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I am submitting herewith a thesis written by Meg E. Howard entitled "Geochemical Characterization of Coastal Pond and Adjacent Soil Organic Matter from Two Distinct Field Areas of the McMurdo Dry Valleys, Antarctica". I have examined the final electronic copy of this thesis for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Master of Science, with a major in Geology.

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GEOCHEMICAL CHARACTERIZATION OF COASTAL POND AND
ADJACENT SOIL ORGANIC MATTER IN TWO DISTINCT FIELD
AREAS OF THE MCMURDO DRY VALLEYS, ANTARCTICA

A Thesis
Presented for the
Master of Science
Degree
The University of Tennessee, Knoxville

Meg Elizabeth Howard
August 2006

Acknowledgements

Without the help and support of faculty, family, and friends, the completion of this thesis would not have been possible. I would like to thank my previous major advisor, Dr. Maria Uhle, for giving me the opportunity to work on this research. I would also like to thank my committee members, Dr. Claudia Mora, Dr. Linda Kah and Dr. Mark Radosevich for their support and interest in both this project, and my personal and academic progress. Many thanks need to be given to Dr. Zheng Hua Li for his instruction, patience and time with me in the isotope extraction and analysis lab. Thanks to Dr. D.C. White at the Center for Biomarker Analysis (CBA), Knoxville, Tennessee, for use of their facilities, and to Aaron Peacock and Amanda Smithgall, also at CBA, for their instruction and help with the lipid extraction and analysis procedures. To all my true friends not mentioned above, you know who you are and your help with keeping me sane over the past years are not forgotten.

My greatest thanks I owe to my family and my husband. Mom, Dad and Kim, without your continued support and belief in me, I would not be where I am today. To my husband, I give the greatest thanks. You put up with many months apart so I could finish. Words can't express my gratitude for all the seemingly limitless patience and understanding you possess and so freely give to me.

This research was supported by the National Science Foundation Office of Polar Programs Grant # 0230237 awarded to Drs. Maria Uhle and Peter Doran.

Abstract

The McMurdo Dry Valleys (MDV), Antarctica contains some of the few ice-free oases on the continent, and is one of the coldest, driest places on earth. Despite the harsh conditions, the MDV supports an abundance of biological communities within soil and aquatic systems. Bioavailable carbon is present in these systems in the form of ancient and modern sources. An additional source of bioavailable carbon that has largely been ignored may be represented by desiccated and disseminated microbial mats (coastal pond organic matter, or CP-OM) originating in ephemeral coastal meltwater ponds of the MDV. The goal of this study is to more fully characterize CP-OM so that it may be recognized in a variety of environmental samples. Modern (active) mat, relict (desiccated) mat, and soil samples were collected from four ponds and along transects adjacent to these ponds at two field localities, Hjorth Hill Camp and Garwood Valley Camp. Bulk isotopic, elemental and phospholipid fatty acid (PLFA) analyses of the three sample types were performed. Results indicate that CP-OM is present in the soil reservoir at both localities, even at sample locations distant from coastal ponds. The soil reservoir at Garwood Valley has a greater contribution of CP-OM than at Hjorth Hill. Total organic carbon (TOC) measurements show high concentrations of organic matter close to pond edges, with TOC concentrations decreasing with distance. PLFA analyses demonstrate all three sample types are composed of a three-tiered community system dominated by cyanobacteria. Additionally, a shift from minor bacterial community composition in modern and relict mats towards greater community composition in soil samples is evident. Bulk carbon and nitrogen isotopic signatures vary between sample types and field locations, however large-scale implications indicate nitrogen-fixing cyanobacteria are present within ponds under CO₂-limited conditions. Variations in carbon and nitrogen isotopic values for relict mat and soils are a result of varying degrees of in situ microbial processes and bulk source matter utilization. A baseline geochemical characterization for CP-OM and adjacent soils has been created, and can be used in conjunction with previous work for future studies of ecosystem functioning and linkages within the MDV.

TABLE OF CONTENTS

Chapter	Page
I. Introduction	1
II. Description of Study Area and Field Sites	4
III. Background	
A. Sources of Organic Matter to Dry Valleys Soils	6
B. Coastal Pond Mats	7
C. Analytical Framework of the Study	8
1. Previous Isotopic and Geochemical Characterization of Cyanobacterial Mats	9
2. Phospholipid Fatty Acids as Biomarkers	9
IV. Methodology	
A. Field Work - Collection of Samples	12
B. Laboratory Analysis	
1. Bulk Isotopic Analysis	12
2. PLFA Extraction and Analysis	14
3. Total Organic Carbon and Total Nitrogen Analysis	15
V. Results	
A. Total Organic Carbon	16
B. Bulk Carbon Isotopes	16
C. Bulk Nitrogen Isotopes	18
D. Carbon to Nitrogen Ratios vs. $\delta^{13}\text{C}$ Values	18
E. $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ Values	19
F. PLFA Data	20
VI. Discussion	26
VII. Conclusions	37
List of References	40
Appendices	47
Vita	95

LIST OF TABLES

Table	Page
Table 1: Descriptions of samples and sample locations.	49
Table 2: Carbon and nitrogen bulk and isotopic compositions of soils, relict and modern mat samples collected from Hjorth Hill and Garwood Valley Camp, McMurdo Dry Valleys, Antarctica.	51
Table 3: Averages of TOC, TN, C:N Ratios, $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ for samples by sample type, pond location, field site, and as both field sites averaged together.	53
Table 4: Community composition structural approach by sample type.	54
Table 5: Community composition structural approach by sample type and field area.	54

LIST OF FIGURES

Figure	Page
Figure 1: Map of the continent of Antarctica showing the location of the McMurdo Dry Valleys.	56
Figure 2: Locations of two field sites, Hjorth Hill Camp (HHC) and Garwood Valley Camp (GVC).	57
Figure 3: Photo of Big Sister/Little Sister Pond at HHC looking north.	58
Figure 4: Photo of Tom Pond at HHC looking east.	58
Figure 5: Photo of Marina Pond (in foreground) at GVC looking south.	59
Figure 6: Photo of Susan Pond at GVC looking northeast.	59
Figure 7: Diagram of a PLFA structure showing polar phosphate head.	60
Figure 8: Diagram of PLFA bilayer membrane structure.	60
Figure 9: Total organic carbon content distribution at (a) Big Sister/Little Sister Pond (HHC), (b) Tom Pond (HHC), (c) Susan Pond (GVC), and (d) Marina Pond (GVC).	61
Figure 10: Distributions of stable carbon isotopes at (a) Big/Little Sister Pond (HHC), (b) Tom Pond (HHC), (c) Susan Pond (GVC), and (d) Marina Pond (GVC).	65
Figure 11: $\delta^{13}\text{C}$ vs. C:N ratios for all three sample types and compared to previous Burkins et al. (2001) soil data.	69
Figure 12: $\delta^{13}\text{C}$ vs. $\delta^{15}\text{N}$ data for modern and relict mat samples from this research and Lawson et al. (2004).	69
Figure 13: Modern mat biomass abundances for GVC and HHC field sites.	70
Figure 14: Relict mat biomass abundances for GVC and HHC field sites.	70
Figure 15: Soil biomass abundances for GVC and HHC field sites.	71
Figure 16: Eukaryotic vs. prokaryotic signature PLFA abundances.	71
Figure 17: Breakdown of modern mat structural groups based on PLFA type.	72
Figure 18: Breakdown of relict mat structural groups based on PLFA type.	72
Figure 19: Breakdown of HHC soil structural groups based on PLFA type.	73
Figure 20: Breakdown of GVC soil structural groups based on PLFA type.	73
Figure 21: Typical PLFA profiles for each of the three sample types.	74
Figure 22: The 15 most abundant PLFAs for all three sample types.	75

I. Introduction

The McMurdo Dry Valleys, Antarctica, contain some of the few ice-free oases on the continent. This ecosystem is among the coldest and driest places on earth, with a mean annual air temperature of -20°C and an annual precipitation rate of 10 cm (Treonis et al., 2002). Despite these conditions, the Dry Valleys ecosystem supports an abundance of life. Biological communities within aquatic and soil environments include cyanobacteria, bacteria, algae, fungi, and nematodes, with photoautotrophic production providing heterotrophic communities with a source of labile, or bioavailable, carbon. Whereas communities found in aquatic environments are dominated by filamentous cyanobacterial mat communities, the soil reservoir is dominated by higher trophic levels consisting primarily of rotifers, tardigrades, and nematodes (Moorehead and Priscu, 1998). Algal and bacterial communities, as well as encrusting cyanobacteria are likely present.

Previous efforts to understand ecosystem functioning, linkages, and organic carbon dynamics within the various reservoirs of the McMurdo Dry Valleys (MDV) ecosystem have focused on interactions between soils, glaciers, ice-covered lakes, and ephemeral meltwater streams (e.g. Bishop et al., 2001; Burkins et al., 2000; Burkins et al., 2001; Doran et al., 1998; Fritsen et al., 2000; Moorehead and Priscu, 1998; Parker et al., 1982a; Priscu et al., 1998; Venkatesan and Mirsadeghi, 1992; Wharton et al., 1993). A potentially important source of organic carbon to the soil reservoir of the Dry Valleys are abundant mats which thrive in ephemeral meltwater ponds found in coastal regions. Whereas previous studies have focused on mats found in meltwater streams, ice-platform ponds, and lakes within the Dry Valleys (i.e., Howard-Williams et al., 1986; Lawson et al., 2004; Vincent and Howard-Williams, 1986), the mats of the Dry Valleys coastal ponds have largely been ignored. These mats are the focus of the present study.

The formation of ephemeral coastal meltwater ponds likely results from seasonal melting of ice buried within glacial till. The average size of ponds (a few to several meters in diameter) is small compared to perennially ice-covered lakes within the

ecosystem (i.e. Bonney, Hoare, Fryxell and Vanda lakes). Collectively, however, these ponds have a substantial surface area, and have been observed to generate large quantities of stranded (i.e., relict) mat material as they shift position on the landscape (Wharton et al., 1983). Previous studies have shown that communities which make up mats found in streams and lakes can undergo recovery following long periods of desiccation (Hawes et al., 1992). The transient nature of coastal ponds, however, renders their organic matter vulnerable to transport, and this organic material likely represents a significant source of labile organic carbon that supports heterotrophic communities within the soil reservoir (Burkins et al., 2000; Moorehead and Priscu, 1998; Priscu et al., 1998).

In order to gain insight into the role of coastal pond organic matter (CP-OM) within the MDV, this study examines linkages between Dry Valleys CP-OM and adjacent soils. Specifically, the focus of this research is the geochemical characterization of active coastal pond mats and their communities, and comparison of these results to similarly characterized relict (desiccated) mats and soils found in close proximity to active ponds. Questions posed include:

1. What communities make up the coastal pond mats?
2. How do they compare to communities present in relict mats and soils in close proximity to the coastal ponds?
3. What types of isotopic and chemical signatures characterize soils, relict and modern mats in and adjacent to coastal ponds in the study area?
4. What processes and organic matter source utilization is indicated by these signatures?
5. Is viable coastal pond organic matter making its way into the soil reservoir?
6. How do these results compare to previously published data on lacustrine cyanobacterial mats and MDV soils characterizations?

To help answer these questions, this study focuses on (1) biomass measurements and distributions of organic matter within the soil reservoir, (2) characterization of active coastal pond mats through bulk carbon and nitrogen isotopic analysis and analysis of phospholipid fatty acid (PLFA) biomarkers, (3) characterization of changes in community structure and isotopic compositions with distance from the perimeters of

active coastal ponds through isotopic and PLFA analysis of relict mats and soils, and (4) identification of compositional ranges for CP-OM bulk organic matter using bulk carbon and nitrogen isotopic analysis, total organic carbon and nitrogen measurements (TOC and TN) and carbon to nitrogen (C:N) ratios. Observations will be used to construct a preliminary understanding of the characteristics of CP-OM and adjacent soils near coastal ponds, and geochemical processes at work in each reservoir.

II. Description of Study Area and Field Sites

Research for this project took place in the MDV, Antarctica (Figure 1, all Figures Appendix B). Field sites for this research include two areas, located along a latitudinal gradient from Taylor Valley along the Ross Sea coast to Garwood Valley (Figure 2).

Site 1: Hjorth Hill - The northernmost site is an area adjacent to Hjorth Hill between Cape Bernacchi and the eastern end of Taylor Valley (Figure 2, 77°30' S, 163°49' E), and is referred to within this paper as Hjorth Hill Camp (HHC). Two ponds at HHC, Big Sister/Little Sister Pond and Tom Pond, were chosen for sample collection (Figures 3 and 4). The surficial geology of HHC consists of four major unconsolidated drift sheets (Ross Sea, Wilson, Alpine I and Bonney) of Quaternary and Late Tertiary age (Hall et al., 2000). Ponds occur within the Ross Sea drift sheet which consists of sandy, poorly sorted, and poorly to non-stratified till. The Ross Sea till presumably formed from landward-flowing ice that was part of a grounded ice-sheet (Hall et al., 2000).

Site 2: Garwood Valley - The southernmost site is located in Garwood Valley, approximately 55 km south of Taylor Valley near the Garwood Glacier (Figure 2, 78°02' S, 164°19' E). This site is referred to within this paper as Garwood Valley Camp (GVC). Two ponds at GVC, Marina Pond and Susan Pond, were chosen for sample collection (Figures 5 and 6). Morphologic features of GVC include active and relict sandar (outwash plains and fans). Pond strandlines occur on the lower moraine slopes and well-developed, braided stream channels flow over the sandar surfaces (Rains et al., 1980). The surficial geology of the area is dominated by glaciofluvial outwash consisting of sand, granule and fine pebbles. Also present is a thin veneer of basalt, presumably originating from Mt. Erebus and deposited by the Ross ice sheet.

Coastal soils of the MDV have previously been described as young, cold desert soils with little to no pedogenic development (Campbell et al., 1998). Recently, Dry Valleys soils have been classified according to requirements of the Soil Survey Staff as Gelisols, characterized as soils containing gelic materials (cryoturbated or within a seasonal thaw layer) and permafrost between 100 and 200 cm of the surface (Bockheim,

1997). Parent materials are sandy to silty, bouldery till which generally includes marble, schist and gneiss (Campbell et al., 1998), as well as volcanic rocks derived from the Mt. Erebus (active) and Mt. Discovery (dormant) volcanoes. Soil features include pebble to boulder surface pavement, and alkaline pH values up to 9.8 (Campbell et al., 1998). The soils generally consist of 95-99% sand by weight with low concentrations of organic matter, and are thus considered poorly weathered (Treonis et al., 2002).

III. Background

A. Sources of Organic Matter to Dry Valleys Soils

The accumulation and distribution of organic matter to MDV soils is attributable to both modern and ancient sources (Burkins et al., 2000). Ancient sources of organic matter that may be present in the soils include detrital organic matter from glaciomarine and glaciolacustrine deposits. This organic matter was derived from glacial tills scoured from McMurdo Sound and deposited in the Dry Valleys, as well as organic matter produced in glacial Lake Washburn and other ancient lakes resulting from the damming of glacial meltwaters (Burkins et al., 2000, Kellogg et al., 1978). Previous workers have also found low concentrations of recalcitrant terrestrial organic matter (i.e., vascular plant debris), that was presumably weathered from sedimentary units and coal beds located at higher elevations (Matsumoto et al., 1990). In general, these organic materials are not very bioavailable.

Modern sources of organic matter include active micro-invertebrate communities consisting of nematodes, rotifers and tardigrades (Priscu et al., 1998), bacteria, and possibly organic matter originating from coastal pond mats. Additional modern sources of organic matter include particulate and dissolved organic carbon (DOC) produced in streams, lakes, and coastal ponds. Modern organic matter is likely disseminated throughout the ecosystem via changes in hydrologic conditions and subsequent aeolian distribution. Stream-derived organic matter consists primarily of material sourced from soils and epilithic communities, which are dominated by cyanobacteria (Aiken et al., 1996; Vincent and Howard-Williams, 1986; Vincent et al., 1993). Leaching of existing biomass in stream channels by glacial meltwater generates relatively labile DOC, but the total DOC content of these waters is extremely low (0.2 to 9.7 mg C/l; Aiken et al., 1996). Of the two field sites in this study, only GVC appeared to have a historical linkage to large stream or river systems, namely Garwood River, a large meltwater river associated with the Garwood Glacier and located approximately 4 miles inland of the GVC coastal ponds. During the 2003-2004 field season, however, coastal ponds at GVC

were not directly linked to this river. At HHC, local streams were clearly ephemeral meltwater streams related to snowfall that occurred during the 2003-2004 season, and likely shifted position on the landscape seasonally.

In modern MDV lakes, between 20% and 80% of the organic material is refractory humic materials (Aiken et al., 1996). Although phytoplankton, cyanobacteria, and bacteria are the predominant sources of labile, dissolved organic carbon to the MDV lakes (Aiken et al., 1996; Laybourn-Parry et al., 1997; Lyons et al., 1992; McKnight et al., 1994; McKnight et al., 2000; Priscu et al., 1998), a substantial amount of the organic matter in lakes is also derived from the leaching of relict carbon from soils as the lakes increase in size. This organic carbon is physically isolated from the soil reservoir unless hydrologic shifts, i.e. sub aerial exposure, renders the organic matter vulnerable to aeolian or fluvial transport.

Previous studies of lacustrine environments in the MDV have shown that lacustrine mats are typically dominated by cyanobacteria, pennate diatoms, and various bacterial communities (Wharton et al., 1983). Phytoplankton within pond waters may also be a source of carbon to the soil reservoir, however, only low standing stocks of phytoplankton are typically observed in the Ross Ice Shelf ponds (Hawes, 1983; Hawes et al., 1993; Howard-Williams et al., 1989).

Coastal pond organic matter has been ignored as a potential source to MDV soils. As such, a baseline approach to the chemical characterization of CP-OM will be as a first approach at being able to identify such material in soils of the MDV.

B. Coastal Pond Mats

Although input of CP-OM into soils proximal to ponds may be extremely important to the support of microbial communities present, no detailed study has yet examined the communities which make up the mats within the MDV coastal ponds. Previous work focused on freshwater ponds on the McMurdo ice shelf, Ross Island coastal ponds, glacial ponds, and lake systems within the MDV, has shed light on community composition in mats within these aquatic environments, and likely are similar to coastal pond communities (Hawes et al., 1993; Howard-Williams et al., 1989; Parker

et al., 1982b; Vincent and James, 1996; Wharton et al., 1983). These studies indicated a predominance of filamentous cyanobacterial populations, as well as diatoms, bacterial populations, and minor yeasts and bryophytes. PLFA analysis will allow more in-depth identification of communities within the coastal pond mats. The communities present may be an important source of labile carbon for higher trophic levels within the aquatic and soil ecosystems of the MDV.

An interesting characteristic of MDV mats studied to date is their ability to undergo prolonged desiccation and subsequent recovery following periods of environmental stress brought on by changing hydrologic conditions, i.e., drops in water levels or physical shifts in pond positions on the landscape. Hawes et al. (1992) investigated the ability of a variety of mat types to recover following prolonged desiccation, and found that after as much as three years of drying, all studied mats contained viable organic matter, suggesting that relict (desiccated) mat material may thus act as a propagule reservoir, reestablishing mats either *in situ* or upon wind dispersal and rewetting. The current study presented here characterizes modern or active mats using PLFAs and stable isotopic analysis and compares results to PLFAs and stable isotopic compositions found in relict mat and soils to investigate the possibility of viable mat material being present within soils near coastal ponds, and to gain insight to geochemical processes occurring in various locations proximal to coastal ponds and across the study area.

C. Analytical Framework of the Study

A major objective of this research includes characterizing organic matter from three sample “pools”, i.e. the (1) modern (active) pond mat, (2) relict pond mat, and (3) soil samples collected along a gradient adjacent to pond locations. Such characterization is accomplished using bulk $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ isotopic analysis, and total organic carbon (TOC) and total nitrogen (TN) measurements. PLFAs are extracted to identify community composition variations across field areas and sample types. Origins of specific lipids have been investigated by previous workers (i.e., Findlay et al., 1993, Ringelberg et al., 1989, and White et al., 1997), and are fairly specific to microbial and

higher trophic level sources. The distribution of CP-OM within the soil reservoir is established by contouring TOC values and bulk carbon isotope values.

1. Previous Isotopic and Geochemical Characterization of Cyanobacterial Mats.

Previous work by Lawson et al. (2004) looked at cyanobacterial mats as benthic organic matter from moat (shallow) locations within four Taylor Valley lakes of the MDV. Depths of these moat mats are similar to the depths of the coastal ponds (0.01 to 2 meters). Analysis of stable carbon and nitrogen isotopes of lacustrine moat mats indicate it is characterized by $\delta^{13}\text{C}$ (PDB standard) and $\delta^{15}\text{N}$ (atmospheric air standard) values of -3‰ to -13‰ , and $+1\text{‰}$ to -7‰ , respectively. Values for CP-OM are expected to be similar to the values given for lacustrine mat communities presented by Lawson et al. (2004), because of the similarity between these cyanobacterial-dominated aquatic mats and those found in coastal ponds. The values of samples analyzed for this research will be plotted against modern and relict lacustrine moat mat values determined by Lawson et al. (2004) in an effort to create a field indicative of CP-OM derived organic matter as a means to distinguish lacustrine mat organic material from CP-OM.

Previous work by Burkins et al. (2001) geochemically characterized soils from various MDV locations using bulk $\delta^{13}\text{C}$ and C:N ratios. These locations were not proximal to coastal ponds or cyanobacterial mat input. Soil samples adjacent to coastal ponds from this research will be plotted against the Burkins et al. (2001) data for comparison. In addition, modern and relict mat samples will also be plotted in order to discern a range of compositions characteristic of CP-OM, although no known current research has characterized non-marine sediment materials in this manner.

2. Phospholipid Fatty Acids as Biomarkers.

Lipids are one of four chemical components of all cells, playing a crucial role in the structures of cell membranes and as storage products, and within *Bacteria* and *Eukarya* are composed primarily of fatty acids. Lipids can be subdivided into three type groups: neutral, glyco-, and polar lipids. PLFAs belong to the polar group of lipids owing to their highly polar phosphate “heads” (Figure 7). Upon death of a cell, the

phosphate “head” of a PLFA is cleaved off due to weak bonds, thus becoming a neutral or “free” fatty acid (Bligh & Dyer, 1959).

PLFAs are essential components of cell membranes of living cells, forming bilayers within cell membrane walls (Figure 8). Unlike other lipids, PLFAs are not present in dead cells, or as storage products (Zelles, 1999), and thus represent viable biomass. Furthermore, these compounds are widely distributed biomarkers that are characteristic of various microbial and higher trophic communities including cyanobacteria, bacteria, algae, fungi, diatoms, and protozoa (White et al., 1997). The presence and ratios of types and structures of specific fatty acids (i.e., ratios of *trans* and *cis* types of PLFAs) give clues to the health of a given microbial community (White et al., 1997). Analysis of PLFAs in soils and sediments can thus be used to (1) establish microbial community compositions (i.e., prokaryotic vs. eukaryotic taxa), (2) quantitatively estimate the amount of total viable microbial biomass in a sample, and (3) gain insight on the physiological status of the community by identifying shifts in PLFA compositions that are indicative of various environmental stressors (White et al., 1997).

There are two systems for the nomenclature of PLFAs used in current literature. Within this paper, the nomenclature system used for PLFAs is in the form A:B ω C, where A is the number of carbons, B is the number of double bonds, and ω C is the distance of the closest unsaturation from the carboxyl group end of the molecule. The suffixes *c*- and *t*- (for *cis* and *trans*) refer to the positions of geometric isomers on the molecule. Prefixes such as “a-”, “br-”, “i-”, “cy”, and “me” refer to anteiso-, branching-, isomethyl-, cyclo- and mid-chain methyl branching fatty acids, respectively, which are descriptive of their structures (Pombo et al., 2002).

As a result of their ubiquity and genus level specificity (Findlay et al., 1993), identification of PLFAs in environmental samples can help establish community composition within each sample, the conditions under which they thrive and, for this research, may act as tracers of CP-OM within the soil reservoir. For example, the PLFA 18:3 ω 3 suggests the presence of the cyanobacteria *Nostoc commune* (Findlay et al., 1993). The presence of this biomarker within both coastal pond mats and peripheral soils

would suggest transport of this labile organic matter from the ponds into the soil reservoir.

In this study, specific PLFA biomarkers were used to identify cyanobacterial, bacterial, algal, and higher (fungi, bryophytes, etc.) organisms present in modern and relict mats and soils. Common PLFAs to cyanobacteria include large quantities of 16:1 ω 7c and 18:1 ω 7c (Brinis et al., 2004). Bacteria originating from the CP-OM, as well as populations already present in the soils, may be a significant source of organic carbon to the soil reservoir. PLFAs of bacteria vary widely, depending on specific genus, however major PLFAs include terminally branched saturated PLFAs for gram positive bacteria, and monounsaturates for gram negative bacteria. Algae, including diatoms, may also be a significant source of organic carbon within coastal ponds and soils of the MDV. The biomarker 16:4 ω 1 and large abundances of 16:0, 16:3, and 20:5 ω 3 PLFAs are important biomarkers for diatoms (Findlay and Dobbs, 1993). Although higher terrestrial plants are absent in Antarctica, terrestrial land plant PLFAs are characterized by long chain-length compounds (20 and greater). Limited investigations of nematode PLFAs suggest common biomarkers for fungal feeding nematodes include 16:0, 18:0, 18:1 ω 7,9, 18:2, and 18:2 ω 6,9 (Chen et al., 2001, Ruess et al., 2002 and 2005). These biomarkers, however, are also observed in a variety of microbial communities, and do not serve as good biomarkers strictly for nematodes in the species-mixed soil ecosystem of the MDV.

