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USE OF MACROINVERTEBRATES IN BIOASSESSMENT OF LAND USE AND WATER QUALITY IN NORTHERN MONGOLIA

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USE OF MACROINVERTEBRATES IN BIOASSESSMENT OF LAND USE AND
WATER QUALITY IN NORTHERN MONGOLIA

A Dissertation
Presented to
the Graduate School of
Clemson University

In Partial Fulfillment
of the Requirements for the Degree
Doctor of Philosophy
Entomology

by

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August 2014

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ABSTRACT

Land-use practices in Mongolia lead to habitat degradation and consequently affect the structure and function of biological communities. There is no accepted bioassessment technique for determining the ecological consequences of habitat degradation on biological communities and water quality in Mongolia, such that a monitoring and management program suitable for Mongolia is sorely needed.

Both a trait-based approach and the North American Rapid Bioassessment Protocol (RBP) metrics were tested with macroinvertebrates to determine the performance and applicability of these approaches for predicting general ecological responses of freshwater and terrestrial communities to habitat variation due to overgrazing and mining in northern Mongolian streams. Significant declines in functional diversity were observed by TBA with greater levels of land use intensity (more grazing and mining), and 13 of 16 traits (such as reproduction, life stages, resistant form, dissemination method, locomotion and substrate relation, feeding habit, food, saprobity, temperature, trophic level, current velocity, and substrate preferendum) varied significantly among different levels of land-use intensity. There were no significant differences observed among traits associated with an r/K reproductive strategy among the sites.

In addition, complying with the RBP protocols, taxonomic richness and diversity and the number of taxa deemed intolerant to disturbance were significantly lower in sites with more grazing and mining than in more natural sites. However, despite the fact that

mayflies are generally associated with low levels of disturbance, the abundance of mayflies (Ephemeroptera) and the percentage of taxon richness and abundance of mayflies was higher in sites with greater land-use intensity. Also, the RBP biotic index classification system for water quality was not well suited for use with Mongolian taxa.

To determine the level of taxonomic resolution needed for accurate functional description, I compared functional diversity and trait responses from a coarse taxonomic level and from species-level resolution in one genus of macroinvertebrates (*Simulium*). Species-level resolution provided more information than genus-level resolution for some traits related to habitat association, but species-level resolution did not improve discrimination of land-use impacts substantially.

Furthermore, I assessed land-use effects on terrestrial communities. Crane flies (Diptera: Tipuloidea) are a diverse group and vulnerable to habitat destruction because of their semi-terrestrial habit. Livestock grazing effects on crane fly diversity were tested among sites with different levels of grazing intensity. Species richness and diversity of crane flies were lower for moderately and highly grazed valleys than for the lightly grazed valleys. Soil moisture, plant biomass, and livestock number were the most significant predictors of variation in crane fly diversity across the grazing gradient.

Overall, my study showed a strong relationship between functional and taxonomic structure of the macroinvertebrate community and habitat conditions. Generally, TBA and taxonomic approaches discriminated seminatural sites from sites with greater levels of land-use intensity. However, TBA provided a more direct explanation for macroinvertebrate responses to land-use and therefore may be more reliable for a future

freshwater biomonitoring program in Mongolia. Species-level resolution may not be necessary for discriminating intensities of grazing and mining. Semiterrestrial crane fly community responses accurately reflected intensities of grazing in northern Mongolia.

Among the results, there is a strong relationship between community structure and habitat condition. Habitat filtering determines variability of macroinvertebrate community observed among sites.

DEDICATION

I dedicate this dissertation to my family for their endless love, support and inspirations. A special thanks to my husband Khishigbold for his tireless support while doing hard inexperienced jobs here in the US and standing by me through the good times and bad; my beloved daughters Tsomorlig, Erdem and Uyaral for being such good girls and always cheering me up spiritually throughout my life; my parents and siblings for all their love and encouragements.

I also dedicate this work and express my heartfelt gratitude to Mrs. Suzanne Morse and Dr. John Morse for being my daughters' grandparents and sharing my overwhelming family responsibilities throughout these years.

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CHAPTER ONE

INTRODUCTION

Freshwater systems of Mongolia

Mongolia is a landlocked country in north central Asia far from oceanic influences and comprises a high plateau surrounded by mountain ridges in the transition between Siberian taiga forest and Central Asian desert (Nandintsetseg et al. 2007). Mongolia has a severe continental climate with large daily and seasonal temperature amplitudes and low precipitation. The increase of aridity from north to south causes an uneven development of river networks. Rivers are concentrated in the northern part of the country (Hilbig 1995).

There are over 4000 rivers in Mongolia originating from the Central Asian high mountain ranges and over 3500 lakes located mainly in the mountains and intermountain depressions belonging to three international river basins: the Arctic Ocean Basin, the Pacific Ocean Basin, and the Central Asian Internal Drainage Basin (Hilbig 1995; Davaa 2007) (Fig.1.1). The Arctic Ocean Basin covers about 68 percent of Mongolia's territory including the Selenge River, Hövsgöl Lake, and Tuul River basins; the Pacific Ocean Basin covers 20 percent of Mongolia's territory including the Kherlen, Onon, Ulz, and Khalkh River basins; the Central Asian Internal Drainage Basin covers 12 percent of Mongolia's territory including the Great Lakes, Northern Gobi, and Southern Gobi basins (Asia Foundation 2009).

The total volume of surface water in Mongolia has been estimated as 599 km³ per year and includes 83.7% in lakes, 10.5% in glaciers and 5.8% in rivers

(Batnasan 2003). Mongolia is one of 60 countries with limited water resources and total water consumption is approximately 540 million m³ per year, with over 80% percent consumed by industrial and agricultural uses and 20% by domestic uses (UNEP 2011).

Major land use issues

At present, both the aquatic and terrestrial ecosystems are being degraded by anthropogenically induced impacts of overgrazing, irresponsible mining, deforestation, urbanization, inefficient water management, and climate change (Asia foundation 2009). In recent years, mining activities have increasingly affected water quantity and quality by using large amounts of ground and surface water (Javzan et al. 2004); using outdated extraction methods such as dredging or diverting rivers, resulting in dry or intermittent small streams (Byamba and Todo 2011); and by contaminating waterways with toxic substances including heavy metals (Inam et al. 2010). In addition, overgrazing has decreased plant biomass and diversity and tends to shift grassland to more desert like conditions (Altanbagana and Chuluun 2010) with impacts to surface waters. Major land use impacts on freshwater ecosystems result especially from overgrazing, and mining throughout Mongolia.

Mongolians have practiced a nomadic lifestyle for over 3000 years. Livestock husbandry is the mainstay of the Mongolian economy and accounts for 80% of agricultural output; pasturelands cover 75% of the total Mongolian territory (1,565,000 km²). A total of 40.9 million livestock were counted at the end of 2012 (Info Mongolia 2013).

During Communist rule, the government strictly regulated the allocation of pasture, the size and type of herds, and the rotation of pastures. After the collapse of the Communist system in Mongolia in 1991 and the resulting privatization of livestock, the number of pastoral households doubled and the animal stocking rate has been increasing over time significantly. As a result, the traditional rotation pattern of grassland use and pasture management practices has been abandoned because of a number of economic, political, social, and environmental factors (MoMo Consortium 2009). Traditional herd composition has also shifted, and the number of goats has almost doubled due to the increased price of cashmere (Lise et al. 2006). Uniquely among all Mongolian livestock, goats uproot vegetation; for this reason, they have the most negative impact on pastures of all of the livestock (Batnasan 2003). The combination of overstocking, overgrazing, and changes in traditional livestock herding practices have increased the ecological vulnerability of Mongolian grasslands (Altanbagana and Chuluun 2010).

Mining has been a rapidly growing industry for the last two decades in Mongolia, accounting for 30% of the gross national product and 81% of exports, with the most important commodities being copper, molybdenum, gold, coal, and fluorspar concentrates. The majority of Mongolia's mines are placer, or surface mines, which mine alluvial deposits of minerals—primarily in the sand and gravel of rivers and streams. Mongolia has issued 4,706 valid mineral licenses, of which 3,610 are exploration permits and 1,096 are mining licenses (Mining technology 2010). Many smaller mining activities, including illegal mining activities, are being

undertaken, particularly in stream and river beds (Tumurchudur and Davaa 2012).

Mining industries consume water chiefly for the washing of deposits; 63% of this is from groundwater and 37% from surface water (Mun et al. 2008).

Effects of overgrazing and mining on freshwater ecosystems

Overgrazing. Livestock grazing can have direct effects on watersheds, such as plant biomass reduction, alteration of plant species composition, increased nitrates from dung and urine, soil erosion, soil compaction, habitat diversity reduction and water turbidity resulting from livestock trampling (Reeves and Champion 2004).

Overgrazing has significant consequences for stream ecosystems, including flooding, loading of sediments and nutrients such as nitrogen and phosphates (Quinn and Stroud 2002, Maasri and Gelhaus 2011), and alteration of stream food webs through changing light, nutrient, and organic-matter dynamics (Dolédec et al. 2006).

Overgrazing can affect either negatively or positively the densities of certain taxa associated with habitat modifications (Quinn 1992), community structure (Scrimgeour and Kendall 2003), and functional traits of macroinvertebrates (Dolédec et al. 2006). Sensitive aquatic organisms can be eliminated by eutrophication, substrate simplification, algal mat formation, bacterial pollution, acute toxicity, increased insolation, loss of riparian vegetation and other harborage for adults, dominance of burrowing taxa due to burying of solid substrate habitat, increase of suspended solids, and burial of hyporheic zone (Strand and Merritt 1999).

Mining. In placer mining operations, vegetation and fertile topsoil are removed and river-bed morphology is changed (Tumurchudur and Davaa 2012).

Mining increases turbidity (by input of suspended mineral particles), sediment deposition (Wagener et al. 1985), introduction of nutrients especially phosphorus (Stubblefield et al. 2005), contamination with heavy metals (Inam et al. 2010), all of which degrade habitat quality (Wood and Armitage 1997). Fine sediment loads affect benthic macroinvertebrate communities in several different ways, such as altering suitability of substrate for some taxa (Richard and Bacon 1994), increasing drift (Culp et al. 1986), affecting respiration due to low concentrations of oxygen (Erikson 1968), and interfering with feeding activities by impeding filter feeding (Aldridge et al. 1987) or reducing food availability (Graham 1990). However, positive effects of increases of fine sediments have been observed for some taxa such as Chironomidae midges (Dudgeon 1994), Oligochaeta worms, and Sphaeriidae fingernail clams (Armitage 1995). Metal can have toxic effects on aquatic organisms through absorption from heavy metal contaminated water, sediments, or food (Rainbow 1996). Furthermore, the increased suspended solids, fine sediments, and heavy metal contamination reduce density, biomass, diversity, and taxonomic composition of invertebrates (Wagener et al. 1985, Quinn et al. 1992, Avlyush 2011).

Water quality monitoring perspectives

Mackie (2004) stated, “Bioassessment is the evaluation of water quality based on analysis of species assemblages of communities of aquatic organisms, or of their products (e.g., chlorophyll a).” Biomonitoring is a biological assessment of environmental changes, due mainly to anthropogenic causes, in order to keep under

systematic review the quality of the environment over a period of time. Traditional physical-chemical and more modern biomonitoring approaches have their own strengths and weakness. While the physical-chemical approach can identify the type of stressor, biomonitoring can detect cumulative or synergetic effects of multiple stressors and magnitude of the effects (Mackie 2004). Rosenberg and Resh (1993) made the analogy that a physical-chemical approach is like a photographic snapshot, describing instantaneous conditions when the sample is collected, whereas biomonitoring is more like a continuous video because resident organisms “sample” conditions continuously over long periods of time.

The most commonly used groups of organisms for biomonitoring are benthic macroinvertebrates (Mackie 2004). Benthic macroinvertebrates are a useful group of organisms for biomonitoring because they are ubiquitous, diverse (with a wide range of environmental requirements), and abundant (providing statistically meaningful numbers of individuals in samples); they are relatively sedentary (unable to avoid unfavorable environmental changes); they have long life cycles relative to other aquatic organisms (thereby reflecting environmental conditions over longer periods of time), and they are highly responsive to environmental stress (Rosenberg and Resh 1993). Biomonitoring can be accomplished by (1) surveillance before and after an impact (Smith 1993), (2) comparing a test site with water quality standards (Yoder and Rankin 1998), or (3) comparing a test site with a reference (control) site (Charvet et al. 2000, Dolédec et al. 2006).

There are two main bioassessment approaches using benthic macroinvertebrates: a taxonomic approach including single metric and multimetric indices and a trait-based approach.

The taxonomic approach is derived from the “niche concept.” An ecological niche is a multi-dimensional hypervolume, and it includes all of the factors that a species needs to survive, grow and reproduce (Hutchinson 1957). According to the niche concept, each species has special abilities to exploit resources (Schmidt-Kloiber and Nijboer 2004).

Single Metric Indices: Many different single metrics and indices as well as multimetric indices have been developed and used for biomonitoring programs based on the benthic macroinvertebrate community in different countries. They include the saprobic system, Biological Monitoring Working Party Score, the Average Score per Taxon and biotic index. Each is described below.

Saprobic System: This is based on an organism's tolerance limits to organic pollution within different saprobic levels or gradually self-purifying habitat zones downstream of a pollution source: The polysaprobic zone (most polluted), the α - mesosaprobic zone, the β -mesosaprobic zone, and the oligosaprobic zone (least polluted). The sum of saprobic values multiplied by the number of individuals for each of the indicator taxa (identified at family or genus or species level) at the sampling point is divided by the sum of the frequency (percentage of occurrence) for the indicator taxa, providing a mean saprobic value for the sample (Mackie 2004).

Biological Monitoring Working Party Score (BMWP, 1978): A score system between 1 and 10 based on an organism's tolerance value to organic pollution was developed in the UK and has been adjusted for the different faunas of many different countries (Birk and Hering 2006). The greater the tolerance of a taxon for pollution, the lower the BMWP scores.

The Average Score per Taxon (ASPT): The average tolerance score of all taxa (family level) within the community ranges from 0 to 10 and is calculated by dividing the BMWP by number of taxa represented in the sample (Armitage et al. 1983).

Biotic index (BI): classifies the organisms according to their tolerance to water pollution. The Biotic Index provides a single 'tolerance value', which is the average of the tolerance values of all taxa within the community. The Biotic Index was subsequently modified and expanded by many workers to provide, for example, The Trent Biotic Index (Woodiwiss 1964); Chandler's Biotic Score (Chandler 1970); Hilsenhoff's Family Biotic Index (Hilsenhoff 1988); Biotic Index (genus/species level) (Lenat 1993).

Multimetric Index: provides a score that represents the overall relationship between the combined values of multiple metrics observed in a given site and expected values under reference conditions. A variety of metrics can be used, such as taxa richness, composition, and functional feeding group metrics (Barbour and Yoder 1999, Hering et al. 2006, Stoddard et al. 2008, Angradi et al. 2009).

A number of standardized biomonitoring techniques are in common use and most of them are multimetric or multivariate predictive models based on the taxonomic composition of communities. Rapid Bioassessment Protocols (RBPs; RBP I, II and III), which are based on benthic macroinvertebrates, were developed in the USA. They allow rapid screening of a large number of sites. Several candidate metrics including taxon richness, taxon composition, tolerance, and functional feeding group metrics are recommended by the US Environmental Protection Agency (Barbour et al. 1999). The United Kingdom River Invertebrate Prediction and Classification System (RIVPACS), with standardized biomonitoring protocols, implements multivariate models to compare the observed fauna of macroinvertebrates at a test site with the expected fauna of reference sites, such that discrepancies between the two can be used to assess the biological impairment of that site. Often this comparison is made in terms of one or more metrics that summarize the community composition (Wright et al. 2000). The Australian River Assessment System (AUSRIVAS) is a rapid bioassessment protocol used to evaluate the biological health of Australian rivers; it incorporates water chemistry, physical form, hydrology, stream side vegetation, and aquatic organism assessments. AUSRIVAS is a predictive model based on RIVPACS (Simpson and Norris 2000). European Union Water Framework Directive (WFD). RIVPACS provided the basic principles of the WFD, which adjusts the national programs of EU member countries into an integrated framework and assesses the water quality status of water bodies

based on multivariate and multimetric quantification of aquatic organisms, including phytoplankton, macroalgae, macroinvertebrates and fish (Furse et al. 2006).

A Trait-Based Approach (TBA) is an alternative to traditional taxonomic approaches and is based on the functional differences among the species in a community associated with habitat characteristics; it is a potential method to reveal changes in communities due to disturbance and define structure of biological communities (Dolédec et al. 1999, 2008; Charvet et al. 2000; Usseglio-Polatera et al. 2000; Statzner et al. 2001; Gayraud et al. 2003; Bady et al. 2005; Poff et al. 2006). TBA was developed in Europe and has been an increasingly applied biomonitoring practice there (Dolédec et al. 1999, 2000, 2008; Charvet et al. 2000, Usseglio-Polatera et al. 2000; Statzner et al. 2001; Gayraud et al. 2003; Bady et al. 2005; and Díaz et al. 2008). TBA has also been explored in North America (e.g., Poff et al. 2010; Vieira et al. 2006), Australia (Chessman and Royal 2004), and New Zealand (Dolédec et al. 2006, 2011).

TBA was derived from a “habitat template” concept (Southwood 1977, Townsend and Hildrew 1994). Southwood (1977) outlined the habitat template concept, which states that ecological strategies of a species have evolved in response to the characteristics of habitat, and that these strategies are reflected in quantifiable life-history and biological traits. Townsend and Hildrew (1994) made the *a priori* prediction (hypothesis) of expected species traits in terms of autoecological interaction between organism and their abiotic environment. The main hypothesis

was that present-day habitat conditions should be matched by present-day traits in the organisms. The habitat template concept specifies two basic dimensions: Temporal heterogeneity indicates frequency of disturbance, and spatial heterogeneity indicates the provision of refugia for buffering against disturbance. The general prediction is that traits conferring population resilience (promoting refuge use and recolonization success, such as r- selected traits including many descendants per reproductive cycle, short generation time, small body size, short life span, parental care, or presence of relatively invulnerable life stages, asexual reproduction, etc.) or resistance (related to survival, such as firm attachment to substrates, high body flexibility, streamlined or flattened body form, dormancy or diapause, housing against desiccation, etc.) would be more common in temporally variable and spatially homogeneous habitat (Townsend and Hildrew 1994). Poff (1997) described the function of trait filters across hierarchical landscape scales ranging from microhabitat to watershed or basin for a mechanistic understanding of species-environment relationship. Only species possessing appropriate traits are likely to filter into certain environmental conditions at different scales (Poff 1997).

Species traits can also be used as measures of community functional diversity (Petchey & Gaston 2006). The Functional Diversity index (FD) is a functional trait measurement usually described by three indices: functional richness, evenness, and divergence that can describe how much volume of functional space is occupied by species, how much space is filled, and how traits deviate from the center of trait space (Mason et al. 2005). A number of different FD indices have been

proposed to quantify different aspects of functional diversity (Mouchet et al. 2010, Schleuter et al. 2010, Casanoves et al. 2011).

Mongolian bioassessment status

There is no Asian-specific bioassessment technique for water quality assessment. Some Asian countries have adjusted North American or European bioassessment methods for water quality (Morse et al. 2007). Hydrobiological studies have been conducted by several Russian and Mongolian cooperative expeditions since the late 1800s and these have focused mostly on faunistic discovery. In the late 1900s, with the introduction of courses on aquatic insects taught by J Morse at the Mongolian National University and Mongolian State Pedagogical University (Morse et al. 2007), bioassessment methods that are used in Mongolia, including aquatic insect species tolerance indices and water quality classifications, were developed based on North American protocols (Yadamsuren 2001, Erdene 2010). In recent years, Mongolian researchers and institutions have been focused on biomonitoring methods to evaluate water quality in an effort to develop a management program suitable for Mongolia.

The following research projects have been carried out and still continue with respect to water resource management and biodiversity inventory in Mongolia: The Mongolian Aquatic Insect Survey project (MAIS), in cooperation with the Institute of Meteorology, Hydrology and Environment of Mongolia (IMHE), conducted substantial work to inventory the country's aquatic insect diversity, biology, and geographical distributions and to report impacts of livestock grazing on biodiversity

through a series of field expeditions between 2003 to 2011(MAIS 2011). The Asia Foundation promoted responsible mining and natural resource management and enhanced public awareness for environmental protection (Asia Foundation 2013). The Integrated Water Resources Management (IWRM) project implemented by the Water Authority of Mongolia developed water resource plans at the national level between 2007-2012 (Deltares 2007). Surface water monitoring has been conducted through the IMHE at a total of 142 gauging stations (Fig. 1.2) on 75 streams and 12 lakes throughout Mongolia since the late 1900s. Water regime measurements are being recorded from 120 stations; water chemical samples are being taken from all 142 stations on a regular schedule (Davaa 2007), with water quality monitoring mostly relying on hydrological and chemical monitoring. For biomonitoring, benthic and planktonic samples are taken each month from April to October by staff from 64 of the 142 stations and sent to the IMHE office in Ulaanbaatar. There are two permanent, full-time aquatic biologists at the Water Division of IMHE who are responsible for processing biological samples and providing annual reports to IMHE; IHME then compiles an integrated report that is sent to the Ministry of Environment and Green Development of Mongolia for future regulatory decisions. In 2009, in order to improve the national biomonitoring program, MAIS and The Asia Foundation organized training for local IMHE field staff regarding benthic macroinvertebrate sampling techniques and provided modern field equipment.

Currently, biomonitoring results are mostly limited to taxon surveys and application of family-level (Hilsenhoff 1987) and genus-level (Lenat 1993) biotic indices (Erdene 2010). Although, Mongolia already has established a water quality monitoring system, the country is not using a national biomonitoring protocol suitable for the geographical region of Mongolia.

Structure of the dissertation

The dissertation is subdivided into five chapters. This Chapter 1 provides background information of the land use practice of Mongolia and its major effects on ecosystems and then introduces bioassessment methods and Mongolian bioassessment status. Chapter 2 examines land-uses with regard to livestock grazing and mining by comparing a trait-based and taxonomic approach. A total of 86 trait categories of 16 traits related to morphology, life history, and habitat association, in a mixture of genus or higher taxonomic levels, were used for estimating functional structure of macroinvertebrate community among three different levels of land-use intensity. Also, taxonomic richness, composition, tolerance and diversity measures were used for estimating taxonomic structure of macroinvertebrate communities. Chapter 3 presents a species-level resolution of TBA for a genus of macroinvertebrate (Simuliidae: *Simulium*) to test accuracy of community description and discrimination of land-use intensity at the species level of resolution in comparison with results from use of more inclusive taxa. The same set of traits and site categories was used in this comparison. Chapter 4 uses a taxonomic approach to determine the effects of livestock grazing on the semi-terrestrial crane fly

community, comparing sites with different levels of grazing intensity. In this study, I did not consider mining effects. Crane fly species diversity was measured through species richness, evenness, and diversity indices. Sample-based rarefaction analysis was performed to predict rarified and estimated species richness. Finally, chapter 5 includes a brief summary of the study and summarizes overall findings of this research, limitations, and future directions.

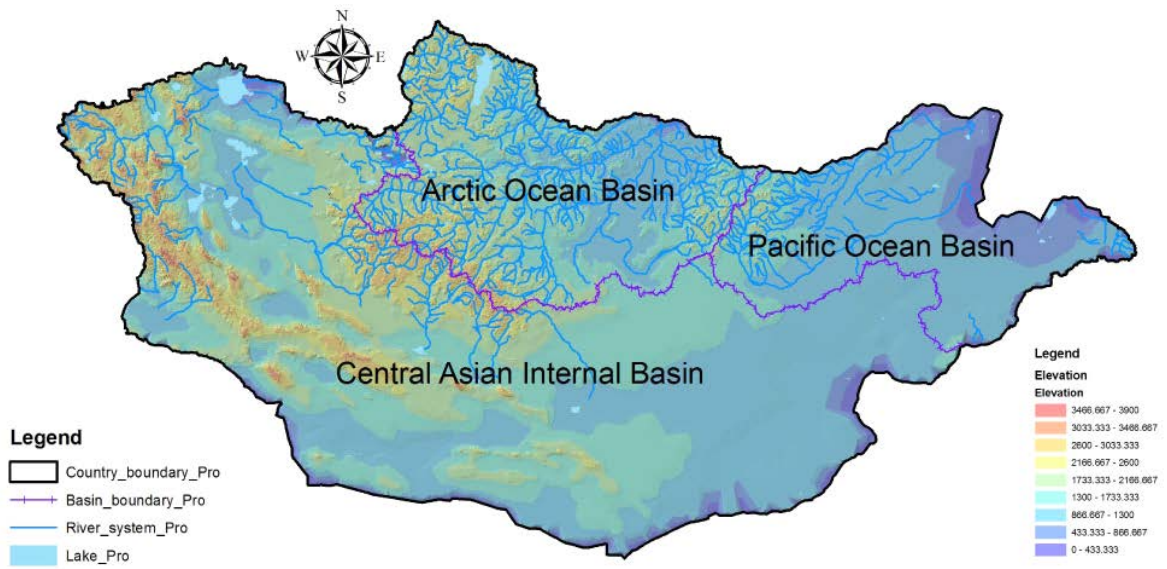


FIG. 1.1 Map of Mongolia showing major river basins and elevation range.

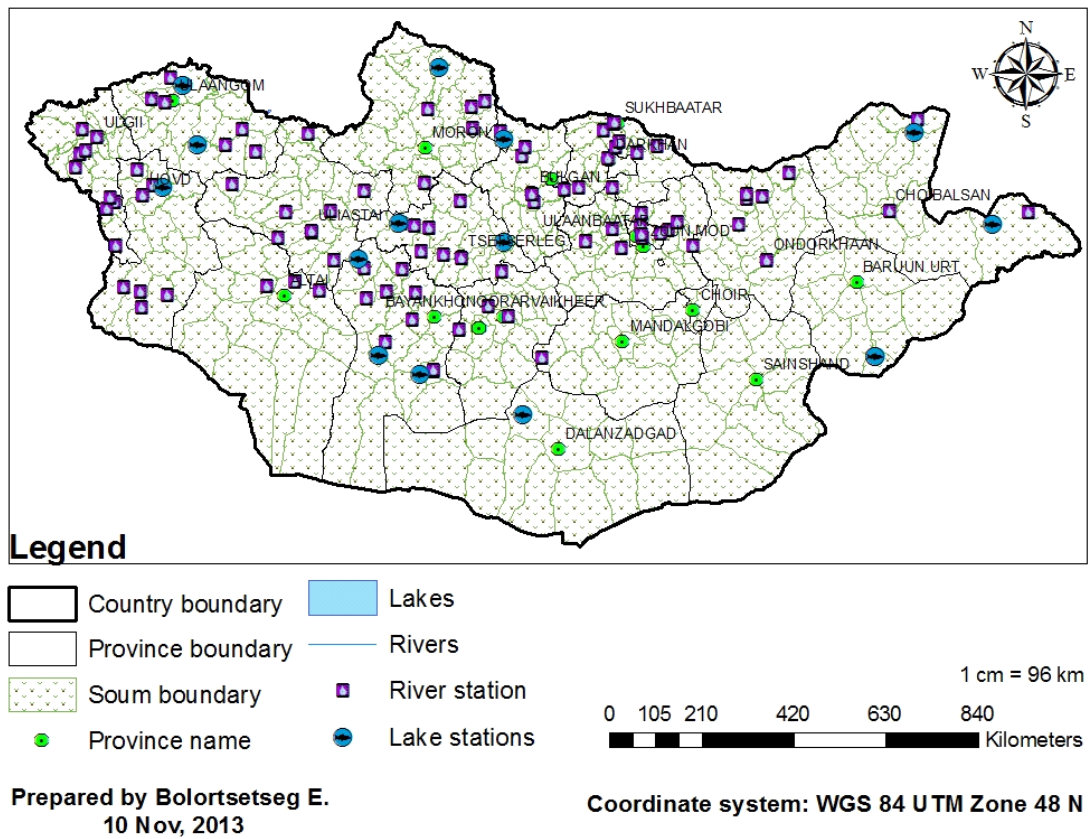


FIG. 2.2 Map of Mongolia showing the location of water quality monitoring stations of Mongolia.

CHAPTER TWO

MACROINVERTEBRATE COMMUNITY RESPONSES TO LAND USE IMPACTS: COMPARISON TRAIT-BASED AND TAXONOMIC APPROACHES FOR FRESHWATER BIOMONITORING IN MONGOLIA

Abstract

There is no accepted bioassessment technique for determining ecological consequences on freshwater biological communities in Mongolia, such that a water quality and management program suitable for Mongolia is sorely needed. The study aim was to examine macroinvertebrate community responses to grazing and mining in order to determine land-use effects on macroinvertebrate communities, to compare trait-based and taxonomic approaches, and to evaluate the applicability of these bioassessment approaches in northern Mongolia. The functional structure of macroinvertebrate communities was examined using 86 categories of 16 traits. Significant declines in functional diversity were observed with increased land-use (grazing coupled with mining) intensity. Functional diversity was highest for seminatural sites, intermediate for moderate land-use intensity, and lowest for high land-use intensity. A total 13 of 16 traits varied significantly among different levels of land-use intensity. There were no significant differences observed among traits associated with r/K reproductive strategy (body size, life span and number of reproductive cycles) among the sites. A majority of variation of community traits was explained by local environmental variables. The study results showed a strong relationship between the functional structure of the macroinvertebrate community and habitat conditions.

The taxonomic structure of macroinvertebrate communities was examined using taxonomic richness, composition, and percentage of tolerance taxa, biotic index, an exponential of the Shannon diversity index, and an evenness index. Overall taxonomic richness and diversity decreased with greater levels of land-use intensity. Intolerant taxa were generally significantly lower with increased land-use intensity, but taxonomic diversity and abundance of the insect order Ephemeroptera were higher in the greater levels of land-use intensity sites than in the seminatural sites. Three different taxa belonging to Ephemeroptera were the most dominant taxa in each of the three levels of land-use intensity. There were no differences in abundance of tolerant taxa among sites. The study sites were classified into four levels of water quality (excellent, good, good-fair, fair) according to the North American biotic index classification system, but the three levels of land-use intensity in this study were mixed among those categories for water quality; thus, this classification system was not well suited for Mongolian taxa.

Generally both TBA and the taxonomic approach discriminated seminatural sites from sites with greater levels of land-use intensity, but TBA was a more reliably consistent indicator of land use according to trait responses and, because traits are specifically correlated with environmental conditions, their presence and frequency provided a more direct explanation for macroinvertebrate responses to land-use. Therefore, TBA may be a more applicable and effective approach for freshwater biomonitoring in Mongolia.

Introduction

At present, the quality and quantity of Mongolia's water resources are being degraded by certain land uses, especially overgrazing and mining (Asia Foundation 2009). Biodiversity is an important component of the ecosystem and higher diversity maintains ecosystem processes (Cardinale 2002). Land-use modification is the major force of environmental change that affects the structure and function of biological communities (Vitousek et al. 1997, Dolédec et al. 2011). Along with physical and chemical assessment, bioassessment is required to manage ecosystem health and conserve biodiversity.

Freshwater biomonitoring programs using benthic macroinvertebrates are usually more reliable and more cost-effective for assessing water quality than traditional physical-chemical analyses (Barbour et al. 1999; Dolédec et al. 1996, 2006). Bioassessment with living organisms has several other advantages over traditional physical-chemical methods, such as (1) reacting to all biologically relevant environmental conditions, (2) detecting cumulative or combined effects of multiple stressors, and (3) responding to relevant conditions continuously over long periods of time (Mackie 2004; Rosenberg and Resh 1993; Morse et al. 2007). In contrast, physical-chemical analyses demonstrate conditions only for the time of sampling. Benthic macroinvertebrates are a useful group of organisms for biomonitoring because they are ubiquitous, diverse and abundant, they are relatively sedentary, they have long life cycles relative to other aquatic organisms, and they are highly responsive to environmental stress (Rosenberg and Resh 1993).

So-called taxonomic approaches have been widely used in many countries, including Australia (Simpson and Norris 2000), the European Union (Furse et al 2006), United Kingdom (Wright et al. 2000), and the US (Barbour et al. 1999). These approaches identify certain groups of freshwater organisms generally to family or genus and then characterize that part of the community with a single metric, such as a biotic index (mean organic pollution tolerance value for a sample), or with multiple metrics, such as measures of taxa richness, percent of Ephemeroptera/Plecoptera/Trichoptera composition, numbers or percent of tolerant/intolerant taxa, percent of selected feeding strategies, and percent of selected habitat optima (Barbour et al. 1999).

In recent years, the trait-based approach has been described as an alternative to the traditional taxonomic approach for assessing disturbance responses in stream communities (Dolédéc and Statzner 2010) and has been identified as one of the most promising tools for biomonitoring freshwater ecosystems (Menezes et al. 2010). A trait-based approach (TBA) is based on ecological theory, the River Habitat Template Concept, which provides a mechanistic framework for relating community responses to environmental characteristics (Southwood 1977, Townsend and Hildrew 1994). While taxonomic biomonitoring approaches focus on changes in community structure, trait-based approaches focus on function (functional diversity and trait composition) related to altered environmental conditions. In a given environment, only taxa possessing certain traits pass through the habitat filter (Keddy 1992), and those traits can be diagnostic of the stressors (Vieira et al. 2006).

