ASSESSING THE POTENTIAL OF NATURAL MICROBIAL COMMUNITIES TO IMPROVE A SECOND-GENERATION BIOFUELS PLATFORM

A Dissertation

by

AMY JO MACBEY HAMMETT

Submitted to the Office of Graduate Studies of
Texas A&M University
in partial fulfillment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

August 2011

Major Subject: Plant Pathology

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Approved by:

Chair of Committee,	Heather H. Wilkinson
Committee Members,	Daniel J. Ebbole
	Terry J. Gentry
	Mark T. Holtzapple
Head of Department,	Leland S. Pierson III

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ABSTRACT

Assessing the Potential of Natural Microbial Communities to Improve a Second-Generation Biofuels Platform. (August 2011)

Amy Jo MacBey Hammett, B.S., Texas Woman's University

Chair of Advisory Committee: Dr. Heather H. Wilkinson

Naturally occurring microbial communities from high-salt and/or high-temperature environments were collected from sites across the United States and Puerto Rico and screened for their efficacy in the MixAlco™ biofuel production platform. The MixAlco™ process, based on the carboxylate platform, is a sustainable and economically viable platform for converting lignocellulosic biomass to biofuels. Using a mixed culture of anaerobic organisms, lignocellulosic biomass is fermented into carboxylic acids, which are neutralized to their corresponding carboxylate salts. These salts can then be converted into a wide variety of chemical products and fuels (alcohols, gasoline, diesel, jet fuel). The central hypothesis is that microbial communities from relatively extreme environments, having evolved to withstand selection pressures similar to the conditions in the carboxylate platform, will exhibit high rates of biomass conversion. A total of 559 soil communities was screened as inocula in established laboratory-scale fermentations. We used pyrotag sequencing of 16S rRNA genes to characterize the bacterial components of the best-performing microbial communities. The best performing communities converted up to 3 times more biomass to acids than a

standard marine community inoculum. The community analyses have allowed us to determine the extent to which the same functional types are favored during fermentation, at both laboratory and demonstration plant scales. In all cases, we observed a shift from the more diverse sediment community to post-fermentation communities with relatively low diversity dominated by organisms in the phylum *Firmicutes*, specifically *Bacilli* and *Clostridia* classes. Despite the fact that the inoculum sources were both geographically and ecologically diverse, all of the post-fermentation communities were more similar to each other in community structure than to the corresponding original inoculum community. In addition, studies of the sediments used as inocula revealed that environmental parameters, such as pH and water content, were significantly correlated with bacterial community composition. The wealth of data provided by current sequencing technologies allowed us to question whether communities with high process performances tend to achieve that performance with similar community structures.

DEDICATION

I would like to dedicate this body of work to my family (Alice Hammett, Gary Hammett, Jennifer, Briana, Michaela, and Caitlyn Moores, Rebecca and Corky Childers), friends (Gabriel Gomez, Nani Cooper, Dottie and Duane Vigus), and to Robert Vigus for their unyielding support and love. I also dedicate this to Dr. Sarah McIntire, Biology Department Chair of Texas Woman's University, for her exemplary dedication to advancing the role of women in science and inspiring me to become a microbiologist.

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I would like to thank my committee chair, Dr. Heather H. Wilkinson, and my committee members, Dr. Daniel Ebbole, Dr. Terry Gentry, and Dr. Mark Holtzapple for their guidance and support throughout the course of this research. I would also like to thank Dr. Thomas DeWitt for assistance with biological statistics and Dr. Emily Hollister for instructing me in microbial community analysis.

Thanks also go to my friends and colleagues and the department faculty and staff in the Plant Pathology and Microbiology Department for making my time at Texas A&M University memorable. I would like to acknowledge the following colleagues for their assistance with this project: Julia Cope, Abria Haynes, Dr. Charles Greenwald, Elena Kolomiets, and Pedro (Ismael) Pesquera. Finally, I would like to acknowledge Howard Schultz for his inspiration and energy.