IV. Methodology

A. Field Work - Collection of Samples

Samples from within ponds (modern mat) were recovered during the 2003-2004 field season by Melissa M. Hage. Samples were immediately placed in one-liter Nalgene bottles and kept frozen until processed. Soil and relict mat samples from the top 3 to 5 cm of substrate were collected using a stainless steel shovel. Following sample collection, sample depths were recorded. Samples were placed in pre-ashed, acetone-cleaned aluminum foil packets. The shovel was cleaned thoroughly with acetone between sample locations. Samples were recovered along transects that ran perpendicular to the north, south, east and west of coastal pond perimeters. Samples were composed of three types; modern mat, relict mat, and bulk soil. Modern mat samples were collected from active mats material from within the ponds. Relict mat samples are defined as samples containing a majority of desiccated coastal pond mat material. Soil samples are those that contained no visible relict mat material. Select sampling locations were recorded using a GPS system accurate to approximately 5m. Samples were placed in whirlpaks and kept frozen until processed. Table 1 in Appendix A (all Tables Appendix A) gives descriptions and locations of those samples analyzed for TOC, TN, bulk nitrogen and carbon isotopes, and includes many of the samples analyzed for PLFAs.

B. Laboratory Analysis

1. Bulk Isotopic Analysis

Measurements of modern mat, relict mat and soil sample bulk organic carbon isotope ratios were accomplished following standard methods. Lyophilized soil samples were dried overnight in an oven at 110°C and homogenized by crushing to a fine powder using a mortar and pestle. The mortar and pestle were cleaned between samples with tap water and Alconox, followed by three rinses each of tap water and Milli-Q water. Both acetone and methanol were used as a final rinse. Inorganic carbon in the form of CaCO_3 was removed from each sample by adding a minimum of 20 mL of 10% HCl to each

sample, stirring, and allowed to sit for at least 1.5 hours. Following acidification, samples were centrifuged and supernatant HCl decanted. Each sample was then rinsed using a minimum of 40 mL Milli-Q water, centrifuged and decanted. This procedure was repeated a minimum of three times or until the pH of the supernatant was between 6 and 7. Once neutralized, samples were dried overnight in an oven at 110 °C and rehomogenized.

In order to assure that enough sample was present for analysis of carbon isotopic measurement, an aliquot of each was used to estimate TOC content using a Loss-On-Ignition technique. Approximately 20g of sample were placed in a pre-weighed crucible. Crucibles were re-weighed with the sample and weights recorded. Crucibles were then placed into a 550 °C furnace for one hour. Crucibles were subsequently removed from the furnace and cooled to room temperature in a desiccator. Crucibles with combusted samples were reweighed and the weights recorded. The estimated TOC content was then: (original weight of sample – combusted sample weight)/original sample weight.

Following TOC analysis, approximately 100 to 1100 mg of sample, or enough to assure the presence of approximately 2 micrograms of pure organic carbon, was placed in either 6 or 9 mm quartz reaction tubes along with 500 mg CuO and Cu, and platinum wire. Tubes were evacuated and sealed on a vacuum line and combusted at 800 °C for 3 hours. The extracted CO₂ gas was cryogenically cleaned of H₂O and non-condensable gases and collected in glass vessels. Carbon isotope compositions of CO₂ gas was measured using a dual inlet Finnigan-MAT DELTA Plus mass spectrometer at the University of Tennessee.

Carbon isotopic ratios are denoted in delta notation (δ) in units of per mil (‰) relative to the Pee Dee Belemnite (PDB) standard:

$$\delta^{13}\text{C} \text{ ‰ [std]} = [(R_{\text{sample}} - R_{\text{std}})/R_{\text{std}}] \times 1000, \text{ where}$$

$$R = {}^{13}\text{C}/{}^{12}\text{C}$$

For analysis of bulk nitrogen isotopes, samples were freeze dried and homogenized using a mortar and pestle. Crushing of samples < 250 μm size was

achieved using a SPEX ball mill. 25-30 mg of the resulting powder was sealed in 5 x 9 mm tin capsules and analyzed by EA-IRMS at the Stable Isotope Ecology Lab at the University of Georgia. Nitrogen isotopic ratios are denoted in standard delta notation as reported above, where:

$$\delta^{15}\text{N in } \text{‰} = [(R_{\text{sample}} - R_{\text{std}})/(R_{\text{std}})] \times 1000, \text{ where}$$

$$R = (^{15}\text{N}/^{14}\text{N})$$

Carbon and nitrogen isotopic compositions, TOC, TN and C:N ratios are reported in Table 2 and average values are reported in Table 3.

2. PLFA Extraction and Analysis

PLFAs from modern mat, relict mats, and soil samples were extracted following a modified Bligh and Dyer technique (White et al., 1979). Total lipids were extracted from lyophilized sediment samples using methanol, chloroform, and phosphate buffer in a 2: 1: 0.8 ratio (75 mL, 37.5 mL, and 30 mL, respectively). Sample aliquots of 75 grams were used for samples containing TOC <1%, whereas smaller aliquots (5-10 grams) were used for organic-rich samples (i.e., relict and modern mat). After extracting in first phase for 4-6 hours, samples were centrifuged and the supernatant decanted into separatory funnels. A maximum of 37.5 mL of chloroform were added to the centrifuge bottles, centrifuged, and the supernatant decanted. 37.5 mL of H₂O were then added to each funnel, giving a final solvent ratio of 1: 1: 0.9. The extract was allowed to sit overnight (maximum of 18 hours). The organic (lower) phase was then transferred to new vials and dried under a stream of N₂ at 37 °C using a Roto-Vap. Dried samples were transferred to test tubes using 2 mL chloroform washes repeated 3 times, and re-dried under a stream of N₂ at 37 °C. Once dry, approximately 150 µl of chloroform were added to each sample, and at least two subsequent 150 µL chloroform washes were used to transfer samples onto silicic acid columns. Samples were loaded onto pre-ashed columns, and separated by elution into hexane cleanup, neutral lipid, glycolipid, and polar lipid fractions by adding 2.5 mL of hexane, chloroform, acetone, and methanol

twice, respectively, for a total of 5 mL (polar lipids were eluted with a total of 10 mL of methanol). The effluent was captured in new labeled vials.

Polar lipids were methylated to fatty acid methyl esters (PLFAs) by drying under a stream of dry N₂ in a 37°C bath. Methanolic KOH, methanol and chloroform were added to sample vials, sealed and reacted in a 60°C bath for thirty minutes. The reaction was quenched and 2 mL each of hexane and DI water, and 200 µL of acetic acid in water was added to adjust the pH. Samples were centrifuged, and the upper aqueous phase transferred to new vials. All samples were dried under an N₂ stream, re-suspended in the appropriate solvent, and transferred to GC-MS vials prior to analysis. PLFA methyl esters were separated, quantified and identified by GC-MS on a Hewlett Packard HP5890 Series II GC interfaced with a HP5972 series mass selective detector. Fatty acids were identified using FID ranges, as described by Ringelberg et al. (1988). Resultant raw data are attached as Appendix C.

3. Total Organic Carbon and Total Nitrogen Analysis

For analysis of total organic carbon and nitrogen, 5 to 10 grams of lyophilized and homogenized samples were pre-treated with 10% HCl to remove inorganic carbon. Samples were loaded onto sample boats and analyzed using a Thermo Electron Corporation FlashEA 1112 series CHN analyzer at the Biosystems Engineering and Soil Science Laboratory at the University of Tennessee. Approximately 50-100 milligrams of sample were analyzed for total organic carbon and nitrogen and reported as a weight percent of the sample.

V. Results

A. Total Organic Carbon

Weight percent TOC for 56 samples and averages for each field site and sample type are presented in Tables 2 and 3. TOC for all samples ranged between 0.01 and 7.2%. Generally hi organic carbon concentrations (0.1 to 7.2%) were found in both active and relict mat samples, whereas lower TOC values (0.01 to 0.15%) occur in soils. Higher TOC values are found in the soils, relict and modern mats samples collected from GVC in comparison to HHC.

TOC distributions for the soils (often including lenses of relict mat) in close proximity to each pond are contoured and are presented in Figure 9a, b, c, and d. At HHC, Big Sister/Little Sister ponds have approximately concentric distributions of TOC, with the exception of an organic-rich swath running from the saddle between Big and Little Sister, to the northeast edge of Little Sister (Figure 9a). Tom Pond has the highest TOC concentrations along the western transect (Figure 9b). This was the most gently sloping of the four transects sampled, and coincided with the location of an ephemeral meltwater stream flowing into the pond and originating from snow-pack. At GVC, Susan Pond had the highest TOC concentrations along the east transect, and was also the most gently sloping transect sampled (Figure 9c). The highest TOC concentrations at Marina Pond were along the east and south transects, with the exception of a “hot spot” along the west transect (Figure 9d). At all ponds, the greatest TOC was found at the very periphery of each pond edge, and typically coincided with relict mat locations.

B. Bulk Carbon Isotopes

Bulk isotope data for field site and sample type, as well as averages for the 56 samples analyzed, are given in Tables 2 and 3, respectively. Isotopically lighter values characterize HHC samples when compared to GVC samples, with an average difference of 6.7‰. The average $\delta^{13}\text{C}$ value for all samples at HHC was -16.5‰ (Table 3). Isotopic values for all HHC samples range between -10.8‰ and -24.0‰ . HHC soils are,

on average, 5‰ lower than average modern mat samples, and 1‰ lower than average relict mat values (Tables 2 and 3). At GVC, the average $\delta^{13}\text{C}$ value for all samples was -11.7‰ (Table 3). Isotopic values for all samples ranged between -6.6‰ and -17.5‰ . The soils, relict mat and modern mat samples had similar average values ranging between -11.7‰ and -12.8‰ (Table 3). Soils at GVC average 2‰ and 0.2‰ lighter than modern and relict mat samples, respectively (Table 3). Relict mat samples averaged approximately 1.1‰ heavier than modern mats (Table 3). At HHC, Big/Little Sister Pond isotopic values for all samples were generally lower than Tom Pond, and at GVC, Susan Pond values for all samples were generally lower than those for Marina Pond. Across site location, isotopic values for Tom and Susan ponds were similar, Big/Little Sister values were the lowest and Marina Pond the highest (Tables 2 and 3).

Distributions of bulk isotope values are shown in Figure 10a, b, c, and d. At HHC, $\delta^{13}\text{C}$ values for relict mat and soils collected from the Big Sister/Little Sister pond site are lower than the modern mat value. Isotopic values get progressively lower with distance from the periphery of the pond (Figure 10a). A seemingly anomalous value (approximately -24‰) occurs at sample BS-RMS 3. This relict mat sample was observed to have mosses utilizing relict mat as substrate at this location. At Tom Pond, $\delta^{13}\text{C}$ values were also lower than the modern mat value of -10.8‰ , with generally lower isotopic values with distance from pond periphery (Figure 10b). Additionally, two lobes of heavier values (values closer to the modern mat isotopic value) occur along the east and west transects.

At GVC, bulk $\delta^{13}\text{C}$ distributions are much different than those at HHC ponds. For Susan Pond, $\delta^{13}\text{C}$ values generally become heavier with distance from pond periphery (Figure 10c). The exception to this is the east transect which exhibits, overall, the lowest values, some of which are lighter than the modern mat value of approximately -15.0‰ . Much heavier values, enriched by a minimum of 5‰, are found on the south transect. Samples collected at pond edges are slightly (0.2‰ to 0.7‰) lower than modern mat. At Marina Pond, $\delta^{13}\text{C}$ values are also progressively more enriched in ^{13}C with distance from pond periphery, but this enrichment is much more exaggerated than at Susan Pond (Figure 10d). All samples, except one, are heavier than the modern mat

value of -10.6‰ . A low value (-14.6‰) is present at sample location MPW-11. This is the only sample collected from Marina Pond that did not contain visible relict mat.

C. Bulk Nitrogen Isotopes

Bulk nitrogen isotope data for 19 samples analyzed are given in Table 2, and Table 3 contains averages of values based on site and sample type. Samples with $\text{TOC} < 0.06\%$ were outside of the analytical capabilities of the EA-IRMS to determine $\delta^{15}\text{N}$. Samples run were either modern mat, relict mat, or had visible quantities of relict mat within the soil matrix. Thus, bulk soil samples were not analyzed. Bulk nitrogen isotopic values ranged across the sample set between $+18.4\text{‰}$ and -0.6‰ . Samples analyzed from HHC were much heavier than those from the GVC, with an average difference of over 9‰ . The average $\delta^{15}\text{N}$ value for all HHC samples was 9.7‰ . At GVC, the average $\delta^{15}\text{N}$ value for all samples was 0.6‰ . Each modern mat collected showed strikingly variable $\delta^{15}\text{N}$ signatures, with values ranging between -0.63‰ and 8.99‰ . Distributions of $\delta^{15}\text{N}$ values were not plotted due to the sparse data, however some trends are apparent. At both HHC and GVC, relict mat samples are enriched in ^{15}N relative to the modern mat isotopic value from each pond.

D. Carbon to Nitrogen Ratios vs. $\delta^{13}\text{C}$ Values

Total organic carbon and nitrogen data (TOC and TN) and C:N ratios for 24 of 56 samples analyzed are reported in Table 2 with averages for each sample and by sample type and location presented in Table 3. In the remaining 32 samples, all of which have $\text{TOC} < 0.1\%$ (with the exception of soil sample WTP-50, a soil sample), fell below the analyzer's TN detection limit. Thus, results were acquired mainly on modern and relict mat samples, with only three soil samples. Previous work has focused on C:N ratios for marine, lacustrine and terrestrial organic matter coupled with bulk $\delta^{13}\text{C}$ values to help delineate sources of organic matter found in soils and sediments. However, as previously mentioned, only three soil samples were analyzed for TN. These results are compared against values of samples collected by Burkins et al. (2001) for soil samples at various locations in the MDV (Figure 11). Values for the three soil samples collected for this

research are isotopically heavier and have a narrower range of C:N ratios than the Burkins et al. (2001) values. Although the number of soil samples is small, their C:N ratios may be indicative of overall trends of the geochemical characterization of soils in close proximity to CP-OM relative to other MDV soils. Values for modern and relict mat samples are also plotted in an effort to further characterize actual CP-OM material. Samples analyzed cluster at the isotopically heavy end of the scale ($> -17\text{‰}$), and are coupled with low (approximately 6 to 17) C:N ratios. These C:N ratios are similar to previous results given for marine, lacustrine and soil-inhabiting cyanobacterial-dominated communities (Acea et al., 2003; Bertilsson et al., 2003; Elser et al., 1995). Soils generally have higher C:N ratios than do modern mats, which generally have higher C:N ratios than relict mat. Relict mats also have the narrowest range of C:N ratios when compared to the other three sample types collected by this study, and compared to the soils collected by Burkins et al. (2001). Two outliers in the present dataset are both for relict mat samples (Figure 11). While one has values similar to the Burkins et al. soil data, the other is a true outlier with the highest C:N ratio within this sample set (31.3) and one of the isotopically heaviest values (-7.64‰).

E. $\delta^{13}\text{C}$ vs. $\delta^{15}\text{N}$ Values

Bulk $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values are presented in Table 2, with averages for each sample and by sample type and location presented in Table 3. Only 19 samples had both values for bulk $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ as the remainder of samples to be analyzed were too low in total nitrogen (<0.004 wt. %) to run nitrogen isotopic analysis. Bulk $\delta^{13}\text{C}$ values were plotted against bulk $\delta^{15}\text{N}$ values for samples where both values were analyzed and are shown in Figure 12. The range of values characteristic of lacustrine moat cyanobacterial proposed by Lawson et al. (2004) is shown by comparison to the measured range of CP-OM derived material, including relict mat samples (Figure 12) measured in this study. As can be seen, the CP-OM data are somewhat different than data given by Lawson et al. (2004) for moat (shallow) lacustrine cyanobacterial mat material. Both a wider range of $\delta^{15}\text{N}$ values and substantially more positive $\delta^{15}\text{N}$ values characterize the CP-OM data when compared to the lacustrine moat mat data. $\delta^{13}\text{C}$ values for the CP-OM falls into a

narrower range, compared to the Lawson et al. data, however their isotopic values are somewhat similar. There is some overlap between the two fields however it appears that relict mat, in particular, is isotopically distinct from relict mat originating from a MDV lacustrine source.

F. PLFA Data

General. Raw data for PLFAs extracted from 35 samples, including modern mat, relict mat, and soil samples, are presented in Appendix C. A total of 64 individual PLFAs were identified within the sample set, with carbon chain-lengths ranging between 14 and 21. PLFAs were present in every sample analyzed. In all samples, there is a clear predominance in mol% of fatty acids having even over odd numbered carbon chain lengths.

Biomass Abundance. Biomass abundances (pmol of PLFA per gram of sample) for every PLFA identified in each sample, and thus a total for each sample, were calculated using the following:

$$((A_{pk}/A_{std}) \times (50 \text{ pmol}/\mu\text{L}) \times \text{dilution factor } (\mu\text{L}))/ \text{sample weight (g)},$$

Where:

A_{pk} = area of the peak for each individual PLFA identified

A_{std} = average area of external, known standard

Dilution factors were known prior to injection for analysis, as were total sample weights. The total biomass of PLFA for each sample was then calculated by summing the biomasses of each PLFA identified in each sample.

Biomass abundances in modern mats were relatively similar at each pond, with the exception of Marina Pond (GVC) which had an order of magnitude greater biomass than the other three modern mat samples (Figure 13). Total viable biomass in relict mat samples was greater than in soils, but less than in modern mat, with values ranging between 3500 and 185500 pmol/g sample (Figure 14). In general, greater biomass abundances are present in relict mat samples from GVC than those from HHC. Total biomass abundances in soil samples were comparable between sites, with most

containing less than 4000 pmol/g sample (Figure 15), however a few exceptions are noted. Samples ETP-23 and SBS-0 from HHC have more than double the biomass of all other soil samples.

Community Composition based on Structural Groups. A community composition approach to PLFA analysis can be examined in two ways. The first and most basic approach is to look at the amount of PLFA representing eukaryotes versus those representing prokaryotes. With the data collected for this research, the sum of pmol/g of sample of polyunsaturated PLFAs as an indicator of the amount of eukaryotes was compared to the sum of pmol/g of normal saturates, mono-branched saturates, terminally branched saturates, and branched monounsaturates as an indicator of the amount of prokaryotes. Prokaryotic taxa clearly dominate the communities in all samples collected (Figure 16), with the exception of sample BS-RMS-3. Since moss was present at this location, it is reasonable that this sample would have a strong eukaryotic signature.

The second, more in-depth approach looks more closely at community composition. This is accomplished by comparing the mol% of total biomass of six different PLFA structural groups. Relative amounts of varying microbial and higher trophic communities within each sample type can therefore be established by comparing relative amounts of these six PLFAs. The six group PLFAs represent certain bacterial consortia, but are not necessarily indicative of algae, fungi, and other taxa that may be present, with the exception of the polyunsaturates. These six groups are interpreted to represent specific organisms, and are shown in Tables 4 and 5 (after Navarrete et al., 2000). Averages for each sample type and each sample type by location were calculated to look at both large-scale and site-to-site trends in community composition using this approach.

All three sample types from both field areas are characterized predominantly by PLFAs for cyanobacterial and gram-negative bacteria (Table 4). The second most abundant group for modern and relict mats is characterized by PLFAs that are ubiquitous (bacteria in general). In soil, the second most abundant group are PLFAs for gram positive bacteria. For modern mats, the third most abundant PLFAs represent cyanobacterial and microeukaryotic consortia, whereas in relict mats it is gram-positive

bacteria. For soils, ubiquitous sources (all bacterial types) comprise the third most abundant PLFAs. All three sample types at both field areas have lesser amounts of PLFAs representing anaerobes, including sulfate reducers and the bacterium *actinomycetes* (Table 4).

In an effort to realize trends that may differ between field sites, averages for each sample type from each field area were also compared (Table 5). For modern mats, the distributions of PLFA biomarkers were nearly identical, with the three highest mol% PLFA being of the same type (Table 5) as described above. However, at GVC, there is a slightly higher mol% of microeukaryotic/cyanobacterial PLFA, and a slightly lower mol% of gram-positive PLFA when compared to HHC (Table 5). Relict mats at both field sites also looked quite similar, with one exception. A larger percentage (nearly 10%) of microeukaryotic/cyanobacterial PLFAs characterize GVC relict mat, while HHC relict mat has a greater abundance of gram positive PLFAs. In addition, GVC soils contained slightly less cyanobacterial/gram negative PLFA biomarkers, but slightly more PLFA biomarkers for sulfate reducing bacteria. PLFAs indicative of anaerobic groups become increasingly more prevalent with distance from active ponds.

By plotting these mol% PLFA groups per sample in graph form, more specific anomalies that would be hidden in the averaging approach were identified (Figures 17 through 20). Looking at specific profiles for each mat sample, BSMM differs greatly from the other three modern mat samples. BSMM is characterized by PLFA for gram-positive bacteria comprising the second highest mol%, with ubiquitous structural group signatures following (Figure 17). In the other three mats, the second and third highest mol% PLFA are characterized by ubiquitous followed by cyanobacterial/microeukaryotic signatures (Figure 17). Whereas PLFA community composition analysis of relict mat samples indicates a predominance of gram-negative/cyanobacterial PLFA, variations in the second and third highest mol% PLFA by sample location was evident (Figure 18). In general, the second and third greatest mol% were identified as ubiquitous and gram-positive PLFA. Variations between which PLFA group was at a greater percentage from location to location do not appear to have a particular trend. Soils at HHC all looked similar with the greatest percentage of PLFAs characterized by gram

negative/cyanobacterial populations followed by gram positive bacteria (Figure 19). Exceptions occur with sample NLS-10, which is characterized by a second highest percentage of PLFA indicative of anaerobic populations, and ELS-7 and WBS-7, which have the second highest percentage of PLFA indicative of cyanobacteria and microeukaryotes. GVC soils look very similar to each other and to the HHC soils, with greatest percentage of PLFAs also characterized by gram-negative/cyanobacterial populations followed by gram positive bacteria (Figure 20). Exceptions here include PCR-2, which is characterized by cyanobacteria/microeukaryotic PLFAs as the second greatest abundance, and PCR-3 which looks nothing like the other samples, and contains the first and second greatest abundances of gram-positive bacteria and gram-negative bacteria/cyanobacteria, respectively (Figure 20).

PLFA Profiles and Specific Biomarkers. Along with the structural approach discussed above, PLFA profiles (i.e., the identification and concentration of specific biomarkers) for modern mats, relict mats and soil samples were constructed to examine specific biomarkers that may be recurring in particular sample types and locations that would not be identified through the structural analysis discussed above. Figure 21a, b, and c illustrates typical PLFA profiles for modern mat, relict mat, and soil samples, respectively. Based on these profiles, the 15 most abundant individual PLFAs within the three sample types were identified, and the distributions of these biomarkers are presented as Figure 22. The microbial communities they represent are labeled so that community distribution could be compared between sample types.

In general, biomarkers for cyanobacterial and algal populations dominate all three sample types. *Cytophaga flexibacter bacteroides* populations are most important in soil samples. Bacterial PLFAs are also important for all three sample types, but there is a slightly greater abundance of biomarkers indicative of gram positive rather than gram-negative bacteria. The largest percentage of gram positive bacterial PLFAs were found in relict mat samples, while the greatest abundance of gram-negative bacterial PLFAs were found in modern mats. Soils contained the least amount of both gram positive and negative bacteria within the three sample types. It is also apparent that PLFA for fungi are present in this analysis (Figure 23).

The PLFA 16:1 ω 7 is a major biomarker for cyanobacterial populations (Brinis et al., 2004; White et al., 1997). Since previous work has shown mat communities of the MDV to be dominated by cyanobacteria, and such populations are also present in soils in this area, this biomarker likely identifies such populations. Figure 24 illustrates the predominance of this biomarker for all three sample types. Individual PLFA profiles for each sample show that this biomarker is a major PLFA in all samples except PCR-3 and BS-RMS 3.

The PLFA 16:0 is a ubiquitous biomarker, and thus its predominance among all three sample types, although expected, cannot be used to identify a particular group of organisms within the community. Collectively, this biomarker is present in cyanobacteria, algae and bacteria, which are the dominant three groups of community types within these samples.

The biomarkers 18:3 ω 3, 18:1 ω 9c and 18:1 ω 7c are associated with cyanobacteria and algae (Brinis et al., 2004). All three biomarkers are present as a high percentage of total biomass in both modern and relict mat and soils, with lesser amounts of 18:3 ω 3 in soils (Figure 23). Current literature has also linked the biomarkers 18:2 ω 6, and i18:0 to fungi and algae (White et al., 1997). Both biomarkers were relatively abundant in all three sample types, with the decreasing amounts from modern to relict mat to soils, respectively.

The PLFA a17:0 and i17:0, which are indicative of the bacterium *cytophaga flexibacter Bacteroides* (D. Hedrick, personal communication), show a marked presence in terrestrial soils (Figure 23), and are a major fatty acid in soil samples collected at distal locations from the pond edges. This shift indicates that *cytophaga flexibacter Bacteroides* populations become more important in distal soil samples. Through analysis of individual PLFA profiles, it was found that a17:0 and i17:0 are major PLFAs particularly for the PCR samples, which were collected from terraces along the northwest side of Pond City at GVC. Soil samples collected from the above identified sample locations occur in moister soils compared to other distal samples. Small quantities (between 1 and 2 mol% of sample) of a17:0 and i17:0 are present in modern and relict mat samples.

The remainder of the 15 most abundant PLFAs are associated with other gram-negative and gram-positive bacteria, and comprise the lowest percentage of the 15 PLFAs. The biomarkers i15:0 and a15:0 are attributed to most gram positive bacteria, including the genera *Bacillus* and *Arthrobacter* in terrestrial soils (White et al., 1997). *Bacillus* has only been identified in geothermal soils of Antarctica (Hudson et al., 1988 and 1989), however, previous work has identified *Arthrobacter* in MDV soils (Cameron et al., 1972).