Species traits can also be used as measures of community functional diversity (Petchey & Gaston 2006). In biomonitoring programs, multiple traits are being used to determine expected biological conditions under reference conditions (Vieira et al. 2006). Most traits are affected in predictable ways by various types of stressors (Dolédec et al. 2006, Dolédec and Statzner 2008). Thus, TBA should be able not only to determine intensities of disturbance (Gayraud et al. 2003), as do taxonomic approaches, but also to discriminate the effects of different stressors on macroinvertebrate communities (Dolédec et al. 1999). Also, species traits are less constrained by biogeography (Dolédec et al. 2011) and are more stable among seasons than species composition (Culp et al. 2010) because species traits should vary across environmental gradients but trait patterns will be similar in different spatial scales (Statzner et al. 2001).

The current surface water-quality monitoring system in Mongolia mostly relies on hydrological and chemical monitoring. There is no widely accepted biomonitoring method for Mongolia. Therefore, it is necessary to develop a national biomonitoring protocol suitable for the geographical region of Mongolia.

The main objectives of this study were 1) to examine community responses to land use disturbances and to determine land use effects on macroinvertebrate communities comparing taxonomic and trait-based approaches and 2) to evaluate whether TBA can provide a more reliable means for discriminating the effects of different land use intensities on Mongolian streams than a taxonomic approach. My basic hypotheses were that 1) macroinvertebrate functional structure would differ in

predictable ways in streams with different levels of land-use intensity according to the river habitat template *a priori* predictions. Specifically, I predicted that species traits associated with resilience and resistance to fine sediment loading and nutrient enrichment would become more common as grazing and mining land-use intensity increased (Table 2.1). 2) Macroinvertebrate taxonomic structure would differ in streams with different levels of land-use intensity. I predicted that there would be lower taxon richness with greater levels of land-use intensity, as only taxa that are pollutant tolerant will persist (Table 2.2). To test this hypothesis, I examined functional and taxonomic structure of benthic macroinvertebrate communities among north-central Mongolian stream sites in areas spanning a range in land-use intensities.

Material and Methods

Study sites

The field sampling occurred in north central Mongolia at 42 sites (Fig. 2.1, Appendix A) from the Orkhon, Kharaa, Yeroo, and Tuul Rivers and their tributaries in the Selenge River Basin, which flows northward into Russia and Lake Baikal. The Selenge River Basin belongs to the Central Asian Internal Basin and is surrounded by the Khentii, Khangai, and Sayan mountain chains, where the average altitude is 1500–2500 m asl. The Selenge Basin includes 30.6 percent of the water resources for Mongolia, with a 425,245 km² catchment area, and covers a wide range of ecoregions including taiga, high mountains, forest-steppe, and steppe (Tumurchudur

and Jadambaa 2012). Grazing sites were impacted by free-ranging horses and ungulates (cattle, sheep, goats, camels), which were often quite dense. Because Mongolian herders are nomadic, and there are no fences to exclude animals from riparian zones or surface waters, grazing sites were variously impacted by these megafauna. Mining sites are sites with mining activity in the watershed. Sites were chosen downstream of the mining. Most mines are surface, placer mines, which use stream water or groundwater resources to sort and extract target minerals (Javzan et al. 2004).

Study sites were categorized in relation to levels of land-use in the watershed as seminatural, moderate, and high land-use intensity sites. Seminatural sites were those with no evident land use activities (no grazing or mining) or with only light grazing. Moderate and high levels of land-use intensity had grazing or grazing coupled with mining impacts except that one site had mining activity but no grazing (Appendix A). Suspended solids, turbidity, and ammonium were significantly higher in high level intensity sites than in moderate level intensity sites (Fig. 2.2).

Macroinvertebrate sampling

Forty-two macroinvertebrate samples were taken using a semiquantitative D-net (500 μ) sampling method within a 50-m reach from each site during late-June to mid-July 2011. In order to reduce time and effort for sorting and identification, I used a fixed-count approach that is the preferred subsampling method for Rapid Bioassessment Protocols (RBPs) (Barbour et al. 1999). Subsamples of 200 organisms were taken from a composite of 20 kicks or jabs taken from the different

macrohabitats (riffle, run, and pool) in accordance with their percentage representation within a reach (modified Barbour et al. 1999). Samples were preserved in 80% ethanol and invertebrates identified to the lowest possible taxonomic levels. Most insect groups of macroinvertebrates were identified to the genus-level except that some water boatmen (Hemiptera: Corixidae), predaceous diving beetles (Coleoptera: Dytiscidae), flies (Diptera), and the non-insect groups were identified only to family level (Appendix B).

Environmental variables

The following physico-chemical parameters were measured using a spectrophotometer Hach DR 2800 Field Water Quality Lab in accordance with procedures described in its accompanying manual (Hach 2008): suspended solids (mg/l), sulfate (mg/l), phosphate (mg/l), nitrite (mg/l), nitrate (mg/l), ammonium (mg/l), salinity (mg/l), water temperature (°C), pH, dissolved oxygen in ppm (DO), conductivity (μ S), and turbidity in Nephelometric Turbidity Units (NTU) (Appendix E). Flow rate was measured at the water surface and at middle and bottom depths at each meter across a stream transect using a FLO-MATE Electromagnetic Flow Meter.

A visual habitat assessment (habitat type, substrate type, stream gradient, stream order, erosion and land use type) was made according to a modified US EPA Rapid Bioassessment Protocol (Barbour et al. 1999). To estimate grazing intensity, a visual assessment of ground cover percentage and a measurement of vegetation height were taken in the riparian zone at 0, 10, and 20 meter distances from the

stream bed along 20-meter perpendicular transects using a randomly tossed 1 m²-frame (Daubenmire 1959). This provided a mean estimate of ground cover percentage and vegetation height for each site.

Trait selection

Species possess biological traits, which are morphological, physiological, behavioral, and ecological features. Two general types of traits are distinguished in current bioassessment programs: biological traits related to life history, mobility, and morphology and ecological traits related to habitats (Charvet et al. 2000, Dolédec et al. 2000, Statzner et al. 2001, and Gayraud et al. 2003).

For 90 taxa, I selected 86 trait categories of 16 traits (Table 2.1) that are related to life history, mobility, morphology, and ecology and that were obtainable from available sources (Bis and Usseglio-Polatera 2004, Schmidt-Kloiber and Hering 2012). The trait matrix was based on European taxa, and since Mongolia has a high proportion of species and genera with widespread Palearctic distributions, it made sense to adopt the already existing European trait database. These traits were associated with the resilience, resistance, and habitat optima relevant to the environmental gradients of interest. Traits were compiled at the family level for non-insect groups and for a few specimens of Corixidae, Dytiscidae, and Ephydriidae. There was no complete trait information available for some insect genera; thus traits were recorded at the subfamily level for *Palpomyia* and all Chironomidae (order Diptera); and at the family level for *Acanthametropus* and *Cynigma* (order Ephemeroptera); *Alloperla*, *Paraperla*, and *Haploperla* (order Plecoptera);

Chaetopteryx (order Trichoptera); and *Anisogomphus* (order Odonata) and at the genus level for all other insect taxa (Appendix C).

Trait-based analytical approaches have categorized traits into categories that are coded in a “fuzzy” manner for each species, as described by Chevenet et al. (1994). Fuzzy coding accommodates trait variation within a species by recording intermediate affinities. Affinity scoring ranges from 0 to 3 where 0 indicates no affinity of a species to a given state and 3 indicates that a species has that particular state exclusively.

Affinity scores were treated as frequency distributions to give the same weight to each taxa and trait so that affinity scores are each equal to 1 for a given trait and taxon (Chevenet et al. 1994).

$$q_k = \frac{a_k}{\sum_{k=1}^h a_k} \text{ with } q_k \geq 0 \text{ and } \sum_{k=1}^h q_k = 1$$

k - a trait category

q_k - frequency of a trait category

a_k - assigned affinity of a trait category

h - total number of categories in a given trait

Taxonomic metrics

The presence of the generally most sensitive groups of macroinvertebrates, such as Ephemeroptera, Plecoptera and Trichoptera (EPT), indicate the cleanest waterways (Lenat 1993). In contrast, generally pollution tolerant groups of macroinvertebrates such as the segmented worms (Oligochaeta) and midges (Insecta: Diptera: Chironomidae) indicate polluted waterways (Myslinski and Ginsburg 1977). Quantifying taxa richness, abundance of intolerant and tolerant organisms, and their proportions in a community are commonly used for bioassessment. Certain stresses may increase or decrease population sizes of certain taxa and their species richness (Resh and Jackson 1993). The most reliable taxonomic candidate metrics of the Rapid Bioassessment Protocol (RBP; Barbour et al. 1999), including taxonomic richness, taxonomic composition, trophic relationship, habit, and tolerance metrics (Table 2.2), were used to examine taxonomic structure of macroinvertebrate communities.

A Biotic Index was calculated based on North American genus-level tolerance values to water pollution. A Biotic Index (BI) is a mean tolerance value that is weighted by abundance for each taxon and its particular tolerance value to the total number of organisms in the sample. The tolerance values for the taxa were assigned mainly with respect to eutrophication, so that this index relies on only a niche dimension-oxygen level. A family-level tolerance value was used for some genera that are not found in North America.

$$BI = \frac{\sum TV_i * N_i}{\sum N}$$

BI- biotic index

TV_{*i*}- tolerance value of *i*th taxa

N_{*i*}- individual number of *i*th taxa

N-total individual number in the sample

In addition to these metrics, an exponential of the Shannon Diversity Index and an evenness index were computed (Table 2.2). The Shannon Diversity Index accounts for both the number of species and their proportional abundances within a community. It assumes individuals are randomly sampled from an infinitely large community and all species are represented in the sample (Shannon 1948).

$$\text{Exp } [H' = -\sum (p_i * \ln p_i)]$$

Exp-exponential

H'-Shannon Diversity Index

p_{*i*} –proportion of individual in *i*th taxa

Ln-natural logarithm

Shannon evenness can be calculated from the Shannon Diversity Index (Pielou 1975) as follows:

$$J = H' / \ln S$$

J-Shannon evenness

S-species number

Statistical analysis

Principle Components Analysis (PCA) is a variable-reduction technique and reorganizes a larger set of variables into smaller set of components that account most of the variance in the original variables (Manly 2004). Environmental variables met assumptions (linear relationship, multiple normality, and no significant outlier) for PCA. PCA was performed using a correlation matrix of environmental variables to discriminate primary environmental gradients and co-varying components among sites. A linear combination of an Eigen value of the correlation matrix among the variables was taken to calculate each principle component. The Eigen values indicated the variability of each component (SAS institute 2012).

Functional diversity (FD) was quantified within each site using a functional richness index (Petchy and Gaston 2002, 2006) based on trait incidence (present/absent). This index is most commonly used and gives a meaningful measure of functional diversity (Pla et al. 2012). The functional diversity index is defined as the sum of branch lengths linking species belonging to the same community on the functional dendrogram built on a regional species pool based on incidence data (Petchy and Gaston 2002, 2006).

$$FD=i' \cdot h2$$

i' - branch presence/absence row vector

$h2$ - branch length vector

Canonical correspondence analysis (CCA) was used to compare trait composition of macroinvertebrate communities to variation in the environment

among sites. CCA is a constrained-ordination technique defined by best explanatory variables (Ter Braak 1986). The frequencies of each trait category per trait were multiplied by the relative abundance of taxa at the site and summed by sites to create a trait-by-site array and this array was used for CCA analyses (Dolédec et al. 2011). CCA was run for all traits together and each trait category separately. Permutational multivariate analysis of variances (MANOVA), based on a dissimilarity matrix using a Euclidean distance measure, was used to test for significance of trait variation explained by environmental variables among land use intensity gradients. It partitions dissimilarities among any objects and uses permutation tests to explore significance of those partitions (Oksanen 2013). The site scores derived from the CCA was used in permutational MANOVA.

Individual trait category differences across the land-use intensity gradients were determined by a community-weighted mean (CWM) trait value. It is a mean trait value weighted by relative abundance (Díaz et al. 2007) and represents the expected functional value of a random community sample (Casanoves et al. 2011).

$$CWM = \sum_{i=1}^S p_i x_i$$

p_i -relative abundance of i^{th} species

x_i - trait value of i^{th} species.

A one-way analysis of variance (ANOVA) was conducted to test whether functional diversity, CWM and taxonomic metrics varied significantly among the land use categories. For pair-wise *post hoc* comparisons, a t-test was used.

I used JMP software version 9.0.2 (SAS Institute Inc. 2010) for PCA, f-diversity software (Casanoves et al. 2011) for computing functional diversity indices, and R software version 3.0.1 for conducting a vegan package (R Development Core Team 2010) for CCA analysis and permutational MANOVA.

Results

The sites clustered into three areas of the PCA (Fig. 2.2), which corresponded with the low (seminatural), moderate and high levels of land-use intensity. Generally land use intensity segregated by grazing intensity for moderate and heavy grazing, either alone or coupled with mining impacts. The Eigen values of the first two axes accounted for most of the variability and are used for graphical representation. The first axis of the PCA explained 21.9% of the variation, and the second axis explained 14.7% (Fig. 2.2). Greater altitude, coarser substrate type, dissolved oxygen, vegetation height, and vegetation cover correspond with seminatural sites. Greater conductivity, salinity, sulfate, and temperature were associated with a moderate level of land-use intensity. Also, a site with recent mining activity and no grazing had greater vegetation height, vegetation cover, and dissolved oxygen with moderate land-use intensity. Mining activity in the watershed had started recently, such that impacts may not have happened yet. Greater values of turbidity, suspended solids, ammonium, and stream depth were associated with a high level of land-use intensity (Fig. 2.2).

Functional structure

Overall functional diversity was significantly different ($P < 0.02$) among the levels of land-use intensity (Fig. 2.3). Functional diversity was highest for seminatural sites, intermediate for moderate land-use intensity, and lowest for high land-use intensity (Fig. 2.3).

CCA showed that overall traits were significantly explained by land-use intensity (permutations=2000, $F=1.7$, $P < 0.0005$). Constrained variance, which is trait composition explained by environmental variables, represented 63% of total variance (Table 2.3). The first two canonical components of CCA accounted for 48% of the constrained variance (Fig. 2.4). For individual traits, 54–77% of total variability was captured in the CCA. A total of 12 of 16 traits varied significantly among the sites. Aquatic stages, reproduction, dissemination, locomotion and substrate relationship, food, feeding habit, substrate, velocity, trophic level, temperature optima, and saprobity showed significant deviance across land-use intensity gradients (Table 2.3, Fig. 2.4).

Individual traits responded differently to the different levels of land-use intensity. The CWM of 19 trait categories for 11 traits was significantly different among sites (Fig. 2.5).

With increased land-use intensity, there was a tendency for greater frequency of ovoviviparity and lower frequency of non-holometabolous taxa, aquatic-active dissemination, and predators. The frequency of taxa with deposit feeding, detritus food, aerial respiration, slow water velocity optima, mesotrophic-level optima,

eurhythmic temperature regime, and mesosaprobism increased directly with greater land-use intensity. In contrast, frequency of coarse-substrate habitat, living-macrophyte food, and oligotrophic level, fast-water-flow, cold-adapted, and xenosaprobic taxa decreased with increased land-use intensity (Fig. 2.5).

The CWM results supported the outcomes of CCA except with respect to two traits (resistant form, locomotion and substrate relations). In the CCA, resistant forms, such as housing against desiccation, pupal cocoons, and dormancy or diapause, were more common in sites with grazing and mining. Also, traits associated with mobility and dispersion, such as flying, surface swimming, fully submerged swimming, use of interstitial habitats, and burrowing and permanent attachment were common in sites with greater levels of land-use intensity. Respiration method differences were not captured by CCA, but in CWM, frequency of aerial respiration was significantly higher in sites with the highest levels of land-use intensity.

There was no significant difference observed in reproductive strategy traits (body size, life span and potential number of reproductive cycle) among the sites with either CCA or CWM.

Taxonomic structure

Overall macroinvertebrate taxa richness ($P < 0.002$) and diversity ($P < 0.01$) were significantly different among the levels of land-use intensity (Figs. 2.6, 2.7). Taxon richness and the exponential of the Shannon Diversity Index were highest in the seminatural sites, intermediate in moderate level of land-use intensity and lowest

in the high level of land-use intensity (Figs. 2.6, 2.7). Evenness was not significantly different among the sites (Table 2.2).

EPT richness was significantly higher ($P < 0.04$) in the seminatural sites and lowest in the high land-use intensity sites (Fig. 2.6). Taxon richness for Diptera and non-insect groups was significantly higher ($P < 0.01$) in seminatural sites than in those with greater levels of intensity (Fig. 2.6, Table 2.2), and their percentage in total taxa and total number of organism was not different among the sites (Table 2.2). The percentage of EPT taxa and abundance was not significantly different among sites, but the percentage and abundance of Ephemeroptera taxa was significantly higher in the greater levels of land-use intensity. The dominant taxa were three different genera of Ephemeroptera, with *Hexagenia* spp. (17% TV=6) dominant at sites with high level of land use intensity, *Serratella* spp. (10% TV=2) in the moderate level of land use intensity, and *Drunella* spp. (8% TV=6) in seminatural sites.

The percentage of intolerant taxa with tolerance values 0–4.9 was significantly higher in seminatural sites than in those with greater levels of land-use intensity, whereas the percentage of tolerant taxa with tolerance values of 8–10 did not differ significantly among the sites.

The Biotic Index varied significantly among levels of land-use intensity (Fig. 2.9). According to the Biotic Index criteria for the North Carolina mountain ecoregion in the USA, which recognizes 5 categories of impairment (excellent, good, good-fair, fair, poor; Lenat 1993), the Mongolian study sites were classified into four

levels of water quality, but the three levels of land-use intensity in this study were mixed among those categories (Table 2.4), and suggesting that the tolerance values for the same genera in Mongolia and North Carolina may differ because of different tolerances of the different species in those regions. Biotic indices ranged between 1.47 and 6.37, and no site was classified as “poor.”

Discussion

Functional structure

Macroinvertebrate communities in the seminatural sites were functionally more diverse than sites with high levels of land use intensity. Previous studies showed substantial loss in functional diversity of biological communities for taxa such as macroinvertebrates, fish, birds, and mammals associated with higher land use intensity (Flynn et al. 2009, Carmona et al. 2012, Colzani et al. 2013, Zhang et al. 2013, and, Wiedmann et al. 2014,).

My study results were consistent with the habitat template concept (Townsend and Hildrew 1994) and habitat filtering (Poff 1997), which predicted that traits associated with population resilience and resistance would be correlated with higher land-use intensity. Most individual traits had a predictable response related to altered environmental conditions, and some of the results supported my predictions that greater population resilience and resistance would be evident in the greater levels of land-use intensity (Table 2.3; Figs. 2.3, 2.4).

Resilience features include high mobility, prolonged presence of relatively invulnerable life stages, and the ability to regenerate after damage (Townsend and Hildrew 1994). With increased levels of land-use intensity, I observed increased ovoviviparity, decreased aquatic-active dissemination, and non-holometabolous aquatic stages, resulting from their increased vulnerability to increased environmental fluctuation. Traits associated with mobility and dispersion, such as flying, surface swimming, fully submerged swimming, use of interstitial habitats, and burrowing, were common in greater land-use intensity sites.

Decreased frequency of predators in the sites with greater levels of land-use intensity is possibly explained by biomagnification of toxic substances. Concentrations of toxic substances may have been higher in the sites as evidenced by increased conductivity in those sites. Also, reduced predator frequency may relate to decreased species diversity and reduced prey abundances of macroinvertebrates in the sites with greater land-use intensity. The current study did not test this possibility because of the subsampling method I used.

According to the r/K reproductive strategy model, r -selected species with traits of small body size, short life span and rapid growth rate thrive in temporally unstable environments (McArthur and Wilson 1967). There was no trade-off between r and K reproductive strategies among the sites. This may possibly be explained as a consequence of climate change.

Ecological traits such as food, feeding habit, saprobity, temperature, current velocity, substrate, and trophic level association all responded in a predictable

manner to land-use impacts. A majority of community variation in terms of trait composition was explained by local environmental variables (Table 2.3, Fig. 2.4).

Consequently, it can be concluded that fine-sediment deposition, suspended solids, and nutrient enrichment increased with land-use intensity and resulted in higher temperatures, stagnant conditions, organic pollution, and more detritus food resources in the moderate and high land-use intensity sites based on the ecological-trait responses. TBA clearly discriminated seminatural sites from sites with greater levels of land-use intensity using mixed genus- and family-level resolution and provided a mechanistic interpretation for the underlying changes in community structure due to land use. Another advantage of TBA that this study has shown includes detection of different types of stressors and intensities of land use and consistent community descriptors less constrained by biogeography (Menezes et al. 2010), a distinct benefit for bioassessment across an area with such a large spatial scale as Mongolia.

There are several challenges for TBA, including inconsistency of trait terms, a need for descriptions of trait modalities applicable for all taxa, and inadequate knowledge of trait differences (Culp et al. 2010). Lack of ecological and biological knowledge has resulted in incomplete trait information, requiring extrapolation of traits from confamilials (Lenat and Resh 2001) or from a few representative species or genera, generalizing those traits for entire genera or families. The “trait-syndrome” or inferring the co-occurrence of phylogenetically constrained traits in

closely related taxa is another issue (Poff et al. 2006); phylogenetically decoupled and more plastic traits are more robust for bioassessment (Vieira et al. 2005).

Not all trait patterns matched habitat conditions. It may take time for environmental drivers to influence the fitness of organism and filter less fit taxa from the community. Also, organisms with higher dispersal abilities may occur randomly in certain habitats and not necessarily indicate a trait-habitat relationship. Dispersal ability also commonly can be included among biological traits to predict changes in a community. Finally, natural variation in habitat (e.g., minerals, acidity in water or rainfall) rather than land-use modification may affect community assembly (Heino. 2007). Natural habitats may differ depending on climate, altitude and geology among catchments, ecoregion or basins. Thus natural habitat variability is needed to be considered.

Taxonomic structure

Higher taxonomic diversity was supported in spatially heterogeneous environments with higher niche space than habitats that had become more homogeneous as the level of disturbance increased. EPT are sensitive groups of organisms that usually inhabit cleaner waterways and give early warning of water pollution like “canaries in a coal mine.” Generally, most individuals in the communities were EPT for all levels of land-use intensity. There were no differences for relatively tolerant Diptera and non-insect groups among the sites. Higher taxa richness, abundance, and dominance of Ephemeroptera were observed in the greater levels of land-use intensity. However, tolerance values are variable among Ephemeroptera species and some

genera are relatively tolerant to pollution, with medium tolerance values. Many species of the Ephemeroptera genus *Hexagenia* are relatively tolerant and dominated in the highest level of land-use intensity; species of Ephemeroptera genera *Serratella* and *Drunella* dominated in moderate and low levels of land-use intensity.

The three levels of land-use intensity were not reliably segregated by the water quality classification of the North Carolina Biotic Index and most study sites, including some with a high level of land use intensity, were classified as having excellent water quality (Table 2.4). Generally the Biotic Index varied among levels of land-use intensity within a smaller range (Fig. 2.9), which may indicate that there was a low level of organic pollution overall at the study sites. Tolerance values may vary among Mongolian genera more than among North American genera because tolerance values are highly variable among species within the same genus (Resh and Unzicker 1975; Resh and Lenat 2001), or the Biotic Index categories for the mountains of North Carolina are not well suited for Mongolia. The tolerance values of the organisms are based primarily on their oxygen requirements to indicate organic pollution (Bonada et al. 2007). Thus, a Biotic Index is not able to indicate levels of land-use intensity when oxygen is not highly variable. In contrast, according to results of the trait-based approach, there was an indication of lower oxygen levels in sites with a high level of land-use intensity evidenced by a higher frequency of aerial respiration. In summary, with the taxonomic approach, macroinvertebrate taxa richness and diversity, including EPT, decreased in association with increased land use intensity and discriminated three levels of land-

use intensities. However, it did not provide any explanation for the changes in macroinvertebrate communities.

Overgrazing has significant consequences for stream ecosystems, including flooding and loading of sediments and nutrients such as nitrogen and phosphate (Quinn and Stroud 2002, Maasri and Gelhaus 2011). Mining caused increased turbidity (from suspended mineral particles), increased sediment deposition (Wagener et al. 1985), and transfer of nutrients, especially phosphorus (Stubblefield et al. 2005), and metal contamination (Inam et al. 2010). In this study, major impacts of livestock grazing and mining were increased suspended particles, fine sediments, and eutrophication (primarily ammonia in the chemical measurements), all of which were detected by the trait-based analysis. Mining may also have resulted in some metal contamination as indicated by higher conductivity, but that possibility needs further analysis.

Overall findings suggest that macroinvertebrate communities were affected by land use. Seminatural sites had a greater diversity of habitats supporting functionally diverse communities, whereas sites with greater land-use intensity tended toward communities that were more tolerant of eutrophication and fine sediment deposition and less functionally diverse. Trait-based patterns of macroinvertebrate community were defined by local habitat conditions; in other words, habitat filtering determines variability of the macroinvertebrate community. Generally both TBA and the taxonomic approach discriminated seminatural sites from sites with greater levels of land-use intensity, but TBA was a reliably consistent

indicator of land-use changes. Traits responded in a predictable way in accordance with the “habitat template concept’s” *a priori* prediction. Presence of particular traits and their frequency indicate particular habitat conditions and they provide a more direct explanation for macroinvertebrate responses to land-use. Therefore, TBA may be a more applicable and effective approach for freshwater biomonitoring in Mongolia.

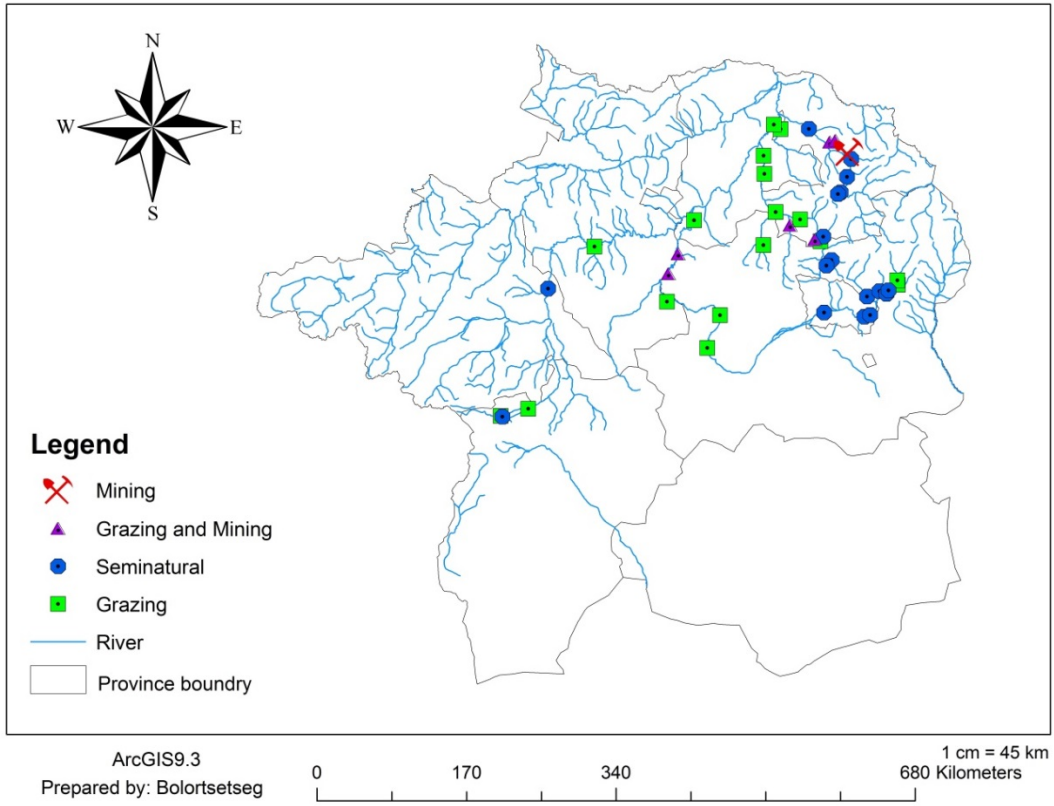


FIG.2.1 The location of the study sites in the Selenge River basin, Mongolia.

Table 2.1 Biological and ecological traits (Bis and Usseglio-Polatera 2004), with trait rationale (Bonada et al. 2007, Statzner and *Bêche* 2010, and Maasri and Gelhaus 2012).

| Traits | Code | Trait categories | Explanation | Rationale |
|-----------------------------|--------|-----------------------------|--|--|
| Maximal potential body size | Size-1 | ≤ .25 cm | Body length from tip of the head to the tip of the abdomen | Smaller sizes provides better resilience capacity after disturbances |
| | Size-2 | > .25-.5 cm | | |
| | Size-3 | > .5-1 cm | | |
| | Size-4 | > 1-2 cm | | |
| | Size-5 | > 2-4 cm | | |
| | Size-6 | > 4-8 cm | | |
| Life span | Life-1 | ≤ 1 year | Life cycle duration | Shorter life cycles provides better resilience capacity after disturbances. |
| | Life-2 | > 1 year | | |
| Voltinism | Volt-1 | Semivoltine | < 1 reproductive cycle per year | Frequent reproduction provides better resilience capacity after frequent disturbance |
| | Volt-2 | Univoltine | 1 reproductive cycle per year | |
| | Volt-3 | Bivoltine | > 1 reproductive cycle per year | |
| Aquatic stages | Aqua-1 | egg | presence of the life stage | Presence of life stages in relatively invulnerable condition |
| | Aqua-2 | larva | | |
| | Aqua-3 | nymph | | |
| | Aqua-4 | adult | | |
| Reproduction | Repr-1 | ovoviviparity | produce hatched larvae | Ovoviviparity and asexual reproduction provide better resilience after disturbance. |
| | Repr-2 | isolated eggs, free | free eggs | |
| | Repr-3 | isolated eggs, cemented | stick eggs on the substrate | |
| | Repr-4 | clutches, cemented or fixed | egg mass stick on substrate | |
| | Repr-5 | clutches, free | egg mass on water surface | |
| | Repr-6 | clutches, in vegetation | egg mass on vegetation in water | |
| | Repr-7 | clutches, terrestrial | egg mass on vegetation edge of the water | |
| | Repr-8 | asexual reproduction | produce egg without fertilization | |
| Dissemination | Desi-1 | aquatic passive | disperse passively via drift | Aquatic passive and areal dispersal will increase with increased disturbance |
| | Desi-2 | aquatic active | disperse actively via swimming or crawling | |
| | Desi-3 | aerial passive | disperse passively via wind in the air | |
| | Desi-4 | aerial active | disperse actively via flying | |

| Traits | Code | Trait categories | Explanation | Rationale |
|-----------------------------------|-------------|------------------------------|--|--|
| Resistant form | Resi-1 | eggs, statoblasts | Resisting in the egg stages | Resistant form will be more common against nutrient enrichment and fine sediment loading |
| | Resi-2 | cocoons | Case for prepupal and pupal stage | |
| | Resi-3 | housings against desiccation | Protective layer against desiccation | |
| | Resi-4 | diapause or dormancy | Physiological suspension of growth and development | |
| | Resi-5 | none | No resistance strategy | |
| Respiration | Resp-1 | tegument | Respire through tegument | Oxygen uptake will require a specialized technique in higher temperature and stagnant condition. |
| | Resp-2 | gill | Using gills | |
| | Resp-3 | plastron/aerial | Using thin layer of air around the body or alternative respiration with atmospheric oxygen | |
| | Resp-4 | spiracle | Using small opening on the body surface | |
| | Resp-5 | hydrostatic vesicle | Using air within a small blister | |
| Locomotion and substrate relation | Habi-1 | flier | Fly in adult stage | High mobility provides better resilience capacity and substrate attachment tend to be common. |
| | Habi-2 | surface swimmer | Swim in the surface of water | |
| | Habi-3 | full water swimmer | Swim in water column | |
| | Habi-4 | crawler | Crawling to aquatic vegetation or substrates | |
| | Habi-5 | burrower | Burrow very fine sediment | |
| | Habi-6 | interstitial | Crawling between small minerals and coarser substrate | |
| | Habi-7 | temporarily attached | Temporarily attached to the substrate | |
| | Habi-8 | permanently attached | Permanently attached to the substrate | |
| Feeding habits | Trop-1 | absorber | Absorb plant fluid | Response to more-abundant food source |
| | Trop-2 | deposit feeder | Feed on sedimented fpm | |
| | Trop-3 | shredder | Shred fallen leaves, plant tissue and cpm | |
| | Trop-4 | scraper | Scrape algal tissue biofilm, partially pom | |
| | Trop-5 | filter-feeder | Food is filtered from water column such as suspended fpm and cpm | |
| | Trop-6 | piercer | Pierce and suck plant or animal tissue | |
| | Trop-7 | predator | Feed on prey | |
| | Trop-8 | parasite | Feed on host | |

| Traits | Code | Trait categories | Explanation | Rationale |
|-----------------------------------|---------|--------------------------------|---|--|
| Food | Food-1 | microorganisms | Optimal food source | Response to more-abundant food source |
| | Food-2 | detritus (< 1mm) | | |
| | Food-3 | dead plant (>= 1mm) | | |
| | Food-4 | living microphytes | | |
| | Food-5 | living macrophytes | | |
| | Food-6 | dead animal (>= 1mm) | | |
| | Food-7 | living microinvertebrates | | |
| | Food-8 | living macroinvertebrates | | |
| | Food-9 | vertebrates | | |
| Substrate (preferendum) | Subs-1 | flags/boulders/cobbles/pebbles | Optimal substrate relation | Taxa adapted to fine sediment will increase with increased fine sediment loading |
| | Subs-2 | gravel | | |
| | Subs-3 | sand | | |
| | Subs-4 | silt | | |
| | Subs-5 | macrophytes | | |
| | Subs-6 | microphytes | | |
| | Subs-7 | twigs/roots | | |
| | Subs-8 | organic detritus/litter | | |
| | Subs-9 | mud | | |
| Current velocity (preferendum) | Velo-1 | null | Optimal water flow range | Response to water flow |
| | Velo-2 | slow (< 25 cm/s) | Optimal water flow range | |
| | Velo-3 | medium (25-50 cm/s) | Optimal water flow range | |
| | Velo-4 | fast (> 50 cm/s) | Optimal water flow range | |
| Trophic level (preferendum) | Tro_p-1 | oligotrophic | Having low levels of nutrients and high levels of dissolved oxygen (DO) | Mesotrophic and eutrophic taxa will increase with increased nutrient enrichment |
| | Tro_p-2 | mesotrophic | Having intermediate levels of nutrients and intermediate levels of DO | |
| | Tro_p-3 | eutrophic | Having high levels of nutrients and negligible DO | |
| Temperature (preferendum) | Temp-1 | cold | Optimal temperature range (< 10°C) | Eurythermic taxa will increase with increased water temperature and stagnant condition |
| | Temp-2 | warm | Optimal temperature range (10-18°C) | |
| | Temp-3 | eurythermic | Wide temperature range | |

| Traits | Code | Trait categories | Explanation | Rationale |
|---------------|-------------|-------------------------|---|---|
| Saprobity | Sapr-1 | xenosaprobic | Unpolluted with high do content | Meso and polysaprobic taxa will increase with increased nutrient enrichment |
| | Sapr-2 | oligosaprobic | Adapted to clear, with no or only slight pollution and still relatively high DO content | |
| | Sapr-3 | β -mesosaprobic | Tolerant to moderately polluted with still medium DO | |
| | Sapr-4 | α -mesosaprobic | Tolerant to polluted with not low DO | |
| | Sapr-5 | polysaprobic | Tolerant to strongly polluted, with negligible DO | |

