurata Rob.-Desv.	3	PA	1	0	0	0	0	0	0	0	0
	Jurinia pompalis (Reinhard)	2	PA	0	0	0	1	0	0	0	0	0
	Lixophaga opaca Reinhard	2	PA	10	9	21	1	0	3	0	1	5
	?Lixophaga spp.	2	PA	6	4	7	0	0	2	0	0	1
	Lydina americana complex	2	PA	0	7	1	5	1	0	1	0	0
	Lypha sp.	1	PA	0	0	0	0	0	0	0	1	0
	Madremyia ?saundersii (Williston)	2	PA	0	0	0	0	1	0	0	0	0
	Myiopharus sp.	1	PA	0	0	0	0	0	0	0	0	2
	Neaera sp.	1	PA	0	0	0	1	1	0	0	0	0
	Neomintha sp.	2	PA	0	0	0	0	1	0	0	0	0
	Nilea sp.	2	PA	0	0	0	0	0	1	0	0	0
	?Opsomeigeinia sp.	1	PA	0	0	0	0	0	0	0	0	1
	Panzeria sp.	2	PA	0	0	0	0	0	0	0	0	1
	Peleteria sp.	2	PA	0	0	0	0	0	2	0	0	0
	Periscepsia helymus (Walker)	1	PA	1	0	0	0	1	2	0	0	0
	Periscepsia laevigata van der Wulp	1	PA	2	1	0	0	0	0	0	0	1
	?Platymya sp.	2	PA	1	30	5	3	2	3	2	0	2
	Phasia sp.	2	PA	1	3	0	2	1	1	0	1	0
	Phebellia sp.	2	PA	1	0	0	0	0	0	0	0	0
	Phorocera sp.	2	PA	0	1	0	0	0	0	0	0	0

Families	Species	Size class	Trophic group	BB-A	BB-R	BB-N	CL-A	CL-R	CL-N	SC-A	SC-R	SC-N
	Phryxe sp.	2	PA	0	1	0	0	2	1	0	0	0
	Prooppia crassiseta (Aldrich & Webber)	2	PA	0	0	0	0	0	0	1	0	0
	Siphona cristata Fabricius	1	PA	0	0	1	0	0	0	0	0	0
	Siphona intrudens Curran	1	PA	0	0	0	0	0	0	1	0	14
	Spallanzania sp.	2	PA	0	0	0	0	1	0	0	0	0
	Tachina sp.	3	PA	0	0	0	1	0	0	0	0	0
	Tachina algens Wiedemann	3	PA	0	1	0	2	2	0	0	0	0
	Tachinomyia panaetius (Walker)	3	PA	1	0	0	0	0	0	0	0	0
	Tachinomyia variata Curran	3	PA	0	0	0	0	0	1	0	1	0
	Winthemia sp. 1	2	PA	0	1	0	0	0	0	0	0	0
	Winthemia sp. 2	2	PA	0	1	0	0	0	0	0	0	0
	Winthemia vesiculata (Townsend)	2	PA	0	0	0	0	1	0	0	0	1
	Xanthomelanodes sp.	2	PA	0	0	0	0	0	1	0	0	1
	Brachycera totals			2809	1741	1251	2687	1635	1435	6025	2969	1674

Appendix 2.2: Soil chemistry (Mean ± SD), pH and field moisture of peat samples collected in each site.