Several less prominent biomarkers are present within samples (i.e., biomarkers whose mol% of total sample was less than the 15 most abundant PLFA identified in Figure 22), and are of interest as biomarkers of microbial and higher trophic communities. The presence of biomarkers such as br17:1 and 12me16:0 indicates a contribution from anaerobic bacteria. Additionally, i17:1, 10me16:0, and cyclo-17:0 indicates contributions from sulphate-reducing bacteria (Boschker et al., 2002). These biomarkers are more prevalent in soil samples, however, their contribution to the total biomass is small when compared to other biomarkers. The biomarker 10me18:0 is indicative of the bacterium *Actinomyces*, which is a common soil-inhabiting organism (Boschker et al., 2002). This biomarker was found as a considerable mol% of total PLFA (approximately 5%) only in one sample, NLS -10. The biomarker 20:4 ω 6, is also indicative of bryophytes such as mosses, which was found in BS-RMS3. The bulk $\delta^{13}\text{C}$ value of this sample (-24.0‰) is similar to carbon isotope ratios found for boreal mosses, which range between -23.4‰ and -29‰ (Menot and Burns, 2001). In addition, Tom Pond and Big Sister/Little Sister modern mats contained the PLFA 20:5 ω 3 at >1%. This PLFA is a biomarker for diatoms (Findlay and Dobbs, 1993; White et al., 1997), thus suggesting that diatoms play a greater role in the mats at the HHC location. Additionally, 18:3 ω 3 is a good biomarker for the cyanobacteria *nostoc commune*, which makes up a large percentage of the total PLFA(> 10%) for modern mat TPMM. This PLFA is lowest in the modern mat sample BSMM .

VI. Discussion

TOC distributions. TOC values ranged dramatically between sites, and with distance from the pond edges (Tables 2 and 3, Figure 9a, b, c, and d). Soil TOC values were similar to values found by previous workers (Burkins et. al, 2001) at sites apart from coastal ponds and cyanobacterial mats. TOC for modern and relict mats were between 2 and 3 orders of magnitude larger than soil TOC. Through visual inspection, mats were found to have windblown silt and sand incorporated into their structures, and therefore translocated inorganic material likely makes up the bulk of the mat samples. The ponds, which are found within unstratified glacial till in areas subjected to significant wind and aeolian transport of materials, likely act as a trap for such windblown material, which thus becomes part of the growing mat structure.

TOC values were highest at GVC, and likely reflect the greater abundance of relict mat preserved in the soil reservoir at this field site. TOC drops considerably with distance from pond periphery, except where snow melt keeps soils moist. This suggests that moisture content greatly influences the abundance of organic carbon, and microbial activity, within the soil reservoir. Soils at HHC, which are predominantly sands, are likely better drained than the glaciofluvial deposits which contain sands, silts and clays at GVC. The greater the moisture content, the greater the amount of microbial activity, and thus organic carbon present in a given sample. This indicates that GVC soils have a greater capacity for moisture retention, and likely accounts for the higher TOC values there. The highest TOC percentages were found in close proximity to ponds where available moisture was more significant than at locations distant from ponds.

Compared to previous investigations of TOC in MDV soils, pure soil samples were found to have similar, low values. However, the coastal ponds clearly represent “hot spots” for sources of organic carbon and, thus, a greater presence of microbial and higher trophic level communities within the soil reservoir. Higher TOC values in soils coincide with greater quantities of nearby relict mat (i.e., GVC site).

Bulk Carbon and Nitrogen Isotopes. Modern mat bulk $\delta^{13}\text{C}$ values varied from pond to pond (Tables 2 and 3), but all exhibited a narrower range of values (-10‰ to -15‰) when compared to previously studied values of cyanobacterial mats collected from similar depths within Dry Valleys lakes (-2.7‰ to -19.2‰ , Lawson et al., 2004). Lawson et al. (2004) found that variation of species composition within the mats was not the likely source of isotopic variation. Thus, it is assumed that species variation within mats between ponds is not the likely reason for the isotopic variation seen in this study. Lawson et al. (2004) note that all the lakes in their study are supplied by glacial meltwater, and have stratified water columns. The supply of waters from glacial meltwater likely contributes to a greater variability in the sources of organic matter utilized by mat communities within the lakes, creating greater isotopic variability. The more hydrologically closed system of the ponds, when compared to the lakes, likely results in a decreased variety of isotopic signatures seen in the coastal pond mats.

Cyanobacteria use the C-3 (Calvin-Benson) pathway to fix carbon, which discriminates against utilization of ^{13}C (Lawson et al., 2004). However, this would indicate that the isotopic values of modern mats at HHC and GVC should be much lighter (somewhere near -24‰) than values seen. In a dissolved CO_2 limited system cyanobacteria cannot readily discriminate, and will take up additional ^{13}C . Studies of hypersaline microbial mats from the Sinai Peninsula revealed $\delta^{13}\text{C}$ values as heavy as -5.4‰ (Schidlowski & Matzigeit, 1984). Schouten et al. (2001) observed that CO_2 -limited systems can result from high growth rates, low CO_2 availability, and light limitation to photoautotrophs. In the coastal ponds, mat growth has been observed to be explosive during the short summer season, and likely results in a rapid drawdown of available dissolved CO_2 . Additionally, thick mat growth likely adds to light limitation to deeper layers of the community. CO_2 limitation may also result from ponds freezing to the bottom during the long winter season, further limiting amounts of dissolved atmospheric CO_2 in the water. Additionally, Filley et al. (2001) cite alkaline waters (>7.5) as possessing lower dissolved CO_2 concentrations. Based on data collected by Hage (2003), the pH of all four ponds were quite alkaline (8.2-11.7). The short growing season in the MDV results in the necessity for these mats to have high growth rates. This

is likely the dominant factor for the CO₂ limitation observed. It is likely that enriched isotopic values of modern mats from Marina Pond (GVC location, -10.6‰) and Tom Pond (HHC location, -10.8‰) relative to Susan Pond and Big Sister/Little Sister Pond are likely more CO₂ limited, although all four ponds exhibit isotopic signatures characteristic of CO₂ limited systems.

Data presented by Lawson et al. (2004) for relict mat samples from the lakes in their studies found that stable carbon isotope values for relict mats were lower than active mat samples. In general, relict mat sample stable carbon isotopic values from this study were also lower relative to active mat samples from ponds where they were collected. However relict mat samples collected from the proximity of Marina Pond were actually enriched relative to modern mat. Relict mat samples indicate previous pond levels within the system, prior to subsidence and/or ground ice melting and shifts in the hydrologic regime. The heavier values in relict mat samples and soils relative to the modern mat collected from the proximity of Marina Pond may indicate that at earlier stages in the pond's development, the system was actually more CO₂ limited than at present. However, intense microbial reworking of the relict mats by communities present within the material is also a likely reason the relict mat from Marina Pond is so enriched in the heavy isotope. As carbon sources are utilized and recycled by microorganisms, carbon isotopic values are enriched. Where isotopic values are heavier than the original material, therefore, it is likely that this organic matter has been recycled extensively by the present microbial and higher trophic level communities.

Conversely, on average, relict mat stable carbon isotope values are all nearly identical or slightly more negative than (by approximately -1‰) than modern mat values from the proximities of the other three ponds. Such values indicate that less intense microbial reworking is occurring within relict mats at these locations. Many of the relict mat samples collected were moist, and the moister conditions at the Marina Pond relict mat locations may have aided the higher microbial activity suggested by the isotopic compositions of these samples.

Soil samples collected from the proximities of the ponds were found, on average, to be isotopically lighter than modern and relict mat samples, with the exception of soil

samples collected around Susan Pond. The lighter values may indicate differences in bulk source at these locations. Since carbon isotopic values of soils within the study area, and specifically at HHC locations, are similar to marine organic matter isotopic values (lighter than -16‰), it seems reasonable to assume that marine organic matter has a greater presence at this field location. Indeed, its proximity to the coast is greater than at GVC, and the tills present are likely scoured from the Ross Sea. At GVC, sediments likely contain lacustrine and riverine organic matter, and thus slightly heavier carbon isotopic values, when compared to marine source values, as a result of waters from Garwood Glacier melt. Garwood Lake and Garwood River are still present in the GVC field area, however they are no longer hydrologically connected to the ponds in this study. At all ponds but Susan Pond, bulk source at distal locations from pond edge appear to be more lacustrine/marine in origin based on $\delta^{13}\text{C}$ values coupled with $\delta^{15}\text{N}$ values (discussed below).

As previously mentioned, Susan Pond shows heavier values in soil samples relative to both modern and relict mat samples. More intense microbial reworking in soils at Susan pond, as within the relict mat at Marina Pond, may potentially result in heavier isotopic values relative to the modern mat material from this location.

In general, heavier $\delta^{15}\text{N}$ values characterize HHC samples relative to GVC samples. Since the samples analyzed for $\delta^{15}\text{N}$ values excluded soil samples, we can assume that the values are tied inherently to the dominance of cyanobacteria within the mats. Many previous workers have attributed lower $\delta^{15}\text{N}$ values ($<2\text{‰}$) in sediments and sapropels to explosive growth rates, or blooms of nitrogen fixing cyanobacteria during the summer season (Meyers and Bernasconi, 2005, Neumann et al., 2002, Struck et al., 2000). A consequence of enhanced primary production within a system is the limitation of nitrate within the water column, which would normally lower nitrate fractionation during photosynthesis and lead to heavier $\delta^{15}\text{N}$ values. It has been proposed that in systems with nitrogen fixing cyanobacteria, the opposite will occur. In systems such as the coastal ponds, based on the presence of cyanobacterial PLFA and bulk nitrogen isotopic data, nitrogen fixing cyanobacteria appear to dominate the system during explosive growth periods. This process is often coupled with heavier $\delta^{13}\text{C}$ isotopic

values which suggests periods of high primary productivity. Such signatures characterize the modern mat isotopic values at Susan and Marina Ponds of GVC, and to some degree Tom Pond at HHC. These signatures have been found in ancient sapropels (Meyers and Bernasconi, 2005), as well as in recent lake sediments (Neumann et al., 2002), and have also been attributed to such a process. The modern mat from Big/Little Sister pond had the heaviest $\delta^{15}\text{N}$ value of all samples analyzed (8.9‰). Based on PLFA data, the prevalence of diatoms within this pond relative to the other three may be the reason for such a heavy $\delta^{15}\text{N}$ value, as algal sources tend to be heavier than cyanobacterial sources. In general, the relict mat $\delta^{15}\text{N}$ values are slightly heavier than modern mat values at GVC. It has been suggested that $\delta^{15}\text{N}$ values of organic matter tend to become more positive during microbial reworking as microbes discriminate against the light isotope during uptake. Together with higher $\delta^{13}\text{C}$ values, the nitrogen isotope values indicate that some microbial reworking is occurring in the relict mats at GVC, and particularly at Marina Pond. The heavier bulk nitrogen values are also likely indicative of trophic level changes that occur from modern to relict mats, and differ between field sites with the heaviest values at HHC. PLFA evidence suggests that samples containing lower TOC have a higher percentage of gram-positive bacteria. TOC values for relict mats were lower at HHC than GVC, suggesting that as TOC content in relict mats decreases, the amount of microbial recycling increases, resulting in more positive bulk nitrogen isotope values. This effect is especially pronounced at HHC, where TOC values are much lower.

Previous workers found minimal variation in nitrogen isotope values within samples collected from different depths of lacustrine-inhabiting mats (Lawson et al., 2004). The reasons for less variation among the stable nitrogen isotopes of lacustrine inhabiting mats is not clear, but may be related to greater variation of the influence of nitrogen-fixing cyanobacteria in the coastal ponds. As such, $\delta^{15}\text{N}$ coupled with $\delta^{13}\text{C}$ values may be an important proxy for distinguishing CP-OM from lacustrine-derived OM in the future.

Carbon to Nitrogen Ratios and $\delta^{13}\text{C}$ Values. The three soil samples plotted against the previous Burkins et al. (2001) data appear to indicate that soils in close proximity to active coastal ponds and containing CP-OM may tend to be in at the relatively enriched

end of the scale ($>-17\text{‰}$), compared to other soils within the MDV. This is likely an artifact of the CO_2 limited systems from which CP-OM comes. However, such results as presented here may only represent a seasonal-specific signature. It is likely that the degree of CO_2 limitation varies seasonally, reflecting variations in light insolation, hydrologic changes in the ponds, and temperature variations such as greater or fewer days above freezing. Isotopic signatures found in soils in close proximity to coastal ponds may therefore vary from season to season. Additionally, the amount of CP-OM that is being integrated into the soil will also have an effect on the isotopic signatures found. In a field site such as GVC, the relict CP-OM is well-integrated into the soil reservoir, and isotopic values reflect this integration much more than at HHC, where less CP-OM is available to soils as a result of lower biomass and the more transient nature of the landscape at this locale. All of these factors should be taken into account for future soil organic matter studies in close proximity to coastal ponds.

High C:N ratios in soils and the apparent decrease in these ratios from modern to relict mat may be indicative of the relative presence or absence of nitrogen fixing cyanobacteria. If so, this reflects a slightly greater component of these cyanobacteria within the relict mats as compared to modern mats. Two outliers within the dataset were MPN-3 (relict mat) and BS-RMS-3 (relict mat with mosses). While it is unknown why sample MPN-3 has such a high C:N ratio, sample BS-RMS-3 looks like the Burkins et al. (2001) soil data. This $\delta^{13}\text{C}$ value is similar to previously published isotopic values for mosses (Menot & Burns, 2001). The high C:N ratio is typical of higher land plants (Meyers, 1997), and the presence of mosses likely created this signature.

$\delta^{13}\text{C}$ vs. $\delta^{15}\text{N}$ Values. Although overlap appears between the two range fields for lacustrine vs. coastal pond OM, in this instance, they are individually identifiable using bulk isotopic analysis. The main difference between the two data sets presented in Figure 13 is a narrower, but heavier, range of $\delta^{15}\text{N}$ values. $\delta^{13}\text{C}$ values for the CP-OM is virtually indistinct from lacustrine mats. It is therefore assumed that such a difference is a direct result of high activity of nitrogen-fixing cyanobacteria in coastal pond mat communities, which, relatively speaking, do not appear to be as great an influence within lacustrine mat communities. This may be the direct result of greater nutrient inputs to

lacustrine rather than coastal pond systems, as lacustrine systems are often linked directly to glacial meltwater streams (Lawson et al., 2004). The only outlier was again relict mat sample BS-RMS 3 which contained mosses, and its extremely light $\delta^{13}\text{C}$ value shifted its location outside of the proposed CP-OM range.

PLFA Data. The chain lengths identified across the sample set (14 to 21) are indicative of major contributions from cyanobacteria, bacteria, and algal populations such as diatoms. The predominance of even over odd chain lengths of specific biomarkers in the PLFA profiles for most samples analyzed is interpreted as a predominance of gram-negative over gram positive bacteria in the populations as a whole. Furthermore, and perhaps most importantly, the presence of PLFAs in each sample analyzed indicates that viable biomass is present even in samples collected at distal locations from pond perimeters. Additionally, the similarities across sample type profiles thus suggest that CP-OM is making its way into the soil reservoir.

Biomass abundances decrease from modern to relict mat to soils, respectively, indicating that the amount of viable biomass decreases exponentially with distance from the ponds. This likely results from both dissemination of and predation by communities present at each sample type location, with the greatest dissemination and predation occurring at distal soil locations. The greater biomass abundance (pmol of PLFA/g sample) for the Marina Pond modern mat when compared to the other modern mat samples analyzed is likely the result of more favorable growing conditions within this pond. Visual inspection of the pond revealed thicker, more well-established mats at Marina Pond when compared to those present in the other three ponds. Greater biomass abundances for GVC relict mat relative to relict mat from HHC likely result from the established nature of the GVC ponds. Based on the size and shape of the ponds, and the visible amount of relict mat at GVC when compared to HHC, it appears that the GVC CP-OM, and thus the amount of relict mat present, is older, thicker, and more integrated into the soil reservoir. The more transient nature of the HHC landscape results in incorporation of less, or more disseminated, relict mat and leads to lower biomass abundances. While the biomass for soil samples from both field locations were similar, greater total biomass in specific soil samples appear to have been influenced by

proximity to meltwater streams (as for ETP-23) and saturated, rather than dry, sample locations (as for SBS-0).

Structural group analysis (discussed below) indicates that the majority of bacterial consortia in all three sample types were gram-negative/cyanobacterial, but with an increase in gram-positive types within soil samples. Gram-negative bacteria are characterized, in general, as faster growers that can take advantage of rapid nutrient fluxes within a system when compared to gram-positive bacteria. However, gram-positive bacteria are often thought of as “heartier” bacteria when it comes to environmental stress. The increased presence of gram-positive groups in soil samples is not surprising. The soil microenvironment is less buffered from extreme environmental changes that occur throughout the year (i.e., temperature, light, and moisture fluxes) than the pond environment. Most of the bioavailable carbon at soil locations is recalcitrant organic material intrinsic to the glacial till deposits. Therefore, nutrient fluxes are probably low in soils through most of the year, except when soils are relatively warm and moist.

Structural group analysis also indicates that all sample types exhibit the dominance of a three-tiered community system with a clear dominance of cyanobacteria, along with major input from algal and bacterial groups. Shifts in community composition are apparent with respect to sample type, and most usually, distance from pond perimeter. While the modern mats maintain a high input of PLFA from cyanobacterial sources, relict mats are characterized by greater abundances of gram-positive bacteria. Likewise, soil communities have an even greater input of gram-positive PLFAs than relict mats. These populations become more dominant as you move laterally from pond to soil environments, with gram-positive bacterial populations likely thriving and filling niches at greater quantities within the soil reservoir rather than within aquatic environments. Anaerobic bacteria including sulfate-reducing bacteria are most prevalent in soil samples however the reason for this is unknown. Microeukaryotic signatures in modern mats are likely related to aqueous yeasts, and such yeasts have previously been identified within Dry Valleys Lakes. Other microeukaryotic signatures represent higher trophic levels, such as the bryophytes (mosses) visually identified at HHC.

Individual PLFA profiling and analysis of the 15 most abundant PLFAs further supports the structural analysis approach discussed above. Identification of specific (single) biomarkers also indicates a three-tiered community system, with biomarkers specific to cyanobacteria dominating the communities along with lesser amounts of algal and bacterial input. Similarity in PLFA profiles, regardless of sample type, indicate that propagules from modern and relict mats are present in the soil reservoir. Specific biomarker analysis also indicates that diatoms are a more prevalent group within the microbial mat from Big Sister/Little Sister (HHC) pond when compared to the other three mats in this study. This variation shows that coastal pond mat communities differ from location to location with regards to community structure, although the reasons for this are currently unknown. PLFAs specific to fungi were also in all three sample types, although, for the most part, at greater concentrations (mol%) in soils than in modern and relict mat. Previous work has identified fungi as yeasts in both Antarctic soils (Atlas et al., 1978) and within lake microbial mats (Baublis et al., 1991), thus it appears yeasts are likely contributing to these biomarkers.

Relict mat samples collected from the soil reservoir of each pond (i.e., many of the samples collected around Marina Pond such as MPE-8 and MPS-5) had profiles that looked very similar to modern mat profiles. This indicates that the populations present in modern mats can be found as viable biomass within the soil reservoir following exposure and desiccation, but are most prevalent as integrated mat material.

The major contribution of the biomarker for CFB populations, especially in soil samples, was also identified. These bacteria are thought to be major contributors to the digestion of cellulose in oxic environments (Madigan et al., 2003). Cellulose is found in both higher plants and algal materials. Cellulose in Antarctic soils is likely derived from marine and lacustrine algae. Microbial populations that use more recalcitrant material as a food source would be found at greater distances from pond edges as more labile material will be bioavailable at closer pond proximities. Thus the presence of CFB populations should be greater at distal, soil sample locales, and is such in this study. Though present, lower levels of these PLFAs are found at sample locations immediately

adjacent to ponds, indicating that such a community is not as ubiquitous due to proximity to highly labile organics for bacterial and other communities to consume.

An important consideration when looking at PLFA data is to understand the difference between *live* and *viable* organic matter. Within modern and relict mats, the PLFA biomarkers for cyanobacteria and algae likely represent live biomass, which would be present in sample types with greater moisture content. The PLFAs for these two groups found in soils is likely indicative of viable biomass, in the form of CP-OM propagules, rather than living biomass because of the near absence of moisture. Nevertheless, the presence of these biomarkers is further evidence that CP-OM is making its way into the soil reservoir.

Subtle differences in community composition across field areas and from pond to pond within the same field area attest to the complex nature of the ecosystem within the McMurdo Dry Valleys. The reasons for all of these variations are not inherently clear, but point to such variables as source waters, geochemistry of such waters, sources of organic matter within the soil reservoir, moisture levels in soils and relict mat, populations inherently present, and shifts in environmental conditions from season to season.

Differences in CP-OM input between field sites. Based on results presented and visual field inspection, it is clear that CP-OM plays a large role in the amount of organic matter found within the soil reservoir at HHC and GVC. However, the impact of CP-OM is greater at GVC than HHC. During the 2003-2004 field season, the GVC field area was dotted with numerous ponds, and many layers of relict mat were visible within the pond basins and along terraces representing previous water levels. This amount of relict mat was not visible at HHC. This suggests that the ponds at GVC are older and more established than at HHC. The modern mats at GVC also appeared thicker, more well established, and in general to be thriving more than those at HHC. This likely is the result of greater amounts of sequestered organic matter at the GVC location. It may also be due, in part, to variations in aqueous chemistry or availability of carbon in the substrate at the ponds at GVC when compared to HHC that allow for greater growth rates. Additionally, distal soil samples at GVC had PLFA profiles more similar to

modern and relict mat samples than did HHC, and biomass measurements were also generally higher. Isotopic data for soils is also more closely identified with the CP-OM at GVC than at HHC, where distal soils samples begin to have a marine or lacustrine signature.

VII. Conclusions

Bulk carbon isotopic signatures of modern mats from all four ponds suggests the pond systems are CO₂ limited, but especially at Marina and Tom Ponds of GVC. Big Sister/Little Sister did not exhibit as thick of mat growth as the other three ponds, based upon visual observation, and likely had less CO₂ limited conditions as a result of lower growth rates. Explosive growth rates observed in these ponds likely creates a quick drawdown of dissolved atmospheric CO₂, and is the probable driving force behind the CO₂ limited conditions.

Heavier bulk carbon isotopic signatures of relict mats relative to modern mats at both field sites suggests that microbial reworking of labile OM within the relict mats is occurring. This is especially apparent at GVC and indicates greater microbial reworking by active communities within relict mats at this field location. Lower bulk carbon isotopic signatures of soils, compared to that of modern and relict mats, suggests the utilization of marine and lacustrine OM sources at both field sites as less CP-OM, and thus less labile OM, is available with distance from the ponds. Based on stable carbon isotopic signatures, utilization of marine and lacustrine OM sources is most apparent at HHC. The more enriched $\delta^{13}\text{C}$ values in soils at GVC thus point to a greater input of CP-OM to the soil reservoir relative to HHC.

Lighter bulk nitrogen values of modern mats at both GVC ponds, and Tom Pond at HHC, indicate a dominance of nitrogen-fixing cyanobacteria in these locations. PLFA evidence indicates that diatoms appear to play a greater role in the Big Sister/Little Sister modern mat community, imparting heavier bulk nitrogen values. Heavier bulk nitrogen values in relict mats at HHC and GVC relative to the modern mat values indicate trophic level changes and microbial reworking of available OM are occurring in the relict mats, with the heaviest values observed in relict mats from HHC. This again suggests trophic level differences between the communities present in relict mats between the two field sites, as well as differences in OM source utilization.

PLFA data illustrate that modern mat communities are dominated by cyanobacteria, followed by algal, then bacterial communities and the minor presence of fungal communities (likely aqueous yeasts) and anaerobic bacteria. This dominantly three tiered system is similar to other mat communities identified within other aqueous environments of the MDV ecosystem. Evidence of microbial reworking of such material, coupled with high organic carbon contents of the mats relative to surrounding soils, illustrates the important role of CP-OM as a source of labile OM to microbial communities found in soils in close proximity to these ponds. PLFA data for relict mats showed nearly identical community structure to modern mats, indicating that such groups likely survive long periods of desiccation without predation. However a shift towards greater bacterial input (i.e., CFB populations) and lesser algal and cyanobacterial input was seen in soil samples. Since the soil reservoir lacks significant moisture at the two field locations, cyanobacterial and algal PLFAs in soils suggests the presence of propagules, or intact mat material making its way into the soil reservoir through one of two functions: as propagules or *in situ* OM, in the form of relict mat material following a shift in the hydrologic regime of the coastal ponds. At HHC, input of CP-OM in soils is more likely as propagules, while the CP-OM at GVC is more likely *in situ*, relict mat OM. Of the two sites studied here, HHC appears to represent a young coastal pond ecosystem, and thus the CP-OM contribution to the soil reservoir, although clearly important, is not as large a factor as it is at GVC. GVC, on the other hand, appears to be a more established coastal pond ecosystem, and evidence of the active recycling of available CP-OM is evident in the isotopic values for relict mat samples. In addition, unless the relict mat is rooted in place, as was the case at GVC, the amount of CP-OM found in the soils diminishes significantly. It is likely that much of the relict mat exposed at the surface at HHC is disseminated via aeolian transport.

It appears that the shift towards greater presence of bacterial communities in soils is a direct result of the presence of more recalcitrant organics (i.e., intrinsic marine and lacustrine cellulose) at locations distant from the ponds, because highly labile OM in the form of CP-OM (i.e., integrated relict mat material) is intensely reworked in closer

proximity to the ponds. The greater presence of CFBs in soils at HHC attests to the presence of smaller amounts of less highly labile CP-OM at this field location.

Greater TOC values at GVC relative to HHC indicate there is a larger presence of labile OM, in the form of both active microbial communities and deposited OM, at GVC. The soils at GVC consist of glaciofluvial outwash sediments which are less well-drained, and likely contain greater amounts of intrinsic OM compared to the sandy sediments at HHC. The soil TOC content and microbial activity therefore appears to be largely controlled by the amount of available moisture.

Previously published data on bulk sources of OM to MDV soils did not include CP-OM. The limited data presented here indicate that soils in close proximity to coastal ponds are influenced by input of CP-OM, which may be identifiable from other OM sources. Soils containing CP-OM will likely have lower $\delta^{13}\text{C}$ values, where associated with CO_2 limited coastal pond systems. Previous work on chemical signatures of lacustrine and stream cyanobacterial mats indicate that CP-OM is distinct. CP-OM within the MDV is generally characterized by higher $\delta^{13}\text{C}$ values and more variable and generally heavier values of $\delta^{15}\text{N}$, compared to the lacustrine and stream mats. Although the chemical and lipid signatures presented in this study are helpful as a starting point for identifying CP-OM in soils and from other cyanobacterial mats, carbon and nitrogen isotopic signatures likely vary from season to season, reflecting such factors as hydrologic changes, length of growing season, thickness of overlying ice, and input of nutrients due to seasonal meltwaters.