Table 2.2 Description of taxonomic metrics and predicted response to increased land-use intensity (compiled from EPA RBP Barbour et al. 1999). P values of ANOVA are included. Significance was marked by*.

| Taxonomic metrics | Description | Predicted response | P value of ANOVA |
|--------------------------------------|---|---------------------------|-------------------------|
| Taxonomic richness measure | | | |
| Total taxonomic richness | Total number of taxa in the community | Decrease | 0.002* |
| EPT richness | Number of taxa in the Ephemeroptera, Plecoptera and Trichoptera (EPT) | Decrease | 0.04* |
| Dipera and non-insect taxa richness | Number of taxa in the diptera and non-insect groups considered tolerant | Increase | 0.01* |
| Taxonomic composition measure | | | |
| % EPT taxa | Percent of the composite of EPT taxa | Decrease | 0.78 |
| % EPT abundance | Percent of the composite of EPT abundance | Decrease | 0.62 |
| % Ephemeroptera taxa | Percent of the ephemeroptera taxa | Decrease | 0.02 |
| % Ephemeroptera abundance | Percent of the ephemeroptera abundance | Decrease | 0.005* |
| % diptera and noninsect taxa | Percent of the composite of diptera and non-insect taxa | Increase | 0.44 |
| % diptera and noninsect abundance | Percent of the composite of diptera and non-insect taxa abundance | Increase | 0.63 |
| % Dominant taxon | Percent of the dominant taxa | Increase | |
| Tolerance/intolerance measure | | | |
| % intolerant taxa with TV 0-4.9 | Percent of intolerant macroinvertebrates | Decrease | 0.4 |
| % tolerant taxa with TV 8-10 | Percent of tolerant macroinvertebrates | Increase | 0.07 |

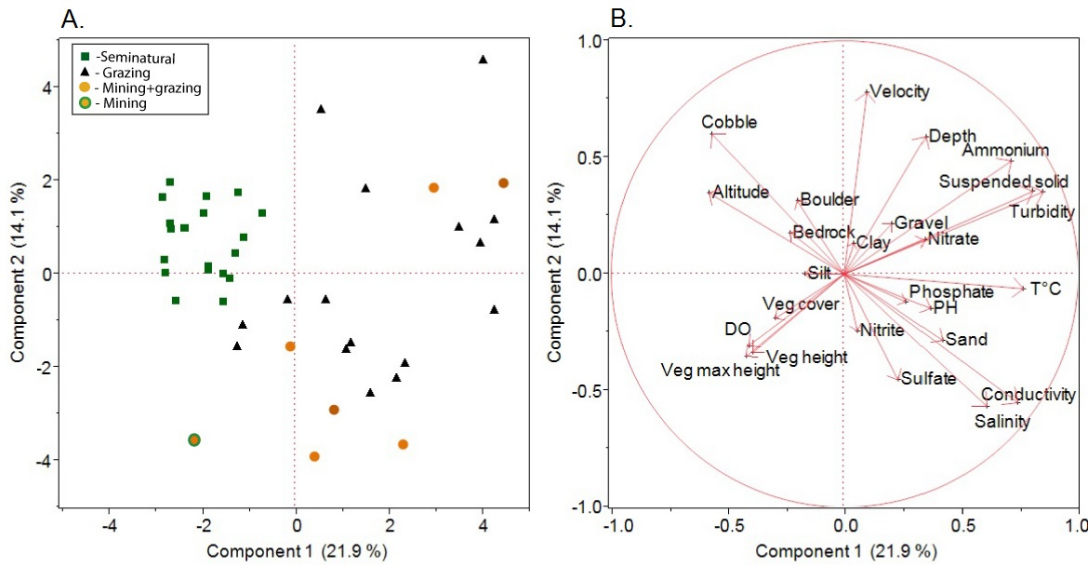


FIG. 2.2. Principle Component Analysis ordination of the 42 study sites. Biplot vectors showing which environmental variables (right) discriminate among land use intensity groups (left). Eigenvalues of the first axis= 5.48 and second axis=3.51. Veg cover= average vegetation cover, veg height= average vegetation height, veg max height= average maximum vegetation height, DO= dissolved oxygen, and T°C = temperature. The value gets closer to 1 indicate greater effect of the component on the variable.

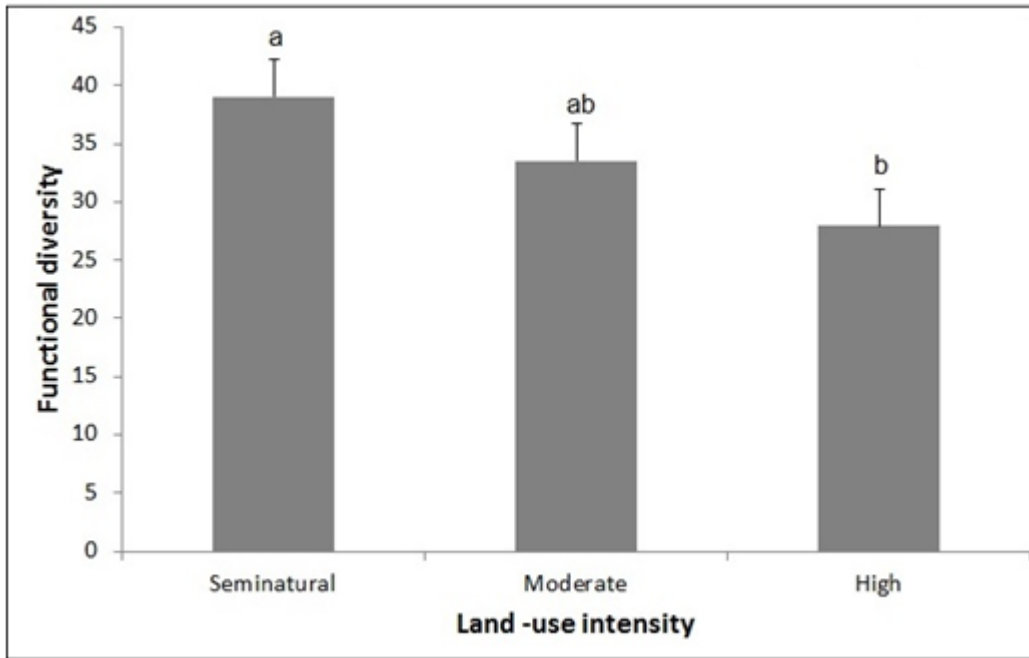


Fig. 2.3 Functional diversity indices among the three levels of land-use intensity.

Standard error of mean taxa richness and pair-wise *post hoc* comparison results are shown with different letters denoting significantly different values.

Table 2.3. Decomposition of the variance of overall trait composition and individual trait composition by canonical correspondence analysis. Significance was marked by*.

| Traits | Total variance | Constrained variance % | P value |
|--|----------------|------------------------|---------|
| Overall trait composition | 0.242 | 0.63 | 0.001* |
| Maximal potential size | 0.315 | 0.66 | 0.1 |
| Life cycle duration | 0.085 | 0.62 | 0.2 |
| Potential number of reproductive cycles per year | 0.229 | 0.77 | 0.1 |
| Aquatic stages | 0.120 | 0.67 | 0.001* |
| Reproduction | 0.638 | 0.60 | 0.005* |
| Dissemination | 0.070 | 0.47 | 0.001* |
| Resistant form | 0.261 | 0.54 | 0.001* |
| Respiration | 0.140 | 0.63 | 0.2 |
| Locomotion and substrate relation | 0.422 | 0.55 | 0.031* |
| Food | 0.254 | 0.70 | 0.001* |
| Feeding habits | 0.516 | 0.63 | 0.006* |
| Substrate (preferendum) | 0.206 | 0.66 | 0.004* |
| Current velocity (preferendum) | 0.211 | 0.70 | 0.003* |
| Trophic level (preferendum) | 0.144 | 0.65 | 0.001* |
| Temperature (preferendum) | 0.122 | 0.54 | 0.001* |
| Saprobity | 0.125 | 0.69 | 0.001* |

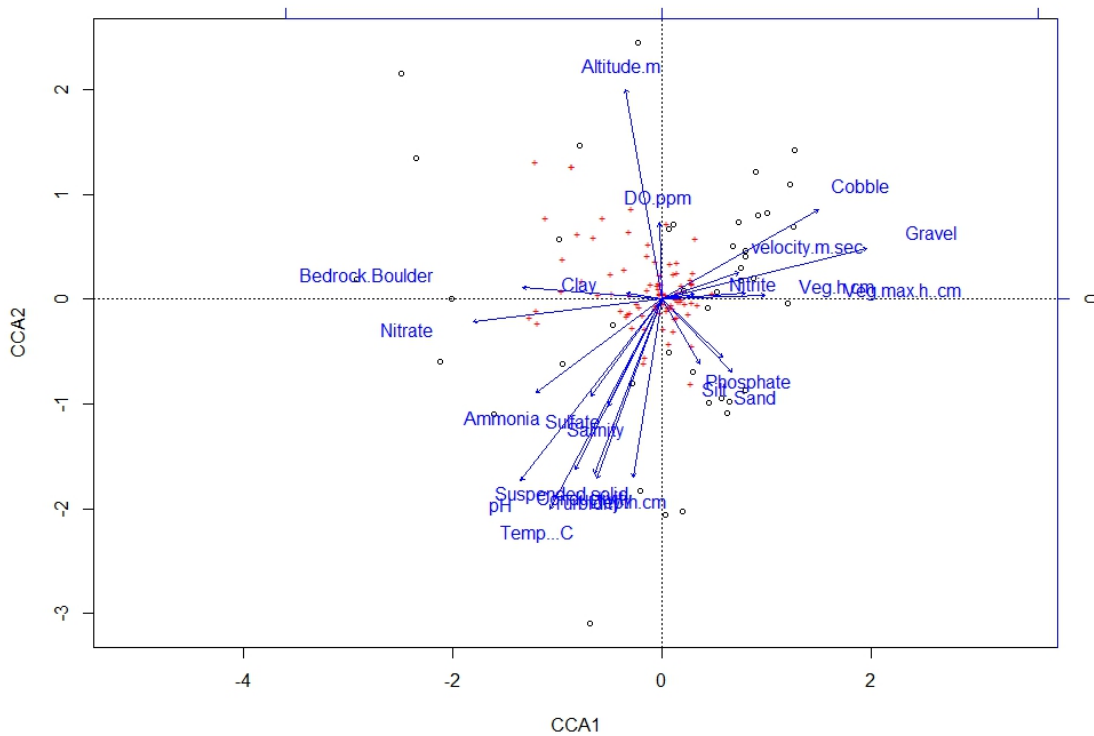


FIG. 2.4. Sample score ordination plot of canonical correspondence analysis on overall trait composition and constraining environmental variables. Axes 1 and 2 from CCA of the trait data set with significant land use gradient sites. Traits are shown as red crosses and sites as black circles.

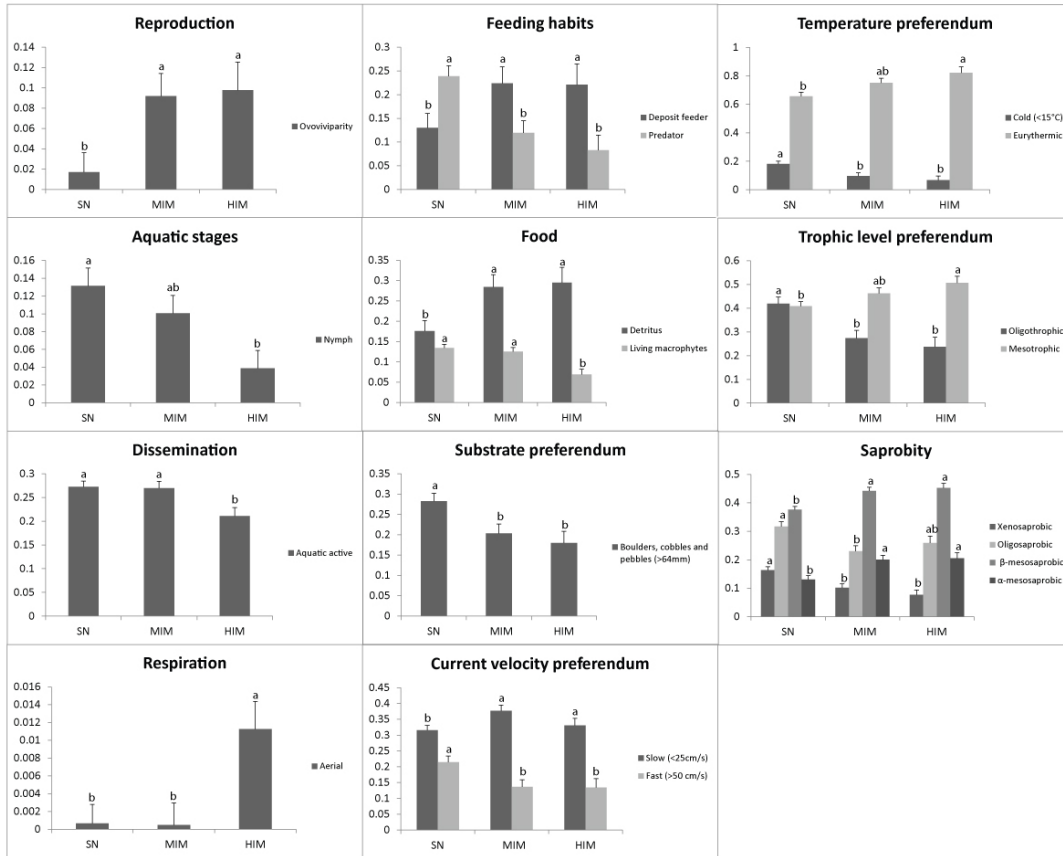


FIG. 2.5. Comparison of the community weighted mean and standard error of individual trait categories among three levels of land use intensity. Only significantly different trait categories among sites are shown pair-wise *post hoc* comparison results are shown with different letters denoting significantly different values.

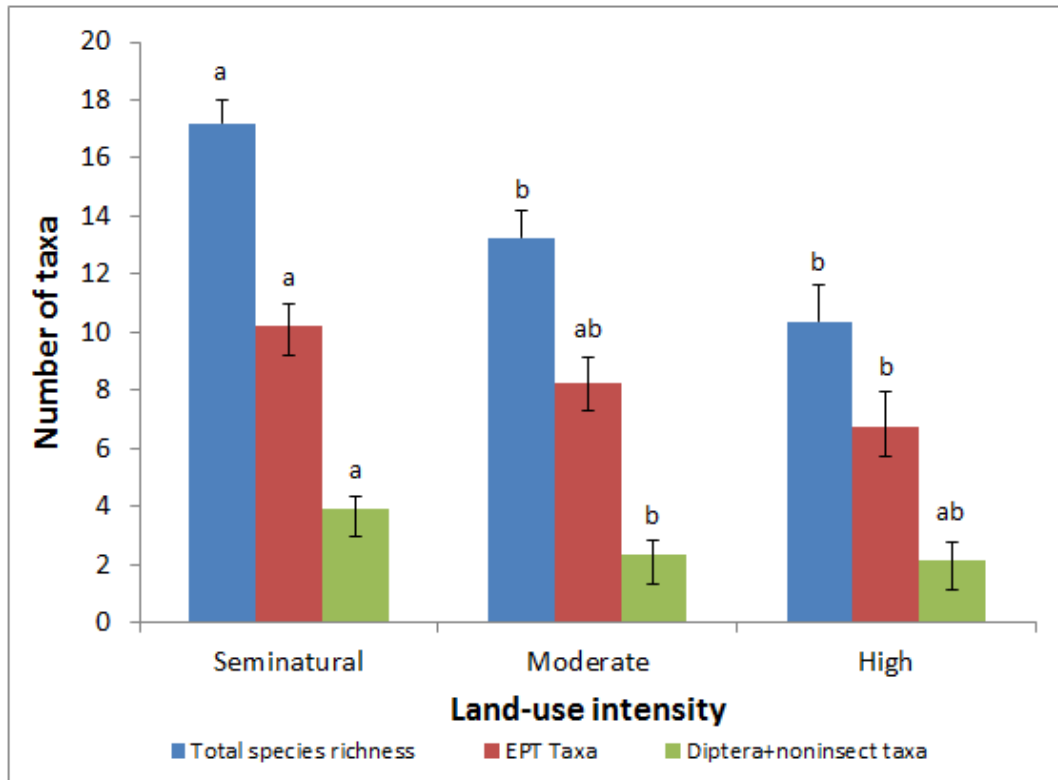


FIG. 2.6. Mean taxa richness of total taxa, EPT taxa, Diptera and non-insect taxa among three levels of land use intensity. Standard error of mean taxa richness and pair-wise *post hoc* comparison results are shown with different letters denoting significantly different values.

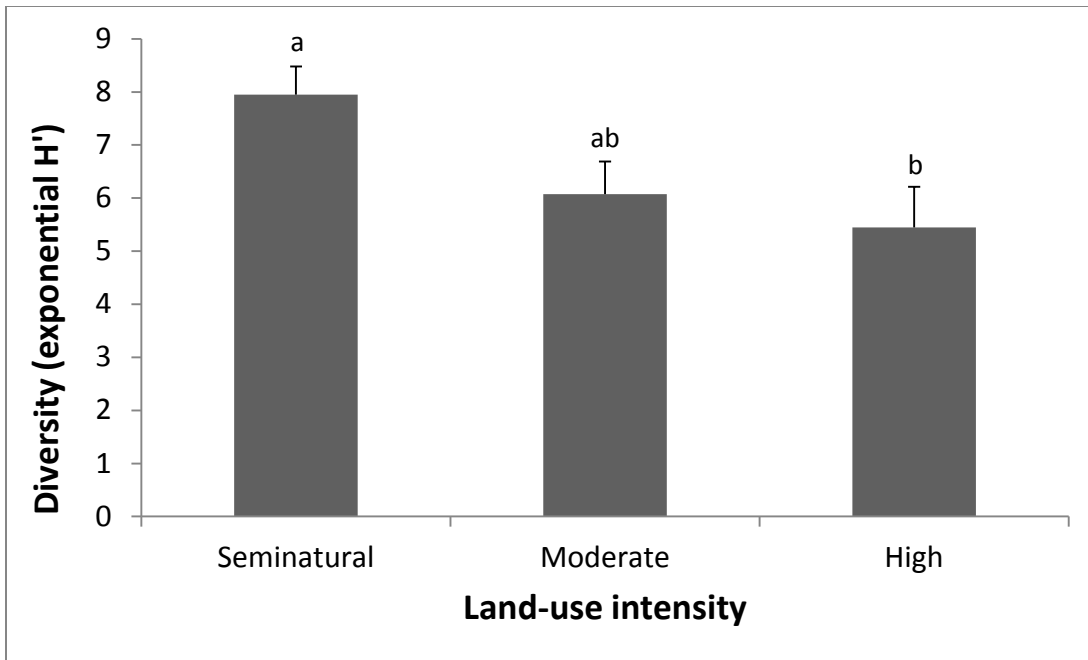


FIG. 2.7. Mean macroinvertebrate diversity among three levels of land use intensity. Standard error of mean diversity (exponential of Shannon diversity index) and pairwise *post hoc* comparison results are shown with different letters denoting significantly different values.

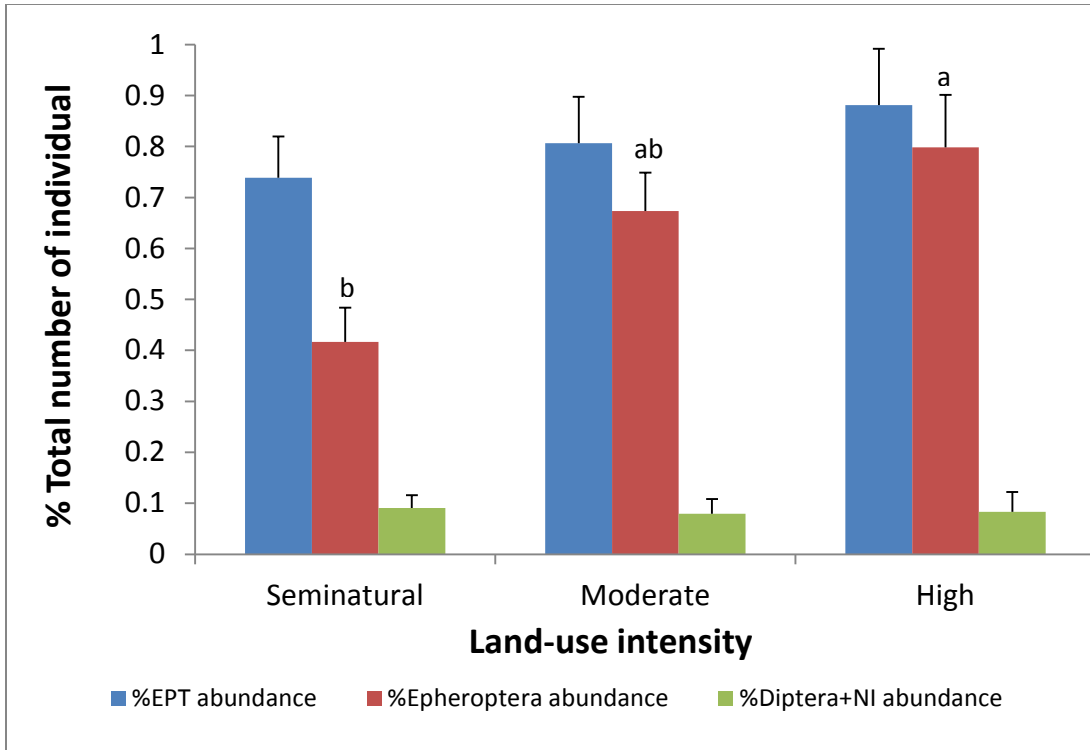


FIG. 2.8. Mean percentage of EPT, Ephemeroptera, Diptera and non-insect abundance among three levels of land use intensity. Standard error of mean percentage of macroinvertebrate abundance and pair-wise *post hoc* comparison results are shown with different letters denoting significantly different values. NI=non-insect group of macroinvertebrates.

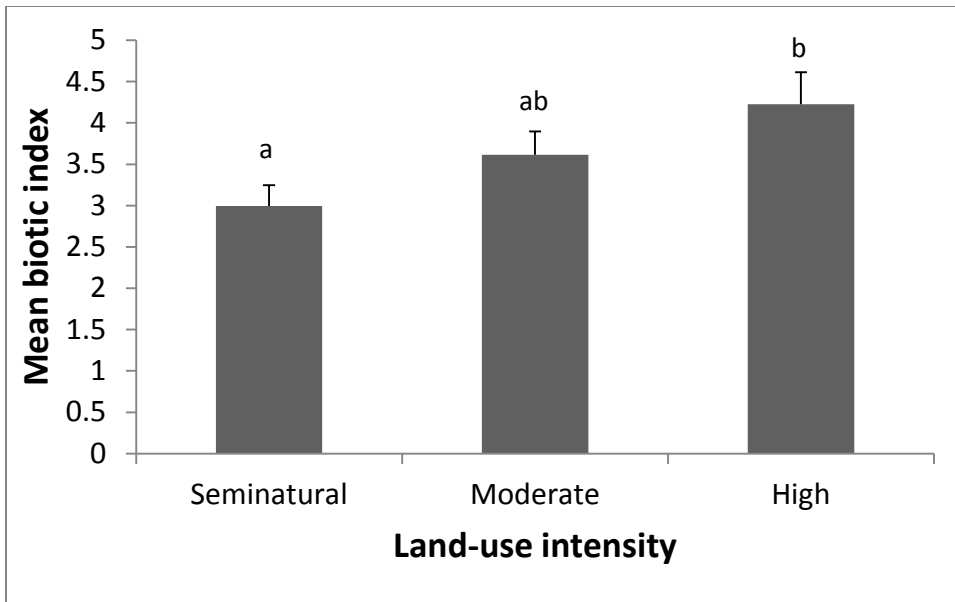


FIG. 2.9. Mean percentage biotic index among three levels of land use intensity. Standard error of mean percentage of macroinvertebrate abundance and pair-wise *post hoc* comparison results are shown with different letters denoting significantly different values.

Table 2.4 Water quality classification for 42 sites based on North American biotic index (Lenat 1993). Biotic index range 0 to 10 and greater value indicate greater tolerance. Water quality classified as Excellent<4.17; Good=4.18-5.09; Good-fair=5.10-5.91; Fair=5.92-7.05; Poor=>7.05 in the mountain ecoregion.

| Land-use intensity | Biotic index | Water quality classification | Land-use intensity | Biotic index | Water quality classification |
|--------------------|--------------|------------------------------|--------------------|--------------|------------------------------|
| High | 2.51 | Excellent | Seminatural | 2.58 | Excellent |
| High | 3.75 | Excellent | Seminatural | 2.60 | Excellent |
| High | 3.85 | Excellent | Seminatural | 2.61 | Excellent |
| High | 3.91 | Excellent | Seminatural | 2.66 | Excellent |
| High | 4.10 | Excellent | Seminatural | 2.71 | Excellent |
| Moderate | 1.55 | Excellent | Seminatural | 3.10 | Excellent |
| Moderate | 2.49 | Excellent | Seminatural | 3.15 | Excellent |
| Moderate | 2.54 | Excellent | Seminatural | 3.17 | Excellent |
| Moderate | 2.75 | Excellent | Seminatural | 3.27 | Excellent |
| Moderate | 3.02 | Excellent | Seminatural | 3.32 | Excellent |
| Moderate | 3.14 | Excellent | High | 4.26 | Good |
| Moderate | 3.27 | Excellent | Moderate | 4.22 | Good |
| Moderate | 3.80 | Excellent | Moderate | 4.80 | Good |
| Moderate | 4.08 | Excellent | Moderate | 5.09 | Good |
| Moderate | 4.11 | Excellent | Seminatural | 4.28 | Good |
| Moderate | 4.11 | Excellent | Seminatural | 4.32 | Good |
| Seminatural | 1.47 | Excellent | Seminatural | 4.54 | Good |
| Seminatural | 1.55 | Excellent | High | 5.15 | Good-fair |
| Seminatural | 1.59 | Excellent | Moderate | 5.39 | Good-fair |
| Seminatural | 1.95 | Excellent | Seminatural | 5.67 | Good-fair |
| Seminatural | 2.29 | Excellent | High | 6.37 | Fair |

CHAPTER THREE

SPECIES-LEVEL RESOLUTION FOR A TRAIT-BASED APPROACH TO BIOMONITORING USING A GENUS OF BLACK FLIES (Simuliidae: *Simulium*)

Abstract

Determining a proper taxonomic resolution is important for bioassessment methods to balance the assessment needs most effectively against effort and funding. I compared efficiencies of species-level versus genus-level resolution to distinguish land use gradients based on the functional structure of black fly assemblages. Black fly qualitative samples were collected from 25 sites and identified to the species level. A total of 86 trait categories of 16 biological and ecological traits were compiled for 16 black fly species. Overall functional diversity distinguished semi-natural sites from the impaired sites. For individual trait categories, no biological traits differed significantly, but some ecological traits related to habitat association and saprobity were significantly different among different level of land-use intensity sites. Species-level resolution provides more information than genus-level, but does not improve discrimination of levels of land-use impacts.

Introduction

Taxonomic resolution of macroinvertebrates has been a controversial topic in stream bioassessment (Lenat and Resh 2001). The main reason for the debate on taxonomic resolution regards possible information loss and accurate biological

assessment versus taxonomic identification difficulty and bioassessment cost (Bouchard et al. 2005). Lower taxonomic levels of identification (i.e. genus or species) are more likely to detect subtle changes in environmental quality than higher taxonomic levels (family or higher) (Hilsenhoff 1988, Bailey et al. 2001, Waite et al. 2004). In particular, some studies have concluded that species-level identification provides a higher predictive success and may be more appropriate for bioassessment (e.g., Giagrande 2003, Schmidt-Kloiber and Nijboer 2004, Drew 2011). Other studies reported that family-level assessment differed only slightly from genus- or species-level assessments in their ability to detect different levels of anthropogenic impacts and may be sufficient for bioassessment (e.g., Ferraro and Cole 1995, Vanderklift et al. 1996). Determining an appropriate level of taxonomic resolution depends on the purpose of the study, the sensitivity required, the type of assessment, and the group of organisms being used (Waite et al. 2004).

For the various taxonomic approaches to bioassessment, species-level resolution is needed for the most accurate description of community structure at large spatial scales while genus- or family-level resolution may be sufficient at a local scale (Dolédéc et al. 2000). Taxonomic structure of communities affected by local physical habitat and ecoregional conditions thus produce different results when different levels of taxonomic resolution are used. In contrast, the functional structure of communities varies across environmental gradients but patterns of ecological function are similar in different spatial scales (Statzner et al. 2001).

According to some authors, for a trait-based approach (TBA), species-level assessment is likely not required and genus- or family-level identifications provide a realistic functional description of the stream invertebrate community regardless of spatial scale (Dolédec et al. 2000, Gayraud et al. 2003). Organisms within a family usually possess similar traits, which provide redundancy of ecological function, such that no more information would be contributed by further taxonomic resolution (Bouchard et al. 2005). In contrast, other authors have noted that environmental requirements, trophic status and tolerance to anthropogenic disturbances are often variable among species (Cranston 1990, Lenat and Resh 2001), such that coarser taxonomic assessment may lead to a wrong classification of ecological quality because of loss of auto-ecological information (Cranston 1990, Schmidt-Kloiber and Nijboer 2004, Jones 2008). These contradicting results raise a question about whether species-level assessment is needed to identify ecological conditions accurately for TBA.

Few studies have examined species-level resolution (Dolédec et al. 2000, Gayraud 2003) because of limited trait information at the species level. In Chapter 2, I examined trait responses to three levels of land-use intensity with a mix of genus- and family-level resolutions; in this chapter, I investigate the importance of taxonomic resolution in TBA to distinguish land use gradients based on the functional structure of black fly assemblages identified to species level.

Material and methods

Black fly samples were obtained from 25 sites in the Orkhon drainage of the Selenge River Basin, northcentral Mongolia, during late June to mid-July 2011 (Fig. 3.1). The Selenge River Basin is surrounded by the Khentii, Khangai, and Sayan Mountain mountain chains and has an average altitude of 1500-2500 MASL. The Selenge Basin includes 30.6% of the water resources for Mongolia with a 425,245 km² catchment area and covers a wide range of ecological regions including taiga, high mountains, forest-steppe and steppe zones (Tumurchudur and Jadambaa 2012). Study sites were categorized in relation to levels of land-use in the watershed as seminatural, moderate, and high land-use intensity sites. Seminatural sites were those with no evident land use activities (no grazing or mining) or with only light grazing present. Moderate and high levels of land-use intensity had grazing or grazing coupled with mining impacts except that one site had mining activity but no grazing. Suspended solids, turbidity, and ammonium were significantly higher in high level land-use intensity sites than in moderate level intensity sites.

Twenty-five qualitative samples were taken using a D-net (500 μ) or by hand sampling from the different microhabitats including rocks, logs and vegetation within a 50-m reach from each site during late June to mid-July 2011. Samples were preserved in Carnoy's solution (one part glacial acetic acid: three parts absolute ethanol) and the fixative was changed twice during the subsequent 12 hours. Simuliids were identified by P.H. Adler to the species level based on polytene chromosome maps (Appendix B).