I would like to acknowledge The Texas Agrilife Research Bioenergy Program and The Texas A&M University Office of the Vice President for Research Energy Resources Program for providing financial support for this work. I would also like to thank Terrabon, Inc. for providing samples and performance data from the Advanced Biofuels Reasearch Facility located in Bryan, TX. MixAlco™ is a registered trademark of Terrabon, Inc. The use of the trademark does not constitute endorsement by Terrabon, Inc. Furthermore, Terrabon, Inc. did not provide any financial support for this work.

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CHAPTER I

INTRODUCTION

There is growing concern over the extensive use of fossil fuels. Energy security is under scrutiny because much of the world's crude oil supply is from regions that are politically unstable and those reserves are finite. Other important considerations that favor the reduction of fossil fuel use are the environmental impacts of drilling, oil spills, and increasing carbon emissions. Collectively, these issues have led to the advocacy of sustainable and renewable energy sources such as wind, solar, and biomass derived energy.

There are two major types of biomass derived fuel platforms in extensive use today (Agler *et al.,* 2011). One is the sugar platform; this platform uses purified enzymes to convert biomass to simple sugars that can then be fermented aseptically to fuels. This platform is heavily based on the use of starches from corn and is problematic due to its contention with food supplies. The other widely used platform is thermochemical conversion of biomass to syngas (e. g., CO_2, H, CO). The syngas is used as feedstock for conversion to fuels (Holtzapple and Granda, 2009). Although both of these platforms are viable, they are fraught with high costs associated with fuel production (Verbruggen *et al.*, 2010).

Another, well-established but lesser-known, renewable fuel production source is

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This dissertation follows the style of the *ISME Journal.*

the carboxylate platform (MixAlco™), which is a sustainable and economically viable platform for converting lignocellulosic biomass to biofuels. Using a mixed-culture of microorganisms, lignocellulosic biomass (i.e., dedicated energy crops, agricultural waste, or municipal waste) is fermented into carboxylic acids. These acids can then be neutralized to their corresponding salts and converted into a wide variety of chemical products (ketones, aldehydes, etc.) and fuels (alcohols, gasoline, diesel, jet fuel) (Holtzapple *et al.,* 1997; Granda *et al.,* 2009; Pham *et al.,* 2010). In the future, this platform and other similar technologies have the potential to supplement a portion of petroleum-based fuels with fuels from sustainable biomass sources at a cost that is potentially lower than current market prices (Fu and Holtzapple, 2010a; Granda *et al.*, 2009).

Pursuant to optimization of this process, naturally occurring microbial communities from high-salt and/or high-temperature environments were collected from sites across the United States and Puerto Rico and screened for their efficacy in this platform. The environmental conditions in which an organism evolves determines what processes are thermodynamically possible and the environment selects for organisms with enzymatic capabilities under such conditions (Hanselmann, 1991). The central hypothesis is that microbial communities, that evolved to withstand environmental conditions similar to those that occur in the fermentation platform, should exhibit superior performances. To date, 559 samples from 78 geographically distinct sites have been collected and screened for efficacy in the carboxylate platform (Figure 1; Appendices B, C, and D). Throughout this dissertation, a site is defined as one of the 78

distinct places and a locale, or sampling point, is a sample within a site. Results show that some of these communities can convert up to 3 times more biomass to acids in laboratory-scale screens than a control inoculum based on an established marine community (Figure 2).

Figure 1 Locations in the United States and Puerto Rico visited for the purpose of screening in the MixAlco™ process. In the figure above, which was obtained from Google Maps™ mapping service (January 2011), dark blue tacks indicate sites with salinities above 7 S m^{-1} (hypersaline). The sites with light blue tacks have salinities that range from 0 to 3.5 S m^{-1} (similar to seawater) and red tacks indicate thermal areas. The sites with sample sequences analyzed in this proposal are represented with dotted tacks. The tacks correspond to the 78 sites in this study. Due to scale, some single tacks represent multiple sites (e. g., there were 4 sites in Puerto Rico)

In the carboxylate process screen, we used conversion to rank the performance of the communities. Conversion is the ratio of the amount of volatile solids (combustible materials) that are digested to products by the microbial community to the amount of volatile solids added to the screen (Fu and Holtzapple, 2010a). To date, the most-studied microbial community used in this platform was collected from Galveston, Texas. The