The isotopic and geochemical data presented here can be used in future work of bulk organic matter source identification. Initial lipid work provides a starting point for identifying microbial composition in varying ecosystems within the MDV. PLFA profiles add to the understanding of variations between isotopic signatures seen in this study, and indicate a complex interaction between community types present (i.e., greater nitrogen fixing cyanobacteria vs. greater diatom input), geochemical processes that occur at varying locations (i.e., greater CO_2 limitation due to more explosive growth), and microbial processes (i.e., amount of microbial reworking) that occurs in various sample types and locations.

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Appendices

Appendix A

Table 1.

Descriptions of samples and sample locations. Does not include sample descriptions for all samples run for PLFA analysis.

Site	Sample ID*	Transect/Location	Sample Type**
<i>Hjorth Hill Camp</i>	SBS-0	south	soil/D
Big Sister Pond	SBS-8	south	soil/W
77°30'36" S	SBS-14	south	soil/D
163° 49'56" E	EBS-3	east	soil/D
	EBS-6	east	soil/D
	WBS-3	west	soil/W
	WBS-7	west	soil/D
	BS-RMS3	3m south of w transect	relict mat
	BSMM	pond	modern mat
Little Sister	NLS-0	north	soil/W
77°30'36" S	NLS-6	north	soil/D
163° 49'56" E	NLS-10	north	soil/D
	ELS-3	east	soil/D
	ELS-7	east	soil/D
	WLS-3	west	soil/W
	WLS-7	west	soil/D
	BS-2	saddle between ponds	relict mat
	BST2 (0-5cm)	saddle between ponds	relict mat
	BST2 (5-7cm)	saddle between ponds	relict mat
Tom Pond	NTP-8	north	soil/W
77°30'39" S	NTP-21	north	soil/W
163°49'49" E	STP-4	south	soil/W
	STP-10	south	soil/D
	ETP-0	east	relict mat/W
	ETP-17	east	soil/D
	ETP-23	east	soil/W
	WTP-0	west	relict mat/W
	WTP-20	west	soil/D
	WTP-50	west	soil/W
	TPMM	pond	modern mat

* Numbers following sample ID letters indicate distance in meters from pond edge along transect.

** W and D stand for wet and dry, respectively

Table 1., Continued

Site	Sample ID*	Transect/Location	Sample Type**
<i>Garwood Valley Camp</i>	MPN-0.5	north	relict mat/W
Marina Pond	MPN-3	north	relict mat/D
78°02'06" S	MPS-3	south	relict mat/W
164°19'19" E	MPS-5	south	relict mat/W
	MPE-0	east	relict mat/W
	MPE-4	east	relict mat/D
	MPE-8	east	relict mat/D
	MPW-0	west	relict mat/W
	MPW-6	west	relict mat/D
	MPW-11	west	soil/D
	MPMM	pond	modern mat/W
Susan Pond	SPN-4	north	soil/D
78°01'59" S	SPN-15	north	soil/D
164°19'58" E	SPS-4	south	soil/D
	SPS-20	south	soil/D
	SPE-0	east	relict mat/W
	SPE-5	east	soil/D
	SPE-10	east	soil/D
	SPW-0	west	relict mat/W
	SPW-4	west	soil/D
	SPW-11	west	soil/W
	SPMM	pond	modern mat/W
Met Station Pond	GMM-1	adjacent to west	relict mat/D
Pond City	PCR-1	first terrace above west transect of Marina Pond	soil/D
	PCR-2	second terrace above west transect of Marina Pond	soil/D
	PCR-3	third terrace above west transect of Marina Pond	soil/D

* Numbers following sample ID letters indicate distance in meters from pond edge along transect.

** W and D stand for wet and dry, respectively

Table 2.

Carbon and nitrogen bulk and isotopic compositions of soils, relict and modern mat samples collected from Hjorth Hill and Garwood Valley Camp, McMurdo Dry Valleys, Antarctica.

Site	Sample	TOC (wt. %)	TN (wt. %)	C:N	Bulk $\delta^{13}\text{C}$	Bulk $\delta^{15}\text{N}$
Hjorth Hill Camp	SBS-0	0.048	BDL		-18.987	
Big Sister Pond	SBS-8	0.051	BDL		-16.022	
77°30'36" S	SBS-14	0.028	BDL		-20.109	
163° 49'56" E	EBS-3	0.012	BDL		-17.538	
	EBS-6	0.041	BDL		-17.517	
	WBS-700	0.039	BDL		-19.967	
	WBS-300	0.068	0.004	16.414	-15.279	
	BS-RMS3	0.207	0.008	26.948	-24.039	11.48
	BSMM	1.810	0.240	7.542	-14.296	8.99
Little Sister Pond	NLS-0	0.055	BDL		-13.661	
77°30'36" S	NLS-6	0.072	BDL		-23.146	
163° 49'56" E	NLS-10	0.038	BDL		-20.27	
	ELS-3	0.045	BDL		-15.925	
	ELS-7	0.101	BDL		-17.187	
	WLS-3	0.047	BDL		-15.299	
	WLS-7	0.028	BDL		-15.366	
	BS-2	0.807	0.092	8.783	-15.1	14.82
	BST2 (0-5CM)	1.378	0.176	7.817	-15.558	
	BST2 (5-7CM)	0.761	0.100	7.631	-16.793	18.4
Tom Pond	NTP-8	0.031	BDL		-15.11	
77°30'39" S	NTP-21	0.039	BDL		-19.573	
163°49'49" E	ETP-0	0.055	BDL		-14.12	
	ETP-17	0.043	BDL		-18.158	
	ETP-23	0.027	BDL		-12.132	
	STP-4	0.027	BDL		-12.841	
	STP-10	0.032	BDL		-15.486	
	WTP-0	0.794	0.089	8.904	-12.157	10.29
	WTP-20	0.070	BDL		-15.232	
	WTP-50	0.100	0.004	25.091	-14.858	
	TPMM	2.060	0.130	15.898	-10.877	1.78

Table 2., Continued

Site	Sample	TOC (wt. %)	TN (wt. %)	C:N	Bulk $\delta^{13}\text{C}$	Bulk $\delta^{15}\text{N}$
<i>Garwood Valley Camp</i>	MPN-0.5	7.454	0.955	7.808	-8.587	0.860
Marina Pond	MPN-3	0.126	0.004	31.297	-7.635	1.530
78°02'06" S	MPS-3	2.692	0.274	9.816	-8.877	2.210
164°19'19" E	MPS-5	1.452	0.133	10.920	-7.384	2.270
	MPE-0	4.174	0.490	8.510	-10.832	0.810
	MPE-4	3.491	0.398	8.760	-7.375	1.970
	MPE-8	2.005	0.226	8.855	-7.246	-0.610
	MPW-0	0.748	0.063	11.928	-9.326	2.640
	MPW-6	7.509	0.801	9.376	-6.659	-0.420
	MPW-11	0.059	BDL		-14.668	
	MPMM	7.196	0.932	7.721	-10.637	-0.640
Susan Pond	SPN-4	0.039	BDL		-15.597	
78°01'59" S	SPN-15	0.044	BDL		-14.513	
164°19'58" E	SPS-4	0.031	BDL		-10.027	
	SPS-20	0.029	BDL		-10.528	
	SPE-0	7.972	1.176	6.781	-15.271	0.020
	SPE-5	0.054	BDL		-16.361	
	SPE-10	0.058	0.004	14.487	-15.502	
	SPW-0	4.223	0.491	8.602	-15.775	0.360
	SPW-4	0.033	BDL		-13.603	
	SPW-11	0.046	BDL		-9.851	
	SPMM	4.626	0.386	11.974	-15.028	-0.370
Additional Samples	PCR-1	0.022	BDL		-17.523	
	PCR-2	0.023	BDL		-6.823	
	PCR-3	0.039	BDL		no	
	GMM-1	10.666	1.109	9.616	-11.475	

Table 3.

Averages of TOC, TN, C:N ratios, $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ for samples by sample type, pond location, field site, and as both field sites averaged together.

Site/Pond	Sample Type	TOC (wt. %)	TN (wt. %)	C:N	Bulk $\delta^{13}\text{C}$ (‰)	Bulk $\delta^{15}\text{N}$ (‰)
HHC - Big/Little Sister	all three types	0.313	0.103	12.52	-18.45	13.42
	soils only	0.048	0.004	16.41	-17.48	NA
	relict mat only	0.788	0.094	12.79	-17.87	14.90
HHC - Tom Pond	all three types	0.298	0.074	16.63	-14.59	6.04
	soils only	0.046	0.004	25.09	-15.42	NA
	relict mat only	0.425	0.089	8.90	-13.14	10.29
HHC - both sites	all three types	0.306	0.089	14.58	-16.52	9.73
	soils only	0.047	0.049	14.60	-17.68	NA
	relict mat only	0.607	0.092	10.85	-15.51	12.60
	modern mats	1.935	0.185	11.72	-12.59	5.39
GVC - Marina Pond	all three types	3.355	0.428	11.50	-9.02	1.06
	soils only	0.059	BDL	ND	-14.67	NA
	relict mat only	3.295	0.372	11.92	-8.21	1.25
GVC - Susan Pond	all three types	1.559	0.514	10.46	-13.82	0.19
	soils only	0.042	0.004	14.49	-13.25	NA
	relict mat only	6.097	0.833	7.69	-15.52	0.19
GVC - both sites	all three types	2.457	0.684	10.53	-11.73	0.63
	soils only	0.051	0.004	14.49	-13.07	NA
	relict mat only	4.696	0.771	9.74	-11.74	0.72
	modern mats	5.911	0.659	9.85	-12.83	-0.32
HHC and GVC Combine	all three types	1.381	0.386	12.55	-14.13	5.18
	soils only	0.049	0.026	14.55	-15.37	NA
	relict mat only	2.652	0.431	10.30	-13.62	6.66
	modern mats	3.923	0.422	10.78	-12.71	2.53

Numbers identified in bold and italics are not averages, but represent a single sample.

NA = not analyzed

Table 4.

Community composition structural approach by sample type. Averages represent mol% of total PLFA in each group for that particular sample type. Numbers were calculated using the total mol% of each PLFA group per sample divided by total biomass of the sample. Averages were then calculated for each sample type.

PLFA Type	Representative Group	Sample Type		
		Modern Mat	Relict Mat	Soils
Monosaturates	Gram Negative/Cyanobacteria	47.22	47.20	43.30
Normal Saturates	ubiquitous/all bacteria	19.37	16.79	10.61
Polysaturates	Cyanobacteria/Microeukaryotes	15.29	11.91	8.44
Terminally Branched Saturates	Gram-positive bacteria	12.68	15.44	20.92
Branched monosaturates	anaerobes (sulfate reducers)	3.09	4.79	6.72
Mid-Chan Branched Saturates	anaerobes (actinomycetes)	1.35	2.26	6.29

Table 5.

Community composition structural approach by sample type and field area. Averages represent mol% of total PLFA in each group for that particular sample type at that particular field location. Numbers were calculated using the total mol% of each PLFA group per sample divided by total biomass of the sample. Averages were then calculated for each sample type at both the HHC and GVC field locations.

PLFA Type	Representative Group	Sample Type and Field Location					
		Modern Mat		Relict Mat		Soils	
		HHC	GVC	HHC	GVC	HHC	GVC
Monosaturates	Gram Negative/Cyanobacteria	48.26	46.18	49.25	43.62	45.30	41.30
Normal Saturates	ubiquitous/all bacteria	18.06	20.68	16.59	17.14	10.71	10.51
Polysaturates	Cyanobacteria/Microeukaryotes	14.35	16.22	8.68	17.56	7.25	9.63
Terminally Branched Saturates	Gram-positive bacteria	13.53	11.82	16.24	14.04	19.99	21.86
Branched monosaturates	anaerobes (sulfate reducers)	2.85	3.33	5.13	4.21	6.24	7.20
Mid-Chan Branched Saturates	anaerobes (actinomycetes)	1.80	0.91	2.43	1.95	6.50	6.08

Appendix B

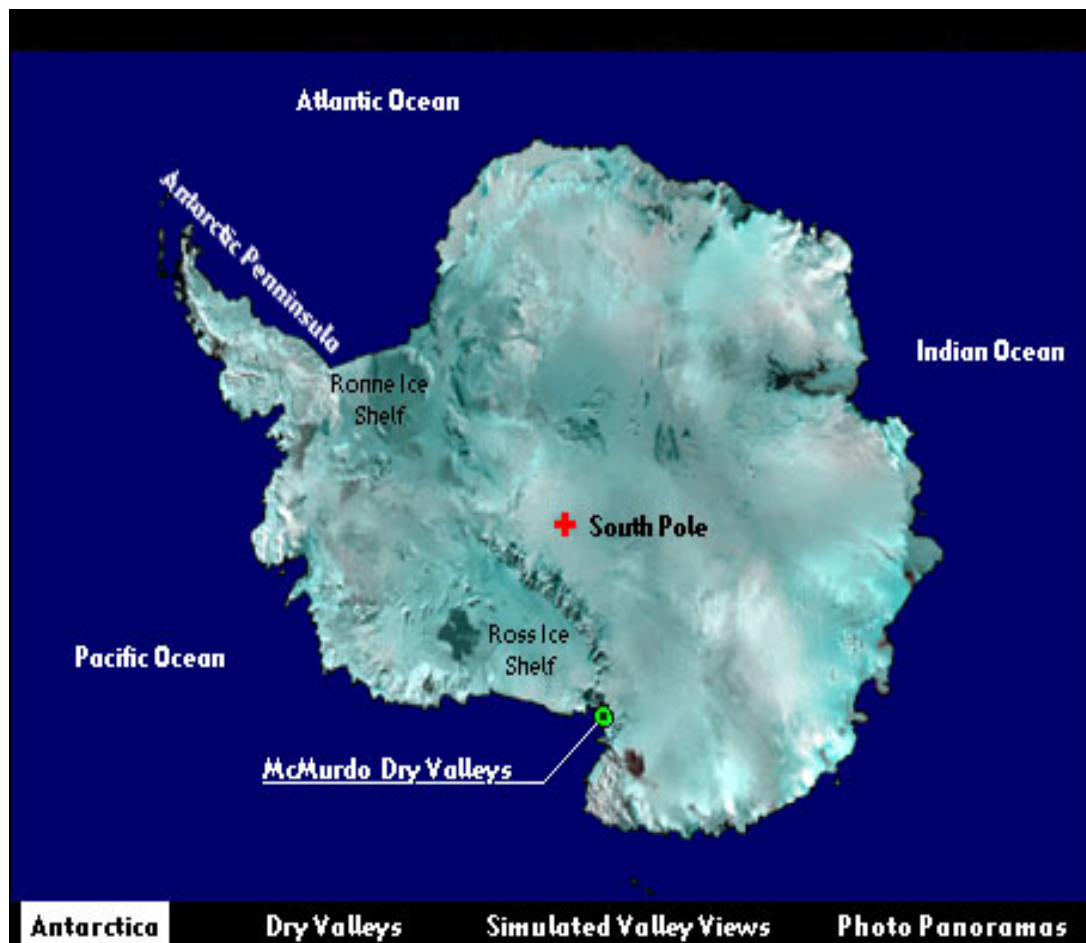


Figure 1. Map of the continent of Antarctica showing the location of the McMurdo Dry Valleys. The area is indicated as a green circle at the bottom of the picture. From <http://huey.colorado.edu/77degreesSouth/Images/map00.jpg>

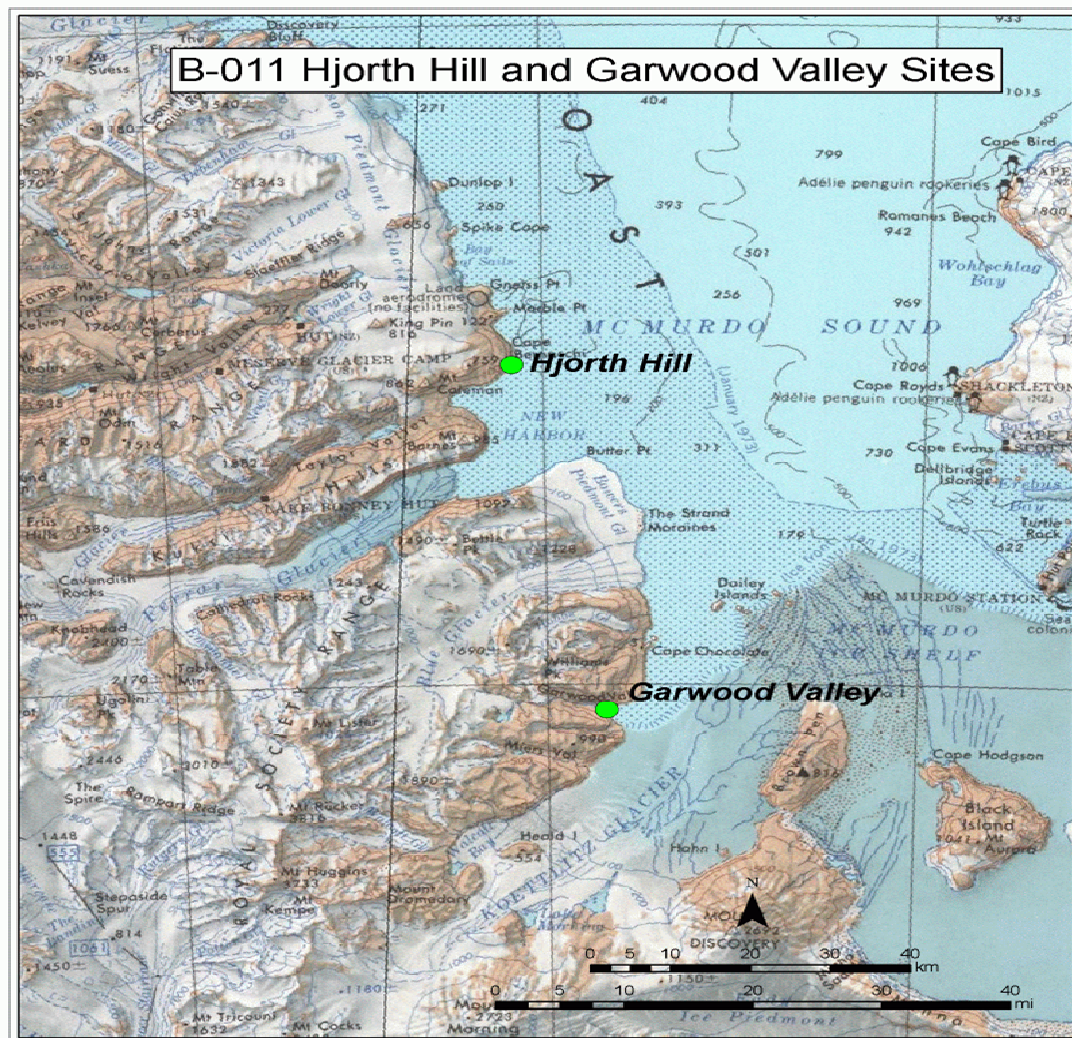


Figure 2. Locations of two field sites, Hjorth Hill Camp (HHC) and Garwood Valley Camp (GVC). Taken from <http://huey.colorado.edu/diatoms/about/maps.php>



Figure 3. Photo of Big Sister/Little Sister Pond at HHC looking north. Notice the saddle in the center that separates the two ponds.



Figure 4. Photo of Tom Pond at HHC looking east. Figures in center for scale. The pond surface was frozen at this date. Notice the meteorological station on far left.



Figure 5. Photo of Marina Pond (in foreground) at GVC looking south. Backpack included for scale. Notice the thick mat growth visible in this pond.

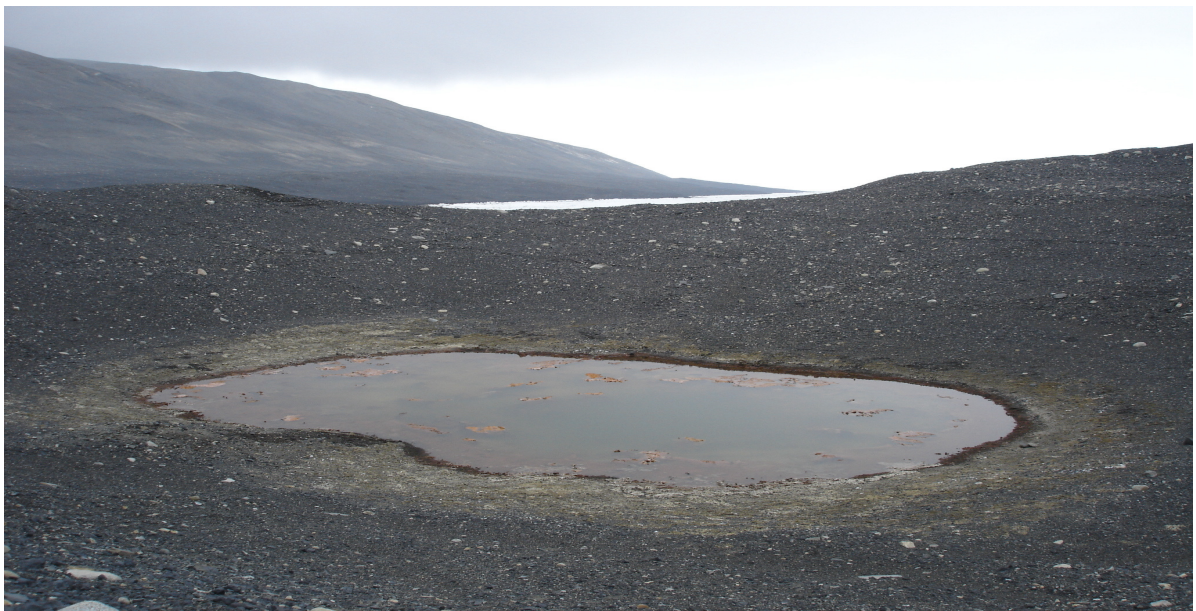


Figure 6. Photo of Susan Pond at GVC looking northeast. Relict mat is visible in a ring around the outer perimeter of the pond, and mats can be seen growing at the surface.

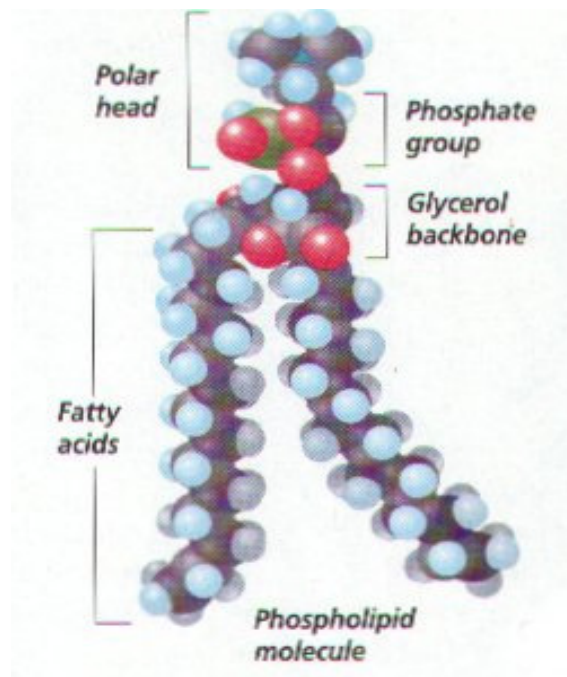


Figure 7. Diagram of a PLFA structure showing polar phosphate head. Taken from <http://www.sirinet.net/~jgjohnso/biochemistry.html>

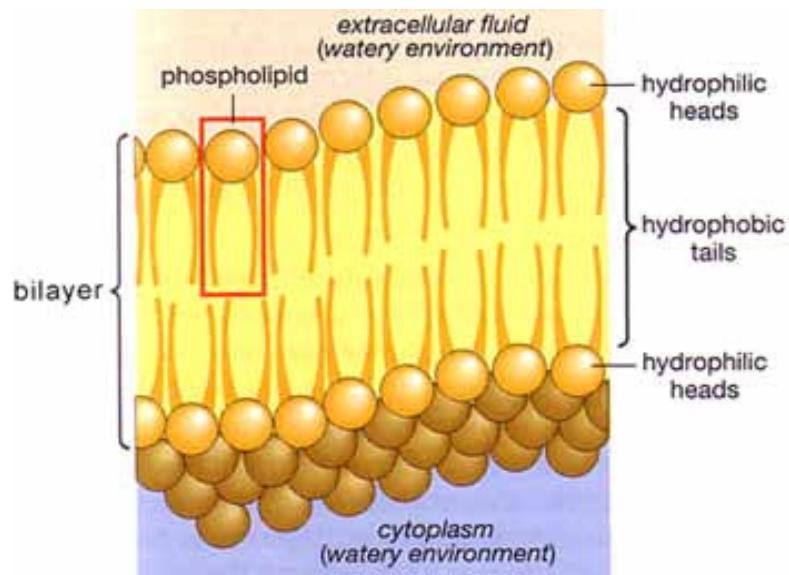


Figure 8. Diagram of PLFA bilayer membrane structure. Taken from http://lhs.lps.org/staff/sputnam/Biology/U3Cell/Unit3Notes_cell.ht

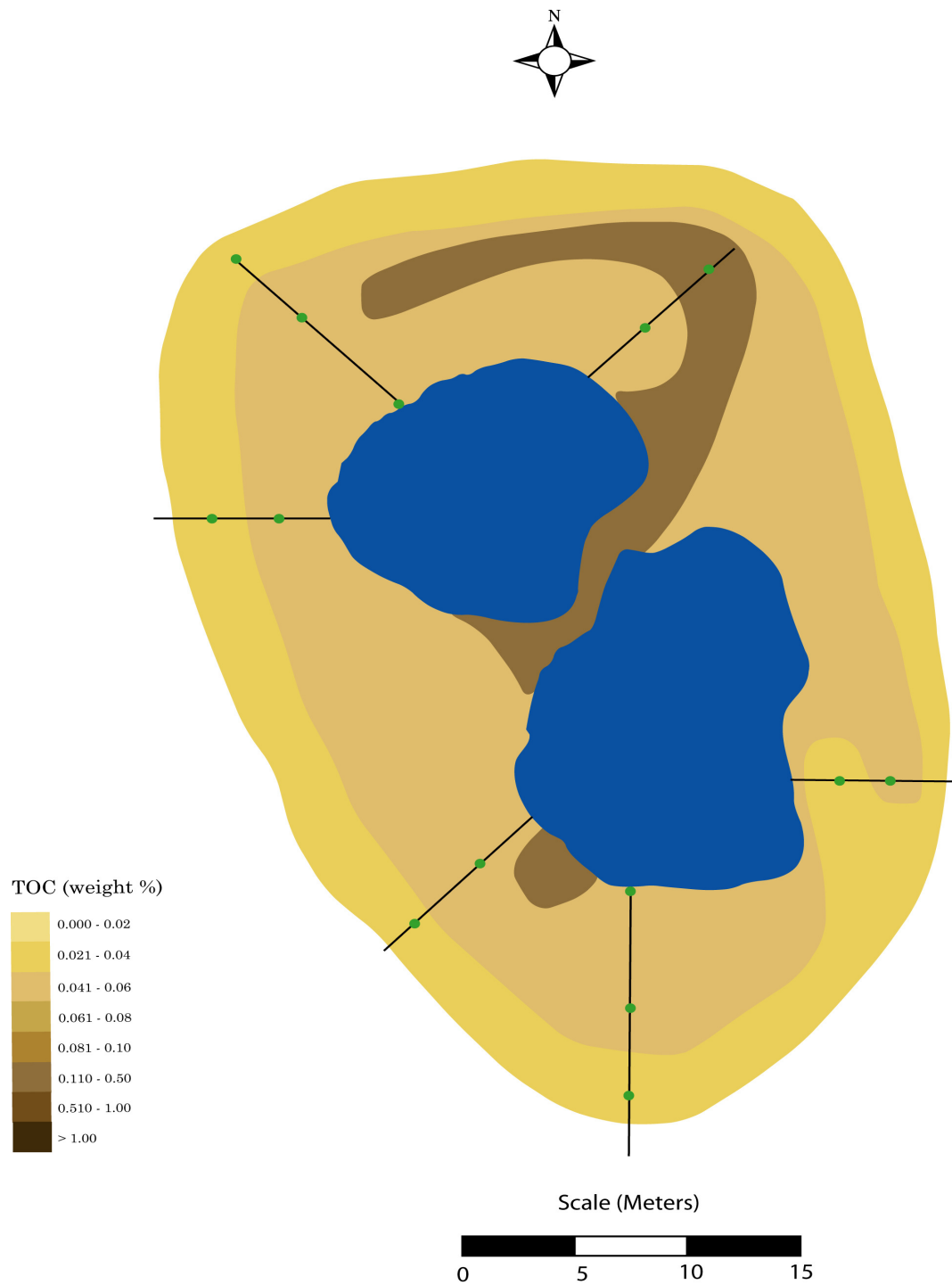


Figure 9. Total organic carbon content distribution at (a) Big Sister/Little Sister Ponds (HHC). Contours established based on TOC values at sample locations, shown in green, along transects. Sample locations and pond perimeters plotted using GPS data collected in the field.