I compiled 86 trait categories of 16 traits related to life history, mobility, and morphology for 16 black fly species of the single genus *Simulium* based on experts' experience (Table 3.1, Appendix C). Trait-based analytical approaches have categorized traits into categories, which are coded in a “fuzzy” manner for each species as described by Chevenet et al. (1994). Fuzzy coding characterizes the affinity of each state to account for trait variation within a species. Affinity scoring ranges from zero to three, where zero indicates no affinity of a species to that state and the highest affinity level indicates that a species has that particular state exclusively.

Affinity scores were treated as frequency distributions to give the same weight to each species and trait so that affinity scores are equal to 1 for a given trait and species (Chevenet et al. 1994).

$$q_k = \frac{a_k}{\sum_{k=1}^h a_k} \text{ with } q_k \geq 0 \text{ and } \sum_{k=1}^h q_k = 1$$

k- a trait category

q_k - frequency of a trait category

a_k - assigned affinity

h- total number of categories in a given trait

Statistical analysis

Functional diversity was measured by computing a functional diversity index (Petchy and Gaston 2006) within land use intensity gradients. This index is the most commonly used and gives a meaningful measure of functional diversity (Pla et al.

2011). Functional diversity was defined as the sum of the branch lengths linking species belonging to the same community on the functional dendrogram built from a regional species pool based on incidence data (Petchy and Gaston 2002, 2006).

$$FD = i' \cdot h2$$

i' - branch presence/absence row vector

$h2$ - branch length vector

A one-way analysis of variance (ANOVA) was conducted to test whether functional diversity varied significantly between the sites with different levels of land-use intensity. In pair-wise *post hoc* comparisons, Fisher's exact test was used (Table 3.2).

Pearson's Chi square test was used to test how the frequency of each trait category differed among the levels of land-use intensity.

Correspondence analysis (CA) is an indirect ordination technique commonly used to explore trait composition across a set of sites (Heino et al. 2013). CA is a graphical method exploring the relationship between categorical variables based on *Chi squared* distance and is a favorite tool for present and absent data (Borcard et al. 2011). CA was used to test the variation in trait composition of black fly species among the levels of land-use intensity (Figs. 3.3). The frequencies of each trait category per trait were multiplied by the incidence of each species at the site to create a trait-by-site array.

I used FDiversity software (Casanoves et al. 2011) for computing functional diversity indices and JMP software version 9.0.2 (SAS Institute Inc. 2010) for

ANOVA and Pearson's *Chi square* test and R software version 3.0.1 for conducting a vegan package (R Development Core Team 2010) for CA.

Results

Functional diversity indices were significantly different between semi-natural sites and sites with greater levels of land-use intensity ($P < 0.004$), but there were no differences between moderate and high levels of land-use intensity (Fig. 3.2). A total of 13 trait categories were used to compute the functional diversity indices, as 73 of the 86 traits were excluded from the analysis because of a lack of range of traits among the species in the genus.

Only five ecological traits belonging to trophic-level (mesotrophic, eutrophic level), temperature (warm temperature), and saprobity (oligosaprobic and β - mesosaprobic) were significantly different (Pearson's chi-square < 0.001) along the land-use intensity gradient. (Table 3.1)

The CA analysis shows the pattern of trait distribution among three levels of land-use intensity. Species more commonly found in warm temperatures and eutrophic conditions occurred more frequently in sites with moderate and high land-use intensity than in seminatural sites (Figs. 3.3). Oligosaprobic species were more common in seminatural sites than in moderate land-use intensity sites while no oligosaprobic species were found in high land-use intensity sites (Fig. 3.3). In contrast, species more commonly occurring in mesotrophic conditions occurred more frequently in seminatural sites than in moderate land-use intensity sites while

none occurred in high land-use sites (Fig. 3.3). Also, mesosaprobic species were more common in high and moderate land-use intensity sites than seminatural sites (Fig. 3.3).

Discussion

Different levels of taxonomic resolution for samples of a biological community may affect the ability of a bioassessment method to detect changes in ecological quality. It is necessary to determine a meaningful compromise for the level of taxonomic resolution by considering all aspects of bioassessment, including potential information loss, accurate biological assessment, species level identification difficulty, and bioassessment cost (Resh and Jackson 1993). This study examined the extent to which species-level resolution can be informative and its potential to discriminate environmental change.

Among my findings, overall functional diversity was significantly different among black fly (*Simulium*) assemblages identified to species along the land use gradient. Also, species-level resolution provided some additional ecological trait information, including differences in saprobity, trophic level, and temperature, capable of discriminating impacted sites from relatively unimpacted sites. According to the niche concept, each species has evolved special abilities to exploit resources and the occurrence of a species indicates the presence of its particularly adapted environmental conditions (Schmidt-Kloiber and Nijboer 2004). Tolerance values to pollution, for example saprobic values or tolerance values as used in Biotic Index

calculations, can be highly variable among species within a genus (Resh and Unzicker 1975). Stubauer and Moog (2000) found a wide range of saprobic values among species of the black fly genus *Simulium*. However, there were no significant differences in biological traits among species of *Simulium*. Closely related species generally have similar biological trait designations (Dolédec et al. 2000) because of phylogenetic constraints (Vieira et al. 2006).

Species-level assessment of species in the black fly genus *Simulium* provided more information related to their habitat association than only genus-level *Simulium* trait information, but these details provided no additional discrimination ability for land-use impact as compared to the results of higher taxonomic resolution (Chapter 2). Genus-level and coarser levels of identification for other macroinvertebrate groups have shown that habitat traits responded similarly to species-level identification, both of which distinguished differences among land-use intensity gradient (Chapter 2). The functional description of the macroinvertebrate community and its potential to discriminate anthropogenic impacts were similar between the genus- or family-level resolutions and the finest taxonomic resolution (Gayraud et al. 2003). Taxonomic resolution for traits had less effect on predictive power than for quantitative information of taxa (Dolédec et al. 2000). Nevertheless, higher taxonomic resolution might be useful to reduce noise derived from environmental heterogeneity (Warwick 1993, Dolédec et al. 2000).

The study result showed that phylogenetically constrained traits co-occur in closely related species while relatively plastic ecological traits vary among species.

Congeneric species may possess similar traits (Poff et al. 2006) or species-level trait information may not be available. Using coarse taxonomic level resolution may reduce “trait syndrome” which is an intercorrelation between phylogenetically constrained traits among closely related taxon.

Species-level resolution may be required depending on study objectives. Species-level resolution may be necessary if a study focuses on adaptive radiation in a highly heterogeneous habitat, if environmental differences occur among only a few species when the overall fauna is poor (Vieira et al. 2006), if ecological specialists are represented at only the species level, or if functional redundancy is being investigated (Bouchard et al. 2005).

This study assessed the importance of species-level analysis for only a single genus. If trait variability in such a restricted sample is low or unknown, it can be problematic to conclude whether species-level resolution is required to assess ecological conditions. Consequently, most successful applications of TBA have been based on genus-level resolution (e.g., Charvet et al. 2000, Díaz et al 2008, Bonada et al. 2007, Dolédec et al. 2006, 2008, 2011, Maasri and Gelhaus 2012). Perhaps the best choice now based on taxonomic knowledge (i.e. ability to identify the macroinvertebrate stages to species) and our knowledge of individual species characteristics (which isn't good) is at genus or family level.

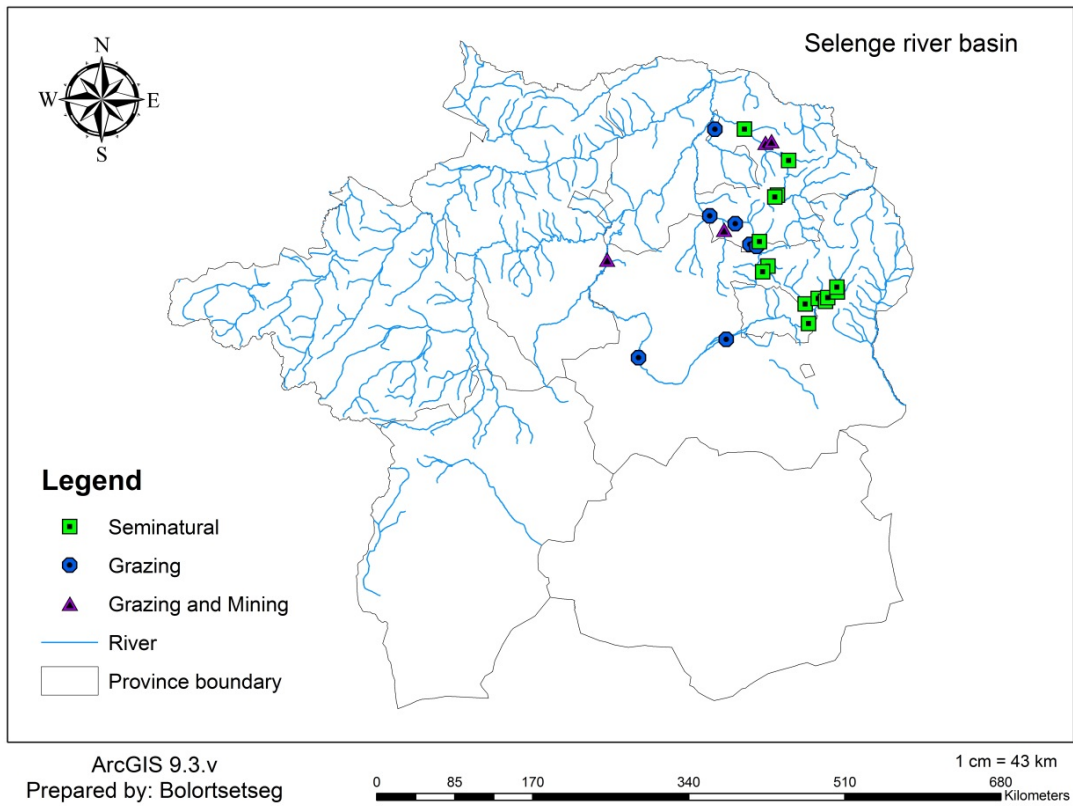


FIG. 3.1. The location of black fly sampling sites in the Selenge basin, Mongolia.

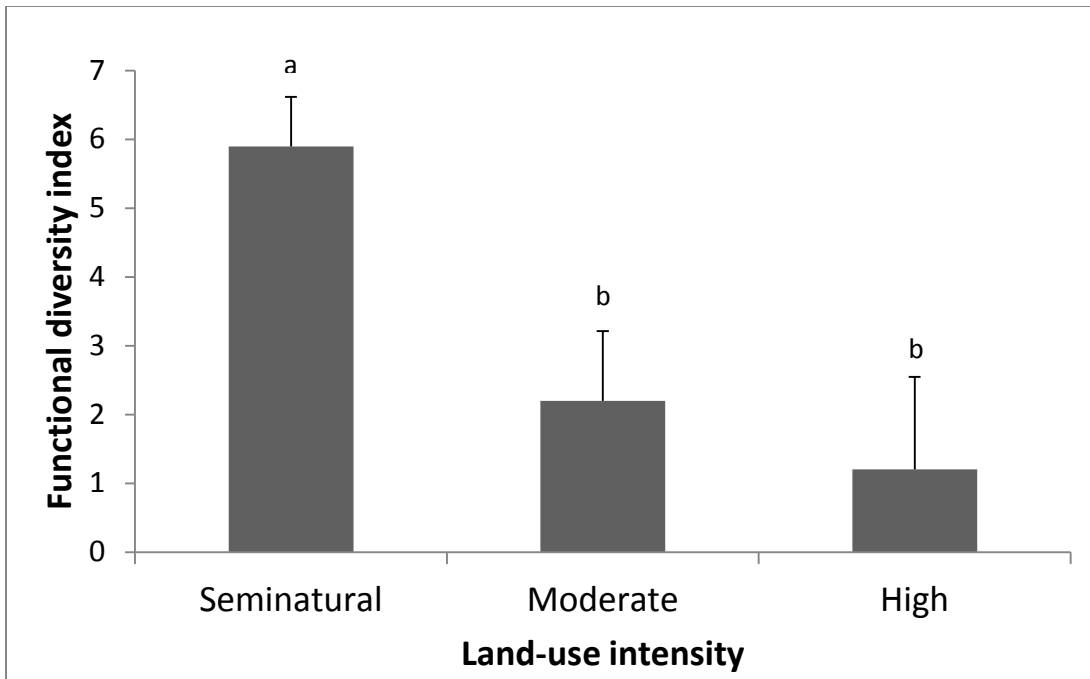


FIG. 3.2 Mean functional diversity among the levels of land use intensity. Standard error of mean functional diversity and pair-wise *post hoc* comparison results are shown with different letters denoting significantly different values.

Table 3.1. Pearson's Chi square test on the trait categories among the levels of land-use intensity and associated P values. Significance was marked by*. There were no variance for all other trait categories.

| Traits | Trait categories | Pearson's Chi square P value |
|-----------------------------|-----------------------------|-------------------------------------|
| Voltinism | univoltine | 0.09 |
| | bivoltine | 0.09 |
| Reproduction | isolated eggs, free | 0.07 |
| | clutches, cemented or fixed | 0.07 |
| Trophic level (preferendum) | mesotrophic | 0.001* |
| | eutrophic | 0.001* |
| | cold | 0.09 |
| Temperature (preferendum) | warm | 0.001* |
| | eurythermic | 0.1 |
| | xenosaprobic | 0.09 |
| Saprobity | oligosaprobic | 0.001* |
| | β -mesosaprobic | 0.001* |
| | α -mesosaprobic | 0.07 |

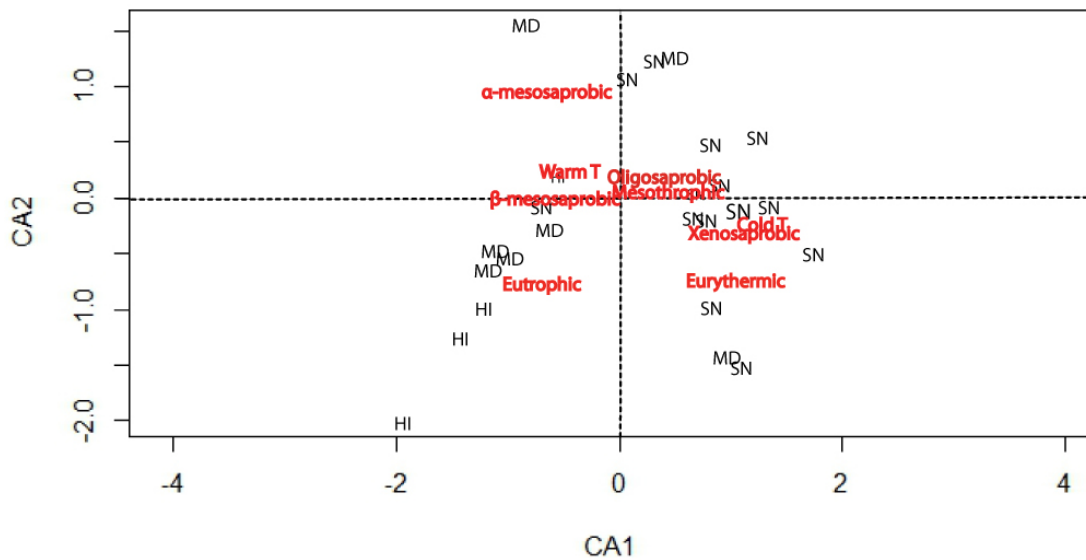


FIG. 3.3 Ordination plot of correspondence analysis showing distribution of temperature, trophic level association and saprobity among the levels of land use intensity. SN=seminatural, MD= moderate, and HI= high level of land-use intensity. Warm T= warm temperature and Cold T=cold temperature. Trait categories scaled proportional to Eigen value. Sites were weighted by averages of trait category scores. Eigen value for first axis=0.26second axis=0.1. The first axis accounted 52% of total variance and second axis 19% of total variance.

CHAPTER FOUR
DECLINES IN DIVERSITY OF CRANE FLIES (DIPTERA: TIPULOIDEA)
INDICATE IMPACT FROM GRAZING BY LIVESTOCK IN THE HÖVSGÖL
REGION OF MONGOLIA

Abstract

Threats to biodiversity are not studied equally among species, leaving some groups, like insects, typically understudied in conservation and management research. Crane flies (Diptera: Tipuloidea) are diverse and important members of the aquatic and terrestrial biotic communities. Increased grazing by livestock in the Hövsgöl region of Mongolia has impacted both the terrestrial and aquatic ecosystems. The purpose of this study was to document biodiversity of crane flies along the east shore of Lake Hövsgöl, Mongolia, and to test whether crane fly diversity differs between valleys with different grazing intensity. Ninety- five species of Tipuloidea were found in this study, nine of these newly recorded for Mongolia, with 21 new records for the Hövsgöl region. Rarefaction curves indicated that predicted diversity is less for moderately and highly grazed valleys than for the less grazed valleys in this region. Results of an analysis of variance indicated that the exponential of Shannon's diversity index was significantly higher in the less grazed valleys. Finally, linear regression analysis indicated that soil moisture, plant biomass, and livestock number were the strongest predictors of variation in crane fly diversity across the grazing gradient.

Introduction

Loss of biological diversity threatens many regions of the globe (Dirzo and Raven 2003), but this threat is not studied equally amongst species, populations, or communities. Insects and other invertebrates are typically understudied groups that may face even greater threats to biodiversity than do vertebrates (McKinney 1999; Strayer 2006). Although some true flies (Diptera) have been studied (e.g. Haslett 2001; McCreddie and Adler 2008), many Diptera are overlooked in biodiversity and conservation research. At just over 15,000 species, crane flies (Tipuloidea) are one of the most diverse groups of Diptera. Crane flies are important members of the aquatic and terrestrial biotic communities (de Jong et al. 2008). Crane fly larvae are fully aquatic to semi-terrestrial and semi-terrestrial species generally associated with humid environments, such as the margins of ponds and streams, but are also found in forests and grasslands (Alexander 1920; de Jong et al. 2008).

In the past two decades, overgrazing has exceeded pasture carrying capacity and has degraded natural habitats of Mongolian grasslands due to increased livestock number and decline of traditional herding practices (Altanbagana 2010). Degradation of grasslands has been accelerated by global climate change leading to a shift from grassland to more desert-like conditions (Batima 2005), and often results in the loss of biodiversity (Watkinson and Ormerod 2001). Grazing along riparian zones can result in habitat modifications such as reduction of vegetative cover, erosion, and stream bed sedimentation (Belsky et al. 1999) which can subsequently lead to a decrease in the density of certain taxa (Quinn et al. 1992) and changes in community

structure (Scrimgeour and Kendall 2003). Overgrazing negatively impacts riparian range health for Mongolia and has been shown to impair dipteran diversity (Hayford and Gelhaus 2010).

Tipulidae are particularly susceptible to soil compaction, drying, and loss of vegetative cover caused by grazing because the larvae generally consume dead organic matter (e.g., usually decaying plant material) and adults have weak flight capabilities (Service 1973, Alexander and Byers 1981) such that they nearly always remain near natal habitats (Barnes 1925, Rogers 1933, Freeman 1968). Crane flies have high levels of endemism in the Hövsgöl region of Mongolia (Gelhaus and Podenas 2006), a region characterized as a biogeographic and ecological transition zone from taiga forest to mountain steppe and Central to East Asia (Lkhagva et al. 2013). Six valleys along the east shore of Lake Hövsgöl exhibit a gradient in conservation management resulting in varying amounts of livestock grazing and thus provide an ideal field laboratory to study the effects of grazing on crane fly diversity.

The purpose of this study is to document biodiversity of crane flies along the east shore of Lake Hövsgöl, Mongolia, to determine whether crane fly diversity differs between valleys with different grazing intensity, and specifically test whether species diversity is inversely related to grazing intensity. More grazing in this study area has been shown to change the dominant plant species and reduced plant cover. The loss of plant cover allows increased evaporation with increased soil temperature and loss of soil moisture (Batkishig 2004, Lkhagva et al. 2013). I expected these impacts to the plant community and edaphic conditions to lead to lower crane fly

species diversity.

Materials and Methods

Study Area

The Hövsgöl region is located in north central Mongolia, about 200 km southwest of Lake Baikal, Russia. It is part of the southern-most zone of the tectonic basins of the Baikal Rift system (Goulden et al. 2006), and its dominant feature is Lake Hövsgöl, a large, deep, ancient lake (Kozhova 1989). The region is characterized by mountain taiga forest and forest steppe plateau in the Lake Hövsgöl watershed.

Six valleys along the northeastern shore of the lake were selected for study by the Hövsgöl Global Environmental Facility (GEF) project, ranging from the heavily grazed northern valleys of Turag (TRG) and Shagnuul (SHL) south of Hanh, the Noyon (NYN) and Sevsuul (SVL) valleys with moderate grazing, and the Dalbay (DLB) and Borsog (BRG) valleys in the south with light or no grazing pressure (Table 4.1; Fig. 4.1).

Livestock number was variable ranging from about 50 to about 3000 livestock (in sheep units) between 2002 and 2005, with the highest density in the Turag and Shagnuul valleys and lowest in the Borsog valleys. Pasture carrying capacity estimates suggested that the two northern valleys were overgrazed, the middle two valleys were beyond their carrying capacity, and the southern two

valleys had low to no grazing (Bayasgalan 2005). Further details about the study area were reported in Puntsag et al. (2010).

Sampling

Sampling for adult crane flies was accomplished through monthly timed sweeps (1 hr) and weekly samples from permanent Townes-style Malaise traps in each valley from June to August 2002–2005. Adult crane fly samples were taken by two methods from the six stream valleys in 2002, 2003, 2004, and 2005: (1) by monthly, timed aerial sweep netting in the riparian zone of three sites (upper, middle, lower reach) in each valleys in 2002, 2003, 2004, and 2005, and (2) by weekly collections from Malaise traps set in two positions (riparian and steppe-forest edge) at middle reach of each valley in 2003, 2004, and 2005 (Table 4.1). The position of the middle site of timed sweep and malaise trap in riparian zone was overlapped. A total of 129 sweep net samples and 286 Malaise-trap samples were collected. Sample sizes for the two methods were unequal in the six study valleys. A total of 17 to 24 timed sweep net samples and 38 to 54 Malaise trap samples were taken in each of the six study valleys. These two sampling methods were analyzed separately because different sampling methods lead to different sets of individuals being observed for the sampling units and the species diversity of each set may be different (Tuomisto 2010).

In addition to insect collections, associated data on vegetative cover and soil moisture were taken regularly at the middle sites in each valley. All plants within a randomly chosen quadrant were harvested at ground level and used to estimate the

total above-ground plant biomass during 2002–2005 (Lhagva et al. 2013). Soil moisture and temperature were measured using a Time-Domain Reflectometer (TDR), soil moisture and temperature probes at 20 cm soil depth in all sampling quadrants during 2003-2004 (Lkhagva et al. 2004). Air temperature, relative humidity, and precipitation were measured in the six valleys every hour with mini-meteorological stations and Hobo data loggers (company, location) during 2003-2005 (Nandintsetseg 2004).

Identification

Crane fly species identifications were accomplished in the laboratories of the Institute of Meteorology and Hydrology, Hövsgöl GEF offices, the University of Vilnius, Lithuania, and the Academy of Natural Sciences, Philadelphia, USA (now Academy of Natural Sciences of Drexel University), using standard taxonomic references (Savchenko 1972; Alexander and Byers 1981; Brodo 2000; Gelhaus et al. 2000; Gelhaus 2001; Podenas and Gelhaus 2001; Oosterbroek 2007).

Voucher collections of crane flies were deposited in the Mongolian Insect Survey Project Laboratory at the Institute of Meteorology and Hydrology and Mongolian Academy of Sciences, Ulaanbaatar. Representatives of selected taxa were also deposited in the Academy of Natural Sciences of Drexel University.

Statistical analysis

Principle Component Analysis (PCA) was performed using plant biomass, soil moisture, and livestock number to discriminate primary grazing gradients (Fig.4.2). A variety of richness estimates were used to describe variation of crane fly

diversity between the sites under different levels of grazing as discriminated by the PCA (Fig.4.2). Crane fly species diversity was measured through species richness, evenness, and diversity indices. Sample-based rarefaction analysis was performed to predict rarefied species richness. Estimated species richness (Chao 1 estimator) was used to demonstrate the asymptotic relationship between the increase in sample size and cumulative number of species. EstimateS v.8.20 software (Colwell 2009) was used to calculate the diversity indices; Mau Tao rarefaction was based on 50 runs considering the number of singletons, doubletons, and unique species; and the Chao 1 asymptotic estimator of species richness was calculated from two datasets collected by the different methods. Species evenness in the assemblages was quantified by Simpson's evenness (Simpson 1949) and the Berger-Parker dominance index (Berger and Parker 1970). The exponential of Shannon's index (Shannon 1948) provides a meaningful measure of true diversity (Jost 2006) and is popular in scientific literature (Maurer and McGill 2011). For this reason, we used the exponential of Shannon's index of diversity for ANOVA and regression analysis.

Diversity values were pooled within the high grazed, medium grazed, and low grazed sites (Fig. 4.2), and a one-way analysis of variance (ANOVA) was used to test whether crane fly diversity varied significantly between these grazing regimes. In pair-wise *post hoc* comparisons, Tukey's HSD test was used. We ran a stepwise multiple linear regression analysis to model response of crane fly diversity to a suite of environmental variables related to grazing (Table 4.2). The middle sites collected in each valley represented the most evident grazing and so were used in the

analysis. We only had field data from two years, 2003 and 2004, for the entire suite of environmental variables (Table 4.2). We pooled these data and used means in the linear regression analysis. Variables met assumptions of normality and heteroskedasticity prior to analysis and in *post hoc* tests for the regression analysis. ANOVA and linear regression analyses were performed using the JMP statistical software package version 9.0.2 (SAS Institute Inc. 2010). Statistical significance was set at $P < 0.05$.

Results

A total of 5829 specimens were identified and comprised 95 species of crane flies (Tipuloidea) from the six study valleys of this study. Nine of these were new records in Mongolia, and 22 were new records for the Hövsgöl region (see Appendix F). Observed species richness was higher in lightly grazed sites than in moderately grazed and heavily grazed sites in both sweep-net and Malaise-trap datasets (Table 4.3, Fig. 4.3). The difference between the observed and estimated number of species was greatest for moderately grazed sites. Based on the Chao 1 estimator of species richness, moderately grazed sites were predicted to have more species than other sites in both datasets. A significant number of rare species (singleton, doubleton, and unique species) occurred at all sites but more singletons and unique species were observed at moderately grazed sites, which contributed to the greater Chao 1 value at moderately grazed sites. Rarified species richness was greatest at the low-grazed sites in the sweep net and Malaise-trap datasets (Table 4.3). In the combined sweep

net and Malaise-trap data set, 8 unique species were found from each low-grazed or moderately grazed site, 10 species were recorded from both low-grazed and moderately grazed sites, and a total of 26 species were found only at low-grazed and moderately grazed sites. In contrast, two species were unique for heavily grazed sites (Appendix F).

Species diversity of crane flies (the exponential of Shannon's index) was significantly different among the sites ($P < 0.001$) with the highest number of species in the low-grazed sites. The *post hoc* test showed that the species diversity of crane flies from the low-grazed sites was significantly higher ($P < 0.001$), whereas there were no significant differences ($P < 0.8$) between moderately and heavily grazed sites (Fig. 4.4).

Three variables, soil moisture ($P < 0.04$, $R^2 = 0.68$), plant biomass ($P < 0.02$, $R^2 = 0.79$) and livestock number ($P < 0.01$, $R^2 = 0.82$), were strong, significant predictors of variation in crane fly diversity in the linear regression model (Table 4.4, Fig. 4.5). There were no relationship between the crane fly diversity and soil temperature, air temperature, relative humidity and precipitation (Table 4.4).

Discussion

A total of 95 species of crane flies have been identified from this study making a total of over 134 species from Hövsgöl region of Mongolia (this study, Gelhaus and Podenas 2006, Gelhaus et al. 2007, Boldgiv 2006). For this study, 9 species are new records for Mongolia, and 22 are new records for the Hövsgöl

region of Mongolia (Appendix E). After extensive sampling, the estimated species richness approached the predicted asymptotic species richness in all sites except one moderately grazed site. Overall, the crane fly fauna in Hövsgöl region was not highly diverse compared to the global fauna in relation to the region's continental location, high elevation, and latitude (Gelhaus and Podenas 2006). However, crane fly diversity was high relative to other insects surveyed in the region that have been sampled over larger areas or longer periods of time. For example, 118 species of non-biting midges (chironomidae) were identified from the Hövsgöl region over 30 years of sampling (Hayford et al. 2006, Erbaeva et al. 2006), and 101 species of caddisflies (trichoptera) were identified from 156 sites across central Mongolia (Chuluunbat and Morse 2007). Crane flies were more diverse than grasshoppers (give scientific name), of which only 20 species of grasshoppers were sampled at the same sites as this study. As a group, crane fly larvae inhabit a wide range of aquatic to moist terrestrial environments and can be found in a variety of soils including muddy, sandy, gravely and loamy soil, such as those found in the study sites (Alexander and Byers 1981; Podenas et al. 2013). Some species of crane flies were also found at nearly every one of the hundreds of aquatic site sampled in Mongolia during recent MAIS studies (Hayford and Gelhaus, 2010) indicating that the group is a common and characteristic faunal element in Mongolian riparian zones. While crane fly diversity relatively high, it appeared to decline with greater grazing intensity in this study, despite the relatively high diversity.

Over-grazing by livestock has been shown to affect terrestrial and aquatic

ecosystems along the six study valleys of this study (Nandintsetseg et al. 2007, Sharkhuu et al. 2007; Otgonsuren et al. 2008; Puntsag et al. 2010). Lower diversity of crane flies was associated with higher soil moisture, plant biomass and livestock number (Table 4.4), which are the first two variables affected by grazing (Batkhisig 2004 and Lkhagva et al. 2013). Livestock grazing resulted in a decrease of the total plant biomass along the grazing gradients (Lkhagva et al. 2013) and consequently soil microclimate alteration caused surface soil temperature to increase and soil moisture content to decrease in the same sites as this study (Batkhisig 2004).

The most important habitat requirement is moisture for both immature and adult (Rogers 1933). Experimental manipulation has shown that high soil moisture is a necessary condition for crane fly population growth because it reduces susceptibility of immature crane fly to desiccation in England (Carroll et al. 2011). Another field experiments have indicated that abundance and distribution of larval crane flies were affected by soil moisture and organic content (Merritt and Lawson 1981). The main cause of mortality of many crane fly species is desiccation of their immature stages (Pritchard 1983). Resistance to desiccation of immature crane fly is generally correlated to the moisture and temperature of both soil and air (Freeman 1967; Jackson and Campbell 1975). Adults crane flies have weak flight capabilities (Alexander et al. 1981, Gelhaus 2006) nearly always remaining near natal habitats (Rogers 1933). Other studies have shown a direct relationship between the impact of grazing by livestock on vegetative structure, plant diversity, and plant biomass and the subsequent impact on grassland insects (Shiemann et al. 1998, Kruess and

Tscharntke 2002, Yoshihara et al. 2008). However, most of these studies examined herbivorous insects impaired by loss of food abundance and quality. Crane flies are short lived as adults (Byers and Gelhaus 2008) and eat little or not at all living vegetation (Hofsvang 1997; Newton 2005), possibly sheltering under vegetation to avoid desiccation during the heat of the day is explaining why plant biomass was a strong or significant driver of variation in crane flies diversity in the linear regression model. Presence of a suitable habitat determines whether a crane fly species can persist in a given area (Roger 1933). Larvae of many species of crane flies inhabit moss (Alexander and Byers 1981). Moss biomass was a significant portion of total plant biomass in lightly grazed sites and was significantly reduced at moderately grazed sites and lost in heavily grazed sites (Lkhagva et al. 2013). Mosses form a thick layer on the soil, which restricts soil evaporation and permafrost thaw, leading to high soil moisture content (Lkhagva et al. 2013) and consequently low soil temperature (Batkishig 2004). As mosses were degraded by grazing, soil temperature increased, which impaired crane fly communities and specifically destroyed larval habitat for some of the species found in this study. Livestock can have direct effects on watersheds soil erosion, soil compaction, and habitat diversity reduction resulted from livestock trampling besides plant biomass reduction (Reeves and Champion 2004). Trampling pressure from grazing increases soil bulk density, decreases water infiltration rate, and increases surface runoff (Rieterk et al. 2000; Savadogo et al. 2007).

Our results corroborate research showing that semi-aquatic fly diversity

(including crane flies) decreases with increased livestock grazing in the Selenge River basin in Central Mongolia (Hayford and Gelhaus 2010).

The ecological effect of habitat destruction and degradation cause species decline, extirpation, and possibly extinction (Lande 1999). Loss of species diversity may also impair ecosystem function (Brussaard et al. 1997, Balvanera et al. 2006). Like many other species of insects, crane flies serve as bioturbators by turning over, aerating, and cycling nutrients as they move through the soil (Brussaard et al. 1997) and are important decomposers, particularly of leaf litter (Pritchard 1983, Cheshire and Griffiths 1989). The results of our study indicate that crane flies are being lost as a result of increased grazing. The loss of crane fly bioturbators and decomposers may exacerbate these physical impacts of grazing on the soils in the Hövsgöl region.