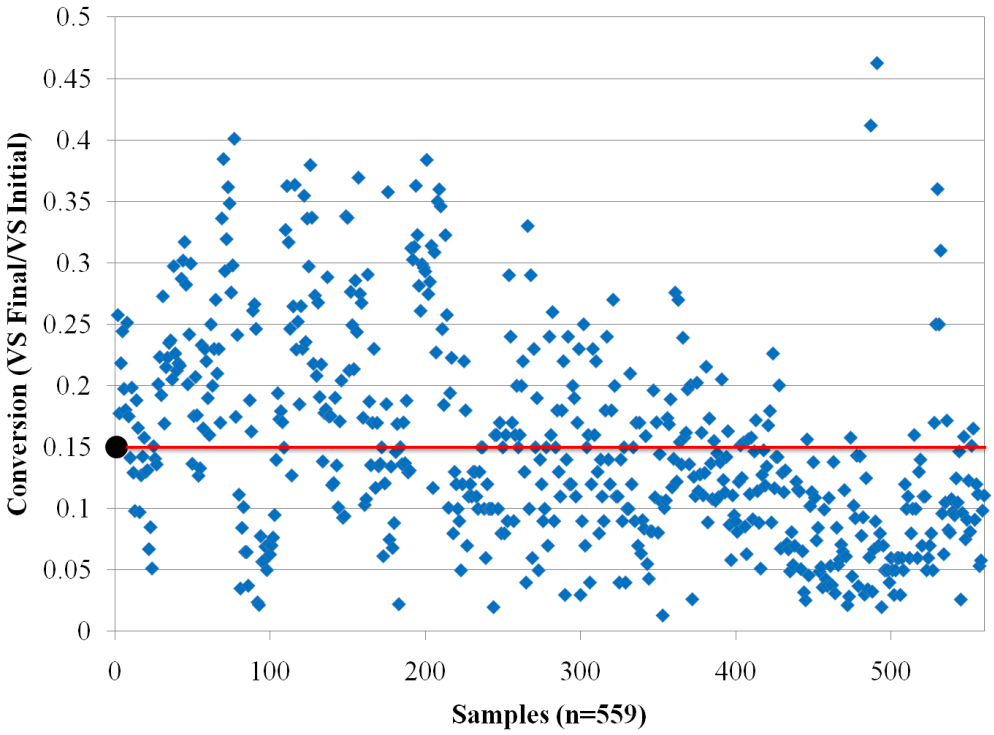

Figure 2 Conversion performances of all samples screened in the carboxylate platform fermentations. A total of 559 samples from 78 geographically distinct sites were collected and screened for efficacy in the carboxylate platform. The control inocula based on a marine community is shown by the black circle and red line. (VS, volatile solids)

community from this marine sand has an average conversion value of 0.15 (0.04 to 0.37). By way of comparison, the range of the top 10% of conversion performances for 559 communities collected from nature is from 0.28 to 0.46, which represents 1.9 to 3.1 times the average performance by the Galveston community (Appendix D).

Although the chemistry of the carboxylate platform is well understood (Holtzapple *et al.,* 1997), the microbial processes and community dynamics involved are largely unknown. There exists a great need to understand which organisms are responsible for the conversion of biomass to carboxylic acids and also what compositional shifts these communities undergo in the process. The communities with the best performances in the screen have been characterized for bacterial species composition using cultivation-independent methods. Some of those communities, with an emphasis on those from saline environments, are the focus of this dissertation.

In the carboxylate platform, salts of the carboxylic acids accumulate and thereby inhibit or kill members of the community that are not "pre-adapted" for process conditions. Therefore, we predict that communities that perform well in the platform will need to tolerate this selective pressure. Halophilic (requiring high concentrations of salts) and halotolerant (able to withstand a range of salinities) organisms are sought after for their extreme adaptability to conditions that would limit the application of many known useful organisms today. In nature, microorganisms able to thrive under high salinities have evolved a diverse array of special adaptations to cope with the extreme osmotic pressures in their surroundings, such as sodium ion transporters and high intracellular concentrations of osmotic solutes like glycerol and other sugar alcohols

(Gunde-Cimerman *et al.,* 2005; Rodriguez-Valera, 1986; Oren, 2002). These traits make them superlative for use in industrial processes, which tend to involve harsh chemical treatments such as large amounts of salts or acids (Oren, 2010). It is ideal in these cases to have organisms that can survive these conditions and still be biologically active to make desired products. Indeed, we found that communities collected from high-salinity sediments could perform quite well in the laboratory screen with performances above what is seen for the control marine community (Chapters II, III, and V).