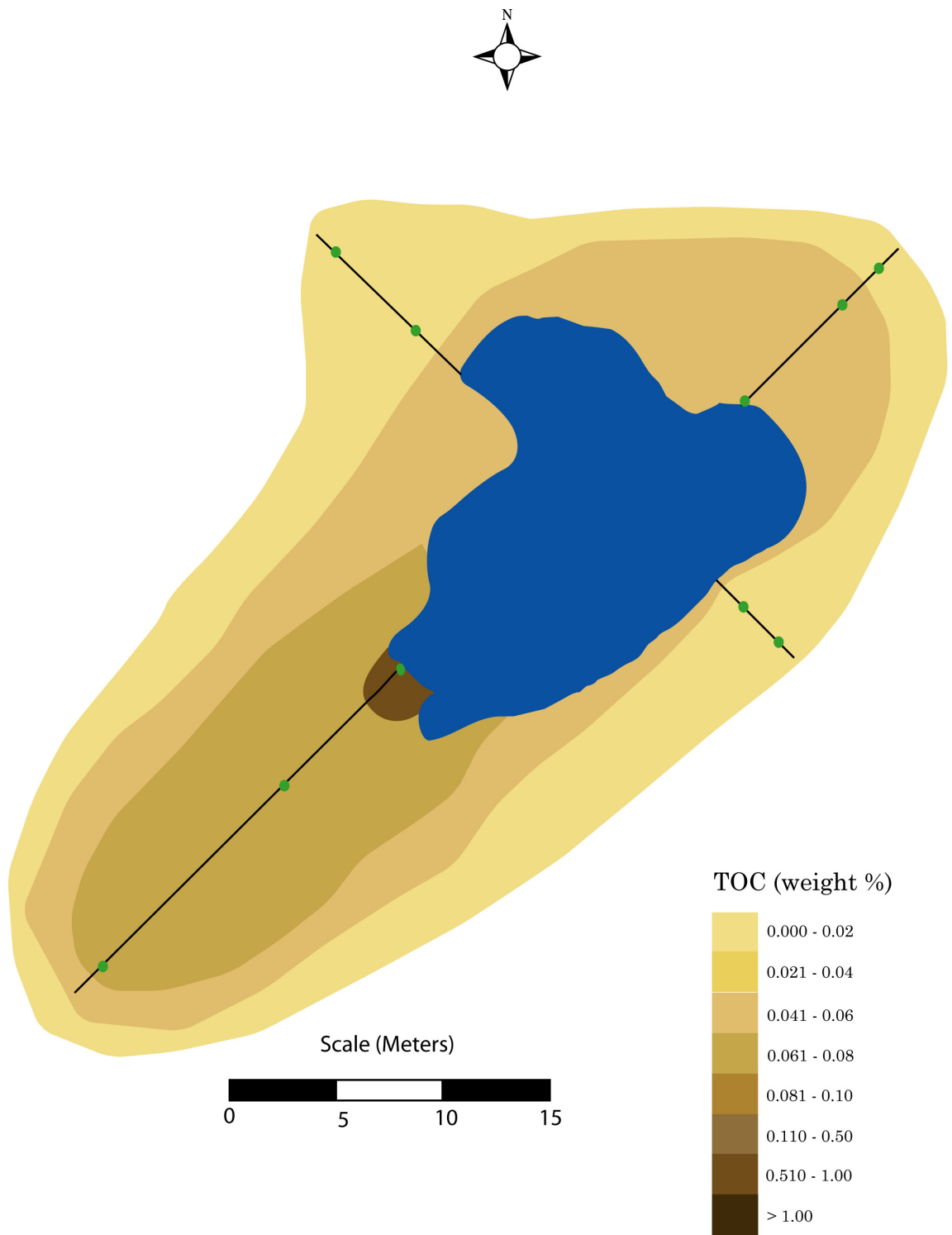


Figure 9., Continued. (b) Tom Pond (HHC).

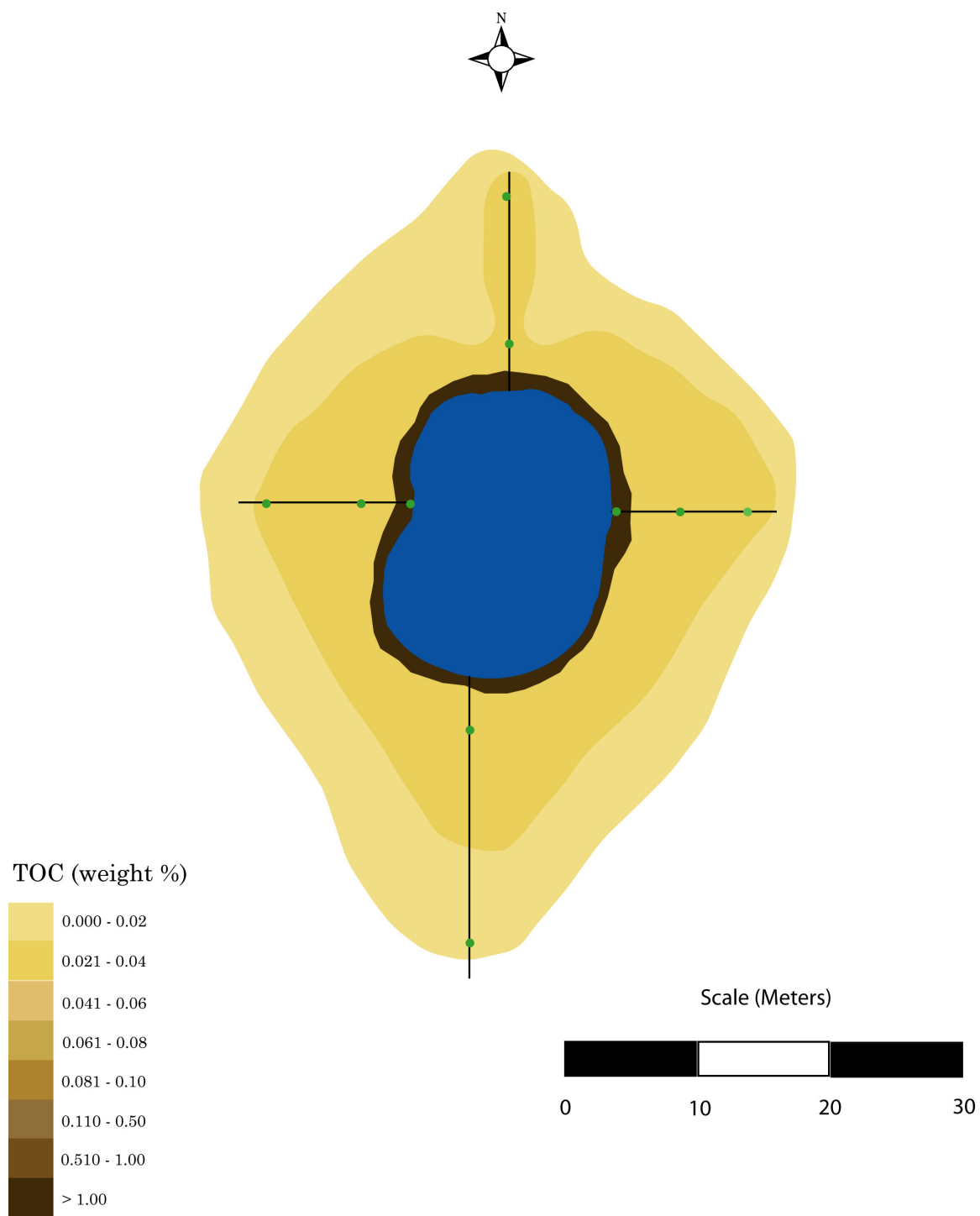


Figure 9., Continued. (c). Susan Pond (GVC). .

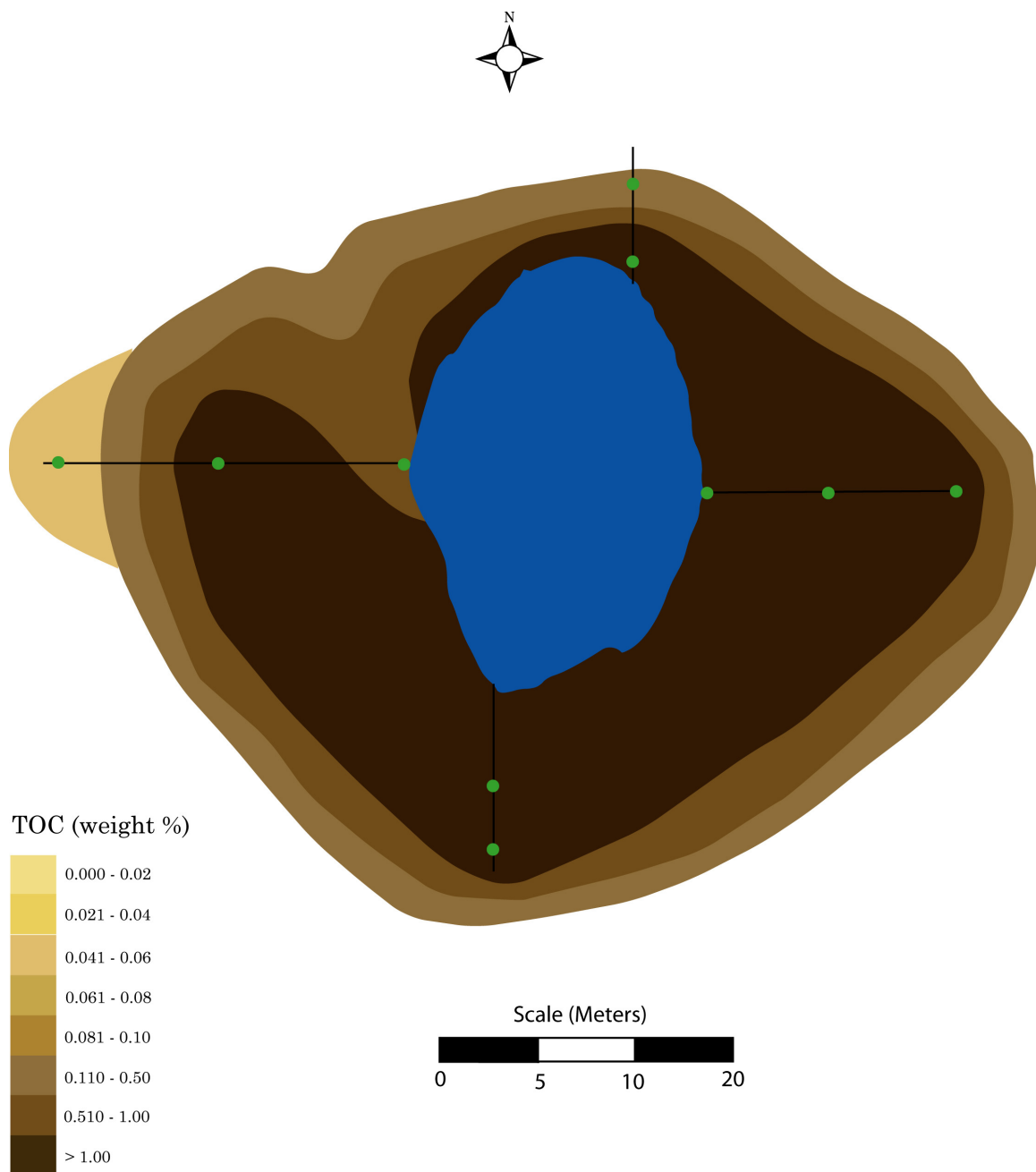


Figure 9., Continued. (d). Marina Pond (GVC).

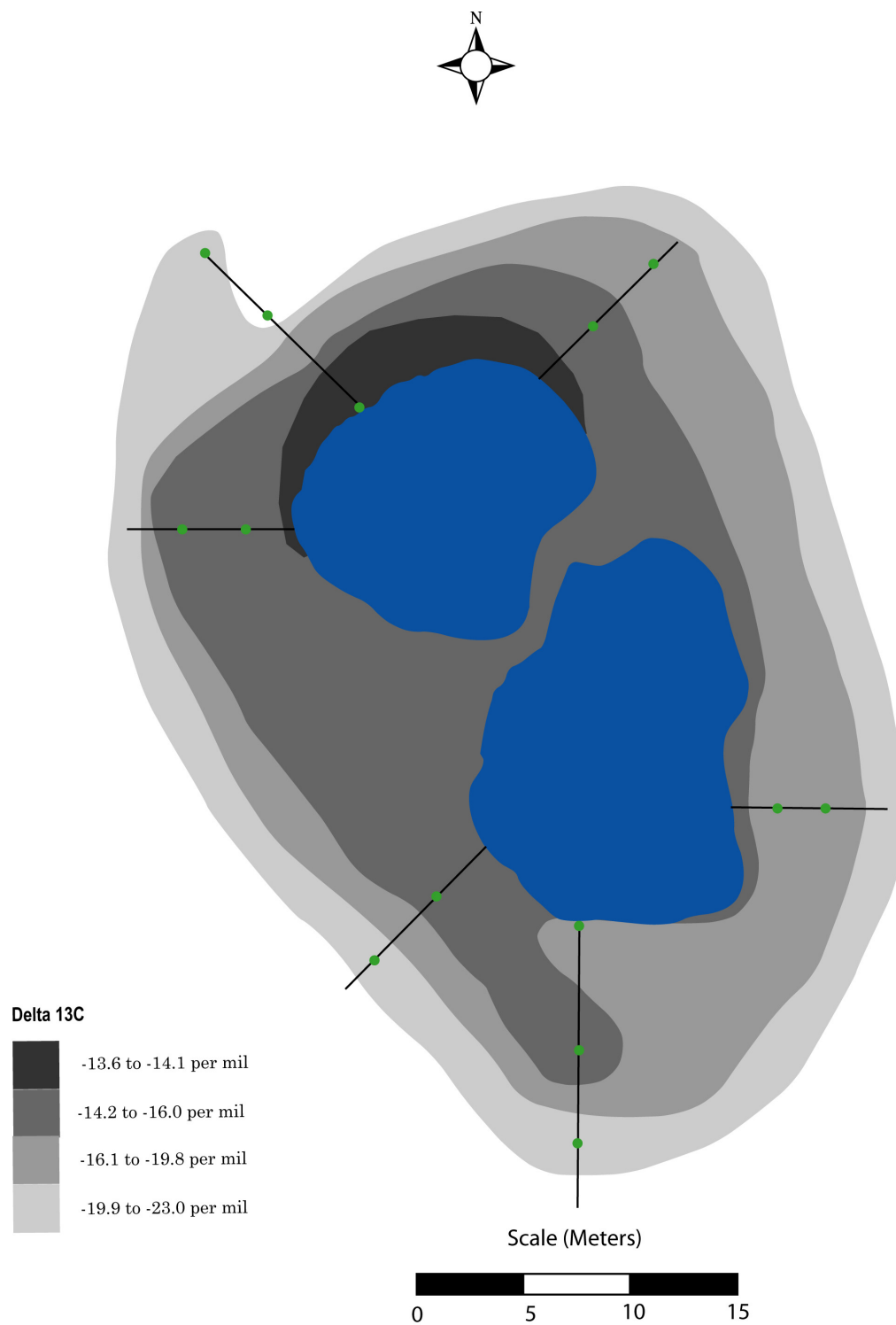


Figure 10. Distributions of stable carbon isotopes at (a) Big/Little Sister ponds (HHC). Contours established based on isotopic values at sample locations, shown in green, along transects. Sample locations and pond perimeters plotted using GPS data collected in the field.

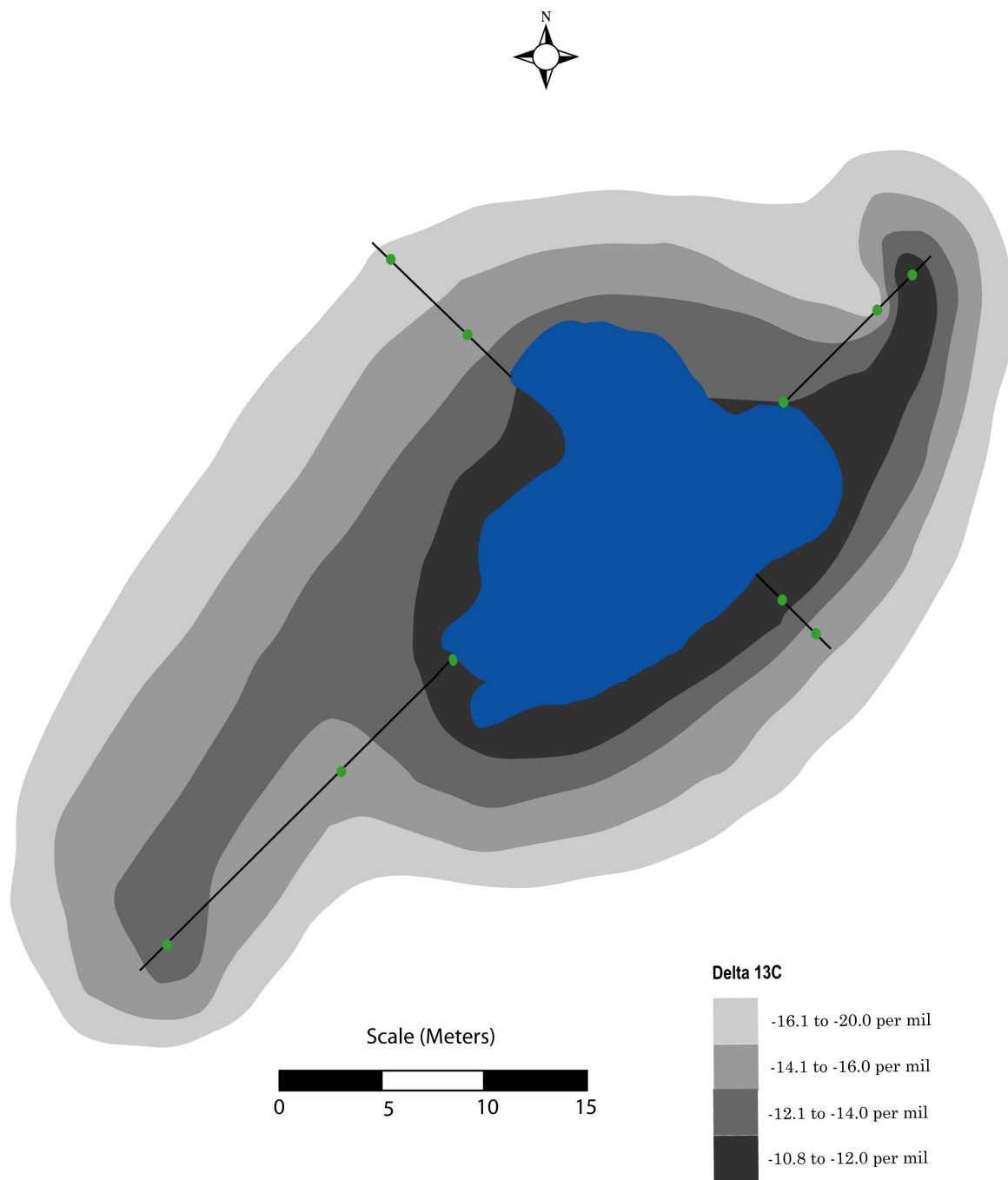


Figure 10., Continued. (b). Tom Pond (HHC).

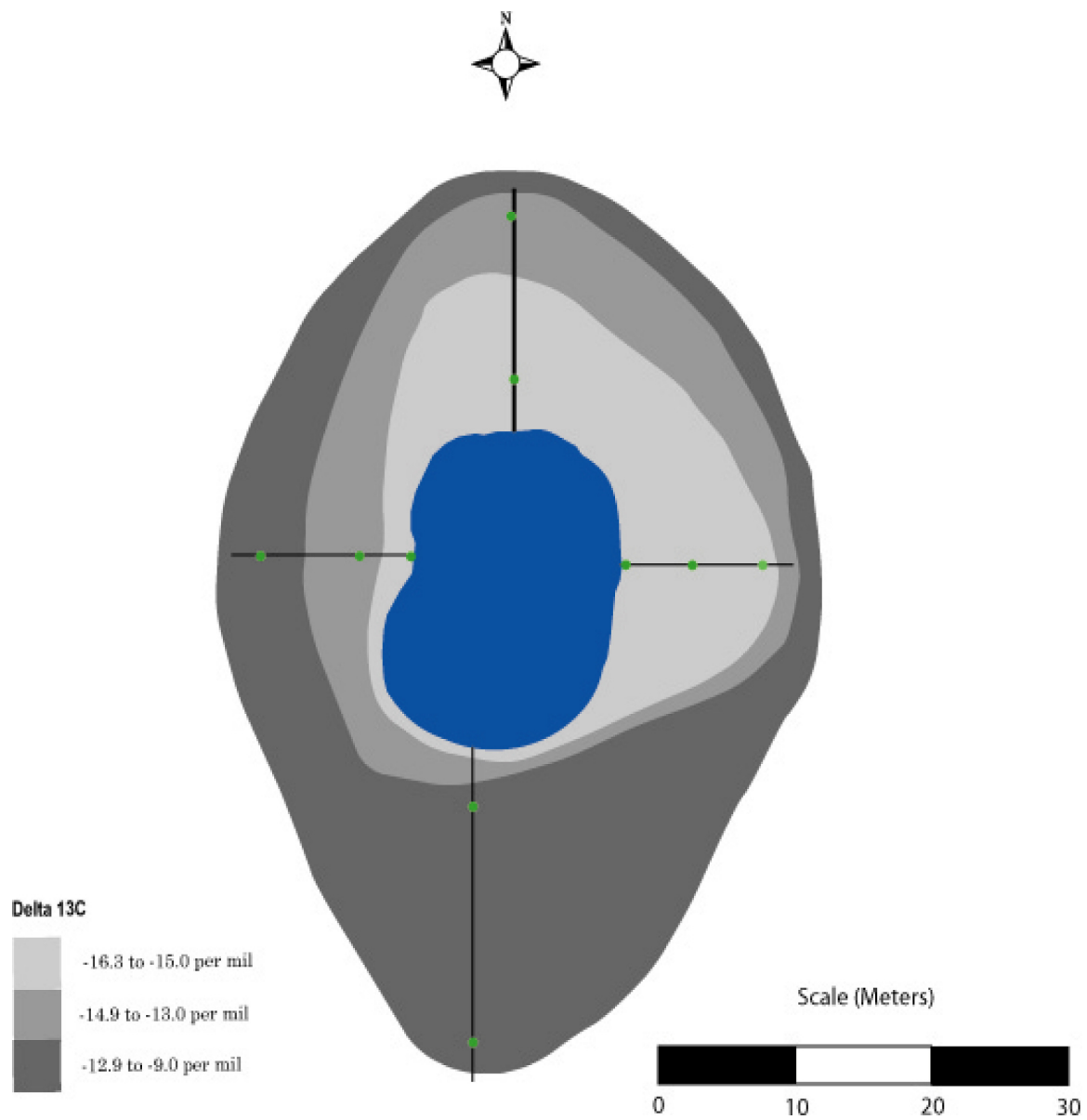


Figure 10., Continued. (c). Susan Pond (GVC).