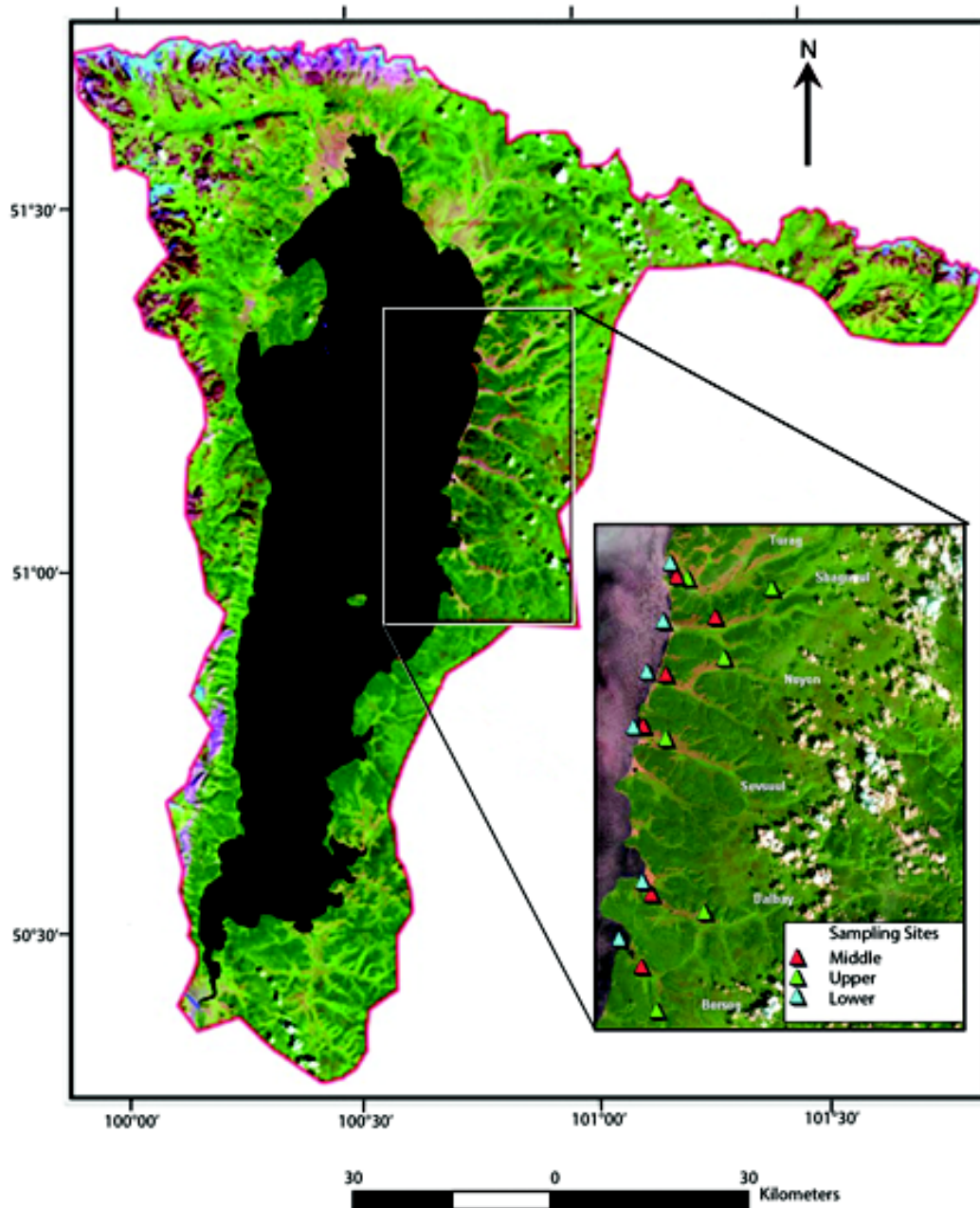


FIG. 4.1. Map of the Hövsgöl region, north central Mongolia. Filled colored triangles indicate upper, middle, and lower sampling sites along the six valleys of this study.

Table 4.1. Six study valleys and sites of the eastern shore of Lake Hövsgöl, their altitudes, coordinates, and collection methods employed.

| Valley | Subsites | Altitude (m) | Longitude (N) | Latitude (E) | Collection method |
|----------|----------------|--------------|---------------|--------------|-------------------|
| Borsog | Upper | 1725 | 50.56 | 100.45 | Timed sweep |
| Borsog | Middle | 1662 | 50.58 | 100.44 | Timed sweep |
| Borsog | Lower | 1656 | 50.58 | 100.44 | Timed sweep |
| Dalbay | Upper | 1727 | 51.00 | 100.50 | Timed sweep |
| Dalbay | Middle | 1662 | 51.01 | 100.45 | Timed sweep |
| Dalbay | Lower | 1660 | 51.02 | 100.44 | Timed sweep |
| Sevsuul | Upper | 1674 | 51.09 | 100.47 | Timed sweep |
| Sevsuul | Middle | 1634 | 51.10 | 100.45 | Timed sweep |
| Sevsuul | Lower | 1631 | 51.10 | 100.46 | Timed sweep |
| Noyon | Upper | 1756 | 51.13 | 100.52 | Timed sweep |
| Noyon | Middle | 1635 | 51.13 | 100.47 | Timed sweep |
| Noyon | Lower | 1649 | 51.12 | 100.46 | Timed sweep |
| Shagnuul | Upper | 1856 | 51.17 | 100.56 | Timed sweep |
| Shagnuul | Middle | 1729 | 51.15 | 100.51 | Timed sweep |
| Shagnuul | Lower | 1668 | 51.15 | 100.47 | Timed sweep |
| Turag | Upper | 1696 | 51.17 | 100.51 | Timed sweep |
| Turag | Middle | 1664 | 51.17 | 100.48 | Timed sweep |
| Turag | Lower | 1637 | 51.18 | 100.48 | Timed sweep |
| Borsog | Riparian Zone | 1681 | 50.96 | 100.73 | Malaise trap |
| Borsog | Edge of Forest | 1689 | 50.96 | 100.73 | Malaise trap |
| Dalbay | Riparian Zone | 1662 | 51.02 | 100.76 | Malaise trap |
| Dalbay | Edge of Forest | 1717 | 51.26 | 100.78 | Malaise trap |
| Sevsuul | Riparian Zone | 1656 | 51.16 | 100.75 | Malaise trap |
| Sevsuul | Edge of Forest | 1687 | 51.16 | 100.75 | Malaise trap |
| Noyon | Riparian Zone | 1626 | 51.20 | 100.81 | Malaise trap |
| Noyon | Edge of Forest | 1709 | 51.20 | 100.81 | Malaise trap |
| Shagnuul | Riparian Zone | 1732 | 51.26 | 100.86 | Malaise trap |
| Shagnuul | Edge of Forest | 1757 | 51.25 | 100.86 | Malaise trap |
| Turag | Riparian Zone | 1667 | 51.29 | 100.83 | Malaise trap |
| Turag | Edge of Forest | 1681 | 51.28 | 100.83 | Malaise trap |

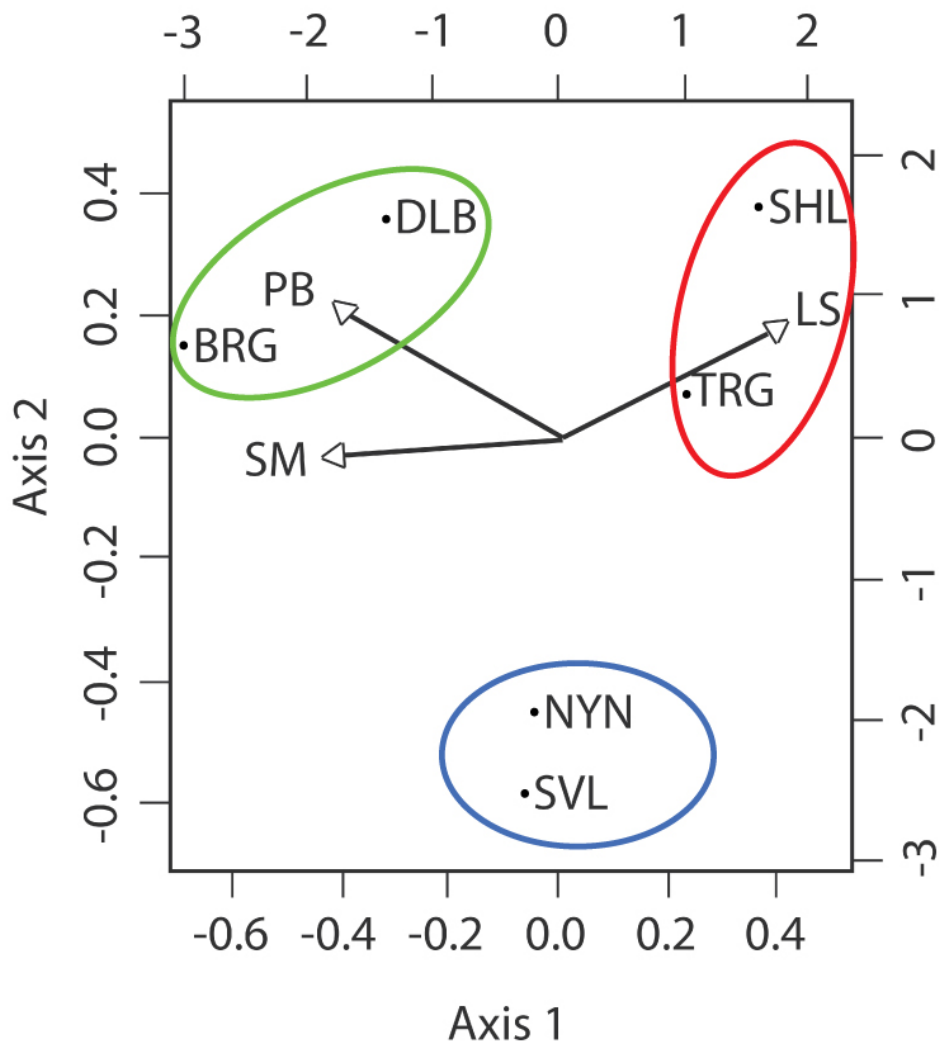


FIG. 4.2. Principle component analysis of six valleys based on three environmental variables. Soil moisture (SM), total aboveground plant biomass (PB) and livestock number (LS). Lines with arrows indicated direction of increasing value for the variables. Sites were segregated by grazing intensity from light (green circle), moderate (blue circle) to heavy (red circle).

Table 4.2. Environmental variables related to grazing in the six valleys of this study for use in the linear regression analysis.

| Environmental variable | Units | Notes about when/how measured |
|-------------------------|----------------------|---|
| Total Plant Biomass | g/0.25m ² | Harvested ground level, classified into functional groups dried and weighted. |
| Livestock Number | Sheep unit | A measurement based on the grazing equivalent of one adult sheep. |
| Soil Moisture | % | Time-Domain Reflectometer (TDR) in 20 cm depth |
| Soil Temperature | °C | Soil Temperature probe in 20 cm depth |
| Atmospheric temperature | °C | Campbell CR10X Meteorological Stations, Hobo Data logger with temperature and relative humidity sensors |
| Precipitation | mm | Campbell CR10X Meteorological Stations, Standard precipitation gauge |
| Relative Humidity | % | Campbell CR10X Meteorological Stations, Hobo Data logger with temperature and relative humidity sensors |

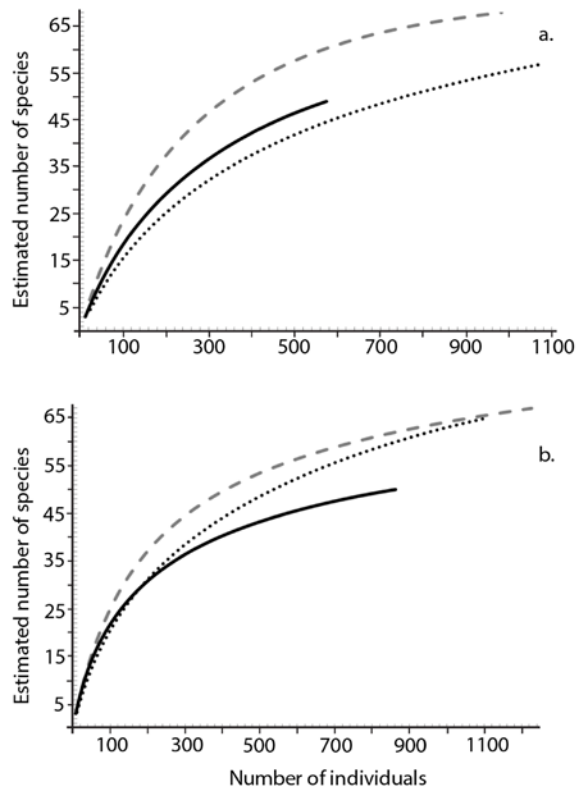


FIG. 4.3. Sample-based species accumulation curves for the six study valleys for a) the sweep-net dataset and b) the malaise-trap dataset. The curves were derived from the Mau Tao function in EstimateS (Colwell 2009). Lightly grazed= dashed, moderately grazed= dotted line, heavily grazed= solid lines.

Table 4.3. Diversity metrics of crane fly assemblages among six study valleys between 2002 and 2005. Sites were ranked by grazing intensity from light (LG), moderate (MG) to heavy (HG). N= total number of animal, S_{obs} =observed species richness, Chao 1 =estimated species richness/asymptotic estimator, $S_{(E\#)}$ = rarified species richness (species richness where number of individuals was standardized), S_1 = number of singletons, S_2 = number of doubletons, S_u = number of unique species, e^H = exponential of Shannon's diversity index, $E_{1/D}$ = Simpson's evenness, and E_{BP} =Berger-Parkerdominance index). Most common species

| Site | N | S_{obs} | Chao1 | $S_{(E\ 574)}$ | S_1 | S_2 | S_u | e^H | $E_{1/D}$ | E_{BP} | Most common species |
|----------------------|------|------------------|-------|----------------|-------|-------|-------|-------|-----------|----------|-------------------------------|
| Timed sweep dataset | | | | | | | | | | | |
| LG | 982 | 68 | 69 | 60 | 3 | 4 | 11 | 39 | 0.36 | 14% | <i>Dicranomyia modesta</i> |
| MG | 1077 | 57 | 70 | 45 | 12 | 4 | 20 | 25 | 0.28 | 14% | <i>Dicranomyia incisurata</i> |
| HG | 574 | 49 | 51 | 49 | 6 | 7 | 18 | 25 | 0.48 | 11% | <i>Dicranomyia modesta</i> |
| Malaise trap dataset | | | | | | | | | | | |
| LG | 1226 | 67 | 70 | 60 | 7 | 7 | 14 | 32 | 0.3 | 12% | <i>Tipula trispinosa</i> |
| MG | 1108 | 65 | 71 | 51 | 12 | 10 | 19 | 25 | 0.23 | 15% | <i>Dicranomyia incisurata</i> |
| HG | 862 | 50 | 51 | 45 | 5 | 13 | 11 | 24 | 0.33 | 10% | <i>Dicranomyia incisurata</i> |

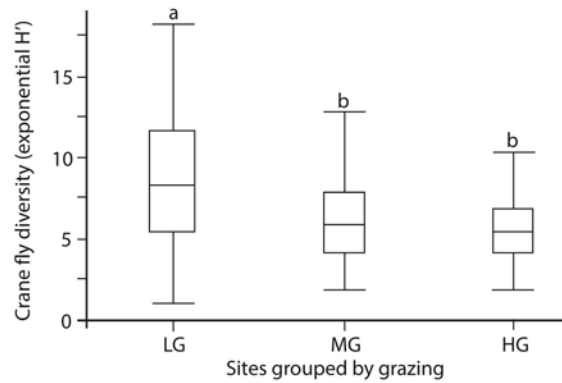


FIG. 4.4 Species diversity of crane flies (exponential of Shannon diversity index) among the valleys along the levels of grazing intensity 2002–2005. Different letters (a and b) represent significant differences in species diversity between the localities. The two datasets from the sweep net and Malaise-trap samples are combined. LG = lightly grazed, MG = moderately grazed, HG = heavily grazed.

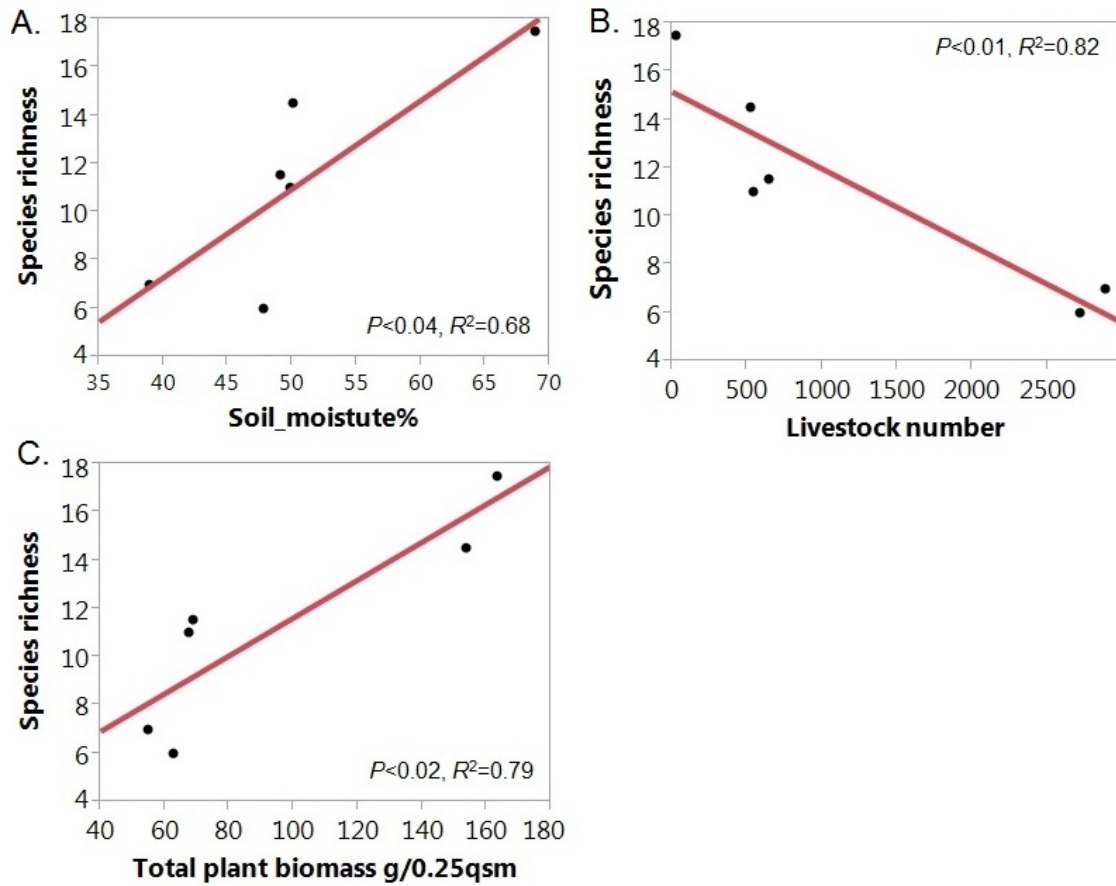


FIG. 4.5 Linear regression analysis between the crane fly diversity by the exponential Shannon's index and, A) soil moisture content, B) plant biomass and C) livestock number among the valleys mean 2003-2004.

CHAPTER FIVE

SYNTHESIS

Mongolia has historically had a nomadic culture so that our lives rely on shared reliance on nature and a substantial part of our economy is based on livestock husbandry. Thus, ecosystem health is a critical theme for politics and public policy of Mongolia. Recently the quantity and quality of water resources and riparian habitats have been degraded dramatically as a consequence of current land use practices coupled with climate change and weak management. To improve water resource management, we need to upgrade the national water quality monitoring program, including development of an appropriate biomonitoring technique for Mongolia.

Why is biological assessment important? Biodiversity has been indentified one of the best descriptor of ecosystem condition as well as playing an important role for ecosystem processes. Hence, alteration of the biological community due to anthropogenic activity may affect the provision of ecosystem goods (e.g., food, timber, clean air, fresh water) and services (e.g., purification of air and water, ground water recharge, soil fertilization, decomposition waste, and soil and vegetation renewal or regeneration) and ultimately will cause negative feedback to our human well-being. Therefore, bioassessment will enhance our understanding of the effects of land use on biological communities and it provides valuable information to any

water quality monitoring programs of Mongolia and to establish appropriate water resource management.

Bioassessment techniques are widely used in water quality monitoring programs all over the world, and environmental policy and management decisions are usually made based on bioassessment results, especially in the USA and other developed countries. Biomonitoring has advantages that detect cumulative or combined effects of multiple stressors and measures their magnitude.

Aquatic and terrestrial ecosystems have been influenced by land use practices in Mongolia thus it is important to examine their effect on both aquatic and terrestrial communities. This study examined land use effects on both aquatic and terrestrial macroinvertebrate communities using traditional taxonomic and trait-based approaches and compared effectiveness and performance of these approaches in Mongolia.

Overall findings demonstrated that diversity of both aquatic and terrestrial macroinvertebrate communities were affected by land-use intensity. Seminatural sites supported more diverse macroinvertebrate communities with a wider range of traits found, indicating a greater diversity of habitats present. Sites with greater land-use intensity had less diverse communities more tolerant of eutrophication and fine sediment deposition and showing less range of traits. The species and functional diversity of macroinvertebrate communities declined with increased land-use intensity; and that decline may result in further loss of ecological function and degradation of ecosystem services and goods.

Generally, major impacts of livestock grazing and mining increased suspended particles and fine sediment loading and eutrophication in the stream ecosystem and caused loss of vegetation cover and soil moisture in terrestrial ecosystem. Loss of soil moisture in the watershed correlated with low diversity of crane flies in the heavily grazed areas. Therefore, from this single study it suggests that crane flies are good indicators of undisturbed habitat including high soil moisture and vegetation cover.

Metal contamination may be another major impact, but that needs further analysis. In this study, greater land-use intensity sites had grazing or grazing coupled with mining impacts, except for one site that had mining activity but no grazing. Hence, it was difficult to distinguish separate impacts of overgrazing and mining, but they are both known to contribute increased fine sediment deposits, suspended solids, and nutrient transfer into streams. A specific effect of mining may be metal contamination in streams. The types of study sites should be expanded in future applications of TBA for biomonitoring in Mongolia, potentially helping to discriminate effects of mining and grazing.

Among the results, there is a strong relationship between community structure and habitat condition. Habitat filtering determines variability of macroinvertebrate community observed among sites. Finally, the study results provide additional support for a habitat template concept and for confirming that the TBA is free of biogeographic constraints. Also, it helped to understand changes in

taxonomic and functional structure of macroinvertebrate communities due to grazing.

Comparison of taxonomic and TBA showed that both approaches discriminated seminatural sites from sites with greater levels of land-use intensity, but TBA was a reliably consistent indicator of land-use changes. As well as TBA provided a mechanistic explanation for macroinvertebrate responses to land-use by presence of particular traits and their frequency indicating particular habitat conditions. The North American biotic index classification for water quality was not well suited for Mongolian taxa. A taxonomic approach is constrained by geography and not applicable for a large spatial scale. This approach can detect overall land-use effects but cannot discriminate different type of stressors (Bonada et al. 2007).

Advantages of TBA include the following: 1) it is derived from ecological theory; 2) it provides an *a priori* prediction for assessment results; 3) it is able to discriminate overall as well as specific types of impacts and their intensity; 4) it is less constrained by biogeography; 5) species-level resolution is not necessary, and 6) it provides mechanistic explanations for changes in community.

There are several challenges for TBA: 1) inconsistency of trait terms; 2) lack of trait information; 3) “trait-syndrome,” inferring the co-occurrence of phylogenetically constrained traits in tandem among closely related taxa; 4) not all trait patterns match habitat conditions because environmental filtering may not have occurred yet; 5) organisms may occupy suboptimal habitat; and 6) certain trait occurrences may be related to the organism’s dispersal ability.

As shown in the single study here looking at the 16 species of *Simulium*, species-level resolution provides more accurate information of community response than genus-level, but does not improve discrimination of land use impacts substantially. The sample size was not enough to conclude whether species-level resolution is required to assess ecological conditions. For future biomonitoring in Mongolia, genus-level resolution may be the best choice, considering the difficulty and cost of species-level identification and general lack of trait information at the species level.

Since Mongolia has a high proportion of species and genera with widespread Palearctic distributions; we can access the European trait database, which includes most of the aquatic invertebrate genera of Europe. Also, Mongolians should continue to improve their knowledge of the Mongolian macroinvertebrate fauna and its life histories and create their own trait database, starting with the available literature. Quantitative data are also important to predict patterns of community structure as well as to improve the power of multivariate statistical analysis. A modified subsampling method using random grids rather than fixed count approach (EPA 2012) needs to be used with future subsampling.

My study results demonstrated that TBA is applicable in further development of the water quality monitoring program currently implemented by the Mongolian Institute of Meteorology, Hydrology and Environment (IMHE). The IMHE already has a well-established system and personnel. Local rangers (macroinvertebrate samplers) at 64 local stations have been trained on sampling technique and have

been supplied with appropriate nets, but they need additional training for subsampling and sampling supplies. Mongolian benthologists already have been trained by the Mongolian Aquatic Insect Survey (MAIS) project so that they are able to identify macroinvertebrates adequately. These benthologists have good microscopes, identification literature, and other supplies in the IMHE lab that were provided by the MAIS but need to be trained for statistical analysis. Implementing TBA will make our bioassessment results productive and meaningful. TBA implementation will not require a lot of money from the Mongolian government, but it will make the money already being spent more helpful for producing assessments that can be used to revise and administer water management policy.

APPENDICES

Appendix A

Study site descriptions

(Referred to chapter 2 and 3)

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| Site ID | Land use type | Land-use intensity level | GPS N | GPS E | Altitude m | Province | County | Stream name |
|------------------|----------------|--------------------------|----------|-----------|------------|-------------|--------------|-----------------------------------|
| MAISOY2011062201 | Grazing | High | 47.70055 | 106.28814 | 1166 | Tov | Altanbulag | Tuul gol |
| MAISOY2011062202 | Grazing | Moderate | 47.86233 | 105.20364 | 992 | Tov | Lun | Tuul gol |
| MAISOY2011062301 | Grazing | High | 47.52788 | 105.01108 | 1017 | Tov | Ondorshireet | Tuul gol |
| MAISOY2011062302 | Grazing | Moderate | 47.99865 | 104.39651 | 956 | Bulgan | Bayannuur | Tuul gol |
| MAISOY2011062303 | Grazing+mining | High | 48.28412 | 104.40328 | 937 | Tov | Zaamar | Tuul gol |
| MAISOY2011062401 | Grazing | Seminatural | 46.79082 | 101.93123 | 1819 | Ovorkhangai | Bat-Olziit | Orkhon gol |
| MAISOY2011062501 | Seminatural | Seminatural | 46.78355 | 101.95715 | 1817 | Ovorkhangai | Bat-Olziit | Ulaan gol |
| MAISOY2011062502 | Grazing | Moderate | 46.87449 | 102.33871 | 1667 | Ovorkhangai | Bat-Olziit | Tsagaan gol |
| MAISOY2011062601 | Seminatural | High | 48.10776 | 102.57946 | 1284 | Arkhangai | Olziit | Orkhon gol |
| MAISOY2011062602 | Grazing | High | 48.54952 | 103.27224 | 1129 | Bulgan | Orkhon | Orkhon gol |
| MAISOY2011062701 | Grazing | High | 48.8315 | 104.80691 | 846 | Selenge | Orkhontuul | Tuul gol |
| MAISOY2011062801 | Grazing+mining | High | 48.48739 | 104.55048 | 939 | Tov | Zaamar | Tuul gol |
| MAISOY2011062802 | Grazing | High | 49.75772 | 106.16899 | 705 | Selenge | Javkhlant | Shariin gol |
| MAISOY2011062901 | Seminatural | Seminatural | 49.75416 | 106.61455 | 669 | Selenge | Eroo | Eroo gol |
| MAISOY2011062902 | Seminatural | Seminatural | 49.43592 | 107.26868 | 776 | Selenge | Eroo | Eroo gol/Buganatai gol confluence |
| MAISOY2011063001 | Seminatural | Seminatural | 49.09894 | 107.08746 | 878 | Selenge | Mandal | Eroo gol |
| MAISOY2011063002 | Seminatural | Seminatural | 49.08269 | 107.04478 | 910 | Selenge | Mandal | Yalbag gol |

| Site ID | Land use type | Land-use intensity level | GPS N | GPS E | Altitude m | Province | County | Stream name |
|------------------|----------------|--------------------------|----------|-----------|------------|-------------|-------------|-------------------|
| MAISOY2011063003 | Seminatural | Seminatural | 49.25584 | 107.19463 | 845 | Selenge | Eroo | Eroo gol |
| MAISOY2011063004 | Mining | Moderate | 49.50716 | 107.23051 | 804 | Selenge | Khuder | Jargalant gol |
| MAISOY2011070101 | Grazing+mining | Moderate | 49.61433 | 106.92656 | 751 | Selenge | /Khuder | Bayan gol |
| MAISOY2011070102 | Grazing+mining | Moderate | 49.6298 | 107.01804 | 820 | Selenge | /Khuder | Bayan gol |
| MAISOY2011070103 | Grazing | High | 49.80436 | 106.06383 | 653 | Selenge | Orkhon | Orkhon gol |
| MAISOY2011070201 | Grazing | Moderate | 49.4888 | 105.89484 | 682 | Darkhan-Uul | Darkhan hot | Kharaa gol |
| MAISOY2011070202 | Grazing | Moderate | 49.30375 | 105.90598 | 710 | Darkhan-Uul | Khongor | Kharaa gol |
| MAISOY2011070204 | Grazing | Moderate | 48.91156 | 106.07141 | 795 | Selenge | Bayangol | Kharaa gol |
| MAISOY2011070301 | Grazing | Moderate | 48.57511 | 105.87609 | 962 | Tov | Jargalant | Jargalant gol |
| MAISOY2011070302 | Grazing+mining | Moderate | 48.77391 | 106.28207 | 859 | Selenge | Mandal | Boroo gol |
| MAISOY2011070303 | Grazing | Moderate | 48.83078 | 106.45015 | 811 | Selenge | Mandal | Kharaa gol |
| MAISOY2011070401 | Grazing+mining | Moderate | 48.6241 | 106.65965 | 1124 | Selenge | Tunkhel | Gatsuurtiin gol |
| MAISOY2011070402 | Grazing | Moderate | 48.60446 | 106.75922 | 1008 | Selenge | Tunkhel | Kharaa gol |
| MAISOY2011070403 | Seminatural | Seminatural | 48.65079 | 106.80056 | 1030 | Selenge | Tunkhel | Tunkhel gol |
| MAISOY2011070501 | Seminatural | Seminatural | 48.40872 | 106.91883 | 1171 | Tov | Batsumber | Sognogor gol |
| MAISOY2011070502 | Seminatural | Seminatural | 48.35418 | 106.8383 | 1145 | Tov | Batsumber | Bayangol |
| MAISOY2011070503 | Seminatural | Seminatural | 47.87445 | 106.78634 | 1300 | Tov | UB | Tuul gol |
| MAISOY2011070601 | Seminatural | Seminatural | 47.82217 | 107.39628 | 1383 | Tov | UB-Terelj | Tuul gol |
| MAISOY2011070602 | Seminatural | Seminatural | 48.02728 | 107.44657 | 1540 | Tov | UB-Terelj | Terelj gol |
| MAISOY2011070603 | Seminatural | Seminatural | 48.07718 | 107.63927 | 1544 | Tov | Erdene | Baruunbayan gol |
| MAISOY2011070701 | Seminatural | Seminatural | 48.04708 | 107.74532 | 1517 | Tov | Erdene | Tuul gol |
| MAISOY2011070702 | Seminatural | Seminatural | 48.08181 | 107.7776 | 1528 | Tov | Erdene | Zuunbayangiin gol |
| MAISOY2011070703 | Seminatural | Seminatural | 48.13485 | 107.92422 | 1565 | Tov | Erdene | Galttayn gol |
| MAISOY2011070704 | Seminatural | Seminatural | 48.18108 | 107.91869 | 1573 | Tov | Erdene | Tuul gol |
| MAISOY2011070801 | Seminatural | Seminatural | 47.83612 | 107.4855 | 1414 | Tov | Erdene | Tuul gol |