	BB-N	BB-R	BB-A	CL-N	CL-R	CL-A	SC-N	SC-R	SC-A
pH	3,71	3,77	3,82	3,5	3,59	4,19	3,69	3,65	3,91
N/NO3 (mg/kg)	4,2 ± 2,1	5,7 ± 1,4	2,4 ± 0,13	4,2 ± 0,039	2,9 ± 0,036	19 ± 2	8 ± 1,3	5,8 ± 1,4	15 ± 0,27
N/NH4 (mg/kg)	12 ± 3,5	12 ± 4,7	14 ± 3	30 ± 0,78	7,9 ± 1,2	41 ± 3,4	32 ± 3,6	13 ± 1,6	17 ± 0,11
N (mg/kg)	16 ± 5,7	17 ± 6,1	16 ± 3,1	34 ± 0,82	11 ± 1,2	60 ± 5,4	40 ± 4,8	19 ± 3	32 ± 0,16
P (mg/g)	0,52 ± 0,002	0,26 ± 0,053	0,33 ± 0,015	0,62 ± 0,052	0,28 ± 0,0097	0,3 ± 0,007	0,58 ± 0,0002	0,27 ± 0,031	0,62 ± 0,01
Ca (mg/g)	1,31 ± 0,46	2,85 ± 0,41	4,24 ± 0,049	2,70 ± 0,41	1,93 ± 0,14	4,57 ± 0,4	1,81 ± 0,3	3,01 ± 0,041	1,35 ± 0,098
Mg (mg/g)	0,69 ± 0,19	1,80 ± 0,46	1,75 ± 0,0014	0,61 ± 0,065	0,4 ± 0,067	1,75 ± 0,0018	0,48 ± 0,033	0,53 ± 0,0017	0,24 ± 0,088
K (mg/g)	0,86 ± 0,25	0,17 ± 0,048	0,37 ± 0,0081	0,54 ± 0,065	0,14 ± 0,069	0,17 ± 0,039	0,72 ± 0,13	0,36 ± 0,36	0,2 ± 0,063
Na (mg/g)	0,29 ± 0,12	0,21 ± 0,052	0,19 ± 0,06	0,16 ± 0,06	0,082 ± 0,026	0,17 ± 0,0005	0,15 ± 0,044	0,095 ± 0,039	0,14 ± 0,04
Zn (mg/kg)	14± 1,9	6,3 ± 2,3	2 ± 2,4	23 ± 3	0,35 ± 0,5	4,4 ± 1,4	55 ± 9,1	6,3 ± 0,7	25 ± 4,6
Fe (mg/g)	0,079± 0,099	0,14 ± 0,094	0,43 ± 0,041	0,24 ± 0,17	0,39 ± 0,026	0,38 ± 0,035	0,20 ± 0,06	0,24 ± 0,0027	0,37 ± 0,059
Mn (mg/kg)	47 ± 3,6	25 ± 7	32 ± 1,6	107 ± 33	16 ± 11	44 ± 8,7	35 ± 9,2	53 ± 1,6	60 ± 15
Field moisture	2	2	1	1	3	1	1	2	1

Appendix 2.3: Vegetation cover at study sites. Cover classes are as follow: 0 (<1%), 1 (1-5%), 2 (6-25%), 3 (26-50%), 4 (51-75%), 5 (76-100%)

	BB-N	BB-R	BB-A	CL-N	CL-R	CL-A	SC-N	SC-R	SC-A
Sphagnum	3	3	0	3	2	0	3	2	0
Other mosses	0	3	1	1	2	1	0	3	2
Lichens	1	0	1	0	0	0	1	0	0
Herbs	0	0	0	0	0	1	0	2	1
Ericaceous shrubs	4	3	2	5	3	0	5	3	0
Trees	4	1	3	2	1	0	4	5	2
Grasses/ Sedges	0	4	2	0	5	2	0	3	4
Horsetails	0	0	3	0	0	1	0	0	0
Bare peat	0	0	3	0	1	4	0	2	3
Open water	0	0	0	0	1	0	1	0	0

CHAPTER 3: GENERAL CONCLUSION

This study contributed to our understanding of Brachycera diversity in southern Quebec peatlands. Currently, only a fraction of the total number of species is described, few studies have examined the arthropod community in peatlands and even fewer have focused on Diptera. Because Brachycera were highly species rich in the three peatlands with more than 700 species identified, the Brachycera community is clearly a major component of peatland diversity that should be taken into account when assessing the success of restoration. This study provided baseline data for future monitoring of Brachycera in restored peatland habitat. By comparing restored areas to disturbed areas and not only to reference areas, it provided valuable information on the resilience of Brachycera and on the impact of peat-mining on community composition.

Given the intensive human activities in Quebec peatlands, we cannot take renewal and reorganization of species for granted even after the restoration processes. The success of restoration in this study was determined on the basis of the recovery of Brachycera community composition and diversity at different organizational levels (taxon, size class, trophic group). Functional diversity is an important component of biodiversity, because functional organization reflects combination of species based on their exploitation of resources, regardless of taxonomic affiliation, and this can lead to different responses to ecosystem changes than taxonomic relationships.

The results from this study showed that Brachycera were resilient to perturbation following peat mining and restoration in the St.Lawrence region, because the overall community composition was not significantly different among the three treatments. On the other hand, the abandoned areas generally supported lower species richness, lower evenness and different species abundance distribution than restored and natural areas, indicating that restoration enhanced the recovery of high species diversity. However, seven years were not sufficient to recover a complete trophic structure or to enable species with low dispersal ability (such as many acalyptrate Diptera) to recolonize to pre-disturbance levels of diversity, because restored areas were not significantly different in trophic, acalyptrate and small size class composition to abandoned areas. However, there was a successful recolonization of saprophages and predators in restored areas as indicated by the diversity estimates. Changes in substrate quality and vegetation structure led to increase abundance of saprophages and predators in the abandoned areas and, to a lesser degree, in the restored areas. Overall, the coverage of bare peat, *Sphagnum* mosses and ericaceous shrubs explained most of the variance in species composition among treatment types. It is clear from observation of the environmental conditions, trophic structure and body size distribution that the restored sites are not fully functioning peatland ecosystems after seven years; although as the sites age they will probably tend toward a natural peatland.