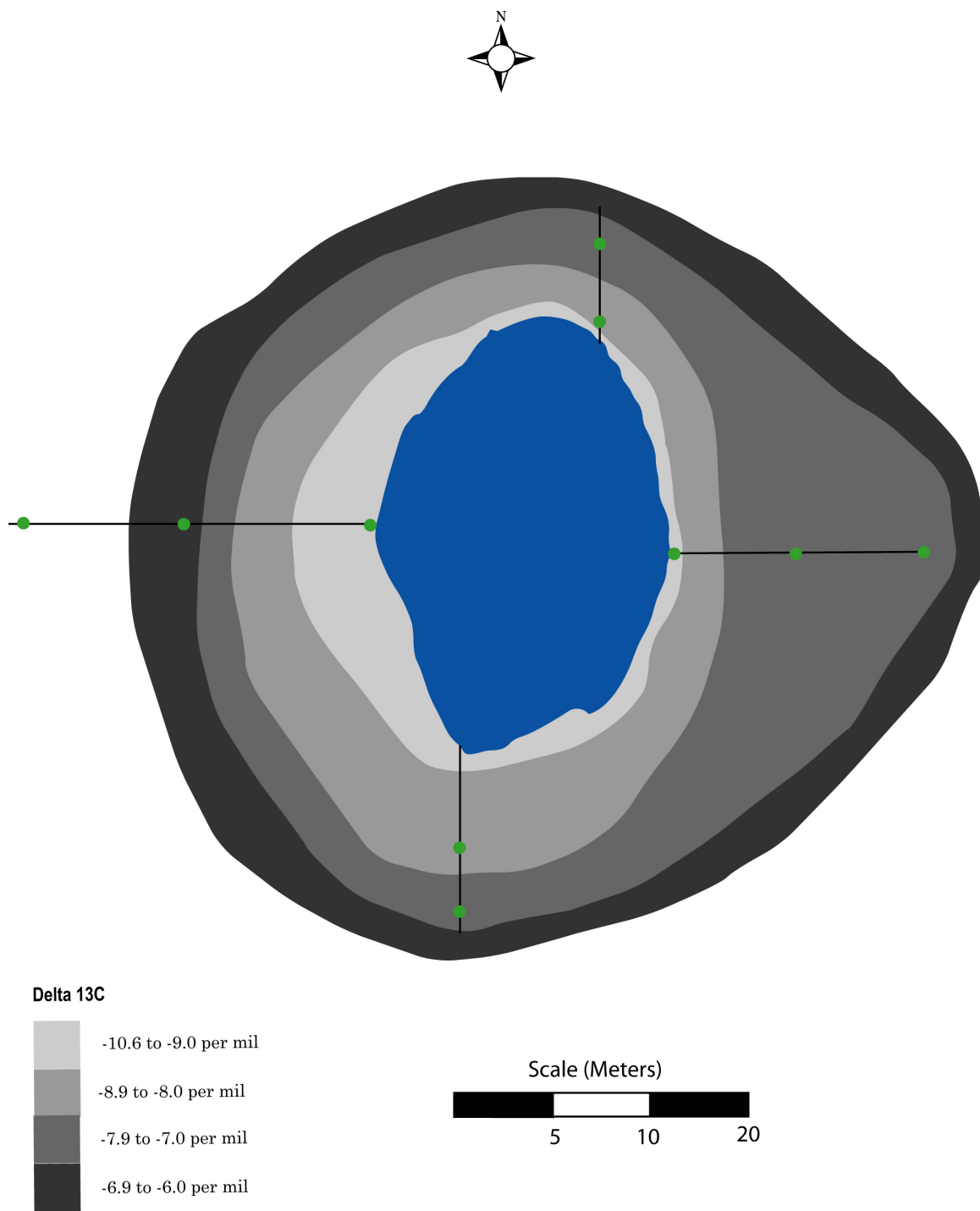


Figure 10., Continued (d). Marina Pond (GVC).

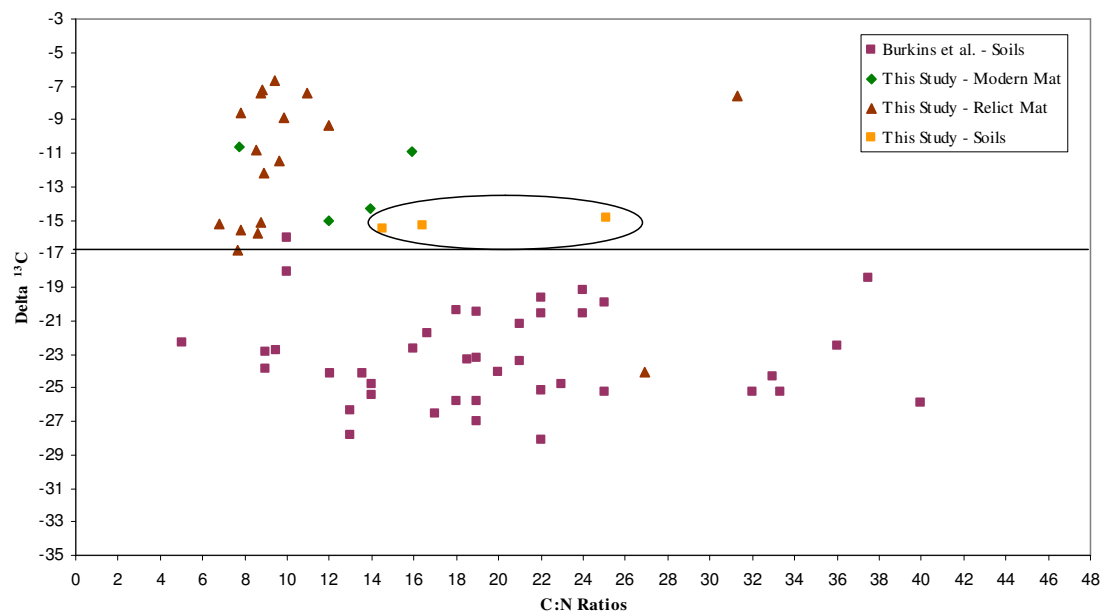


Figure 11. $\delta^{13}\text{C}$ vs. C:N Ratios for all three sample types and compared to previous Burkins et al. (2001) soil data.

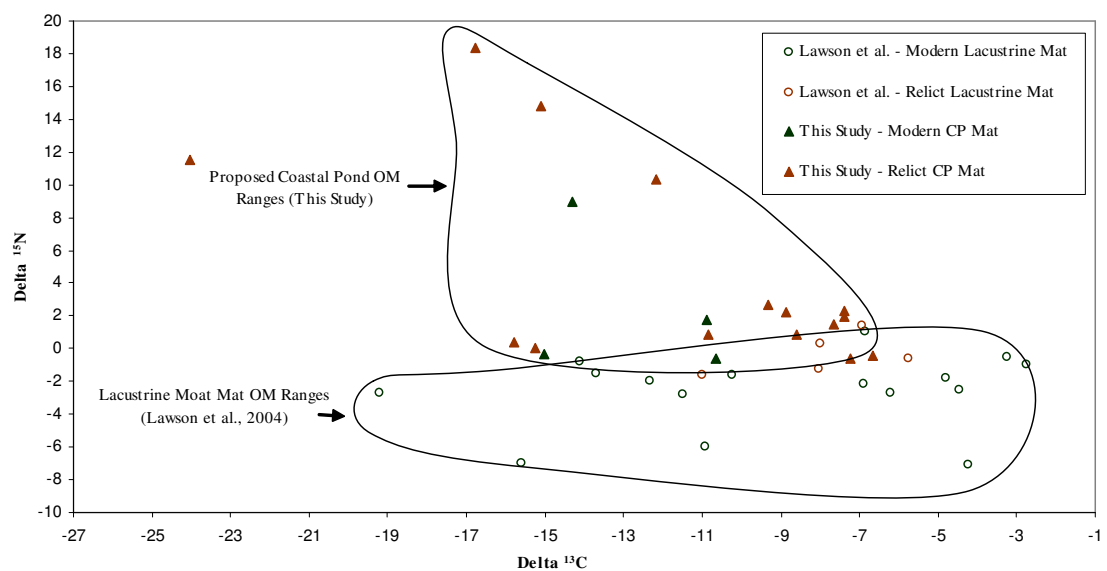


Figure 12. $\delta^{13}\text{C}$ vs. $\delta^{15}\text{N}$ data for modern and relict samples from this research and Lawson et al. (2004). Note the new proposed range for CP-OM (after Lawson et al., 2004).

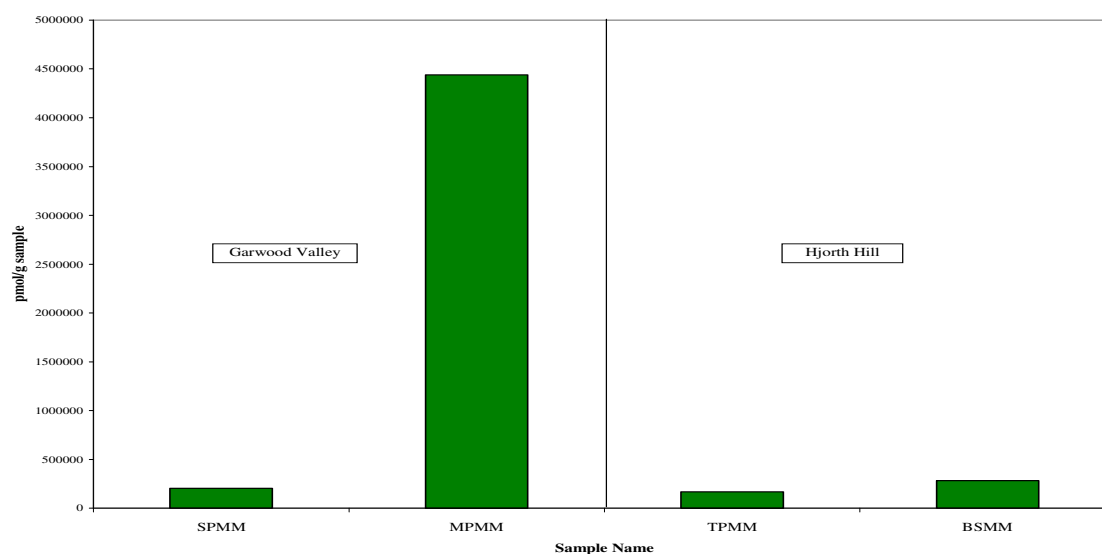


Figure 13. Modern mat biomass abundances for GVC and HHC field sites. SPMM = Susan Pond modern mat; MPMM = Marina Pond modern mat; TPMM = Tom Pond modern mat; BSMM = Big/Little Sister Pond modern mat. These abundances were measured during PLFA analysis.

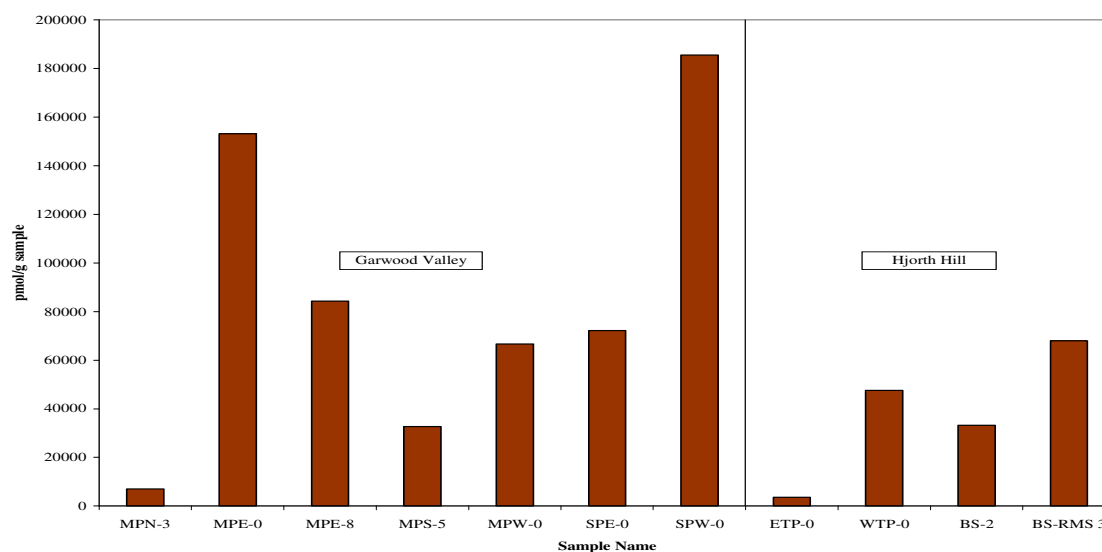


Figure 14. Relict mat biomass abundances for GVC and HHC field sites. Sample names are described in Table 1. Biomass measurements calculated during PLFA analysis.

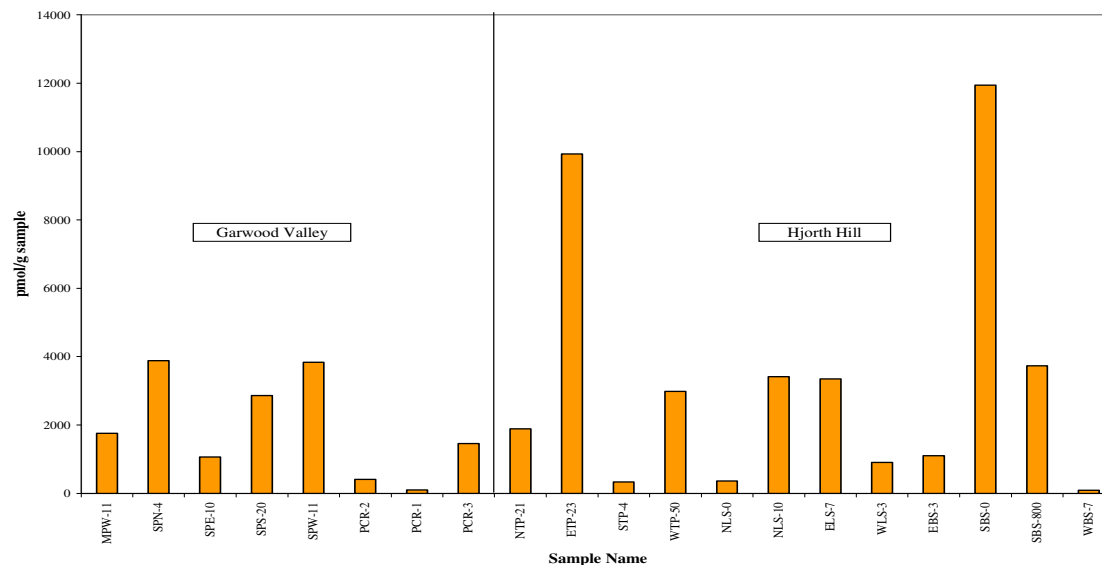


Figure 15. Soil biomass abundances for GVC and HHC field sites. Sample names are described in Table 1. Biomass measurements calculated during PLFA analysis.

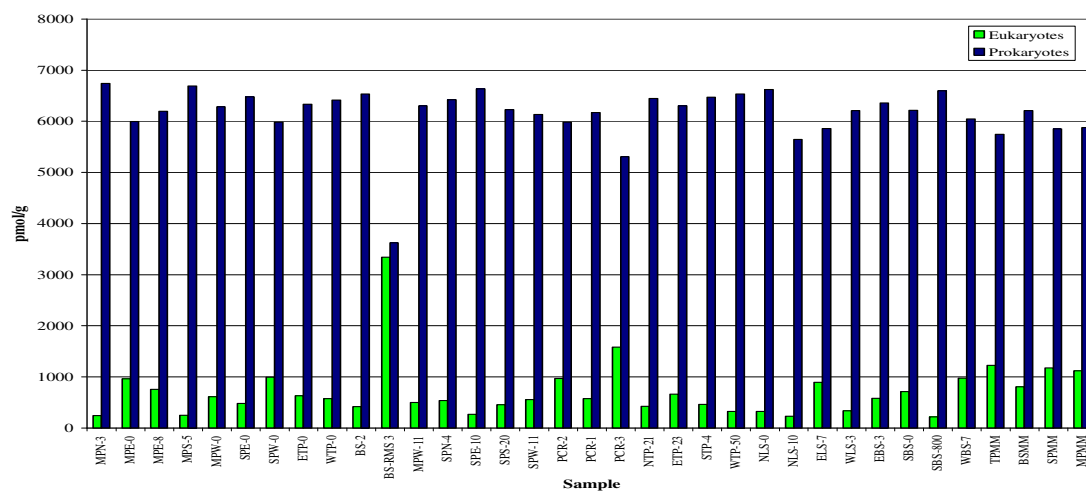


Figure 16. Eukaryotic vs. prokaryotic signature PLFA abundances. The eukaryotic signatures dominate likely due to the dominance of cyanobacteria along with other bacterial consortia. Abundances represent total pmol/g sample of polyunsaturates (eukaryotes) versus total pmol/g sample of normal saturates + mono-branched saturates + terminally branched saturates + branched monounsaturates (prokaryotes). Prokaryotic signatures are likely algal and fungal in origin based on PLFA profiling.

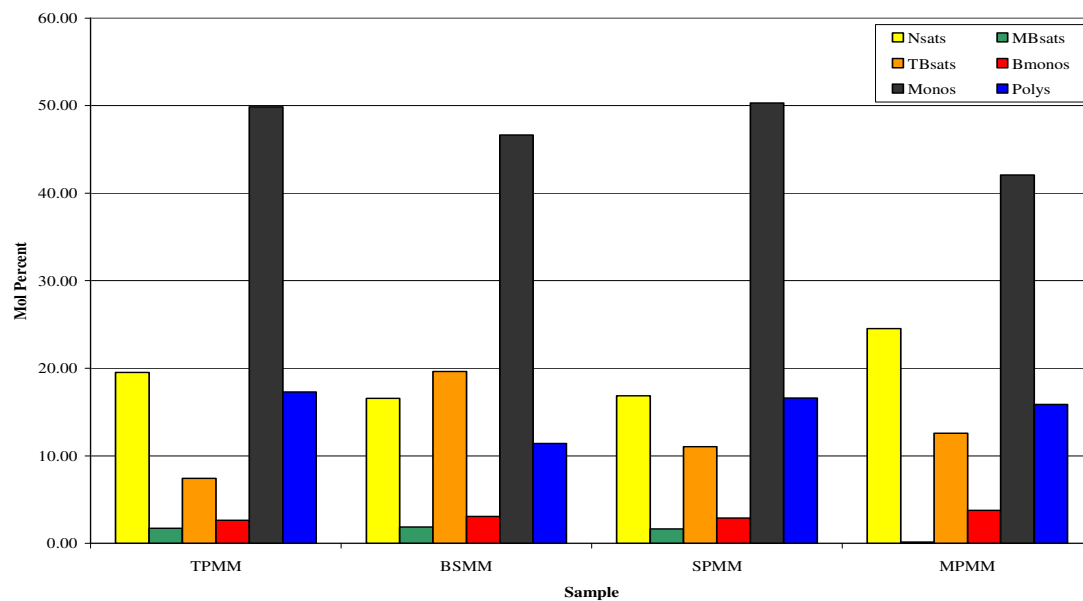


Figure 17. Breakdown of modern mat structural groups based on PLFA type.

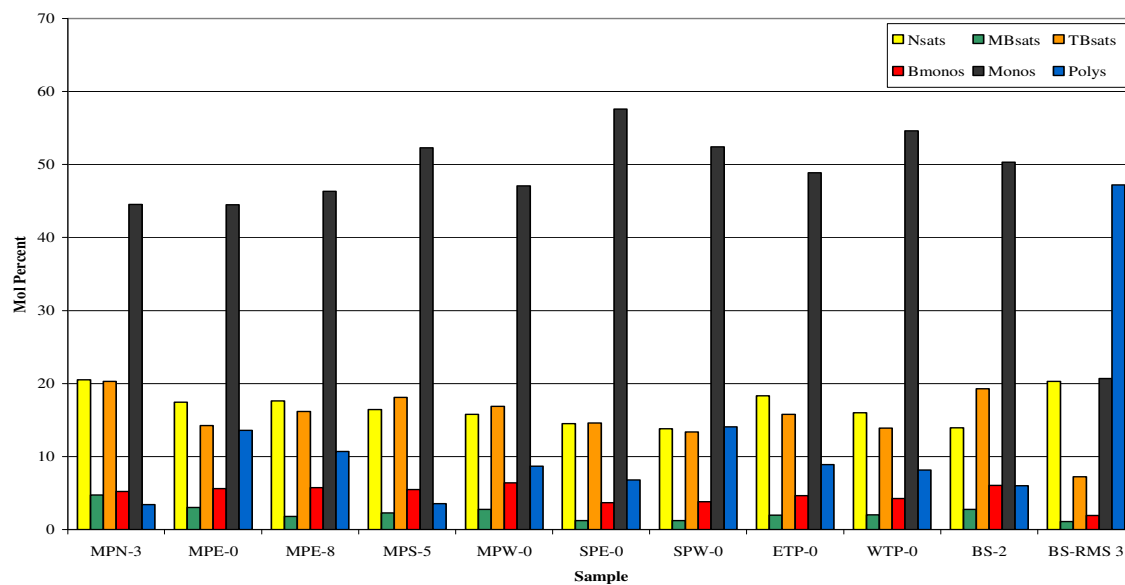


Figure 18. Breakdown of relict mat structural groups based on PLFA type

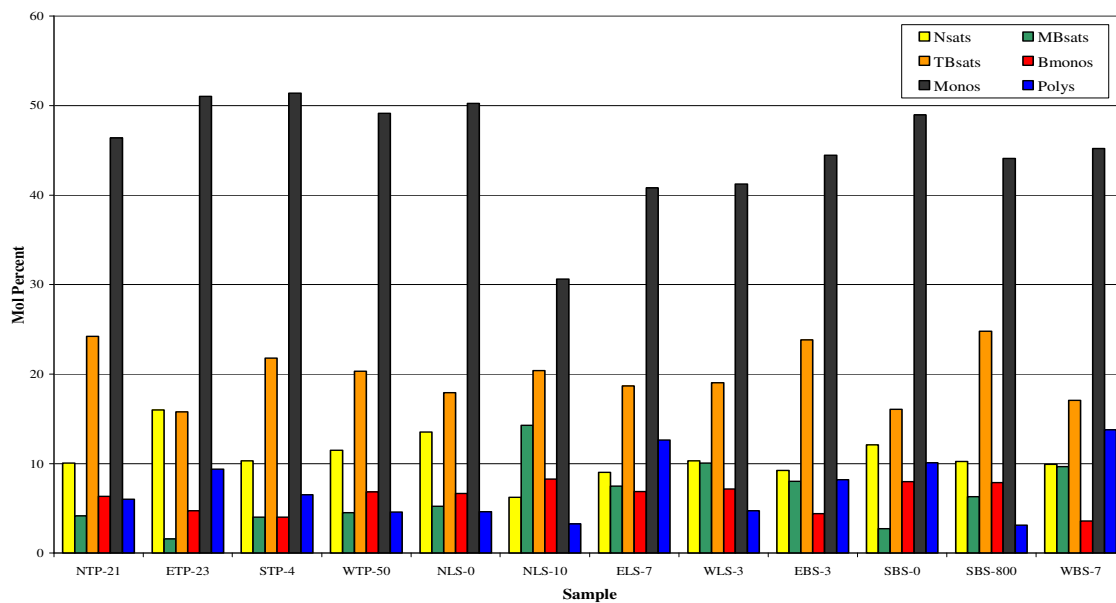


Figure 19. Breakdown of HHC soil structural groups based on PLFA type.