Appendix B

Macroinvertebrate taxon occurrence

HI=high land use intensity, MD=moderate land-use intensity, SN=semi-natural

(referred to Chapter 1 and chapter 2). A new species was marked by*

| Order | Family | Subfamily/Genera | Species | HI | MD | SN |
|---------------|---------------------|------------------|---------|----|----|----|
| Amphipoda | Gammaridae | | | 0 | 1 | 0 |
| Gastropoda | Physidae | | | 0 | 0 | 1 |
| Gastropoda | Planorbidae | | | 0 | 1 | 1 |
| Gastropoda | Sphaeriidae | | | 1 | 1 | 1 |
| Hirudinea | Glossiphoniidae | | | 1 | 1 | 1 |
| Oligochaeta | Tubificidae | | | 1 | 1 | 1 |
| Coleoptera | Hydrophilidae | Crenitis | | 1 | 0 | 0 |
| Coleoptera | Dytiscidae | Agabus | | 0 | 1 | 0 |
| Coleoptera | Dytiscidae | Copelatus | | 0 | 0 | 1 |
| Coleoptera | Dytiscidae | Dytiscidae | | 0 | 1 | 1 |
| Coleoptera | Dytiscidae | Nebrioporus | | 0 | 1 | 1 |
| Coleoptera | Dytiscidae | Stictotarsus | | 0 | 1 | 1 |
| Coleoptera | Halplidae | Halplus | | 0 | 1 | 1 |
| Coleoptera | Hydraenidae | Ochthebius | | 0 | 1 | 0 |
| Coleoptera | Hydrophilidae | Helophorus | | 1 | 0 | 0 |
| Ephemeroptera | Acanthametropodidae | Acanthametropus | | 0 | 1 | 1 |
| Ephemeroptera | Ameletidae | Ameletus | | 0 | 0 | 1 |
| Ephemeroptera | Baetidae | Procloeon | | 0 | 1 | 0 |
| Ephemeroptera | Baetidae | Baetis | | 1 | 1 | 1 |
| Ephemeroptera | Baetidae | Cloeon | | 1 | 1 | 1 |
| Ephemeroptera | Caenidae | Brachycercus | | 1 | 1 | 1 |
| Ephemeroptera | Ephemerellidae | Drunella | | 0 | 1 | 1 |
| Ephemeroptera | Ephemeridae | Ephemerella | | 0 | 1 | 1 |
| Ephemeroptera | Ephemeridae | Hexagenia | | 1 | 1 | 1 |
| Ephemeroptera | Ephemerellidae | Acentrella | | 1 | 1 | 1 |
| Ephemeroptera | Ephemerellidae | Ephemerella | | 1 | 1 | 1 |
| Ephemeroptera | Ephemerellidae | Serratella | | 1 | 1 | 1 |
| Ephemeroptera | Heptageniidae | Ecdyonurus | | 1 | 1 | 1 |
| Ephemeroptera | Heptageniidae | Epeorus | | 0 | 1 | 1 |
| Ephemeroptera | Heptageniidae | Heptagenia | | 1 | 1 | 1 |
| Ephemeroptera | Heptageniidae | Cinygma | | 0 | 0 | 1 |
| Ephemeroptera | Heptageniidae | Rhithrogena | | 0 | 0 | 1 |
| Ephemeroptera | Isonychiidae | Isonychia | | 1 | 1 | 1 |
| Ephemeroptera | Leptophlebiidae | Leptophlebia | | 0 | 0 | 1 |
| Ephemeroptera | Leptophlebiidae | Paraleptophlebia | | 1 | 1 | 1 |
| Ephemeroptera | Metretopodidae | Metretopus | | 0 | 1 | 1 |
| Ephemeroptera | Oligoneuridae | Oligoneuriella | | 1 | 1 | 0 |
| Ephemeroptera | Polymitarciidae | Ephoron | | 0 | 1 | 1 |

| Order | Family | Subfamily/Genera | Species | HI | MD | SN |
|---------------|-------------------|------------------|---------|----|----|----|
| Ephemeroptera | Siphonuridae | Siphonurus | | 0 | 1 | 1 |
| Hemiptera | Corixidae | Corixini | | 0 | 0 | 1 |
| Hemiptera | Corixidae | Micronecta | | 1 | 1 | 0 |
| Hemiptera | Corixidae | Sigara | | 1 | 0 | 1 |
| Hemiptera | Gerridae | Gerris | | 1 | 1 | 0 |
| Hemiptera | Mesoveliidae | Mesovelia | | 0 | 1 | 0 |
| Hemiptera | Nepidae | Nepa | | 0 | 1 | 0 |
| Neuroptera | Sialidae | Sialis | | 0 | 1 | 1 |
| Odonata | Corduliidae | Somatochlora | | 0 | 0 | 1 |
| Odonata | Gomphidae | Anisogomphus | | 0 | 1 | 1 |
| Odonata | Gomphidae | Ophiogomphus | | 1 | 1 | 1 |
| Odonata | Lestidae | Lestes | | 1 | 0 | 0 |
| Plecoptera | Chloroperlidae | Alloperla | | 0 | 0 | 1 |
| Plecoptera | Chloroperlidae | Haploperla | | 0 | 1 | 0 |
| Plecoptera | Chloroperlidae | Paraperla | | 0 | 1 | 0 |
| Plecoptera | Chloroperlidae | Suwallia | | 0 | 1 | 1 |
| Plecoptera | Nemouridae | Amphinemura | | 0 | 1 | 1 |
| Plecoptera | Nemouridae | Nemoura | | 0 | 1 | 0 |
| Plecoptera | Perlidae | Agnetina | | 1 | 1 | 1 |
| Plecoptera | Perlidae | Perla | | 1 | 0 | 0 |
| Plecoptera | Perlodidae | Arcynopteryx | | 0 | 0 | 1 |
| Plecoptera | Perlodidae | Diura | | 0 | 0 | 1 |
| Plecoptera | Perlodidae | Isoperla | | 1 | 1 | 1 |
| Plecoptera | Perlodidae | Skwala | | 0 | 0 | 1 |
| Trichoptera | Lepidostomatidae | Lepidostoma | | 0 | 0 | 1 |
| Trichoptera | Apatanidae | Apatania | | 0 | 0 | 1 |
| Trichoptera | Brachycentridae | Brachycentrus | | 1 | 1 | 1 |
| Trichoptera | Glossosomatidae | Agapetus | | 0 | 1 | 1 |
| Trichoptera | Glossosomatidae | Glossosoma | | 0 | 1 | 1 |
| Trichoptera | Goeridae | Goera | | 0 | 1 | 1 |
| Trichoptera | Hydropsychidae | Hydropsyche | | 1 | 1 | 1 |
| Trichoptera | Leptoceridae | Ceraclea | | 1 | 1 | 1 |
| Trichoptera | Leptoceridae | Mystacides | | 0 | 1 | 0 |
| Trichoptera | Limnephilidae | Anabolia | | 0 | 1 | 1 |
| Trichoptera | Limnephilidae | Chaetopteryx | | 0 | 0 | 1 |
| Trichoptera | Polycentropodidae | Neureclipsis | | 0 | 1 | 0 |
| Trichoptera | Psychomyiidae | Psychomyia | | 0 | 0 | 1 |
| Trichoptera | Rhyacophilidae | Rhyacophila | | 0 | 1 | 1 |
| Diptera | Athericidae | Atherix | | 0 | 0 | 1 |
| Diptera | Blephariceridae | Blepharicera | | 0 | 1 | 1 |
| Diptera | Ceratopogoniidae | Bezzia | | 1 | 1 | 1 |
| Diptera | Ceratopogoniidae | Palpomyia | | 0 | 0 | 1 |
| Diptera | Chaoboridae | Chaoborus | | 0 | 1 | 0 |
| Diptera | Chironomidae | Tanypodinae | | 1 | 1 | 1 |
| Diptera | Dixidae | Dixa | | 0 | 1 | 0 |
| Diptera | Ephydriidae | Ephydriidae | | 1 | 1 | 1 |

| Order | Family | Subfamily/Genera | Species | HI | MD | SN |
|---------|---------------|-------------------|-----------------|----|----|----|
| Diptera | Pediciidae | Dicranota | | 0 | 1 | 1 |
| Diptera | Tabanidae | Hybomitia | | 1 | 1 | 1 |
| Diptera | Tipulidae | Hexatoma | | 0 | 1 | 1 |
| Diptera | Tipulidae | Limnophila | | 0 | 1 | 1 |
| Diptera | Tipulidae | Tipula | | 0 | 1 | 1 |
| Diptera | Chironominae | Cryptochironomus | | 0 | 1 | 1 |
| Diptera | Chironominae | Chironomini | | 0 | 1 | 1 |
| Diptera | Chironominae | Microtendipes | pedellus group | 0 | 1 | 1 |
| Diptera | Chironominae | Polypedilum | | 0 | 1 | 1 |
| Diptera | Chironominae | Paracladopelma | | 0 | 1 | 0 |
| Diptera | Chironominae | Glyptotendipes | | 1 | 0 | 0 |
| Diptera | Chironominae | Micropsectra | | 0 | 1 | 1 |
| Diptera | Chironominae | Robackia | | 0 | 0 | 1 |
| Diptera | Chironominae | Saetheria | | 0 | 1 | 0 |
| Diptera | Chironominae | Stictochironomus | | 1 | 0 | 0 |
| Diptera | Chironominae | Tanytarsus | | 0 | 1 | 1 |
| Diptera | Diamesinae | Diamesa | | 0 | 1 | 1 |
| Diptera | Diamesinae | Pagastia | | 0 | 1 | 1 |
| Diptera | Diamesinae | Pseudodiamesa | | 0 | 1 | 0 |
| Diptera | Orthocladinae | Cardiocladius | | 0 | 0 | 1 |
| Diptera | Orthocladinae | Cricotopus | | 0 | 1 | 1 |
| Diptera | Orthocladinae | Epoicocladius | | 0 | 0 | 1 |
| Diptera | Orthocladinae | Euryhapsis | | 0 | 0 | 1 |
| Diptera | Orthocladinae | Hydrobaenus | | 0 | 0 | 1 |
| Diptera | Orthocladinae | Orthocladius | | 0 | 1 | 1 |
| Diptera | Orthocladinae | Paracladius | | 0 | 1 | 1 |
| Diptera | Orthocladinae | Nanocladius | | 0 | 1 | 0 |
| Diptera | Orthocladinae | Paratrichocladius | | 0 | 0 | 1 |
| Diptera | Orthocladinae | Potthastia | | 0 | 0 | 1 |
| Diptera | Orthocladinae | Potthastia | longimani group | 0 | 0 | 1 |
| Diptera | Orthocladinae | Tvetenia | | 0 | 1 | 1 |
| Diptera | Prodiamesinae | Monodiamesa | | 0 | 1 | 0 |
| Diptera | Tanypodinae | Thienemannimyia | | 0 | 0 | 1 |
| Diptera | Simulidae | Helodon alpestris | alpestris | 0 | 0 | 1 |
| Diptera | Simulidae | Prosimulium | | | | |
| Diptera | Simulidae | hirtipes group | hirtipes group | 0 | 0 | 1 |
| Diptera | Simulidae | Metacnephia | | | | |
| Diptera | Simulidae | edwardsiana | edwardsiana | 0 | 0 | 1 |
| Diptera | Simulidae | Simulium | bicorne | 0 | 0 | 1 |
| Diptera | Simulidae | Simulium | curvans | 0 | 0 | 1 |
| Diptera | Simulidae | Simulium | meigeni | 0 | 0 | 1 |
| Diptera | Simulidae | Simulium | maculatum | 1 | 0 | 1 |
| Diptera | Simulidae | Simulium | acrotrichum | 0 | 1 | 1 |
| Diptera | Simulidae | Simulium | cholodkovskii | 1 | 0 | 1 |
| Diptera | Simulidae | Simulium | decimatum | 1 | 1 | 1 |

| Order | Family | Subfamily/Genera | Species | HI | MD | SN |
|---------|-----------|------------------|---------------|----|----|----|
| Diptera | Simulidae | Simulium | malyschevi | 0 | 0 | 1 |
| Diptera | Simulidae | Simulium | malyschevi* | 0 | 0 | 1 |
| Diptera | Simulidae | Simulium | murmanum | 0 | 1 | 1 |
| Diptera | Simulidae | Simulium | noelleri | 0 | 1 | 1 |
| | | | ornatum | | | |
| Diptera | Simulidae | Simulium | complex | 0 | 1 | 1 |
| Diptera | Simulidae | Simulium | transiens | 1 | 1 | 1 |
| Diptera | Simulidae | Simulium | subvariegatum | 0 | 1 | 1 |
| Diptera | Simulidae | Simulium | vulgare | 0 | 1 | 1 |
| Diptera | Simulidae | Simulium | aemulum | 0 | 1 | 1 |
| Diptera | Simulidae | Simulium | rubtzovi | 0 | 1 | 0 |

Appendix C

Macroinvertebrate trait matrix

| Taxa | Size-1 | Size-2 | Size-3 | Size-4 | Size-5 | Size-6 | Life-1 | Life-2 | Volt-1 | Volt-2 | Volt-3 | Aqua-1 | Aqua-2 | Aqua-3 | Aqua-4 |
|-----------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Acanthametropus | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Acentrella | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Agabus | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.8 | 0.3 | 0.4 | 0.4 | 0.0 | 0.3 |
| Agapetus | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.3 | 0.3 | 0.0 |
| Agnetina | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Ameletus | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Amphinemura | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Anabolia | 0.0 | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.0 |
| Apatania | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.8 | 0.0 | 0.3 | 0.4 | 0.4 | 0.0 |
| Arcynopteryx | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Atherix | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.8 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 |
| Baetis | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.4 | 0.6 | 0.5 | 0.5 | 0.0 | 0.0 |
| Bezzia | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.2 | 0.4 | 0.4 | 0.0 |
| Blepharicera | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.4 | 0.3 | 0.0 |
| Brachycentrus | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.0 |
| Brachycercus | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Ceraclea | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.8 | 0.3 | 0.3 | 0.3 | 0.3 | 0.0 |
| Ceratopogoninae | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.2 | 0.4 | 0.4 | 0.0 |
| Chaoborus | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.4 | 0.4 | 0.0 |
| Chironominae | 0.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 | 1.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.5 | 0.5 | 0.0 |
| Chloroperlidae | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.8 | 0.3 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Cloeon | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.5 | 0.5 | 0.0 | 0.0 |
| Copelatus | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.8 | 0.3 | 0.4 | 0.4 | 0.0 | 0.3 |
| Corixidae | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.4 | 0.4 | 0.0 | 0.3 |
| Crenitis | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.8 | 0.3 | 0.4 | 0.4 | 0.0 | 0.3 |
| Dicranota | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.4 | 0.6 | 0.2 | 0.6 | 0.2 | 0.3 | 0.3 | 0.3 | 0.0 |
| Diura | 0.0 | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.3 | 0.8 | 0.6 | 0.4 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Dixa | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.4 | 0.3 | 0.0 |
| Drunella | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.5 | 0.5 | 0.0 | 0.0 |
| Dytiscidae | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 1.0 | 0.0 | 1.0 | 0.0 | 0.4 | 0.4 | 0.0 | 0.3 |
| Ecdyonurus | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.8 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Epeorus | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Ephemera | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.8 | 0.8 | 0.3 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Ephemerella | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.5 | 0.5 | 0.0 | 0.0 |
| Ephoron | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Ephydriidae | 0.0 | 0.1 | 0.4 | 0.4 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.5 | 0.3 | 0.0 |
| Gammaridae | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 1.0 | 0.3 | 0.3 | 0.0 | 0.3 |
| Gerris | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.4 | 0.6 | 0.2 | 0.4 | 0.0 | 0.4 |
| Glossiphoniidae | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.3 | 0.8 | 0.0 | 1.0 | 0.0 | 0.4 | 0.4 | 0.0 | 0.3 |
| Glossosoma | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.7 | 0.3 | 0.3 | 0.3 | 0.3 | 0.0 |
| Goera | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.0 |
| Gomphidae | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Haliplus | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.3 | 0.8 | 0.4 | 0.4 | 0.0 | 0.3 |

| Taxa | Size-1 | Size-2 | Size-3 | Size-4 | Size-5 | Size-6 | Life-1 | Life-2 | Volt-1 | Volt-2 | Volt-3 | Aqua-1 | Aqua-2 | Aqua-3 | Aqua-4 |
|------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Helophorus | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.8 | 0.3 | 0.3 | 0.3 | 0.0 | 0.5 |
| Heptagenia | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.8 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Heptageniidae/ | | | | | | | | | | | | | | | |
| Cinygma | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.8 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Hexagenia | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.8 | 0.8 | 0.3 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Hexatoma | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.4 | 0.6 | 0.2 | 0.6 | 0.2 | 0.3 | 0.3 | 0.3 | 0.0 |
| Hydropsyche | 0.0 | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.3 | 0.3 | 0.3 | 0.0 |
| Isonychia | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Isoperla | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.3 | 0.8 | 0.4 | 0.6 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Lepidostoma | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.8 | 0.3 | 0.3 | 0.3 | 0.3 | 0.0 |
| Leptophlebia | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Lestes | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.8 | 0.0 | 0.0 |
| Limnephilini | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.0 |
| Limnophila | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.4 | 0.6 | 0.2 | 0.6 | 0.2 | 0.3 | 0.3 | 0.3 | 0.0 |
| Mesovelia | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.2 | 0.4 | 0.0 | 0.4 |
| Metretopodidae | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Micronecta | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.3 | 0.3 | 0.0 | 0.3 |
| Mystacides | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.0 |
| Nebrioporus | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.3 | 0.8 | 0.4 | 0.4 | 0.0 | 0.3 |
| Nemoura | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.5 | 0.5 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Nepa | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.8 | 0.3 | 0.0 | 1.0 | 0.0 | 0.4 | 0.4 | 0.0 | 0.3 |
| Neureclipsis | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.3 | 0.3 | 0.3 | 0.0 |
| Ochthebius | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.8 | 0.3 | 0.6 | 0.0 | 0.0 | 0.4 |
| Oligoneuriella | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Ophiogomphus | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.8 | 0.3 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Orthocladiinae/ | | | | | | | | | | | | | | | |
| Diamesinae | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.2 | 0.3 | 0.5 | 0.0 |
| Paraleptophlebia | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Perla | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Physidae | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.5 |
| Planorbiidae | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.5 | 0.0 | 0.0 | 0.5 |
| Procloeon | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.5 | 0.5 | 0.0 | 0.0 |
| Psychomyia | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.3 | 0.3 | 0.3 | 0.0 |
| Rhithrogena | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.8 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Rhyacophila | 0.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 | 0.6 | 0.4 | 0.3 | 0.5 | 0.3 | 0.3 | 0.3 | 0.3 | 0.0 |
| Serratella | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.5 | 0.5 | 0.0 | 0.0 |
| Sialis | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 | 1.0 | 0.8 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 |
| Sigara | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.5 | 0.5 | 0.4 | 0.4 | 0.0 | 0.3 |
| Simulium | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.4 | 0.6 | 0.3 | 0.4 | 0.4 | 0.0 |
| Siphonurus | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Skwala | 0.0 | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.3 | 0.8 | 0.6 | 0.4 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Somatochlora | 0.0 | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Sphaeriidae | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.3 | 0.8 | 0.0 | 0.5 | 0.5 | 0.3 | 0.3 | 0.0 | 0.3 |
| Stictotarsus | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.3 | 0.8 | 0.4 | 0.4 | 0.0 | 0.3 |
| Suwallia | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.8 | 0.3 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Tabanidae | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 |
| Tanypodinae | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 |
| Tipula | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.4 | 0.6 | 0.2 | 0.6 | 0.2 | 0.3 | 0.3 | 0.3 | 0.0 |
| Tubificidae | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.6 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.3 | 0.3 | 0.0 | 0.3 |

| Taxa | Size-1 | Size-2 | Size-3 | Size-4 | Size-5 | Size-6 | Life-1 | Life-2 | Volt-1 | Volt-2 | Volt-3 | Aqua-1 | Aqua-2 | Aqua-3 | Aqua-4 |
|------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Helophorus | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.8 | 0.3 | 0.3 | 0.3 | 0.0 | 0.5 |
| Heptagenia | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.8 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Heptageniidae/ | | | | | | | | | | | | | | | |
| Cinygma | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.8 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Hexagenia | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.8 | 0.8 | 0.3 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Hexatoma | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.4 | 0.6 | 0.2 | 0.6 | 0.2 | 0.3 | 0.3 | 0.3 | 0.0 |
| Hydropsyche | 0.0 | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.3 | 0.3 | 0.3 | 0.0 |
| Isonychia | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Isoperla | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.3 | 0.8 | 0.4 | 0.6 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Lepidostoma | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.8 | 0.3 | 0.3 | 0.3 | 0.3 | 0.0 |
| Leptophlebia | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Lestes | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.8 | 0.0 | 0.0 |
| Limnephilini | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.0 |
| Limnophila | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.4 | 0.6 | 0.2 | 0.6 | 0.2 | 0.3 | 0.3 | 0.3 | 0.0 |
| Mesovelgia | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.2 | 0.4 | 0.0 | 0.4 |
| Metretopodidae | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Micronecta | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.3 | 0.3 | 0.0 | 0.3 |
| Mystacides | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.0 |
| Nebrioporus | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.3 | 0.8 | 0.4 | 0.4 | 0.0 | 0.3 |
| Nemoura | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.5 | 0.5 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Nepa | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.8 | 0.3 | 0.0 | 1.0 | 0.0 | 0.4 | 0.4 | 0.0 | 0.3 |
| Neureclipsis | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.0 |
| Ochthebius | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.8 | 0.3 | 0.6 | 0.0 | 0.0 | 0.4 |
| Oligoneuriella | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Ophiogomphus | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.8 | 0.3 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Orthocladiinae/ | | | | | | | | | | | | | | | |
| Diamesinae | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.2 | 0.3 | 0.5 | 0.0 |
| Paraleptophlebia | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Perla | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Physidae | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.5 |
| Planorbiidae | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.5 | 0.0 | 0.0 | 0.5 |
| Proclleon | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.5 | 0.5 | 0.0 | 0.0 |
| Psychomyia | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.3 | 0.3 | 0.3 | 0.0 |
| Rhithrogena | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.8 | 0.3 | 0.3 | 0.8 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Rhyacophila | 0.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 | 0.6 | 0.4 | 0.3 | 0.5 | 0.3 | 0.3 | 0.3 | 0.3 | 0.0 |
| Serratella | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.5 | 0.5 | 0.0 | 0.0 |
| Sialis | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 | 1.0 | 0.8 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 |
| Sigara | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.5 | 0.5 | 0.4 | 0.4 | 0.0 | 0.3 |
| Simulium | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.4 | 0.6 | 0.3 | 0.4 | 0.4 | 0.0 |
| Siphonurus | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Skwala | 0.0 | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.3 | 0.8 | 0.6 | 0.4 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Somatochlora | 0.0 | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Sphaeriidae | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.3 | 0.8 | 0.0 | 0.5 | 0.5 | 0.3 | 0.3 | 0.0 | 0.3 |
| Stictotarsus | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.3 | 0.8 | 0.4 | 0.4 | 0.0 | 0.3 |
| Suwallia | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.8 | 0.3 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Tabanidae | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 |
| Tanypodinae | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 |

| Taxa | Repr-1 | Repr-2 | Repr-3 | Repr-4 | Repr-5 | Repr-6 | Repr-7 | Repr-8 | Desi-1 | Desi-2 | Desi-3 | Desi-4 | Resi-1 | Resi-2 | Resi-3 |
|-----------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Tipula | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.4 | 0.6 | 0.2 | 0.6 | 0.2 | 0.3 | 0.3 | 0.3 | 0.0 |
| Tubificidae | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.6 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.3 | 0.3 | 0.0 | 0.3 |
| Acanthametropus | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 |
| Acentrella | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.2 | 0.2 | 0.3 | 0.0 | 0.0 | 0.0 |
| Agabus | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.3 | 0.0 | 0.0 | 0.2 | 0.2 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 |
| Agapetus | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.4 | 0.2 | 0.2 | 0.0 | 0.5 | 0.0 |
| Agnetina | 0.0 | 0.0 | 0.6 | 0.0 | 0.4 | 0.0 | 0.0 | 0.0 | 0.3 | 0.5 | 0.0 | 0.3 | 0.5 | 0.0 | 0.0 |
| Ameletus | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.4 | 0.1 | 0.4 | 0.5 | 0.0 | 0.0 |
| Amphinemura | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.4 | 0.0 | 0.2 | 0.2 | 0.0 | 0.0 |
| Anabolia | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.3 | 0.0 | 0.4 | 0.0 | 0.0 | 0.0 |
| Apatania | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.5 | 0.0 | 0.4 | 0.3 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 |
| Arcynopteryx | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.4 | 0.0 | 0.2 | 1.0 | 0.0 | 0.0 |
| Atherix | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 |
| Baetis | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.2 | 0.1 | 0.3 | 0.5 | 0.0 | 0.0 |
| Bezzia | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.2 | 0.0 | 0.3 | 0.3 | 0.0 | 0.0 |
| Blepharicera | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.3 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 |
| Brachycentrus | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.3 | 0.5 | 0.0 | 0.0 | 0.0 |
| Brachycercus | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.3 | 1.0 | 0.0 | 0.0 |
| Ceraclea | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.3 | 0.1 | 0.1 | 0.4 | 0.0 | 0.0 | 0.0 |
| Ceratopogoninae | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.2 | 0.0 | 0.3 | 0.3 | 0.0 | 0.0 |
| Chaoborus | 0.0 | 0.3 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 |
| Chironominae | 0.2 | 0.0 | 0.0 | 0.2 | 0.6 | 0.0 | 0.0 | 0.0 | 0.3 | 0.1 | 0.4 | 0.1 | 0.0 | 0.0 | 0.0 |
| Chloroperlidae | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.3 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 |
| Cloeon | 0.6 | 0.2 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.3 | 0.2 | 0.3 | 0.0 | 0.0 | 0.0 |
| Copelatus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 |
| Corixidae | 0.0 | 0.0 | 0.3 | 0.5 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.4 | 0.1 | 0.4 | 0.0 | 0.0 | 0.0 |
| Crenitis | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 |
| Dicranota | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.5 | 0.0 | 0.5 | 0.0 | 0.5 | 0.0 |
| Diura | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.3 | 0.5 | 0.0 | 0.3 | 0.6 | 0.0 | 0.0 |
| Dixa | 0.0 | 0.0 | 0.0 | 0.6 | 0.2 | 0.0 | 0.2 | 0.0 | 0.6 | 0.2 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 |
| Drunella | 0.0 | 0.2 | 0.6 | 0.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.2 | 0.3 | 0.1 | 0.3 | 0.5 | 0.0 | 0.0 |
| Dytiscidae | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 |
| Ecdyonurus | 0.0 | 0.4 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.1 | 0.1 | 0.4 | 0.4 | 0.0 | 0.0 |
| Epeorus | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.1 | 0.1 | 0.4 | 0.2 | 0.0 | 0.0 |
| Ephemera | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.2 | 0.5 | 0.4 | 0.0 | 0.0 |
| Ephemerella | 0.0 | 0.2 | 0.6 | 0.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.2 | 0.3 | 0.1 | 0.3 | 0.5 | 0.0 | 0.0 |
| Ephoron | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.4 | 0.1 | 0.4 | 1.0 | 0.0 | 0.0 |
| Ephydriidae | 0.0 | 0.0 | 0.2 | 0.2 | 0.0 | 0.3 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 |
| Gammaridae | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Gerris | 0.0 | 0.0 | 0.2 | 0.3 | 0.0 | 0.0 | 0.5 | 0.0 | 0.2 | 0.3 | 0.0 | 0.5 | 0.3 | 0.0 | 0.0 |
| Glossiphoniidae | 0.7 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Glossosoma | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.4 | 0.2 | 0.2 | 0.0 | 0.5 | 0.0 |
| Goera | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.2 | 0.4 | 0.0 | 0.0 | 0.0 |
| Gomphidae | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.0 | 0.0 | 0.6 | 1.0 | 0.0 | 0.0 |
| Haliplus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 |
| Helophorus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.2 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 |
| Heptagenia | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.1 | 0.1 | 0.4 | 0.2 | 0.0 | 0.0 |

| Taxa | Repr-1 | Repr-2 | Repr-3 | Repr-4 | Repr-5 | Repr-6 | Repr-7 | Repr-8 | Desi-1 | Desi-2 | Desi-3 | Desi-4 | Resi-1 | Resi-2 | Resi-3 |
|------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Heptageniidae/ | | | | | | | | | | | | | | | |
| Cinygma | 0.0 | 0.4 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.1 | 0.1 | 0.4 | 0.4 | 0.0 | 0.0 |
| Hexagenia | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.2 | 0.5 | 0.4 | 0.0 | 0.0 |
| Hexatoma | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.5 | 0.0 | 0.5 | 0.0 | 0.5 | 0.0 |
| Hydropsyche | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.2 | 0.1 | 0.3 | 0.0 | 0.0 | 0.0 |
| Isonychia | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 |
| Isoperla | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.3 | 0.0 | 0.3 | 0.5 | 0.0 | 0.0 |
| Lepidostoma | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.2 | 0.4 | 0.0 | 0.0 | 0.0 |
| Leptophlebia | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.1 | 0.1 | 0.4 | 0.0 | 0.0 | 0.0 |
| Lestes | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.8 | 0.0 | 0.0 |
| Limnephilini | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.3 | 0.0 | 0.7 | 0.5 | 0.0 | 0.0 |
| Limnophila | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.5 | 0.0 | 0.5 | 0.0 | 0.5 | 0.0 |
| Mesovelia | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.7 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 |
| Metretopodidae | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 |
| Micronecta | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Mystacides | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.2 | 0.4 | 0.0 | 0.0 | 0.0 |
| Nebrioporus | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.2 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 |
| Nemoura | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.3 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 |
| Nepa | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.2 | 0.5 | 0.0 | 0.3 | 0.5 | 0.0 | 0.0 |
| Neureclipsis | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.1 | 0.1 | 0.3 | 0.0 | 0.0 | 0.0 |
| Ochthebius | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.2 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 |
| Oligoneuriella | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.1 | 0.1 | 0.3 | 1.0 | 0.0 | 0.0 |
| Ophiogomphus | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.0 | 0.0 | 0.6 | 1.0 | 0.0 | 0.0 |
| Orthocladiinae/ | | | | | | | | | | | | | | | |
| Diamesinae | 0.0 | 0.0 | 0.0 | 0.4 | 0.2 | 0.0 | 0.4 | 0.0 | 0.4 | 0.2 | 0.2 | 0.2 | 0.0 | 0.0 | 0.0 |
| Paraleptophlebia | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.1 | 0.1 | 0.4 | 0.0 | 0.0 | 0.0 |
| Perla | 0.0 | 0.0 | 0.6 | 0.0 | 0.4 | 0.0 | 0.0 | 0.0 | 0.3 | 0.5 | 0.0 | 0.3 | 0.5 | 0.0 | 0.0 |
| Physidae | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.7 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Planorbiidae | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.7 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 |
| Proclleon | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.3 | 0.2 | 0.3 | 1.0 | 0.0 | 0.0 |
| Psychomyia | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.3 | 0.0 | 0.0 | 0.0 |
| Rhithrogena | 0.0 | 0.2 | 0.2 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.2 | 0.1 | 0.3 | 0.5 | 0.0 | 0.0 |
| Rhyacophila | 0.0 | 0.0 | 0.8 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.4 | 0.3 | 0.1 | 0.3 | 0.2 | 0.0 | 0.0 |
| Serratella | 0.0 | 0.2 | 0.6 | 0.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.2 | 0.3 | 0.1 | 0.3 | 0.5 | 0.0 | 0.0 |
| Sialis | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.7 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 |
| Sigara | 0.0 | 0.0 | 0.2 | 0.5 | 0.0 | 0.3 | 0.0 | 0.0 | 0.2 | 0.3 | 0.2 | 0.3 | 0.0 | 0.0 | 0.0 |
| Simulium | 0.0 | 0.2 | 0.0 | 0.5 | 0.2 | 0.0 | 0.2 | 0.0 | 0.3 | 0.3 | 0.4 | 0.1 | 0.5 | 0.0 | 0.0 |
| Siphonurus | 0.0 | 0.2 | 0.6 | 0.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.1 | 0.3 | 0.1 | 0.4 | 1.0 | 0.0 | 0.0 |
| Skwala | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.3 | 0.5 | 0.0 | 0.3 | 0.6 | 0.0 | 0.0 |
| Somatochlora | 0.0 | 0.6 | 0.2 | 0.0 | 0.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 |
| Sphaeriidae | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.2 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 |
| Stictotarsus | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 |
| Suwallia | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.3 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 |
| Tabanidae | 0.0 | 0.0 | 0.0 | 0.6 | 0.0 | 0.0 | 0.4 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 |
| Tanypodinae | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.4 | 0.2 | 0.2 | 0.2 | 0.0 | 0.0 | 0.0 |
| Tipula | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.5 | 0.0 | 0.5 | 0.0 | 0.5 | 0.0 |
| Tubificidae | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.3 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 |