Saline environments are widely distributed in all parts of the world. From seawater and coastal marshes, to solar salterns and inland salt lakes; high-salinity ecosystems represent extreme environments (Ventosa *et al.,* 1998; Rothschild and Mancinelli, 2001). Although limiting to many life forms, saline ecosystems harbor a diverse array of organisms in every domain of life and those organisms are important for the nutrient cycling and productivity of their ecosystems (Oren, 2002). There is substantial evidence that microbial communities in soils and sediments are more taxonomically diverse than any other natural environment and that salinity is a key influence in microbial community composition (Hollister *et al*., 2010a; Lozupone and Knight, 2007). Both environmental factors and geographic distance have been correlated with influences on microbial assemblages (Hollister *et al.*, 2010a; Martiny *et al.,* 2006; Pagaling *et al.,* 2009). To study the influence geographic distance exerts on microbial ecology, the study of microbial biogeography has emerged seeking to examine microbial diversity as it relates to spatial and temporal patterns as well as evolutionary events such as speciation (Martiny *et al.,* 2006; Pagaling *et al.,* 2009). From this, there is evidence to

support the idea that microorganisms vary in abundance, distribution, and diversity across a range of spatial scales and that microbial community composition is non-random (Martiny *et al.,* 2006). Based upon this, the collection of hundreds of samples from varying ecologies across the United States and Puerto Rico represents an attempt to screen as many phylogenetically diverse microorganisms as possible.

It has been estimated that 99% of microorganisms that exist in nature are un-culturable (Schloss and Handelsman, 2005). Previously, culture-independent methods based on sequencing of the hyper-variable regions of the 16S rRNA gene had limitations that only allowed a few hundred to a few thousand sequences to be identified. Though it is impossible to exhaustively describe every sample, these estimations of diversity based on only a few hundred members of the natural community do not accurately reflect the true diversity of the sample, because many members still remain unidentified (Shaw *et al.,* 2008). With the advent of next-generation sequencing techniques, such as 454 sequencing technology, and with the cost of sequencing larger numbers of libraries continually falling, researchers can estimate microbial diversity with greater speed (Rothberg and Leamon, 2008; Shendure and Ji, 2008).

The studies described herein involved pyrosequencing of the 16S rRNA genes using universal bacterial primers and analysis of those sequences using phylogenetic classifications, OTU analyses, and diversity indices (Schloss and Handelsman, 2005, 2008; Shaw *et al*., 2008). The hyper-variable region of the 16S rRNA gene makes it ideal to distinguish between closely related taxa and is the basis of many phylogenetic classification models (Huse *et al.,* 2008*;* Weider *et al*., 2005; Head *et al.,* 1998;

Weisburg *et al.*, 1991). Pyrosequencing, while having a higher error rate than traditional Sanger sequencing, has significant advantages over traditional cloning and Sanger sequencing because more of the community can be uncovered, revealing less dominant members that could have been lost because of cloning bias (Hollister *et al.,* 2010a).

Along with new sequencing technology have come many software advancements more appropriate for large datasets. One open-source software package, MOTHUR (Schloss and Handelsman, 2005, 2008; Shaw *et al*., 2008), is designed to specifically analyze pyrosequencing data for the microbial ecology community. It combines several data analysis tools together to describe and compare microbial communities using robust statistical algorithms. Using this program, we can to analyze communities by creating distance matrices based on pairwise distances and group sequences into operational taxonomic units (OTUs). Using an OTU-based approach to sequence analysis allows us to describe the richness, diversity, and similarity of the soil and fermentation microbial communities. We aim to analyze the alpha-diversity indices for single communities and compare communities using beta-diversity indices (Schloss and Handelsman, 2005, 2008). Alpha-diversity indices (e.g., the observed richness, Shannon index of diversity, and ChaoI richness estimator) enable us to evaluate the relative amount and abundance of species in single communities using well-established algorithms. For comparison of more than one community, beta-diversity indices (e.g., Jaccard and the Yu and Clayton similarity coefficients, θyc) were employed to reveal similarity between the structures and membership of two communities.