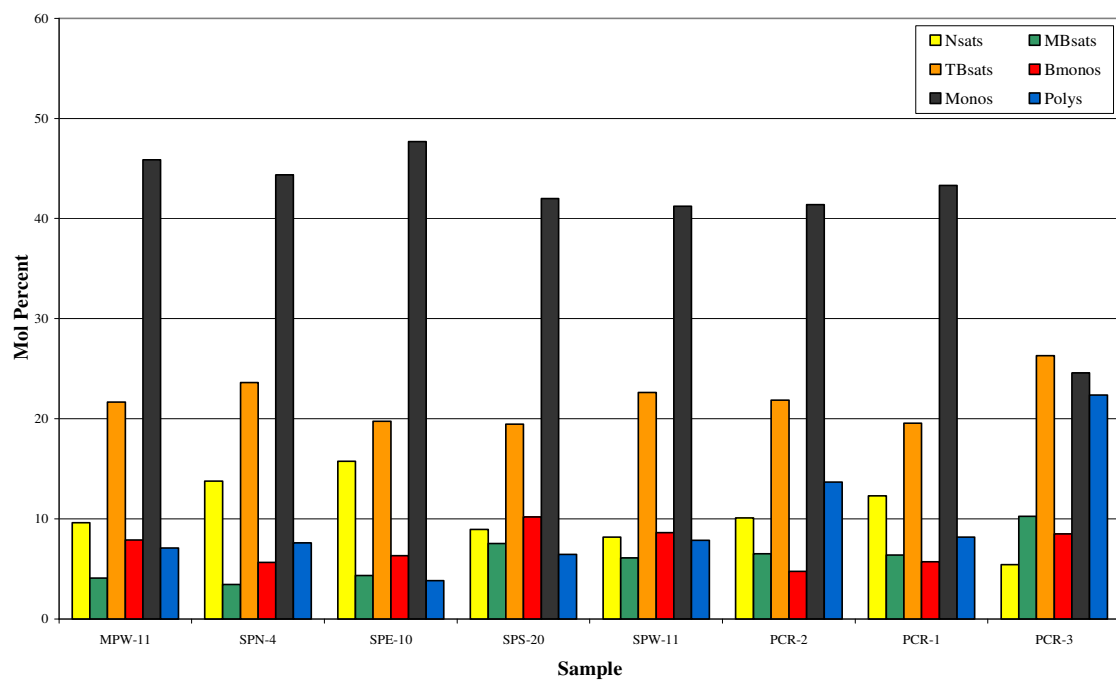
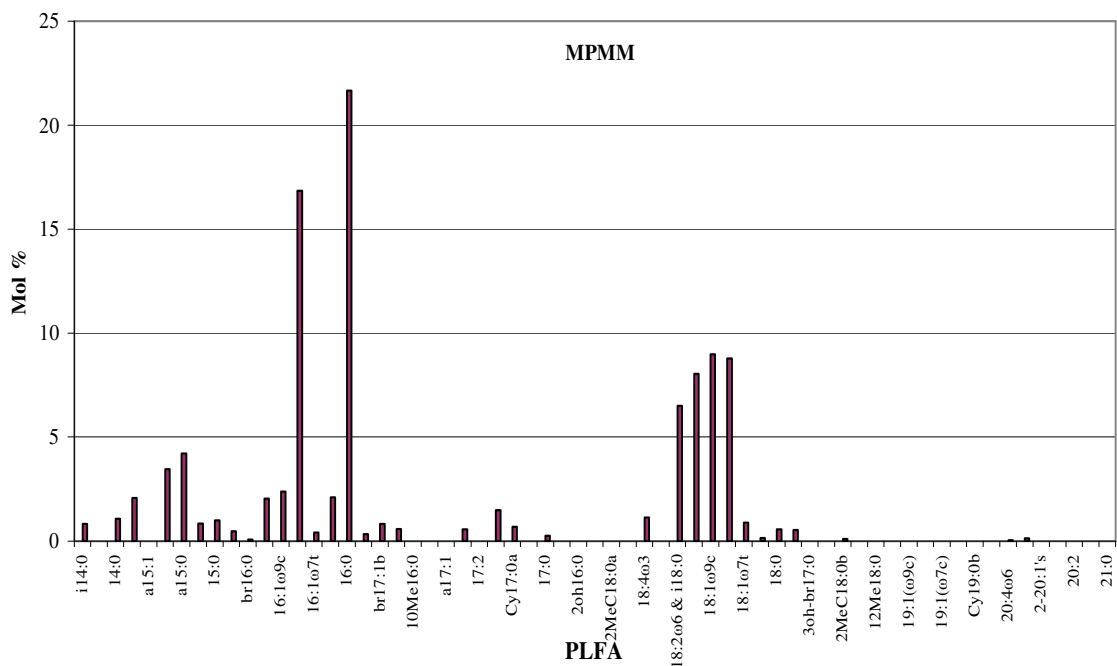
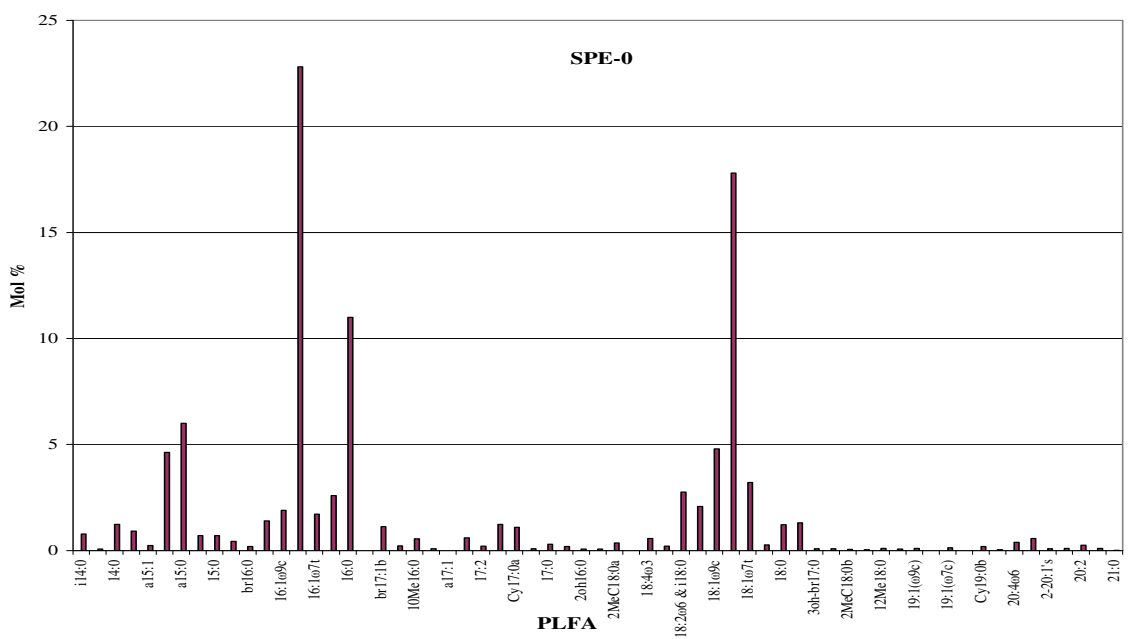


Figure 20. Breakdown of GVC soil structural groups based on PLFA type.



(a)



(b)

Figure 21. Typical PLFA Profiles for each of the three sample types. (a) Modern mat profile and (b) relict mat profile.

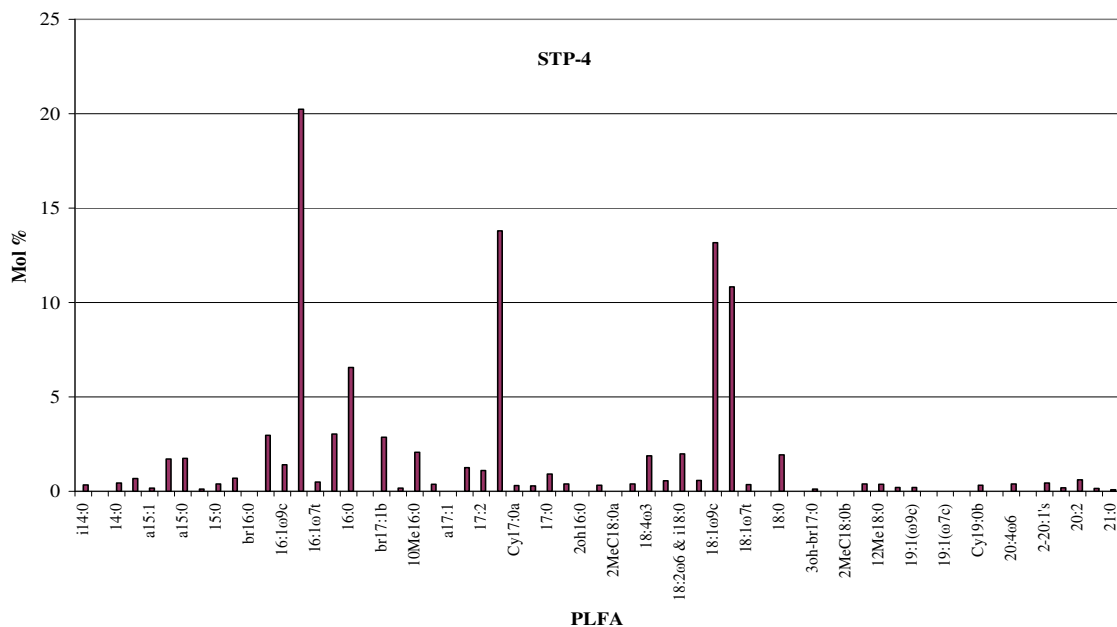


Figure 21., Continued. (c) Soil profile.

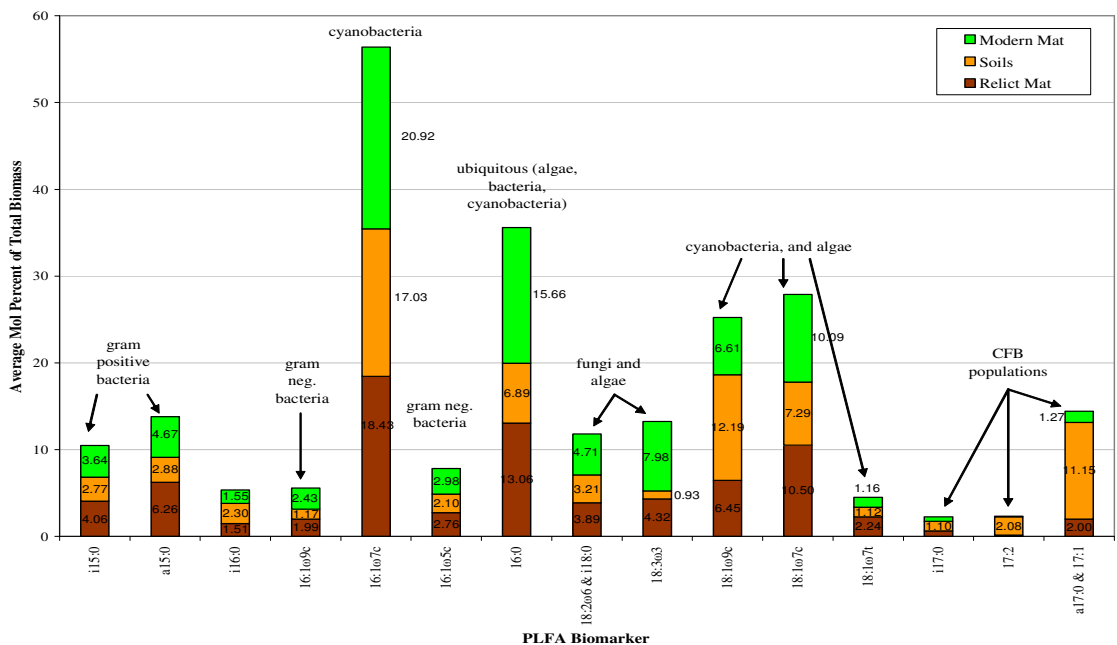


Figure 22. The 15 most abundant PLFAs for all three sample types. PLFA abundance quantified during PLFA analysis. Labels indicate what each biomarker is generally recognized as representing.

Appendix C

Mol% Table		Sample	MPN-3	MPE-0	MPE-8	MPS-5
		weight (g)	11	10	10	10
		dilution	600	600	600	600
PLFA	retention time	Total Biomass	7,072	153,110	84,269	32,699
i14:0	13.64894042	pmol/g	1.16	1.04	1.20	1.14
14:1ω5c	13.8559883		0.08	0.08	0.10	0.08
14:0	14		1.55	1.26	1.67	2.32
5-br15:1's			1.45	1.73	1.72	1.66
a15:1	14.49100469		0.58	0.71	0.66	0.94
i15:0	14.63456269		5.30	3.53	4.23	4.44
a15:0	14.71583243		7.66	6.13	6.78	9.21
2-15:1's			0.39	1.18	1.09	1.00
15:0	15		0.72	0.93	0.97	0.72
i16:1			0.68	0.61	0.62	0.66
br16:0	15.47839585		0.10	0.04	0.06	0.07
i16:0	15.63429732		2.08	1.44	1.56	1.29
16:1ω9c	15.71247294		1.84	2.11	2.28	1.74
16:1ω7c	15.76206021		14.06	15.74	16.00	17.98
16:1ω7t	15.79828736		1.34	0.43	0.74	2.05
16:1ω5c	15.85105235		2.94	3.27	3.37	3.19
16:0	16		15.83	13.98	13.43	12.95
br17:1a	16.29403794		0.00	0.01	0.57	0.36
br17:1b	16.34289784		2.28	1.71	1.09	1.14
i17:1	16.41313603		0.00	0.11	0.14	0.20
10Me16:0	16.44300356		2.51	0.83	1.07	1.70
12Me16:0			0.86	0.09	0.24	0.14
a17:1	16.49743877		0.00	0.00	0.00	0.00
i17:0	16.63733956		1.17	0.50	0.63	0.56
17:2	16.69284508		0.26	0.05	0.19	0.10
a17:0 & 17:1	16.73350911		2.93	1.59	1.77	1.46
Cy17:0a	16.80901386		1.70	1.57	0.46	1.85
Cy17:0b	16.83981216		1.45	0.05	0.04	1.48
17:0	17		0.55	0.39	0.42	0.41
diMe16:0	17.0654758		0.20	0.06	0.06	0.03
2oh16:0	17.162474		0.00	0.04	0.05	0.07
i18:1	17.36156392		0.16	0.08	0.13	0.09
2MeC18:0a	17.39109424		0.00	0.39	0.43	0.18
br18:0	17.42519926		0.34	1.64	0.00	0.00
18:4ω3	17.47966329		0.64	0.59	0.77	0.59
i18:0			0.10	0.21	0.16	0.40
18:2ω6 & i18:0	17.63157053		0.73	5.19	3.86	1.09
18:3ω3	17.67273227		0.89	7.02	5.00	0.82

Mol% Table		Sample	MPN-3	MPE-0	MPE-8	MPS-5
		weight (g)	11	10	10	10
		dilution	600	600	600	600
PLFA	retention time	Total Biomass	7,072	153,110	84,269	32,699
18:1ω9c	17.71877452	pmol/g	6.33	8.48	8.55	5.55
18:1ω7c	17.77417285		7.83	10.08	10.54	10.04
18:1ω7t	17.82311211		4.43	1.05	2.37	4.27
18:1w5c			0.00	0.11	0.08	1.10
18:0	18		1.87	0.84	1.09	0.00
br19:1 & oh18:1	18.05464662		0.75	1.37	1.57	1.30
3oh-br17:0	18.15535016		0.00	0.06	0.05	0.09
Poly1	18.20755168		0.00	0.04	0.02	0.05
2MeC18:0b	18.34277507		0.00	0.17	0.17	0.07
10Me18:0	18.40495673		0.49	0.04	0.07	0.13
12Me18:0	18.43828751		0.24	0.08	0.08	0.07
2-19:1's			0.00	0.08	0.07	0.06
19:1(ω9c)	18.73820878		0.13	0.11	0.13	0.11
FA(250)	18.76675354		0.13	0.00	0.00	0.02
19:1(ω7c)	18.78242381		0.00	0.05	0.05	0.02
Cy19:0a	18.82183529		0.15	0.04	0.05	0.00
Cy19:0b	18.85141353		0.90	0.09	0.23	1.65
19:0	19		0.00	0.04	0.00	0.01
20:4ω6	19.21558249		0.12	0.22	0.25	0.23
20:5ω3	19.26480133		0.44	0.37	0.43	0.48
2-20:1's			0.26	0.05	0.07	0.10
Poly2	19.47501837		0.24	0.09	0.11	0.12
20:2	19.51726672		0.33	0.14	0.19	0.27
20:1(ω9c)	19.78188165		0.84	0.04	0.22	0.13
21:0	21		0.00	0.01	0.02	0.03

Mol% Table		Sample	SPE-10	SPS-20	SPW-0	SPW-11
		weight (g)	75	75	10	75
		dilution	250	250	600	250
PLFA	retention time	Total Biomass	1,064	2,861	185,512	3,836
i14:0	13.64894042	pmol/g	0.73	0.23	0.96	0.55
14:1ω5c	13.8559883		0.06	0.04	0.09	0.04
14:0	14		1.29	0.97	1.28	0.66
5-br15:1's			1.42	0.63	1.24	0.94
a15:1	14.49100469		0.82	0.15	0.38	0.29
i15:0	14.63456269		4.63	2.71	3.71	2.95
a15:0	14.71583243		5.75	1.67	5.16	2.74
2-15:1's			0.37	0.26	0.84	0.20
15:0	15		0.74	0.77	0.76	0.51
i16:1			0.73	3.35	0.38	3.69
br16:0	15.47839585		0.07	0.23	0.35	0.22
i16:0	15.63429732		2.04	2.30	1.74	2.22
16:1ω9c	15.71247294		0.86	0.52	2.49	0.92
16:1ω7c	15.76206021		15.35	16.97	23.49	16.02
16:1ω7t	15.79828736		1.46	0.56	0.87	0.62
16:1ω5c	15.85105235		2.23	1.69	2.92	2.18
16:0	16		10.97	5.17	10.60	5.32
br17:1a	16.29403794		0.46	1.65	0.01	0.27
br17:1b	16.34289784		2.14	6.79	1.30	5.87
i17:1	16.41313603		0.26	1.73	0.16	1.24
10Me16:0	16.44300356		2.38	3.01	0.50	2.26
12Me16:0			0.34	1.38	0.06	1.65
a17:1	16.49743877		0.00	0.00	0.00	0.00
i17:0	16.63733956		0.97	1.18	0.51	1.20
17:2	16.69284508		0.15	1.69	0.04	2.41
a17:0 & 17:1	16.73350911		5.62	11.37	1.30	12.97
Cy17:0a	16.80901386		0.70	0.20	0.86	0.52
Cy17:0b	16.83981216		0.86	0.05	0.07	0.06
17:0	17		0.53	0.72	0.29	0.60
diMe16:0	17.0654758		0.26	0.28	0.12	0.18
2oh16:0	17.162474		0.10	0.06	0.04	0.04
i18:1	17.36156392		0.39	0.68	0.07	0.92
2MeC18:0a	17.39109424		0.00	0.00	0.39	0.00
br18:0	17.42519926		0.43	0.93	0.00	0.71
18:4ω3	17.47966329		1.26	0.70	0.67	1.02
i18:0			0.55	0.09	0.18	0.13
18:2ω6 & i18	17.63157053		0.94	3.54	5.30	3.18
18:3ω3	17.67273227		0.78	0.36	6.79	0.83

Mol% Table		Sample	SPE-10	SPS-20	SPW-0	SPW-11
		weight (g)	75	75	10	75
		dilution	250	250	600	250
PLFA	retention time	Total Biomass	1,064	2,861	185,512	3,836
18:1 ω 9c	17.71877452	pmol/g	7.93	15.85	6.03	12.94
18:1 ω 7c	17.77417285		8.81	4.80	12.99	6.41
18:1 ω 7t	17.82311211		7.10	0.48	1.32	0.54
18:1 ω 5c			0.00	0.01	0.06	0.05
18:0	18		2.08	1.19	0.82	0.99
br19:1 & oh1	18.05464662		1.09	0.28	0.80	0.32
3oh-br17:0	18.15535016		0.09	0.04	0.01	0.07
Poly1	18.20755168		0.05	0.02	0.01	0.05
2MeC18:0b	18.34277507		0.00	0.05	0.08	0.06
10Me18:0	18.40495673		0.43	1.24	0.03	0.67
12Me18:0	18.43828751		0.32	0.36	0.02	0.28
2-19:1's			0.15	0.14	0.07	0.21
19:1(ω 9c)	18.73820878		0.26	0.12	0.10	0.17
FA(250)	18.76675354		0.20	0.06	0.00	0.05
19:1(ω 7c)	18.78242381		0.00	0.00	0.07	0.00
Cy19:0a	18.82183529		0.12	0.11	0.02	0.07
Cy19:0b	18.85141353		0.57	0.10	0.12	0.12
19:0	19		0.13	0.06	0.04	0.05
20:4 ω 6	19.21558249		0.26	0.01	0.41	0.14
20:5 ω 3	19.26480133		0.29	0.03	0.64	0.11
2-20:1's			0.24	0.04	0.09	0.13
Poly2	19.47501837		0.18	0.04	0.11	0.07
20:2	19.51726672		0.16	0.11	0.20	0.14
20:1(ω 9c)	19.78188165		0.90	0.15	0.03	0.17
21:0	21		0.00	0.06	0.01	0.04

Mol% Table		Sample	MPW-0	MPW-11	SPN-4	SPE-0
		weight (g)	10	75	75	10
		dilution	600	250	600	600
PLFA	retention time	Total Biomass	66,686	1,759	3,880	72,150
i14:0	13.64894042	pmol/g	1.31	0.61	0.89	0.78
14:1ω5c	13.8559883		0.07	0.06	0.06	0.07
14:0	14		1.19	0.94	1.06	1.23
5-br15:1's			2.16	1.13	1.41	0.92
a15:1	14.49100469		2.00	0.44	0.67	0.23
i15:0	14.63456269		3.79	2.70	3.70	4.62
a15:0	14.71583243		7.42	2.83	6.04	6.01
2-15:1's			0.38	0.27	0.35	0.69
15:0	15		0.62	0.50	0.53	0.71
i16:1			0.67	1.87	0.57	0.43
br16:0	15.47839585		0.09	0.12	0.12	0.18
i16:0	15.63429732		1.82	2.84	2.79	1.39
16:1ω9c	15.71247294		2.54	1.15	1.59	1.90
16:1ω7c	15.76206021		19.62	19.07	18.27	22.81
16:1ω7t	15.79828736		0.61	0.75	0.65	1.72
16:1ω5c	15.85105235		2.85	2.03	2.47	2.60
16:0	16		12.87	6.28	9.89	11.00
br17:1a	16.29403794		0.03	0.15	0.06	0.00
br17:1b	16.34289784		0.91	5.29	2.21	1.14
i17:1	16.41313603		0.36	0.82	0.26	0.22
10Me16:0	16.44300356		2.26	1.83	1.68	0.55
12Me16:0			0.09	0.74	0.26	0.08
a17:1	16.49743877		0.00	0.00	0.00	0.00
i17:0	16.63733956		0.57	1.07	0.82	0.59
17:2	16.69284508		0.26	2.95	1.16	0.21
a17:0 & 17:1	16.73350911		1.96	11.62	9.35	1.22
Cy17:0a	16.80901386		0.71	0.50	0.80	1.09
Cy17:0b	16.83981216		0.05	0.03	0.28	0.08
17:0	17		0.31	0.62	0.69	0.30
diMe16:0	17.0654758		0.02	0.20	0.58	0.18
2oh16:0	17.162474		0.01	0.03	0.06	0.06
i18:1	17.36156392		0.19	0.41	0.31	0.07
2MeC18:0a	17.39109424		0.43	0.00	0.00	0.36
br18:0	17.42519926		0.00	0.43	0.35	0.00
18:4ω3	17.47966329		1.33	0.95	0.72	0.56
i18:0			0.47	0.40	0.47	0.21
18:2ω6 & i18	17.63157053		3.75	1.94	2.28	2.76
18:3ω3	17.67273227		2.61	0.55	2.49	2.07

Mol% Table		Sample	MPW-0	MPW-11	SPN-4	SPE-0
		weight (g)	10	75	75	10
		dilution	600	250	600	600
PLFA	retention time	Total Biomass	66,686	1,759	3,880	72,150
18:1 ω 9c	17.71877452	pmol/g	8.09	12.67	9.48	4.79
18:1 ω 7c	17.77417285		9.90	7.85	8.05	17.81
18:1 ω 7t	17.82311211		1.38	0.70	1.49	3.21
18:1 ω 5c			0.00	0.00	0.10	0.26
18:0	18		0.81	1.14	1.58	1.21
br19:1 & oh1	18.05464662		1.10	0.48	0.98	1.31
3oh-br17:0	18.15535016		0.09	0.10	0.06	0.08
Poly1	18.20755168		0.00	0.05	0.00	0.09
2MeC18:0b	18.34277507		0.10	0.09	0.14	0.06
10Me18:0	18.40495673		0.06	0.46	0.14	0.03
12Me18:0	18.43828751		0.14	0.18	0.15	0.10
2-19:1's			0.08	0.17	0.12	0.07
19:1(ω 9c)	18.73820878		0.10	0.23	0.16	0.10
FA(250)	18.76675354		0.00	0.09	0.00	0.00
19:1(ω 7c)	18.78242381		0.03	0.00	0.05	0.13
Cy19:0a	18.82183529		0.04	0.07	0.06	0.00
Cy19:0b	18.85141353		0.32	0.19	0.25	0.19
19:0	19		0.00	0.03	0.04	0.04
20:4 ω 6	19.21558249		0.15	0.25	0.27	0.39
20:5 ω 3	19.26480133		0.32	0.23	0.45	0.56
2-20:1's			0.14	0.10	0.17	0.08
Poly2	19.47501837		0.33	0.23	0.04	0.11
20:2	19.51726672		0.25	0.22	0.24	0.25
20:1(ω 9c)	19.78188165		0.27	0.25	0.11	0.09
21:0	21		0.00	0.09	0.00	0.02

Mol% Table		Sample	PCR-2	PCR-1	PCR-3	NTP-21
		weight (g)	75	75	75	75
		dilution	250	250	250	250
PLFA	retention time	Total Biomass	413	97	1,456	1,895
i14:0	13.64894042	pmol/g	0.13	0.71	0.05	0.65
14:1ω5c	13.8559883		0.00	0.00	0.03	0.05
14:0	14		0.58	0.99	0.53	0.65
5-br15:1's			0.54	0.25	0.55	1.73
a15:1	14.49100469		0.14	0.00	0.13	0.27
i15:0	14.63456269		1.07	2.16	1.47	2.72
a15:0	14.71583243		1.33	1.66	0.51	2.48
2-15:1's			0.22	0.00	0.09	0.19
15:0	15		0.73	0.65	0.57	0.39
i16:1			0.68	0.98	0.95	1.21
br16:0	15.47839585		0.23	0.00	0.42	0.08
i16:0	15.63429732		1.44	2.52	1.29	3.03
16:1ω9c	15.71247294		0.34	1.41	0.24	1.25
16:1ω7c	15.76206021		16.95	16.60	8.31	19.08
16:1ω7t	15.79828736		0.39	0.27	0.26	0.64
16:1ω5c	15.85105235		0.83	1.14	0.56	3.68
16:0	16		6.36	8.20	2.10	6.78
br17:1a	16.29403794		1.02	0.00	3.50	0.11
br17:1b	16.34289784		2.48	4.73	3.82	3.51
i17:1	16.41313603		0.93	0.61	1.47	0.64
10Me16:0	16.44300356		3.45	2.36	5.11	1.81
12Me16:0			0.27	0.44	0.45	0.50
a17:1	16.49743877		0.00	0.00	0.00	0.00
i17:0	16.63733956		0.43	1.31	0.35	0.92
17:2	16.69284508		3.88	2.48	10.26	1.18
a17:0 & 17:1	16.73350911		17.47	11.21	22.64	14.42
Cy17:0a	16.80901386		0.39	1.73	0.30	0.30
Cy17:0b	16.83981216		0.36	0.00	0.10	0.21
17:0	17		1.21	0.75	1.14	0.68
diMe16:0	17.0654758		0.06	0.34	0.45	0.36
2oh16:0	17.162474		0.00	0.00	0.23	0.02
i18:1	17.36156392		0.47	0.00	0.43	0.36
2MeC18:0a	17.39109424		0.00	0.00	0.00	0.00
br18:0	17.42519926		1.60	0.78	2.46	0.58
18:4ω3	17.47966329		1.31	0.69	1.47	1.03
i18:0			0.00	0.79	0.03	0.37
18:2ω6 & i18	17.63157053		8.29	3.38	10.57	1.43
18:3ω3	17.67273227		0.20	0.00	0.06	1.32