| Taxa | Resi-4 | Resi-5 | Resp-1 | Resp-2 | Resp-3 | Resp-4 | Resp-5 | Habi-1 | Habi-2 | Habi-3 | Habi-4 | Habi-5 | Habi-6 | Habi-7 | Habi-8 |
|---------------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Acanthametropus | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.3 | 0.0 | 0.0 | 0.4 | 0.0 |
| Acentrella | 0.0 | 1.0 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |
| Agabus | 0.0 | 1.0 | 0.3 | 0.0 | 0.0 | 0.8 | 0.0 | 0.1 | 0.0 | 0.4 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 |
| Agapetus | 0.5 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.8 | 0.0 |
| Agnetina | 0.0 | 0.5 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Ameletus | 0.0 | 0.5 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 |
| Amphinemura | 0.4 | 0.4 | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Anabolia | 0.8 | 0.3 | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Apatania | 0.7 | 0.3 | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.2 | 0.0 |
| Arcynopteryx | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Atherix | 0.0 | 1.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.7 | 0.0 | 0.3 | 0.0 | 0.0 |
| Baetis | 0.0 | 0.5 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.5 | 0.0 | 0.1 | 0.0 | 0.0 |
| Bezzia | 0.0 | 0.8 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.4 | 0.1 | 0.4 | 0.0 | 0.0 | 0.0 |
| Blepharicera | 1.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.5 | 0.0 |
| Brachycentrus | 0.0 | 1.0 | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.0 | 0.0 | 0.6 | 0.0 |
| Brachycercus | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Ceraclea | 0.5 | 0.5 | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Ceratopogoninae | 0.0 | 0.8 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.4 | 0.1 | 0.4 | 0.0 | 0.0 | 0.0 |
| Chaoborus | 0.5 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.1 | 0.7 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 |
| Chironominae | 0.3 | 0.8 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.3 | 0.2 | 0.1 | 0.2 | 0.0 |
| Chloroperlidae | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.7 | 0.0 | 0.3 | 0.0 | 0.0 |
| Cloeon | 0.0 | 1.0 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 |
| Copelatus | 0.0 | 1.0 | 0.3 | 0.0 | 0.0 | 0.8 | 0.0 | 0.1 | 0.0 | 0.4 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 |
| Corixidae | 1.0 | 0.0 | 0.2 | 0.0 | 0.3 | 0.5 | 0.0 | 0.2 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Crenitis | 0.0 | 1.0 | 0.2 | 0.0 | 0.2 | 0.6 | 0.0 | 0.1 | 0.0 | 0.4 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 |
| Dicranota | 0.0 | 0.5 | 0.3 | 0.2 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 |
| Diura | 0.4 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Dixa | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.2 | 0.2 | 0.0 | 0.0 | 0.2 | 0.0 |
| Drunella | 0.3 | 0.3 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |
| Dytiscidae | 0.0 | 1.0 | 0.3 | 0.0 | 0.0 | 0.8 | 0.0 | 0.1 | 0.0 | 0.4 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 |
| Ecdyonurus | 0.2 | 0.4 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |
| Epeorus | 0.2 | 0.6 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Ephemera | 0.6 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 |
| Ephemerella | 0.3 | 0.3 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |
| Ephoron | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 |
| Ephydriidae | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 |
| Gammaridae | 0.0 | 1.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.5 | 0.0 | 0.2 | 0.0 | 0.0 |
| Gerris | 0.5 | 0.2 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Glossiphoniidae | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.3 | 0.0 |
| Glossosoma | 0.5 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.8 | 0.0 |
| Goera | 0.0 | 1.0 | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.2 | 0.0 |
| Gomphidae | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 |
| Halipus | 0.0 | 1.0 | 0.5 | 0.0 | 0.0 | 0.5 | 0.0 | 0.1 | 0.0 | 0.4 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 |
| Helophorus | 0.0 | 1.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.1 | 0.0 | 0.4 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 |
| Heptagenia | 0.4 | 0.4 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |
| Heptageniidae/ Cinygma | 0.2 | 0.4 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |

| Taxa | Resi-4 | Resi-5 | Resp-1 | Resp-2 | Resp-3 | Resp-4 | Resp-5 | Habi-1 | Habi-2 | Habi-3 | Habi-4 | Habi-5 | Habi-6 | Habi-7 | Habi-8 |
|-------------------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Hexagenia | 0.6 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 |
| Hexatoma | 0.0 | 0.5 | 0.3 | 0.2 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 |
| Hydropsyche | 0.0 | 1.0 | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.0 | 0.0 | 0.6 | 0.0 |
| Isonychia | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.3 | 0.0 | 0.0 | 0.4 | 0.0 |
| Isoperla | 0.3 | 0.3 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.2 | 0.0 | 0.0 |
| Lepidostoma | 0.0 | 1.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Leptophlebia | 0.0 | 1.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.6 | 0.0 | 0.1 | 0.0 | 0.0 |
| Lestes | 0.0 | 0.3 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |
| Limnephilini | 0.0 | 0.5 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Limnophila | 0.0 | 0.5 | 0.3 | 0.2 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 |
| Mesovelia | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.7 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 |
| Metretopodidae | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.3 | 0.0 | 0.0 | 0.4 | 0.0 |
| Micronecta | 1.0 | 0.0 | 0.3 | 0.0 | 0.3 | 0.3 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 |
| Mystacides | 0.0 | 1.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |
| Nebrioporus | 0.0 | 1.0 | 0.3 | 0.0 | 0.0 | 0.8 | 0.0 | 0.1 | 0.0 | 0.4 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 |
| Nemoura | 0.3 | 0.8 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Nepa | 0.0 | 0.5 | 0.2 | 0.0 | 0.2 | 0.6 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |
| Neureclipsis | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.0 | 0.0 | 0.6 | 0.0 |
| Ochthebius | 0.0 | 1.0 | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.1 | 0.0 | 0.4 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 |
| Oligoneuriella | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |
| Ophiogomphus | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 |
| Orthocladiinae/ Diamesinae | 0.0 | 1.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.4 | 0.1 | 0.3 | 0.1 | 0.0 |
| Paraleptophlebia | 0.0 | 1.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.7 | 0.2 | 0.0 | 0.0 | 0.0 |
| Perla | 0.0 | 0.5 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Physidae | 0.5 | 0.5 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Planorbiidae | 0.5 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 |
| Procloeon | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 |
| Psychomyia | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.5 | 0.2 |
| Rhithrogena | 0.0 | 0.5 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.7 | 0.0 | 0.1 | 0.0 | 0.0 |
| Rhyacophila | 0.3 | 0.5 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.5 | 0.0 | 0.0 | 0.2 | 0.0 |
| Serratella | 0.3 | 0.3 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |
| Sialis | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.1 | 0.5 | 0.4 | 0.0 | 0.0 | 0.0 |
| Sigara | 1.0 | 0.0 | 0.2 | 0.0 | 0.3 | 0.5 | 0.0 | 0.2 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Simulium | 0.5 | 0.0 | 0.4 | 0.1 | 0.0 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.1 | 0.6 | 0.0 |
| Siphonurus | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 |
| Skwala | 0.4 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Somatochlora | 1.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 |
| Sphaeriidae | 1.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.6 | 0.0 | 0.3 | 0.0 |
| Stictotarsus | 0.0 | 1.0 | 0.3 | 0.0 | 0.0 | 0.8 | 0.0 | 0.1 | 0.0 | 0.4 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 |
| Suwallia | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.7 | 0.0 | 0.3 | 0.0 | 0.0 |
| Tabanidae | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.1 | 0.0 | 0.3 | 0.6 | 0.0 | 0.0 | 0.0 |
| Tanypodinae | 0.0 | 1.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.3 | 0.1 | 0.1 | 0.0 | 0.0 |
| Tipula | 0.0 | 0.5 | 0.3 | 0.2 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 |
| Tubificidae | 0.0 | 0.8 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 |

| Taxa | Food-1 | Food-2 | Food-3 | Food-4 | Food-5 | Food-6 | Food-7 | Food-8 | Food-9 | Trop-1 | Trop-2 | Trop-3 | Trop-4 | Trop-5 | Trop-6 |
|-----------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Acanthametropus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Acentrella | 0.0 | 0.3 | 0.1 | 0.4 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 |
| Agabus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.5 |
| Agapetus | 0.0 | 0.2 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 |
| Agnetina | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 |
| Ameletus | 0.1 | 0.3 | 0.4 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.2 | 0.5 | 0.0 | 0.0 |
| Amphinemura | 0.0 | 0.3 | 0.5 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 |
| Anabolia | 0.0 | 0.1 | 0.3 | 0.3 | 0.3 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 | 0.1 | 0.4 | 0.3 | 0.0 | 0.0 |
| Apatania | 0.0 | 0.1 | 0.1 | 0.5 | 0.1 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 | 0.2 | 0.0 | 0.6 | 0.0 | 0.0 |
| Arcynopteryx | 0.1 | 0.1 | 0.2 | 0.1 | 0.2 | 0.0 | 0.0 | 0.4 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 |
| Atherix | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 |
| Baetis | 0.0 | 0.2 | 0.2 | 0.5 | 0.1 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 |
| Bezzia | 0.0 | 0.1 | 0.0 | 0.2 | 0.0 | 0.1 | 0.4 | 0.2 | 0.0 | 0.0 | 0.2 | 0.2 | 0.0 | 0.0 | 0.0 |
| Blepharicera | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 |
| Brachycentrus | 0.0 | 0.1 | 0.1 | 0.2 | 0.3 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.3 | 0.4 | 0.0 |
| Brachycercus | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Ceraclea | 0.0 | 0.4 | 0.1 | 0.1 | 0.2 | 0.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.1 | 0.4 | 0.1 | 0.0 | 0.0 |
| Ceratopogoninae | 0.0 | 0.1 | 0.0 | 0.2 | 0.0 | 0.1 | 0.4 | 0.2 | 0.0 | 0.0 | 0.2 | 0.2 | 0.0 | 0.0 | 0.0 |
| Chaoborus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Chironominae | 0.0 | 0.5 | 0.0 | 0.2 | 0.2 | 0.0 | 0.1 | 0.1 | 0.0 | 0.0 | 0.3 | 0.2 | 0.1 | 0.2 | 0.0 |
| Chloroperlidae | 0.1 | 0.1 | 0.1 | 0.1 | 0.0 | 0.0 | 0.1 | 0.5 | 0.0 | 0.0 | 0.2 | 0.5 | 0.2 | 0.0 | 0.0 |
| Cloeon | 0.0 | 0.3 | 0.1 | 0.3 | 0.1 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.4 | 0.1 | 0.4 | 0.0 | 0.0 |
| Copelatus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 |
| Corixidae | 0.0 | 0.0 | 0.1 | 0.2 | 0.1 | 0.2 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.0 | 0.6 |
| Crenitis | 0.0 | 0.0 | 0.0 | 0.4 | 0.0 | 0.0 | 0.4 | 0.1 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 |
| Dicranota | 0.0 | 0.2 | 0.3 | 0.2 | 0.2 | 0.0 | 0.1 | 0.2 | 0.0 | 0.0 | 0.3 | 0.4 | 0.0 | 0.0 | 0.0 |
| Diura | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Dixa | 0.0 | 0.4 | 0.0 | 0.5 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.0 | 0.6 | 0.0 |
| Drunella | 0.0 | 0.1 | 0.3 | 0.3 | 0.3 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Dytiscidae | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.5 |
| Ecdyonurus | 0.1 | 0.3 | 0.4 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 |
| Epeorus | 0.0 | 0.2 | 0.0 | 0.6 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 |
| Ephemera | 0.0 | 0.4 | 0.3 | 0.1 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.1 | 0.4 | 0.0 | 0.4 | 0.0 |
| Ephemerella | 0.0 | 0.1 | 0.3 | 0.3 | 0.3 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.2 | 0.3 | 0.3 | 0.0 | 0.0 |
| Ephoron | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.8 | 0.0 |
| Ephydriidae | 0.0 | 0.2 | 0.1 | 0.4 | 0.2 | 0.1 | 0.0 | 0.2 | 0.0 | 0.0 | 0.1 | 0.1 | 0.3 | 0.3 | 0.1 |
| Gammaridae | 0.0 | 0.1 | 0.4 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 |
| Gerris | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 |
| Glossiphoniidae | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 |
| Glossosoma | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 |
| Goera | 0.0 | 0.2 | 0.3 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 |
| Gomphidae | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Haliplus | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.5 |
| Helophorus | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 |
| Heptagenia | 0.1 | 0.2 | 0.2 | 0.3 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.3 | 0.5 | 0.0 | 0.0 |

| Taxa | Food-1 | Food-2 | Food-3 | Food-4 | Food-5 | Food-6 | Food-7 | Food-8 | Food-9 | Trop-1 | Trop-2 | Trop-3 | Trop-4 | Trop-5 | Trop-6 |
|------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Heptageniidae/ | | | | | | | | | | | | | | | |
| Cinygma | 0.1 | 0.3 | 0.4 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 |
| Hexagenia | 0.0 | 0.4 | 0.3 | 0.1 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.1 | 0.4 | 0.0 | 0.4 | 0.0 |
| Hexatoma | 0.0 | 0.2 | 0.3 | 0.2 | 0.2 | 0.0 | 0.1 | 0.2 | 0.0 | 0.0 | 0.3 | 0.4 | 0.0 | 0.0 | 0.0 |
| Hydropsyche | 0.0 | 0.2 | 0.1 | 0.3 | 0.0 | 0.0 | 0.3 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 |
| Isonychia | 0.1 | 0.4 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.0 |
| Isoperla | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.1 | 0.6 | 0.0 | 0.0 | 0.0 | 0.6 | 0.2 | 0.0 | 0.0 |
| Lepidostoma | 0.0 | 0.0 | 0.8 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 |
| Leptophlebia | 0.1 | 0.4 | 0.1 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 |
| Lestes | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Limnephilini | 0.0 | 0.1 | 0.6 | 0.0 | 0.2 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 |
| Limnophila | 0.0 | 0.2 | 0.3 | 0.2 | 0.2 | 0.0 | 0.1 | 0.2 | 0.0 | 0.0 | 0.3 | 0.4 | 0.0 | 0.0 | 0.0 |
| Mesovelia | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.6 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 |
| Metretopodidae | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Micronecta | 0.0 | 0.0 | 0.0 | 0.3 | 0.3 | 0.0 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.3 | 0.0 | 0.4 |
| Mystacides | 0.0 | 0.2 | 0.0 | 0.2 | 0.4 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 | 0.0 |
| Nebrioporus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.5 |
| Nemoura | 0.0 | 0.3 | 0.5 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 |
| Nepa | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 |
| Neureclipsis | 0.0 | 0.0 | 0.1 | 0.1 | 0.1 | 0.0 | 0.4 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 |
| Ochthebius | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 |
| Oligoneuriella | 0.2 | 0.3 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.3 | 0.4 | 0.0 |
| Ophiogomphus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Orthocladiinae/ | | | | | | | | | | | | | | | |
| Diamesinae | 0.0 | 0.3 | 0.0 | 0.5 | 0.1 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.2 | 0.0 | 0.5 | 0.2 | 0.0 |
| Paraleptophlebia | 0.0 | 0.4 | 0.3 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.4 | 0.2 | 0.0 | 0.0 |
| Perla | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 |
| Physidae | 0.0 | 0.0 | 0.2 | 0.3 | 0.3 | 0.1 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 |
| Planorbiidae | 0.0 | 0.0 | 0.4 | 0.3 | 0.3 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 |
| Procloeon | 0.0 | 0.3 | 0.0 | 0.7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.7 | 0.0 | 0.0 |
| Psychomyia | 0.0 | 0.1 | 0.0 | 0.6 | 0.1 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.2 | 0.0 | 0.5 | 0.3 | 0.0 |
| Rhithrogena | 0.0 | 0.2 | 0.0 | 0.6 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.0 |
| Rhyacophila | 0.0 | 0.1 | 0.1 | 0.1 | 0.0 | 0.0 | 0.1 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Serratella | 0.0 | 0.1 | 0.3 | 0.3 | 0.3 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.2 | 0.3 | 0.3 | 0.0 | 0.0 |
| Sialis | 0.0 | 0.1 | 0.1 | 0.0 | 0.0 | 0.1 | 0.1 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Sigara | 0.0 | 0.0 | 0.3 | 0.3 | 0.1 | 0.1 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.3 | 0.0 | 0.3 |
| Simulium | 0.0 | 0.6 | 0.0 | 0.2 | 0.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 |
| Siphonurus | 0.1 | 0.2 | 0.1 | 0.1 | 0.2 | 0.2 | 0.0 | 0.2 | 0.0 | 0.0 | 0.3 | 0.1 | 0.4 | 0.0 | 0.0 |
| Skwala | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Somatochlora | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Sphaeriidae | 0.0 | 0.3 | 0.0 | 0.5 | 0.1 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 |
| Stictotarsus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.5 |
| Suwallia | 0.1 | 0.1 | 0.1 | 0.1 | 0.0 | 0.0 | 0.1 | 0.5 | 0.0 | 0.0 | 0.2 | 0.5 | 0.2 | 0.0 | 0.0 |
| Tabanidae | 0.0 | 0.1 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.7 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.8 |
| Tanypodinae | 0.0 | 0.0 | 0.1 | 0.1 | 0.0 | 0.1 | 0.3 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Tipula | 0.0 | 0.2 | 0.3 | 0.2 | 0.2 | 0.0 | 0.1 | 0.2 | 0.0 | 0.0 | 0.3 | 0.4 | 0.0 | 0.0 | 0.0 |
| Tubificidae | 0.2 | 0.6 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 0.0 |

| Taxa | Trop-7 | Trop-8 | Subs-1 | Subs-2 | Subs-3 | Subs-4 | Subs-5 | Subs-6 | Subs-7 | Subs-8 | Subs-9 | Velo-1 | Velo-2 | Velo-3 | Velo-4 |
|---------------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Acanthametropus | 1.0 | 0.0 | 0.4 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.4 | 0.4 |
| Acentrella | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 |
| Agabus | 0.0 | 0.0 | 0.0 | 0.1 | 0.1 | 0.1 | 0.3 | 0.0 | 0.0 | 0.3 | 0.3 | 0.8 | 0.3 | 0.0 | 0.0 |
| Agapetus | 0.0 | 0.0 | 0.5 | 0.2 | 0.1 | 0.0 | 0.1 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 | 0.4 | 0.4 | 0.2 |
| Agnetina | 0.3 | 0.0 | 0.4 | 0.3 | 0.1 | 0.0 | 0.1 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 |
| Ameletus | 0.0 | 0.0 | 0.3 | 0.1 | 0.1 | 0.1 | 0.0 | 0.0 | 0.2 | 0.1 | 0.2 | 0.2 | 0.2 | 0.5 | 0.2 |
| Amphinemura | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.4 | 0.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.3 | 0.5 | 0.3 |
| Anabolia | 0.1 | 0.0 | 0.3 | 0.0 | 0.2 | 0.0 | 0.5 | 0.0 | 0.0 | 0.1 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 |
| Apatania | 0.2 | 0.0 | 0.2 | 0.2 | 0.2 | 0.1 | 0.2 | 0.0 | 0.0 | 0.2 | 0.1 | 0.0 | 0.4 | 0.3 | 0.3 |
| Arcynopteryx | 0.7 | 0.0 | 0.6 | 0.2 | 0.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.4 | 0.2 |
| Atherix | 0.0 | 0.0 | 0.3 | 0.2 | 0.0 | 0.0 | 0.3 | 0.0 | 0.1 | 0.1 | 0.1 | 0.0 | 0.4 | 0.6 | 0.0 |
| Baetis | 0.0 | 0.0 | 0.3 | 0.1 | 0.1 | 0.0 | 0.3 | 0.0 | 0.2 | 0.1 | 0.0 | 0.0 | 0.3 | 0.4 | 0.3 |
| Bezzia | 0.6 | 0.0 | 0.1 | 0.1 | 0.2 | 0.0 | 0.1 | 0.1 | 0.1 | 0.0 | 0.2 | 0.6 | 0.2 | 0.2 | 0.0 |
| Blepharicera | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 |
| Brachycentrus | 0.1 | 0.0 | 0.3 | 0.1 | 0.0 | 0.1 | 0.3 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.3 | 0.5 | 0.2 |
| Brachycercus | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.2 | 0.1 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 1.0 | 0.0 | 0.0 |
| Ceraclea | 0.1 | 0.1 | 0.3 | 0.1 | 0.1 | 0.1 | 0.1 | 0.0 | 0.2 | 0.1 | 0.1 | 0.2 | 0.5 | 0.2 | 0.2 |
| Ceratopogoninae | 0.6 | 0.0 | 0.1 | 0.1 | 0.2 | 0.0 | 0.1 | 0.1 | 0.1 | 0.0 | 0.2 | 0.6 | 0.2 | 0.2 | 0.0 |
| Chaoborus | 1.0 | 0.0 | 0.0 | 0.1 | 0.1 | 0.1 | 0.1 | 0.0 | 0.0 | 0.0 | 0.5 | 0.8 | 0.3 | 0.0 | 0.0 |
| Chironominae | 0.1 | 0.1 | 0.2 | 0.1 | 0.1 | 0.1 | 0.2 | 0.0 | 0.1 | 0.0 | 0.2 | 0.8 | 0.3 | 0.0 | 0.0 |
| Chloroperlidae | 0.2 | 0.0 | 0.2 | 0.3 | 0.0 | 0.1 | 0.2 | 0.0 | 0.1 | 0.3 | 0.0 | 0.0 | 0.4 | 0.4 | 0.2 |
| Cloeon | 0.0 | 0.0 | 0.1 | 0.0 | 0.1 | 0.1 | 0.5 | 0.0 | 0.0 | 0.2 | 0.1 | 0.8 | 0.3 | 0.0 | 0.0 |
| Copelatus | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.3 | 0.3 | 1.0 | 0.0 | 0.0 | 0.0 |
| Corixidae | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.6 | 0.0 | 0.0 | 0.4 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 |
| Crenitis | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.1 | 0.0 | 0.3 | 0.3 | 1.0 | 0.0 | 0.0 | 0.0 |
| Dicranota | 0.3 | 0.0 | 0.1 | 0.1 | 0.1 | 0.1 | 0.2 | 0.0 | 0.1 | 0.2 | 0.1 | 0.5 | 0.3 | 0.2 | 0.0 |
| Diura | 1.0 | 0.0 | 0.2 | 0.3 | 0.3 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.4 | 0.4 |
| Dixa | 0.2 | 0.0 | 0.4 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.1 | 0.3 | 0.0 | 0.0 | 0.2 | 0.6 | 0.2 |
| Drunella | 1.0 | 0.0 | 0.2 | 0.1 | 0.1 | 0.1 | 0.2 | 0.0 | 0.2 | 0.1 | 0.1 | 0.0 | 0.4 | 0.4 | 0.1 |
| Dytiscidae | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.3 | 0.3 | 1.0 | 0.0 | 0.0 | 0.0 |
| Ecdyonurus | 0.0 | 0.0 | 0.5 | 0.1 | 0.1 | 0.1 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 | 0.1 | 0.3 | 0.4 | 0.3 |
| Epeorus | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 |
| Ephemera | 0.1 | 0.0 | 0.0 | 0.3 | 0.3 | 0.1 | 0.1 | 0.0 | 0.1 | 0.1 | 0.2 | 0.2 | 0.5 | 0.3 | 0.0 |
| Ephemerella | 0.2 | 0.0 | 0.2 | 0.1 | 0.1 | 0.1 | 0.3 | 0.0 | 0.2 | 0.1 | 0.1 | 0.0 | 0.4 | 0.4 | 0.1 |
| Ephoron | 0.0 | 0.0 | 0.1 | 0.3 | 0.4 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 |
| Ephydriidae | 0.0 | 0.1 | 0.2 | 0.1 | 0.1 | 0.0 | 0.3 | 0.0 | 0.1 | 0.1 | 0.2 | 0.3 | 0.3 | 0.3 | 0.0 |
| Gammaridae | 0.0 | 0.0 | 0.2 | 0.1 | 0.1 | 0.0 | 0.1 | 0.1 | 0.2 | 0.2 | 0.0 | 0.1 | 0.3 | 0.4 | 0.1 |
| Gerris | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.4 | 0.1 | 0.1 |
| Glossiphoniidae | 0.0 | 0.3 | 0.4 | 0.3 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.1 | 0.0 | 0.3 | 0.3 | 0.3 | 0.1 |
| Glossosoma | 0.0 | 0.0 | 0.6 | 0.0 | 0.1 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.5 | 0.2 |
| Goera | 0.0 | 0.0 | 0.4 | 0.2 | 0.2 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.3 | 0.4 | 0.1 |
| Gomphidae | 1.0 | 0.0 | 0.2 | 0.0 | 0.2 | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.3 | 0.5 | 0.0 |
| Haliplus | 0.0 | 0.0 | 0.1 | 0.1 | 0.1 | 0.3 | 0.3 | 0.0 | 0.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.2 | 0.0 |
| Helophorus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.3 | 0.0 | 0.3 | 0.3 | 0.8 | 0.3 | 0.0 | 0.0 |
| Heptagenia | 0.0 | 0.0 | 0.5 | 0.2 | 0.1 | 0.0 | 0.1 | 0.0 | 0.1 | 0.1 | 0.0 | 0.0 | 0.3 | 0.4 | 0.3 |
| Heptageniidae/ Cinygma | 0.0 | 0.0 | 0.5 | 0.1 | 0.1 | 0.1 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 | 0.1 | 0.3 | 0.4 | 0.3 |

| Taxa | Trop-7 | Trop-8 | Subs-1 | Subs-2 | Subs-3 | Subs-4 | Subs-5 | Subs-6 | Subs-7 | Subs-8 | Subs-9 | Velo-1 | Velo-2 | Velo-3 | Velo-4 |
|-------------------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Hexagenia | 0.1 | 0.0 | 0.0 | 0.3 | 0.3 | 0.1 | 0.1 | 0.0 | 0.1 | 0.1 | 0.2 | 0.2 | 0.5 | 0.3 | 0.0 |
| Hexatoma | 0.3 | 0.0 | 0.1 | 0.1 | 0.1 | 0.1 | 0.2 | 0.0 | 0.1 | 0.2 | 0.1 | 0.5 | 0.3 | 0.2 | 0.0 |
| Hydropsyche | 0.3 | 0.0 | 0.3 | 0.1 | 0.1 | 0.0 | 0.2 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.2 | 0.6 | 0.2 |
| Isonychia | 0.4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.0 | 0.5 | 0.3 | 0.0 | 0.0 | 0.2 | 0.6 | 0.2 |
| Isoperla | 0.2 | 0.0 | 0.2 | 0.2 | 0.2 | 0.0 | 0.2 | 0.0 | 0.1 | 0.2 | 0.0 | 0.0 | 0.2 | 0.5 | 0.3 |
| Lepidostoma | 0.0 | 0.0 | 0.2 | 0.1 | 0.1 | 0.0 | 0.3 | 0.0 | 0.2 | 0.0 | 0.0 | 0.2 | 0.5 | 0.2 | 0.2 |
| Leptophlebia | 0.0 | 0.0 | 0.2 | 0.1 | 0.1 | 0.0 | 0.3 | 0.0 | 0.2 | 0.3 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 |
| Lestes | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.0 | 0.2 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 |
| Limnephilini | 0.0 | 0.0 | 0.1 | 0.1 | 0.1 | 0.0 | 0.1 | 0.1 | 0.2 | 0.2 | 0.1 | 0.4 | 0.4 | 0.1 | 0.0 |
| Limnophila | 0.3 | 0.0 | 0.1 | 0.1 | 0.1 | 0.1 | 0.2 | 0.0 | 0.1 | 0.2 | 0.1 | 0.5 | 0.3 | 0.2 | 0.0 |
| Mesovelia | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.1 | 0.0 | 0.1 | 0.8 | 0.3 | 0.0 | 0.0 |
| Metretopodidae | 1.0 | 0.0 | 0.4 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.4 | 0.4 |
| Micronecta | 0.0 | 0.0 | 0.2 | 0.1 | 0.1 | 0.1 | 0.2 | 0.0 | 0.0 | 0.1 | 0.2 | 0.5 | 0.3 | 0.3 | 0.0 |
| Mystacides | 0.0 | 0.0 | 0.2 | 0.1 | 0.1 | 0.1 | 0.2 | 0.0 | 0.2 | 0.1 | 0.1 | 0.3 | 0.5 | 0.2 | 0.0 |
| Nebrioporus | 0.0 | 0.0 | 0.1 | 0.3 | 0.3 | 0.1 | 0.1 | 0.0 | 0.0 | 0.1 | 0.0 | 0.5 | 0.3 | 0.2 | 0.0 |
| Nemoura | 0.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.1 | 0.4 | 0.0 | 0.1 | 0.3 | 0.0 | 0.2 | 0.2 | 0.3 | 0.3 |
| Nepa | 0.3 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.3 | 0.3 | 0.6 | 0.4 | 0.0 | 0.0 |
| Neureclipsis | 0.5 | 0.0 | 0.4 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.3 | 0.0 | 0.0 | 0.1 | 0.4 | 0.3 | 0.1 |
| Ochthebius | 0.0 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 | 0.2 | 0.2 | 0.0 | 0.2 | 0.2 | 0.8 | 0.3 | 0.0 | 0.0 |
| Oligoneuriella | 0.0 | 0.0 | 0.4 | 0.0 | 0.0 | 0.0 | 0.4 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.6 |
| Ophiogomphus | 1.0 | 0.0 | 0.0 | 0.0 | 0.4 | 0.3 | 0.0 | 0.0 | 0.3 | 0.0 | 0.1 | 0.0 | 0.4 | 0.4 | 0.2 |
| Orthocladiinae/ Diamesinae | 0.0 | 0.2 | 0.3 | 0.2 | 0.1 | 0.1 | 0.2 | 0.1 | 0.0 | 0.1 | 0.1 | 0.2 | 0.3 | 0.2 | 0.2 |
| Paraleptophlebia | 0.0 | 0.0 | 0.2 | 0.2 | 0.1 | 0.0 | 0.2 | 0.0 | 0.2 | 0.2 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 |
| Perla | 0.3 | 0.0 | 0.4 | 0.3 | 0.1 | 0.0 | 0.1 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 |
| Physidae | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 |
| Planorbiidae | 0.0 | 0.0 | 0.2 | 0.1 | 0.1 | 0.1 | 0.3 | 0.1 | 0.0 | 0.1 | 0.2 | 0.8 | 0.3 | 0.0 | 0.0 |
| Proclleon | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.2 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 |
| Psychomyia | 0.0 | 0.0 | 0.4 | 0.1 | 0.1 | 0.0 | 0.2 | 0.0 | 0.3 | 0.0 | 0.0 | 0.1 | 0.4 | 0.3 | 0.1 |
| Rhithrogena | 0.0 | 0.0 | 0.6 | 0.2 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.4 | 0.6 |
| Rhyacophila | 1.0 | 0.0 | 0.5 | 0.1 | 0.1 | 0.0 | 0.1 | 0.0 | 0.2 | 0.1 | 0.0 | 0.0 | 0.2 | 0.5 | 0.3 |
| Serratella | 0.2 | 0.0 | 0.2 | 0.1 | 0.1 | 0.1 | 0.3 | 0.0 | 0.2 | 0.1 | 0.1 | 0.0 | 0.4 | 0.4 | 0.1 |
| Sialis | 1.0 | 0.0 | 0.1 | 0.2 | 0.2 | 0.2 | 0.1 | 0.0 | 0.0 | 0.1 | 0.1 | 0.4 | 0.4 | 0.3 | 0.0 |
| Sigara | 0.0 | 0.0 | 0.0 | 0.1 | 0.2 | 0.1 | 0.3 | 0.0 | 0.0 | 0.3 | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 |
| Simulium | 0.0 | 0.0 | 0.3 | 0.1 | 0.0 | 0.0 | 0.4 | 0.0 | 0.2 | 0.1 | 0.0 | 0.0 | 0.2 | 0.4 | 0.4 |
| Siphonurus | 0.1 | 0.0 | 0.0 | 0.0 | 0.1 | 0.1 | 0.6 | 0.0 | 0.0 | 0.0 | 0.1 | 0.5 | 0.5 | 0.0 | 0.0 |
| Skwala | 1.0 | 0.0 | 0.2 | 0.3 | 0.3 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.4 | 0.4 |
| Somatochlora | 1.0 | 0.0 | 0.1 | 0.0 | 0.1 | 0.1 | 0.2 | 0.0 | 0.0 | 0.4 | 0.2 | 0.8 | 0.3 | 0.0 | 0.0 |
| Sphaeriidae | 0.0 | 0.0 | 0.1 | 0.0 | 0.3 | 0.1 | 0.1 | 0.1 | 0.0 | 0.0 | 0.3 | 0.5 | 0.3 | 0.2 | 0.0 |
| Stictotarsus | 0.0 | 0.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.4 | 0.0 | 0.0 | 0.2 | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 |
| Suwallia | 0.2 | 0.0 | 0.2 | 0.3 | 0.0 | 0.1 | 0.2 | 0.0 | 0.1 | 0.3 | 0.0 | 0.0 | 0.4 | 0.4 | 0.2 |
| Tabanidae | 0.0 | 0.0 | 0.0 | 0.1 | 0.2 | 0.0 | 0.2 | 0.0 | 0.0 | 0.3 | 0.3 | 0.4 | 0.4 | 0.2 | 0.0 |
| Tanypodinae | 1.0 | 0.0 | 0.1 | 0.1 | 0.2 | 0.1 | 0.2 | 0.0 | 0.1 | 0.1 | 0.2 | 0.0 | 0.2 | 0.4 | 0.4 |
| Tipula | 0.3 | 0.0 | 0.1 | 0.1 | 0.1 | 0.1 | 0.2 | 0.0 | 0.1 | 0.2 | 0.1 | 0.5 | 0.3 | 0.2 | 0.0 |
| Tubificidae | 0.0 | 0.0 | 0.1 | 0.2 | 0.2 | 0.2 | 0.0 | 0.0 | 0.1 | 0.1 | 0.2 | 0.2 | 0.3 | 0.3 | 0.2 |

| Taxa | Tro_p-1 | Tro_p-2 | Tro_p-3 | Temp-1 | Temp-2 | Temp-3 | Sapr-1 | Sapr-2 | Sapr-3 | Sapr-4 | Sapr-5 |
|-----------------|---------|---------|---------|--------|--------|--------|--------|--------|--------|--------|--------|
| Acanthametropus | 0.0 | 0.5 | 0.5 | 0.5 | 0.0 | 0.5 | 0.0 | 0.4 | 0.4 | 0.1 | 0.0 |
| Acentrella | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.2 | 0.6 | 0.2 | 0.0 | 0.0 |
| Agabus | 0.1 | 0.4 | 0.4 | 0.0 | 0.0 | 1.0 | 0.0 | 0.4 | 0.4 | 0.3 | 0.0 |
| Agapetus | 0.8 | 0.3 | 0.0 | 0.3 | 0.0 | 0.8 | 0.3 | 0.4 | 0.4 | 0.0 | 0.0 |
| Agnetina | 1.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.6 | 0.3 | 0.5 | 0.3 | 0.0 | 0.0 |
| Ameletus | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 |
| Amphinemura | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 | 0.0 |
| Anabolia | 0.3 | 0.5 | 0.2 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 |
| Apatania | 0.8 | 0.3 | 0.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.3 | 0.2 | 0.0 | 0.0 |
| Arcynopteryx | 1.0 | 0.0 | 0.0 | 0.8 | 0.0 | 0.3 | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 |
| Atherix | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 1.0 | 0.1 | 0.3 | 0.4 | 0.1 | 0.0 |
| Baetis | 0.3 | 0.3 | 0.3 | 0.0 | 0.0 | 1.0 | 0.1 | 0.3 | 0.4 | 0.1 | 0.0 |
| Bezzia | 0.3 | 0.3 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.1 |
| Blepharicera | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.3 | 0.2 | 0.0 | 0.0 |
| Brachycentrus | 0.5 | 0.3 | 0.3 | 0.0 | 0.0 | 0.0 | 0.1 | 0.3 | 0.4 | 0.1 | 0.0 |
| Brachycercus | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 |
| Ceraclea | 0.3 | 0.3 | 0.5 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 |
| Ceratopogoninae | 0.3 | 0.3 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.3 | 0.3 | 0.1 |
| Chaoborus | 0.1 | 0.4 | 0.4 | 0.3 | 0.0 | 0.8 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 |
| Chironominae | 0.0 | 0.4 | 0.6 | 0.2 | 0.3 | 0.5 | 0.0 | 0.1 | 0.3 | 0.3 | 0.3 |
| Chloroperlidae | 0.8 | 0.3 | 0.0 | 0.5 | 0.0 | 0.5 | 0.2 | 0.5 | 0.3 | 0.0 | 0.0 |
| Cloeon | 0.0 | 0.5 | 0.5 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 |
| Copelatus | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 |
| Corixidae | 0.2 | 0.5 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.3 | 0.5 | 0.0 |
| Crenitis | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.7 | 0.3 | 0.0 |
| Dicranota | 0.5 | 0.3 | 0.2 | 0.3 | 0.0 | 0.8 | 0.2 | 0.3 | 0.3 | 0.1 | 0.0 |
| Diura | 1.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 |
| Dixa | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 |
| Drunella | 0.4 | 0.6 | 0.0 | 0.0 | 0.3 | 0.7 | 0.1 | 0.3 | 0.4 | 0.1 | 0.0 |
| Dytiscidae | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.3 | 0.5 | 0.0 |
| Ecdyonurus | 0.4 | 0.6 | 0.0 | 0.2 | 0.2 | 0.6 | 0.1 | 0.4 | 0.4 | 0.1 | 0.0 |
| Epeorus | 0.8 | 0.3 | 0.0 | 0.5 | 0.0 | 0.5 | 0.3 | 0.5 | 0.2 | 0.0 | 0.0 |
| Ephemera | 0.3 | 0.5 | 0.3 | 0.0 | 0.0 | 1.0 | 0.2 | 0.2 | 0.5 | 0.2 | 0.0 |
| Ephemerella | 0.4 | 0.6 | 0.0 | 0.0 | 0.3 | 0.7 | 0.1 | 0.3 | 0.4 | 0.1 | 0.0 |
| Ephoron | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.7 | 0.3 | 0.0 |
| Ephydriidae | 0.3 | 0.5 | 0.3 | 0.2 | 0.2 | 0.6 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 |
| Gammaridae | 0.5 | 0.5 | 0.0 | 0.3 | 0.0 | 0.8 | 0.1 | 0.3 | 0.4 | 0.3 | 0.0 |
| Gerris | 0.3 | 0.3 | 0.4 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.4 | 0.4 | 0.0 |
| Glossiphoniidae | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 |
| Glossosoma | 0.8 | 0.3 | 0.0 | 0.0 | 0.0 | 1.0 | 0.3 | 0.5 | 0.3 | 0.0 | 0.0 |
| Goera | 0.4 | 0.6 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 |
| Gomphidae | 0.5 | 0.3 | 0.2 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 |
| Haliphus | 0.1 | 0.4 | 0.4 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 |
| Helophorus | 0.2 | 0.2 | 0.6 | 0.0 | 0.0 | 1.0 | 0.0 | 0.1 | 0.4 | 0.4 | 0.0 |
| Heptagenia | 0.0 | 0.8 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 |
| Heptageniidae/ | | | | | | | | | | | |
| Cinygma | 0.4 | 0.6 | 0.0 | 0.2 | 0.2 | 0.6 | 0.1 | 0.4 | 0.4 | 0.1 | 0.0 |
| Hexagenia | 0.3 | 0.5 | 0.3 | 0.0 | 0.0 | 1.0 | 0.2 | 0.2 | 0.5 | 0.2 | 0.0 |

| Taxa | Tro_p-1 | Tro_p-2 | Tro_p-3 | Temp-1 | Temp-2 | Temp-3 | Sapr-1 | Sapr-2 | Sapr-3 | Sapr-4 | Sapr-5 |
|-------------------------------|---------|---------|---------|--------|--------|--------|--------|--------|--------|--------|--------|
| Hexatoma | 0.5 | 0.3 | 0.2 | 0.3 | 0.0 | 0.8 | 0.2 | 0.3 | 0.3 | 0.1 | 0.0 |
| Hydropsyche | 0.2 | 0.5 | 0.3 | 0.2 | 0.2 | 0.6 | 0.1 | 0.3 | 0.4 | 0.3 | 0.0 |
| Isonychia | 0.0 | 0.5 | 0.5 | 0.5 | 0.0 | 0.5 | 0.0 | 0.4 | 0.4 | 0.1 | 0.0 |
| Isoperla | 0.6 | 0.4 | 0.0 | 0.7 | 0.0 | 0.3 | 0.3 | 0.5 | 0.2 | 0.0 | 0.0 |
| Lepidostoma | 0.6 | 0.4 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.7 | 0.0 | 0.0 |
| Leptophlebia | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 |
| Lestes | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 |
| Limnephilini | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 1.0 | 0.3 | 0.3 | 0.4 | 0.1 | 0.0 |
| Limnophila | 0.5 | 0.3 | 0.2 | 0.3 | 0.0 | 0.8 | 0.2 | 0.3 | 0.3 | 0.1 | 0.0 |
| Mesovelia | 0.3 | 0.5 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.5 | 0.3 | 0.0 |
| Metretopodidae | 0.0 | 0.5 | 0.5 | 0.5 | 0.0 | 0.5 | 0.0 | 0.4 | 0.4 | 0.1 | 0.0 |
| Micronecta | 0.5 | 0.3 | 0.2 | 0.0 | 0.0 | 1.0 | 0.0 | 0.4 | 0.4 | 0.2 | 0.0 |
| Mystacides | 0.1 | 0.4 | 0.4 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.6 | 0.4 | 0.0 |
| Nebrioporus | 0.5 | 0.5 | 0.0 | 0.3 | 0.0 | 0.8 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 |
| Nemoura | 0.3 | 0.5 | 0.2 | 0.7 | 0.0 | 0.3 | 0.3 | 0.5 | 0.3 | 0.0 | 0.0 |
| Nepa | 0.2 | 0.6 | 0.2 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.8 | 0.3 | 0.0 |
| Neureclipsis | 0.2 | 0.4 | 0.4 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 |
| Ochthebius | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Oligoneuriella | 0.0 | 1.0 | 0.0 | 0.0 | 0.3 | 0.8 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 |
| Ophiogomphus | 0.3 | 0.3 | 0.3 | 0.3 | 0.0 | 0.8 | 0.0 | 0.3 | 0.5 | 0.2 | 0.0 |
| Orthocladiinae/ Diamesinae | 0.4 | 0.4 | 0.2 | 0.5 | 0.0 | 0.5 | 0.2 | 0.3 | 0.3 | 0.1 | 0.0 |
| Paraleptophlebia | 0.4 | 0.4 | 0.2 | 0.0 | 0.0 | 1.0 | 0.0 | 0.5 | 0.3 | 0.2 | 0.0 |
| Perla | 1.0 | 0.0 | 0.0 | 0.2 | 0.2 | 0.6 | 0.3 | 0.5 | 0.3 | 0.0 | 0.0 |
| Physidae | 0.0 | 0.8 | 0.3 | 0.0 | 0.4 | 0.6 | 0.0 | 0.0 | 0.3 | 0.5 | 0.2 |
| Planorbiidae | 0.0 | 0.6 | 0.4 | 0.0 | 0.3 | 0.8 | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 |
| Procloeon | 0.0 | 0.6 | 0.4 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.4 | 0.4 | 0.0 |
| Psychomyia | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 |
| Rhithrogena | 0.8 | 0.3 | 0.0 | 0.7 | 0.0 | 0.3 | 0.3 | 0.4 | 0.3 | 0.0 | 0.0 |
| Rhyacophila | 0.6 | 0.4 | 0.0 | 0.2 | 0.2 | 0.6 | 0.3 | 0.4 | 0.3 | 0.1 | 0.0 |
| Serratella | 0.4 | 0.6 | 0.0 | 0.0 | 0.3 | 0.7 | 0.1 | 0.3 | 0.4 | 0.1 | 0.0 |
| Sialis | 0.3 | 0.5 | 0.2 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 |
| Sigara | 0.4 | 0.4 | 0.3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.4 | 0.4 | 0.3 | 0.0 |
| Simulium | 0.2 | 0.6 | 0.2 | 0.3 | 0.3 | 0.4 | 0.1 | 0.3 | 0.4 | 0.1 | 0.0 |
| Siphonurus | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 1.0 | 0.0 | 0.4 | 0.4 | 0.1 | 0.0 |
| Skwala | 1.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.8 | 0.5 | 0.5 | 0.0 | 0.0 | 0.0 |
| Somatochlora | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.3 | 0.5 | 0.2 | 0.0 |
| Sphaeriidae | 0.2 | 0.6 | 0.2 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.5 | 0.3 | 0.0 |
| Stictotarsus | 0.3 | 0.8 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.2 | 0.6 | 0.2 | 0.0 |
| Suwallia | 0.8 | 0.3 | 0.0 | 0.5 | 0.0 | 0.5 | 0.2 | 0.5 | 0.3 | 0.0 | 0.0 |
| Tabanidae | 0.0 | 0.5 | 0.5 | 0.0 | 0.3 | 0.8 | 0.0 | 0.3 | 0.4 | 0.3 | 0.0 |
| Tanypodinae | 0.2 | 0.3 | 0.5 | 0.4 | 0.0 | 0.6 | 0.1 | 0.3 | 0.3 | 0.2 | 0.0 |
| Tipula | 0.5 | 0.3 | 0.2 | 0.3 | 0.0 | 0.8 | 0.2 | 0.3 | 0.3 | 0.1 | 0.0 |
| Tubificidae | 0.0 | 0.4 | 0.6 | 0.0 | 0.3 | 0.8 | 0.0 | 0.0 | 0.3 | 0.5 | 0.2 |

Appendix D

Black fly(*Simulium*) species trait matrix

| Trait categories | <i>S. acrotrichum</i> | <i>S. aemulum</i> | <i>S. bicorne</i> | <i>S. cholodkovskii</i> | <i>S. curvans</i> | <i>S. decimatum</i> | <i>S. malyschevi</i> | <i>S. malyschevi*</i> | <i>S. meigeni</i> | <i>S. murmanum</i> | <i>S. noelleri</i> | <i>S. ornatum complex</i> | <i>S. subvariegatum</i> | <i>S. transiens</i> | <i>S. vulgare</i> | <i>S. rubtzovi</i> |
|------------------|-----------------------|-------------------|-------------------|-------------------------|-------------------|---------------------|----------------------|-----------------------|-------------------|--------------------|--------------------|---------------------------|-------------------------|---------------------|-------------------|--------------------|
| Size-1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Size-2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Size-3 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| Size-4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Size-5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Size-6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Life-1 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| Life-2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Volt-1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Volt-2 | 0.0 | 0.0 | 1.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Volt-3 | 1.0 | 1.0 | 0.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| Aqua-1 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 |
| Aqua-2 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 |
| Aqua-3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Aqua-4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Repr-1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Repr-2 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 0.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| Repr-3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Repr-4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Repr-5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Repr-6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Repr-7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Repr-8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Desi-1 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 |
| Desi-2 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| Desi-3 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| Desi-4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 |
| Resi-1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Resi-2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Resi-3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Resi-4 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| Resi-5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Resp-1 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 |
| Resp-2 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 |
| Resp-3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |

| Trait categories | <i>S. acrotrichum</i> | <i>S. aemulum</i> | <i>S. bicornis</i> | <i>S. cholodkovskii</i> | <i>S. curvans</i> | <i>S. decimatum</i> | <i>S. malyschevi</i> | <i>S. malyschevi*</i> | <i>S. meigeni</i> | <i>S. murmanum</i> | <i>S. noelleri</i> | <i>S. ornatum complex</i> | <i>S. subvariegatum</i> | <i>S. transiens</i> | <i>S. vulgare</i> | <i>S. rubtzovi</i> |
|------------------|-----------------------|-------------------|--------------------|-------------------------|-------------------|---------------------|----------------------|-----------------------|-------------------|--------------------|--------------------|---------------------------|-------------------------|---------------------|-------------------|--------------------|
| Resp-4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Resp-5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Habi-1 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 | 0.3 |
| Habi-2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Habi-3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Habi-4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Habi-5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Habi-6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Habi-7 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 |
| Habi-8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Food-1 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 |
| Food-2 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 |
| Food-3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Food-4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Food-5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Food-6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Food-7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Food-8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Food-9 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Trop-1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Trop-2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Trop-3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Trop-4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Trop-5 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| Trop-6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Trop-7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Trop-8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Dist-1 | 0.0 | 0.5 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.3 | 0.5 |
| Dist-2 | 0.0 | 0.5 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.5 | 0.5 | 0.0 | 0.0 | 0.3 | 0.5 |
| Dist-3 | 0.5 | 0.0 | 0.0 | 0.3 | 0.3 | 0.5 | 0.5 | 0.5 | 0.3 | 0.5 | 0.0 | 0.0 | 0.5 | 0.0 | 0.3 | 0.0 |
| Dist-4 | 0.5 | 0.0 | 0.0 | 0.3 | 0.3 | 0.5 | 0.5 | 0.5 | 0.3 | 0.5 | 0.0 | 0.0 | 0.5 | 0.0 | 0.3 | 0.0 |
| Dist-5 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Dist-6 | 0.0 | 0.0 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 |
| Dist-7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Dist-8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Alti-1 | 0.5 | 0.5 | 0.0 | 0.5 | 0.0 | 0.5 | 0.5 | 0.5 | 0.0 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 |
| Alti-2 | 0.5 | 0.5 | 0.0 | 0.5 | 1.0 | 0.5 | 0.5 | 0.5 | 1.0 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 |
| Alti-3 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Subs-1 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 |
| Subs-2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |

| Trait categories | <i>S. acrotrichum</i> | <i>S. aemulum</i> | <i>S. bicornis</i> | <i>S. cholodkovskii</i> | <i>S. curvans</i> | <i>S. decimatum</i> | <i>S. malyschevi</i> | <i>S. malyschevi</i> "2a" | <i>S. meigeni</i> | <i>S. murmanum</i> | <i>S. noelleri</i> | <i>S. ornatum</i> complex | <i>S. subvariegatum</i> | <i>S. transiens</i> | <i>S. vulgare</i> | <i>S. rubtzovi</i> |
|------------------|-----------------------|-------------------|--------------------|-------------------------|-------------------|---------------------|----------------------|---------------------------|-------------------|--------------------|--------------------|---------------------------|-------------------------|---------------------|-------------------|--------------------|
| Subs-3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Subs-4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Subs-5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 |
| Subs-6 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Subs-7 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Subs-8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Subs-9 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Velo-1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Velo-2 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 |
| Velo-3 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 |
| Velo-4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 |
| Tro_p-1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Tro_p-2 | 0.5 | 0.5 | 1.0 | 0.5 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 0.0 | 0.0 | 1.0 | 0.5 | 1.0 | 0.5 |
| Tro_p-3 | 0.5 | 0.5 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 1.0 | 0.0 | 0.5 | 0.0 | 0.5 |
| Sali-1 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| Sali-2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Temp-1 | 0.0 | 0.0 | 1.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Temp-2 | 1.0 | 1.0 | 0.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 0.0 | 1.0 |
| Temp-3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 | 0.0 |
| Sapr-1 | 0.0 | 0.0 | 0.5 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |
| Sapr-2 | 0.0 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.3 | 0.3 | 1.0 | 0.0 | 1.0 | 0.5 |
| Sapr-3 | 1.0 | 0.5 | 0.0 | 0.5 | 0.0 | 0.5 | 0.5 | 0.5 | 0.0 | 0.5 | 0.3 | 0.3 | 0.0 | 1.0 | 0.0 | 0.5 |
| Sapr-4 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.3 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 |

Appendix E

Environmental variables

| Data range | Semi-natural | | | Moderate land-use intensity | | | High land-use intensity | | |
|--------------------------------|---------------------|------------|------------|------------------------------------|------------|------------|--------------------------------|------------|------------|
| | MIN | AVR | MAX | MIN | AVR | MAX | MIN | AVR | MAX |
| Suspended solid (mg/l) | 0.006 | 15.9 | 142 | 4 | 43.5 | 105 | 31 | 183.9 | 355 |
| Nitrite (mg/l) | 0.005 | 0.1 | 1.4 | 0.007 | 3.8 | 57 | 0.003 | 0.04 | 0.1 |
| Ammonia (mg/l) | 0 | 0.05 | 0.3 | 0.02 | 0.06 | 0.16 | 0.15 | 0.3 | 0.4 |
| Nitrate (mg/l) | 0.5 | 1.7 | 4.5 | 0 | 2.0 | 12 | 0.4 | 3.7 | 8 |
| Sulfate (mg/l) | 1 | 19.3 | 90 | 9 | 36.7 | 77 | 14 | 28.5 | 47 |
| Phosphate (mg/l) | 0.1 | 0.6 | 3.9 | 0.2 | 1.2 | 2.9 | 0.5 | 1.1 | 3.3 |
| Turbidity (NTU) | 1.2 | 13.9 | 87.4 | 6.1 | 29.1 | 64.5 | 65.5 | 156.1 | 203 |
| Conductivity (µS) | 24.4 | 62 | 151.2 | 95.9 | 230.8 | 405.5 | 141.1 | 221 | 325.6 |
| Salinity (mg/l) | 0 | 0.03 | 0.1 | 0.1 | 0.1 | 0.3 | 0.1 | 0.1 | 0.2 |
| Temperature (°C) | 0 | 12.2 | 18.8 | 11.4 | 17.4 | 22.3 | 15.4 | 20.9 | 24.7 |
| PH | 7.1 | 7.9 | 8.9 | 7.2 | 8.3 | 9.4 | 7.8 | 8.3 | 8.8 |
| Dissolved oxygen (ppm) | 9.1 | 11.3 | 13.0 | 8.5 | 11.3 | 13.4 | 7.8 | 9.2 | 12.3 |
| Velocity (m/sec) | 0.7 | 1.5 | 2.3 | 0.3 | 0.8 | 1.5 | 1.3 | 1.8 | 2.5 |
| Depth (cm) | 10.2 | 25.1 | 47.5 | 0.2 | 19.7 | 38.6 | 23.1 | 39.5 | 57.4 |
| Altitude (m) | 669 | 1257.3 | 1817 | 682 | 1013.7 | 1819 | 653 | 924 | 1166 |
| Average vegetation height (cm) | 4.9 | 9.7 | 19.8 | 3.7 | 9.6 | 36.6 | 4.6 | 5.7 | 7.7 |
| Maximum vegetation height (cm) | 7.8 | 17.1 | 34.9 | 5.1 | 16.4 | 63.4 | 6.7 | 8.5 | 10.4 |
| Bedrock/Boulder (%) | 0 | 0.06 | 0.4 | 0 | 0.04 | 0.3 | 0 | 0.01 | 0.05 |
| Cobble (%) | 0.2 | 0.31 | 0.5 | 0 | 0.07 | 0.3 | 0 | 0.1 | 0.4 |
| Gravel (%) | 0.1 | 0.28 | 0.4 | 0 | 0.2 | 0.4 | 0.2 | 0.4 | 0.5 |
| Sand (%) | 0 | 0.16 | 0.4 | 0 | 0.2 | 0.5 | 0.05 | 0.3 | 0.6 |
| Silt (%) | 0 | 0.04 | 0.1 | 0 | 0.06 | 0.2 | 0 | 0.04 | 0.08 |
| Clay (%) | 0 | 0.03 | 0.08 | 0 | 0.04 | 0.2 | 0 | 0.3 | 2 |

Appendix F

The species of crane flies (Tipuloidea) in the six study valleys of the eastern shore of Lake Hovsgol.

New records were determined by accessing Oosterbroek (2007). Sweep sample=1, Malaise trap river bank=2, Malaise trap steppe-forest edge=3, new record for Hovsgol region.

| Species name | BRG | DLB | SVL | NYN | SHL | TRG |
|---|-------|-------|-------|-------|-------|-------|
| Tipulinae | | | | | | |
| Angarotipula tumidicornis (Lundstrom, 1907) | | | | | 1 | 1 |
| Nephrotoma aculeata (Loew, 1871) | 1 | 1,3 | | | 1,2 | 2 |
| Nephrotoma erebus Alexander, 1921* | 2,3 | 1,2 | 1,2,3 | 1,2 | 1,2,3 | 1,2,3 |
| Nephrotoma lundbecki (Nielsen, 1907) | 1,2,3 | 1,2,3 | | 2 | 2,3 | 1,2,3 |
| Nephrotoma lunulicornis (Schummel, 1833)** | | 2 | 2,3 | 1 | | 1 |
| Nephrotoma minuticornis Alexander, 1921** | | 2 | | | | |
| Nephrotoma quadristriata (Schummel, 1833) | 2,3 | 1,2 | | 1 | | 1 |
| Nephrotoma ramulifera Tjeder, 1955 | 1,2,3 | 1,2,3 | 1 | 3 | | 2 |
| Nephrotoma stackelbergi (Savchenko, 1957) | 1,2,3 | 1,2,3 | 2,3 | 2,3 | 2,3 | 2,3 |
| Nephrotoma sublunulicornis (Savchenko, 1957) | 2 | 2,3 | 3 | 2 | 3 | 2,3 |
| Prionocera ringdahli Tjeder, 1948** | | | 1 | | | |
| Prionocera serenicola Alexander, 1945 | 1 | 1 | 1 | | 1 | |
| Prionocera subserricornis (Zetterstedt, 1851) | 1,2 | 2 | 2 | 1 | 1 | |
| Prionocera chosenicola Alexander, 1945** | 2 | | 3 | 2 | 1 | |
| Prionocera turcica (Fabricius, 1787) | 1,2 | 1,2,3 | 1,2,3 | 1,2,3 | 2 | 1,2,3 |
| Tipula (Arctotipula) caliginosa Savchenko, 1961 | 2 | 2 | | 2 | 2 | 2 |
| T.(Arctotipula) excelsa Savchenko, 1961 | 1 | | | 1 | 1 | |
| T.(Arctotipula) hovgolensis Gelhaus, Podenas, & Brodo, 2000 | 1,2 | 1,2 | | 1,2 | 1,2 | 2 |
| T.(Arctotipula) quadriloba Savchenko, 1967 | 1,2 | 1 | 1 | | 2 | 2 |

| Species name | BRG | DLB | SVL | NYN | SHL | TRG |
|--|------------|------------|------------|------------|------------|------------|
| T. (Arctotipula) salicetorum Siebke, 1870 | 1 | 1 | 1 | 1 | 1,2 | 1 |
| T. (Beringotipula) unca amuriensis Alexander, 1925 | 1,2,3 | 1,2,3 | 2,3 | 1,2,3 | 1,2,3 | 1,2,3 |
| T. (Lindnerina) dershavini Alexander, 1934 | 1,3 | 2,3 | | 1,3 | 1 | |
| T. (Lunatipula) lunata Linnaeus, 1758 | 1,2 | 1,2,3 | 1,3 | 1,2 | 1 | |
| T. (Lunatipula) recticornis Schummel, 1833 | 2,3 | 1,2,3 | | 2,3 | | 2 |
| T. (Lunatipula) trispinosa Lundstrom, 1907 | 1,2,3 | 1,2,3 | 1 | 1,2 | | 1 |
| T. (Lunatipula) turanensis Alexander, 1934 | 1,2,3 | 1,2,3 | | 1,2 | | 2,3 |
| T. (Odonatisca) kamchatkensis Alexander, 1918 | 1 | | 1 | 1 | | |
| T. (Odonatisca) nodicornis longicauda Matsumura, 1906 | 1,2 | 1,2 | 1,2,3 | 1,2,3 | 3 | 2,3 |
| T. (Odonatisca) nodicornis platyglossa Alexander, 1936 | 1 | 2,3 | | 1,2,3 | 2 | 1 |
| T. (Odonatisca) subarctica Alexander, 1919 | 2,3 | 2 | 2 | | | |
| T. (Odonatisca) timptonensis Savchenko, 1956 | 1 | | | 3 | | |
| T. (Pterelachisus) luridirostris Schummel, 1833* | | 2 | | | | |
| T. (Pterelachisus) winthemi Lackschewitz, 1932 | 2 | | | | | |
| T. (Savtshenkia) gimmerthali Lackschewitz, 1925** | | 1 | | | | |
| T. (Savtshenkia) invenusta Riedel, 1919* | 1 | 1 | 1 | 1 | 1 | |
| T. (Savtshenkia) persignata tofina Alexander, 1945** | | 1 | 1 | 1 | | |
| T. (Savtshenkia) postposita Riedel, 1919 | 1,2,3 | 2,3 | 2,3 | 2 | 2 | 3 |
| T. (Tipula) subcunctans Alexander, 1921 | | | | 1 | | 1 |
| T. (Triplixtipula) justa Alexander, 1935 | | 1 | 1 | 1 | | |
| T. (Vestiplex) kamchatkana Alexander, 1934 | 2,3 | | | | | |
| T. (Vestiplex) kiritshenkoi Savchenko, 1960 | 1 | 1,2,3 | | | 1 | |
| T. (Vestiplex) laccata Lundstrom & Frey, 1916 | | 2,3 | 1,2 | 2 | | |
| T. (Vestiplex) longitudinalis Nielsen, 1929 | 1,2,3 | 1,2,3 | 2 | 1,2,3 | 2,3 | 1,3 |
| T. (Vestiplex) scripta Meigen, 1830** | | | | 3 | | |
| T. (Vestiplex) subcentralis Alexander, 1818* | 1 | 1,3 | 1 | | 2,3 | 3 |
| T. (Vestiplex) virgatula Riedel, 1913 | 1,2,3 | 1,2,3 | 1,2,3 | 1,2,3 | 1,2,3 | 1,3 |
| T. (Yamatotipula) anceps Savchenko, 1965 | 1,3 | 1,2 | 1 | 2,3 | 1 | 1 |

| Species name | BRG | DLB | SVL | NYN | SHL | TRG |
|--|------------|------------|------------|------------|------------|------------|
| T. (Yamatotipula) freyana Lackschewitz, 1936** | 1,2 | 1,2 | 1 | | | |
| T. (Yamatotipula) pierrei Tonnoir, 1921 | 1,3 | 1,2,3 | 1,3 | 1,2 | 1,2,3 | 1,2,3 |
| T. (Yamatotipula) pruinosa Wiedemann, 1817 | 1,2,3 | 1,2,3 | 1,2,3 | 1,2 | 1 | 1,3 |
| T. (Yamatotipula) quadrivittata cinifera Savchenko, 1961 | | 2,3 | 2 | 2,3 | 2 | |
| T.(Yamatotipula) quadrivittata subsulphurea Alexander, 1934* | 1 | 1 | | | | |
| Limoniinae | | | | | | |
| Dicranomyia (Dicranomyia) aperta Wahlgren, 1904 | 1,2,3 | 1,2,3 | 1,2,3 | 1,2,3 | 1,2,3 | 1,2 |
| D. (Dicranomyia) didyma (Meigen, 1804) | 1,2,3 | 1,2,3 | 1,3 | 2,3 | 1 | 1,2,3 |
| D. (Dicranomyia) distendens Lundstrom, 1912* | 1 | 1 | | | | |
| D. (Dicranomyia) frontalis (Staeger, 1840) | 3 | 1,2,3 | 2,3 | 2 | 2,3 | 2,3 |
| D. (Dicranomyia) halterata Osten-Sacken, 1869 | 1 | 1 | 1 | 1,2 | 2,3 | 1 |
| D. (Dicranomyia) hyalinata (Zetterstedt, 1851) | 1,2,3 | 1,2,3 | 1,2,3 | 2,3 | 2,3 | 1,2,3 |
| D. (Dicranomyia) incisurata Lackschewitz, 1928 | 1,2,3 | 1,2,3 | 1,2,3 | 1,2,3 | 1,2,3 | 1,2,3 |
| D. (Dicranomyia) longipennis (Schummel, 1829) | 1 | 1 | 1 | 1 | 1 | 1 |
| D. (Dicranomyia) modesta (Meigen, 1818) | 1,2,3 | 1,3 | 1,2 | 1,2 | 1,2,3 | 1,2,3 |
| D. (Dicranomyia) omissinervis De Meijere, 1818 | 1 | 1 | 1 | 1 | | 1 |
| D. (Dicranomyia) patens Lundstrom, 1907* | 2 | 1 | 1 | 1,2 | | |
| D. (Dicranomyia) reductissima (Alexander, 1952) | 1 | 1 | 1 | 1,2 | 1 | 1 |
| D. (Dicranomyia) sera (Walker, 1848) | | | 1,2 | 1 | 1 | 1 |
| D. (Dicranomyia) tessulata (Savchenko, 1974) | | 1,2,3 | | 2 | 1 | |
| D. (Glochina) schineriana (Alexander, 1964) | | 3 | 3 | 2 | 3 | |
| D. (Glochina) tristis (Schummel, 1829) | | 3 | 2 | 3 | | |
| D. (Idiopyga) ctenopyga (Alexander, 1943) | | 1 | 1,3 | 1 | 1 | |
| D. (Idiopyga) halterella Edwards, 1921* | 1 | 1 | 1,3 | 1,2 | 1,2 | 1 |
| D. (Idiopyga) stigmatica (Meigen, 1830)* | 1 | 1 | 1 | 2,3 | 1 | |
| Limonia annulata Lackschewitz, 1940* | | 2 | | 3 | | 3 |
| Limonia episema Alexander, 1924 | | | 2 | | | |

| Species name | BRG | DLB | SVL | NYN | SHL | TRG |
|--|------------|------------|------------|------------|------------|------------|
| Metalimnobia bifasciata (Schrank, 1781) | 1,3 | 1,2,3 | 1,3 | 1,2,3 | 3 | 3 |
| Metalimnobia quadrimaculata (Linnaeus, 1761)* | | 2 | 2,3 | 2,3 | | 1,2,3 |
| Metalimnobia quadrinotata (Meigen, 1818) | 1,2,3 | 1,2,3 | 2,3 | 1,2,3 | 2,3 | 1,2,3 |
| Rhipidia maculata Meigen, 1818 | | 3 | | | | 3 |
| Chioneinae | | | | | | |
| Arctoconopa zonata (Zetterstedt, 1851) | 1 | 1 | | | | |
| Cheilotrichia (Empeda) areolata (Lundstrom, 1912) | 3 | | | | | |
| Erioptera lutea fuscohalterata Alexander, 1925 | | 1,2 | | 2 | | 1,3 |
| Erioptera (Mesocyphona) testacea (Lackschewitz, 1964) | 2 | 2,3 | 2,3 | 2 | 2 | |
| Gonomyia (Teuchogonomyia) horribilis Alexander, 1941** | 1,2,3 | 1,2,3 | | 2,3 | 2,3 | 2,3 |
| Hoplolabis (Parilisia) estella (Alexander, 1955)* | 1 | 1,2 | 1,2,3 | | | 2 |
| Rhabdomastix (Sacandaga) laeta (Loew, 1873) | 1,2,3 | 1,2,3 | 1,2,3 | 2 | 1,3 | 1,3 |
| Symplecta (Symplecta) hybrida (Meigen, 1804) | 1,2 | 1 | 2 | 1 | 1 | 1 |
| S. (Symplecta) scotica (Edwards, 1938) | 1,2,3 | 1,2,3 | 1,2,3 | 1,2,3 | 1,2,3 | 1,2,3 |
| Limnophilinae | | | | | | |
| Idioptera linnei Oosterbroek, 1992 | | 1 | 1 | | | |
| Limnophila chinggiskhani Podenas & Gelhaus, 2001 | 1 | 1,2,3 | 1,2 | 1,2,3 | 2 | 1,2 |
| Dicranophragma (Brachylimnophila) nemorale (Meigen, 1818) | | | | 2 | | |
| Phylidorea (Macrolabina) temelskin Podenas & Gelhaus, 2001 | 1 | 1 | | 1,2 | 1,2 | 1 |
| P. (Phylidorea) longicornis pietatis (Alexander, 1950) | | | | 2 | | |
| P. (Phylidorea) squalens (Zetterstedt, 1838) | | | | 2 | | |
| Cylindrotomidae | | | | | | |
| Cylindrotoma distinctissima (Meigen, 1818) | 1 | | | | | |
| Cylindrotoma nigriventris (Loew, 1849) | | | | | | 3 |
| Ptychopteridae | | | | | | |
| Ptychoptera scutellaris Meigen, 1818* | 2 | 2,3 | 2 | | 2 | |

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