Mol% Table		Sample	PCR-2	PCR-1	PCR-3	NTP-21
		weight (g)	75	75	75	75
		dilution	250	250	250	250
PLFA	retention time	Total Biomass	413	97	1,456	1,895
18:1ω9c	17.71877452	pmol/g	16.85	12.22	12.76	11.33
18:1ω7c	17.77417285		4.41	8.79	1.56	7.96
18:1ω7t	17.82311211		0.10	0.00	0.00	0.73
18:1ω5c			0.00	0.00	0.04	0.03
18:0	18		1.20	1.69	1.01	1.35
br19:1 & oh1	18.05464662		0.12	0.73	0.07	0.38
3oh-br17:0	18.15535016		0.00	0.58	0.00	0.12
Poly1	18.20755168		0.00	0.00	0.03	0.04
2MeC18:0b	18.34277507		0.00	0.00	0.08	0.09
10Me18:0	18.40495673		0.51	2.07	0.47	0.43
12Me18:0	18.43828751		0.38	0.40	0.58	0.28
2-19:1's			0.23	0.00	0.13	0.17
19:1(ω9c)	18.73820878		0.10	0.72	0.03	0.22
FA(250)	18.76675354		0.00	0.42	0.04	0.12
19:1(ω7c)	18.78242381		0.00	0.00	0.00	0.00
Cy19:0a	18.82183529		0.00	0.00	0.12	0.06
Cy19:0b	18.85141353		0.27	0.44	0.03	0.20
19:0	19		0.00	0.00	0.00	0.06
20:4ω6	19.21558249		0.00	0.54	0.03	0.27
20:5ω3	19.26480133		0.00	0.00	0.00	0.45
2-20:1's			0.00	0.70	0.04	0.15
Poly2	19.47501837		0.00	0.48	0.00	0.10
20:2	19.51726672		0.00	1.07	0.00	0.35
20:1(ω9c)	19.78188165		0.06	0.00	0.03	0.35
21:0	21		0.00	0.00	0.08	0.15

Mol% Table		Sample	ETP-0	ETP-23	STP-4	WTP-0
		weight (g)	75	75	75	10
		dilution	250	600	250	600
PLFA	retention time	Total Biomass	3,510	9,928	337	47,561
i14:0	13.64894042	pmol/g	0.77	0.92	0.34	1.01
14:1ω5c	13.8559883		0.08	0.08	0.00	0.07
14:0	14		1.01	1.10	0.44	1.09
5-br15:1's			2.04	2.39	0.67	2.13
a15:1	14.49100469		0.45	0.56	0.17	0.63
i15:0	14.63456269		5.06	5.16	1.71	4.10
a15:0	14.71583243		5.91	6.13	1.74	5.27
2-15:1's			0.85	0.83	0.12	0.82
15:0	15		0.87	0.82	0.39	0.79
i16:1			0.37	0.35	0.69	0.46
br16:0	15.47839585		0.19	0.18	0.00	0.38
i16:0	15.63429732		1.35	1.33	2.96	1.33
16:1ω9c	15.71247294		1.86	1.91	1.41	2.50
16:1ω7c	15.76206021		23.60	25.68	20.23	25.60
16:1ω7t	15.79828736		0.89	1.14	0.49	1.22
16:1ω5c	15.85105235		2.21	2.32	3.03	2.95
16:0	16		13.52	12.42	6.57	12.79
br17:1a	16.29403794		0.01	0.00	0.00	0.00
br17:1b	16.34289784		1.26	1.10	2.87	0.80
i17:1	16.41313603		0.31	0.28	0.18	0.20
10Me16:0	16.44300356		0.89	0.76	2.07	0.86
12Me16:0			0.35	0.28	0.38	0.18
a17:1	16.49743877		0.00	0.00	0.00	0.00
i17:0	16.63733956		0.74	0.57	1.25	0.56
17:2	16.69284508		0.05	0.15	1.10	0.16
a17:0 & 17:1	16.73350911		1.94	1.66	13.79	1.59
Cy17:0a	16.80901386		1.09	0.97	0.30	1.12
Cy17:0b	16.83981216		0.04	0.03	0.30	0.70
17:0	17		0.49	0.37	0.91	0.35
diMe16:0	17.0654758		0.11	0.05	0.39	0.05
2oh16:0	17.162474		0.03	0.03	0.00	0.03
i18:1	17.36156392		0.14	0.08	0.31	0.10
2MeC18:0a	17.39109424		0.38	0.34	0.00	0.00
br18:0	17.42519926		0.00	0.00	0.40	0.33
18:4ω3	17.47966329		0.84	0.91	1.88	0.77
i18:0			0.22	0.29	0.55	0.24
18:2ω6 & i18	17.63157053		1.85	1.86	1.99	2.79
18:3ω3	17.67273227		4.15	4.34	0.58	3.04

Mol% Table		Sample	ETP-0	ETP-23	STP-4	WTP-0
		weight (g)	75	75	75	10
		dilution	250	600	250	600
PLFA	retention time	Total Biomass	3,510	9,928	337	47,561
18:1ω9c	17.71877452	pmol/g	4.79	4.63	13.17	6.28
18:1ω7c	17.77417285		10.51	11.29	10.83	11.41
18:1ω7t	17.82311211		0.51	0.00	0.36	1.27
18:1ω5c			1.75	1.62	0.00	0.00
18:0	18		2.33	1.24	1.94	0.97
br19:1 & oh1	18.05464662		0.75	0.63	0.00	0.58
3oh-br17:0	18.15535016		0.05	0.03	0.12	0.02
Poly1	18.20755168		0.07	0.03	0.00	0.03
2MeC18:0b	18.34277507		0.15	0.09	0.00	0.07
10Me18:0	18.40495673		0.14	0.10	0.39	0.06
12Me18:0	18.43828751		0.11	0.08	0.37	0.05
2-19:1's			0.07	0.06	0.20	0.07
19:1(ω9c)	18.73820878		0.12	0.09	0.19	0.11
FA(250)	18.76675354		0.00	0.00	0.00	0.00
19:1(ω7c)	18.78242381		0.12	0.09	0.00	0.06
Cy19:0a	18.82183529		0.00	0.03	0.00	0.00
Cy19:0b	18.85141353		0.18	0.16	0.32	0.26
19:0	19		0.04	0.02	0.00	0.01
20:4ω6	19.21558249		0.79	0.86	0.38	0.34
20:5ω3	19.26480133		0.98	1.04	0.00	0.83
2-20:1's			0.12	0.12	0.45	0.06
Poly2	19.47501837		0.02	0.07	0.19	0.06
20:2	19.51726672		0.23	0.22	0.62	0.21
20:1(ω9c)	19.78188165		0.18	0.07	0.15	0.21
21:0	21		0.03	0.01	0.09	0.00

Mol% Table		Sample	WTP-50	NLS-0	NLS-10	ELS-7
		weight (g)	75	75	75	75
		dilution	250	250	250	250
PLFA	retention time	Total Biomass	2,991	362	3,416	3,347
i14:0	13.64894042	pmol/g	0.73	0.38	0.21	0.20
14:1ω5c	13.8559883		0.05	0.00	0.03	0.04
14:0	14		0.88	0.51	0.30	0.61
5-br15:1's			1.35	1.18	0.46	0.50
a15:1	14.49100469		0.27	0.22	0.07	0.12
i15:0	14.63456269		2.96	3.00	2.46	1.85
a15:0	14.71583243		4.50	2.73	1.19	1.18
2-15:1's			0.20	0.11	0.24	0.11
15:0	15		0.32	0.44	0.36	0.44
i16:1			0.73	0.78	8.52	2.71
br16:0	15.47839585		0.08	0.00	0.55	0.23
i16:0	15.63429732		1.94	2.36	2.73	1.99
16:1ω9c	15.71247294		1.25	1.52	0.87	0.91
16:1ω7c	15.76206021		14.61	19.79	9.60	16.36
16:1ω7t	15.79828736		1.11	0.48	0.56	0.52
16:1ω5c	15.85105235		2.13	2.79	0.94	1.33
16:0	16		7.41	9.15	2.80	4.86
br17:1a	16.29403794		0.11	0.00	0.46	0.56
br17:1b	16.34289784		4.21	4.64	6.28	4.78
i17:1	16.41313603		0.71	0.49	5.02	0.93
10Me16:0	16.44300356		1.42	2.24	3.84	2.90
12Me16:0			0.34	0.70	4.00	1.05
a17:1	16.49743877		0.00	0.00	0.67	0.00
i17:0	16.63733956		1.09	1.47	2.17	0.98
17:2	16.69284508		1.39	0.40	0.98	4.64
a17:0 & 17:1	16.73350911		9.12	8.00	11.60	12.48
Cy17:0a	16.80901386		1.10	0.65	0.21	0.48
Cy17:0b	16.83981216		0.05	0.65	0.10	0.07
17:0	17		0.66	0.71	0.91	1.23
diMe16:0	17.0654758		0.74	0.64	0.47	0.25
2oh16:0	17.162474		0.09	0.00	0.09	0.10
i18:1	17.36156392		0.29	0.28	0.83	0.61
2MeC18:0a	17.39109424		0.00	0.00	2.21	0.00
br18:0	17.42519926		0.75	0.42	0.00	1.44
18:4ω3	17.47966329		0.91	0.78	0.71	1.47
i18:0			0.64	0.00	0.08	0.21
18:2ω6 & i18	17.63157053		0.88	1.40	0.91	5.75
18:3ω3	17.67273227		0.42	0.97	0.28	0.27

Mol% Table		Sample	WTP-50	NLS-0	NLS-10	ELS-7
		weight (g)	75	75	75	75
		dilution	250	250	250	250
PLFA	retention time	Total Biomass	2,991	362	3,416	3,347
18:1ω9c	17.71877452	pmol/g	10.56	11.66	13.12	13.68
18:1ω7c	17.77417285		8.41	10.46	3.80	5.86
18:1ω7t	17.82311211		7.03	0.91	0.14	0.34
18:1ω5c			0.00	0.00	0.08	0.06
18:0	18		2.05	2.47	1.48	1.76
br19:1 & oh1	18.05464662		0.62	0.37	0.18	0.31
3oh-br17:0	18.15535016		0.33	0.09	0.05	0.14
Poly1	18.20755168		0.09	0.00	0.02	0.05
2MeC18:0b	18.34277507		0.15	0.00	0.09	0.06
10Me18:0	18.40495673		0.61	0.86	4.81	1.00
12Me18:0	18.43828751		0.34	0.35	0.42	0.43
2-19:1's			0.22	0.13	0.19	0.32
19:1(ω9c)	18.73820878		0.20	0.22	0.19	0.21
FA(250)	18.76675354		0.22	0.00	0.10	0.06
19:1(ω7c)	18.78242381		0.00	0.34	0.00	0.00
Cy19:0a	18.82183529		0.12	0.00	0.07	0.06
Cy19:0b	18.85141353		1.54	0.46	0.29	0.28
19:0	19		0.15	0.00	0.07	0.07
20:4ω6	19.21558249		0.18	0.33	0.12	0.17
20:5ω3	19.26480133		0.39	0.32	0.02	0.07
2-20:1's			0.27	0.11	0.12	0.16
Poly2	19.47501837		0.14	0.14	0.09	0.21
20:2	19.51726672		0.40	0.44	0.25	0.26
20:1(ω9c)	19.78188165		0.48	0.19	0.27	0.19
21:0	21		0.04	0.27	0.31	0.06

Mol% Table		Sample	WLS-3	BS-2	EBS-3	SBS-0
		weight (g)	75	10	75	75
		dilution	250	600	250	250
PLFA	retention time	Total Biomass	905	33,225	1,101	11,950
i14:0	13.64894042	pmol/g	0.51	1.22	0.38	1.75
14:1ω5c	13.8559883		0.08	0.05	0.03	0.13
14:0	14		0.84	1.17	0.36	0.90
5-br15:1's			0.77	1.84	0.44	2.61
a15:1	14.49100469		0.18	1.18	0.13	0.52
i15:0	14.63456269		2.51	4.92	1.39	4.57
a15:0	14.71583243		1.94	8.17	2.56	4.10
2-15:1's			0.18	0.74	0.14	0.29
15:0	15		0.40	0.70	0.43	0.45
i16:1			3.81	0.58	0.68	0.47
br16:0	15.47839585		0.18	0.07	0.09	0.08
i16:0	15.63429732		2.44	1.53	3.01	1.94
16:1ω9c	15.71247294		1.28	2.05	1.01	2.49
16:1ω7c	15.76206021		18.61	18.00	16.06	20.40
16:1ω7t	15.79828736		0.50	1.26	0.37	0.87
16:1ω5c	15.85105235		1.75	2.88	1.38	4.75
16:0	16		6.58	10.19	4.92	9.14
br17:1a	16.29403794		0.12	0.31	0.11	0.01
br17:1b	16.34289784		5.40	1.14	3.27	3.92
i17:1	16.41313603		2.30	0.00	0.00	0.34
10Me16:0	16.44300356		3.00	2.00	4.32	1.59
12Me16:0			1.91	0.10	0.43	0.28
a17:1	16.49743877		0.00	0.00	0.00	0.00
i17:0	16.63733956		1.72	0.73	0.79	1.33
17:2	16.69284508		1.19	0.15	2.39	0.03
a17:0 & 17:1	16.73350911		9.91	2.71	15.70	2.39
Cy17:0a	16.80901386		0.19	1.77	0.29	0.47
Cy17:0b	16.83981216		0.60	0.83	0.11	0.02
17:0	17		0.83	0.44	1.08	0.28
diMe16:0	17.0654758		0.84	0.07	0.45	0.15
2oh16:0	17.162474		0.08	0.07	0.08	0.07
i18:1	17.36156392		0.60	0.32	0.43	0.16
2MeC18:0a	17.39109424		0.00	0.27	0.00	0.44
br18:0	17.42519926		1.18	0.00	1.21	0.00
18:4ω3	17.47966329		0.97	1.03	0.96	1.01
i18:0			0.20	0.36	0.16	0.28
18:2ω6 & i18	17.63157053		1.35	1.92	4.08	2.64
18:3ω3	17.67273227		0.41	1.19	0.20	3.60

Mol% Table		Sample	WLS-3	BS-2	EBS-3	SBS-0
		weight (g)	75	10	75	75
		dilution	250	600	250	250
PLFA	retention time	Total Biomass	905	33,225	1,101	11,950
18:1ω9c	17.71877452	pmol/g	10.88	7.41	18.13	7.68
18:1ω7c	17.77417285		5.90	9.91	5.30	10.05
18:1ω7t	17.82311211		0.23	4.29	0.38	1.05
18:1ω5c			0.08	0.00	0.08	0.04
18:0	18		1.47	1.39	1.70	1.20
br19:1 & oh1	18.05464662		0.10	1.23	0.00	0.79
3oh-br17:0	18.15535016		0.36	0.07	0.29	0.12
Poly1	18.20755168		0.00	0.11	0.02	0.04
2MeC18:0b	18.34277507		0.06	0.15	0.21	0.19
10Me18:0	18.40495673		2.43	0.11	0.76	0.20
12Me18:0	18.43828751		0.36	0.21	0.48	0.20
2-19:1's			0.31	0.13	0.35	0.07
19:1(ω9c)	18.73820878		0.30	0.15	0.26	0.14
FA(250)	18.76675354		0.25	0.00	0.22	0.15
19:1(ω7c)	18.78242381		0.00	0.04	0.00	0.00
Cy19:0a	18.82183529		0.00	0.14	0.00	0.04
Cy19:0b	18.85141353		0.18	0.61	0.22	0.22
19:0	19		0.10	0.02	0.07	0.04
20:4ω6	19.21558249		0.23	0.45	0.10	0.90
20:5ω3	19.26480133		0.06	0.84	0.04	1.58
2-20:1's			0.27	0.11	0.13	0.19
Poly2	19.47501837		0.19	0.12	0.26	0.06
20:2	19.51726672		0.55	0.39	0.43	0.33
20:1(ω9c)	19.78188165		0.21	0.13	0.46	0.21
21:0	21		0.11	0.03	0.65	0.08

Mol% Table		Sample	SBS-800	WBS-7	BS-RMS	TPMM
		weight (g)	75	75	11	5
		dilution	250	250	600	600
PLFA	retention time	Total Biomass	3,735	88	67,876	166,771
i14:0	13.64894042	pmol/g	0.85	0.00	0.32	0.76
14:1ω5c	13.8559883		0.09	0.00	0.02	0.10
14:0	14		0.83	0.44	0.42	1.19
5-br15:1's			1.85	0.00	0.67	1.84
a15:1	14.49100469		0.30	0.00	0.19	0.26
i15:0	14.63456269		4.38	1.23	0.96	2.86
a15:0	14.71583243		5.21	1.30	1.13	1.57
2-15:1's			0.18	0.00	0.23	0.23
15:0	15		0.46	0.45	0.76	0.37
i16:1			1.29	0.47	0.25	0.33
br16:0	15.47839585		0.10	0.00	0.03	1.27
i16:0	15.63429732		3.29	1.58	1.02	1.02
16:1ω9c	15.71247294		1.34	1.09	0.56	2.02
16:1ω7c	15.76206021		18.05	14.56	5.84	25.55
16:1ω7t	15.79828736		0.71	0.00	0.21	0.93
16:1ω5c	15.85105235		2.95	1.87	1.15	2.33
16:0	16		6.64	6.13	16.48	16.34
br17:1a	16.29403794		0.12	0.00	0.00	0.00
br17:1b	16.34289784		4.98	3.01	0.52	0.27
i17:1	16.41313603		1.26	0.00	0.14	0.09
10Me16:0	16.44300356		2.74	4.70	0.47	0.27
12Me16:0			0.70	0.41	0.07	0.08
a17:1	16.49743877		0.00	0.00	0.04	0.00
i17:0	16.63733956		1.63	0.81	0.26	0.36
17:2	16.69284508		0.40	2.86	0.24	0.04
a17:0 & 17:1	16.73350911		9.44	12.16	3.57	0.88
Cy17:0a	16.80901386		0.80	0.28	0.76	0.18
Cy17:0b	16.83981216		0.04	0.00	0.02	0.03
17:0	17		0.46	1.05	0.47	0.22
diMe16:0	17.0654758		0.71	0.35	0.14	0.01
2oh16:0	17.162474		0.06	0.00	0.03	0.01
i18:1	17.36156392		0.25	0.59	0.09	0.06
2MeC18:0a	17.39109424		0.00	0.00	0.47	0.62
br18:0	17.42519926		0.73	1.75	0.00	0.00
18:4ω3	17.47966329		0.69	2.36	0.33	0.49
i18:0			0.21	0.00	0.42	0.18
18:2ω6 & i18	17.63157053		0.68	7.04	13.49	3.14
18:3ω3	17.67273227		0.56	0.48	13.98	10.96

Mol% Table		Sample	SBS-800	WBS-7	BS-RMS	TPMM
		weight (g)	75	75	11	5
		dilution	250	250	600	600
PLFA	retention time	Total Biomass	3,735	88	67,876	166,771
18:1ω9c	17.71877452	pmol/g	10.37	17.79	4.66	5.05
18:1ω7c	17.77417285		7.66	7.61	4.51	12.31
18:1ω7t	17.82311211		0.88	0.00	0.49	0.66
18:1ω5c			0.00	0.00	0.49	0.04
18:0	18		1.60	1.85	2.13	1.35
br19:1 & oh1	18.05464662		0.38	0.00	0.44	0.21
3oh-br17:0	18.15535016		0.18	0.00	0.00	0.02
Poly1	18.20755168		0.02	0.00	0.12	0.00
2MeC18:0b	18.34277507		0.09	0.00	0.10	0.10
10Me18:0	18.40495673		0.78	1.43	0.12	0.01
12Me18:0	18.43828751		0.39	1.04	0.09	0.00
2-19:1's			0.12	0.25	0.09	0.11
19:1(ω9c)	18.73820878		0.20	0.00	0.12	0.09
FA(250)	18.76675354		0.25	0.27	0.00	0.03
19:1(ω7c)	18.78242381		0.00	0.65	0.05	0.03
Cy19:0a	18.82183529		0.07	0.00	0.04	0.00
Cy19:0b	18.85141353		0.32	0.00	0.11	0.00
19:0	19		0.08	0.00	0.02	0.05
20:4ω6	19.21558249		0.32	0.76	7.15	0.90
20:5ω3	19.26480133		0.15	0.00	11.77	1.40
2-20:1's			0.13	1.12	1.14	0.18
Poly2	19.47501837		0.14	0.00	0.00	0.11
20:2	19.51726672		0.34	0.28	0.26	0.37
20:1(ω9c)	19.78188165		0.39	0.00	0.30	0.12
21:0	21		0.16	0.00	0.03	0.01

Mol% Table		Sample	BSMM	SPMM	MPMM
		weight (g)	5	6	1
		dilution	600	600	1000
PLFA	retention time	Total Biomass	282,370	204,954	4,438,138
i14:0	13.64894042	pmol/g	1.20	1.25	0.82
14:1ω5c	13.8559883		0.13	0.07	0.00
14:0	14		1.93	1.11	1.06
5-br15:1's			1.34	1.50	2.07
a15:1	14.49100469		0.16	0.30	0.00
i15:0	14.63456269		5.36	2.89	3.46
a15:0	14.71583243		9.44	3.48	4.21
2-15:1's			2.15	0.55	0.83
15:0	15		2.03	0.64	0.99
i16:1			0.39	0.24	0.47
br16:0	15.47839585		0.22	0.45	0.07
i16:0	15.63429732		1.45	1.68	2.04
16:1ω9c	15.71247294		2.28	3.04	2.38
16:1ω7c	15.76206021		19.51	21.78	16.85
16:1ω7t	15.79828736		0.88	0.89	0.42
16:1ω5c	15.85105235		4.17	3.31	2.11
16:0	16		10.96	13.70	21.66
br17:1a	16.29403794		0.00	0.00	0.33
br17:1b	16.34289784		0.65	0.43	0.82
i17:1	16.41313603		0.13	0.12	0.57
10Me16:0	16.44300356		0.66	0.39	0.00
12Me16:0			0.07	0.07	0.00
a17:1	16.49743877		0.00	0.00	0.00
i17:0	16.63733956		0.67	0.56	0.56
17:2	16.69284508		0.34	0.05	0.00
a17:0 & 17:1	16.73350911		1.51	1.21	1.48
Cy17:0a	16.80901386		1.67	0.55	0.69
Cy17:0b	16.83981216		0.11	0.12	0.00
17:0	17		0.39	0.29	0.25
diMe16:0	17.0654758		0.10	0.07	0.00
2oh16:0	17.162474		0.05	0.03	0.00
i18:1	17.36156392		0.09	0.07	0.00
2MeC18:0a	17.39109424		0.00	0.00	0.00
br18:0	17.42519926		0.53	0.50	0.00
18:4ω3	17.47966329		0.43	0.63	1.13
i18:0			0.03	0.07	0.00
18:2ω6 & i18	17.63157053		4.25	4.98	6.50
18:3ω3	17.67273227		3.77	9.13	8.05

Mol% Table		Sample	BSMM	SPMM	MPMM
		weight (g)	5	6	1
		dilution	600	600	1000
PLFA	retention time	Total Biomass	282,370	204,954	4,438,138
18:1ω9c	17.71877452	pmol/g	5.02	7.37	8.99
18:1ω7c	17.77417285		7.86	11.40	8.79
18:1ω7t	17.82311211		2.26	0.83	0.88
18:1ω5c			0.06	0.07	0.14
18:0	18		1.19	1.04	0.56
br19:1 & oh1	18.05464662		0.82	0.61	0.54
3oh-br17:0	18.15535016		0.04	0.04	0.00
Poly1	18.20755168		0.07	0.03	0.00
2MeC18:0b	18.34277507		0.10	0.10	0.10
10Me18:0	18.40495673		0.05	0.02	0.00
12Me18:0	18.43828751		0.08	0.03	0.00
2-19:1's			0.07	0.06	0.00
19:1(ω9c)	18.73820878		0.11	0.12	0.00
FA(250)	18.76675354		0.00	0.00	0.00
19:1(ω7c)	18.78242381		0.04	0.05	0.00
Cy19:0a	18.82183529		0.04	0.00	0.00
Cy19:0b	18.85141353		0.10	0.06	0.00
19:0	19		0.04	0.05	0.00
20:4ω6	19.21558249		0.80	0.67	0.04
20:5ω3	19.26480133		1.44	0.89	0.13
2-20:1's			0.29	0.10	0.00
Poly2	19.47501837		0.05	0.05	0.00
20:2	19.51726672		0.37	0.24	0.00
20:1(ω9c)	19.78188165		0.03	0.05	0.00
21:0	21		0.03	0.01	0.00

Vita

Meg Elizabeth Howard was born on April 7, 1973 in Lake Forest, Illinois. She is the younger of two daughters born to Jeane and William Howard. She graduated from Libertyville High School in Libertyville, Illinois in June of 1991. Attending college for a year at the University of Illinois, Chicago, she quickly realized city life did not agree with her. For the remainder of her undergraduate education, Meg attended East Carolina University in Greenville, North Carolina. Originally pursuing a degree in English with a focus on Journalism, her interest in Geology happened accidentally while taking an introductory course to fulfill a science requirement. After graduating in the summer of 1997 with a B.S. in Geology, Meg worked the next five years as a hydrogeologist for two different environmental consulting firms. She gained licensure as a Professional Geologist (P.G.) in the state of North Carolina in November, 2001. Becoming disenchanted with the business side of consulting, she decided to pursue a graduate degree and began attending the University of Tennessee at Knoxville in August of 2002. On October 9, 2004, she married Jason Alan Strother of Apex, North Carolina. In August of 2006, she completed her Master's degree in Geology, and currently works and resides in Asheville, North Carolina with her husband, dog Cody, and cat Mooch.