Using MOTHUR, we can identify the OTUs shared among multiple communities. This was particularly useful in the identification of taxa deemed to be important for the conversion of cellulosic materials because of their prevalence in the fermentation communities. Using pyrosequencing technology and a well-established data analysis pipeline developed in the Gentry Lab at Texas A&M University (Hollister *et al.*, 2010a) to survey the best-performing microbial communities allowed us to elucidate the organisms that tend to be present, and thus prescribe the components necessary to optimize the fermentation process, specifically efficient conversion.

In a study of nitrifying microbial diversity in batch reactors, the more diverse the original inoculum community the more stable the community was to making products when adverse conditions were imposed upon it (Daims *et al.,* 2001). This provides rationale to extensively study the diversity within the microbial communities used as inocula in the platform, which can then be compared to the community diversity in the corresponding fermentations. The information gained in the descriptive natural histories of the sediments studied here will also reveal the extent to which geographic distance, salinity and ecological variation influence species composition in a wide array of ecosystems.

A recent review of the carboxylate platform, states that the use of a mixed microbial community is vital to the fermentation process because the variety of metabolic pathways contained therein can handle many types of complex organic substrates (Agler *et al.,* 2011). The authors call for high throughput genomic approaches (e.g., pyrosequencing) to evaluate correlations between the environmental conditions

within the fermentations and microbial community composition. By understanding the community structure changes in both the laboratory-scale fermentations, and also at the demonstration-plant-scale, we can target groups of organisms that may be useful in the conversion process. It is reasonable to expect that some of these functional types of organisms uncovered in the present research could serve as components of a "seed" inoculum to optimize production in biotechnologies that employ the carboxylate platform. We may also be able to influence favorable community compositions by altering the conditions of the platform (e.g., temperature). The information elucidated through these studies will reveal a more detailed picture of the bacterial component of the MixAlco™ process, allowing us to guide our attempts to optimize efficiency and productivity.

CHAPTER II

SHIFTS IN BACTERIAL COMMUNITY COMPOSITION FROM THE INOCULUM SOIL COMMUNITY TO THE LABORATORY-SCALE FERMENTATION COMMUNITY

Introduction

Rising fuel costs and the increasing instability of crude oil production have led to an increased need for inexpensive and renewable sources of fuels. A major hurdle in the introduction of biofuels to mainstream consumption is the availability of economically viable platforms (Verbruggan *et al.,* 2010). Removal of pretreatment inhibitors such as acids, the use of expensive purified enzyme mixtures, and fermentation of cellulose and hemicelluloses under sterile conditions all increase the cost of production and, thus, decrease the profitability of the products. The MixAlco™ process, a carboxylate platform for biofuel production, is both sustainable and economically viable. This process circumvents the needs for the most expensive aspects of biomass processing: extensive biomass pretreatment, limited enzyme sources, and/or use of individual microbes under sterile conditions (Holtzapple *et al.,*, 1997; Holtzapple and Granda, 2009). The MixAlco™ process utilizes a naturally occurring mixed-microbial community to simultaneously hydrolyze cellulosic biomass (e.g., dedicated energy crops, agricultural or municipal wastes) into carboxylate salts (Holtzapple *et al.,*, 1997), which are concentrated and collected. The carboxylate salts are then used as feedstocks

to produce a wide variety of chemical products (e.g., ketones, ethers, esters) and can also be used to make liquid fuel (e.g., gasoline, diesel, and jet fuel).

There is a significant advantage to using a mixed community of organisms to degrade biomass. Naturally occurring microbial communities have evolved synergistic metabolic networks (Rittman *et al.,* 2008). Using mixed naturally co-occurring microbes in this process produces the ability to exploit these synergies and the tolerance conferred by the members to many types of complex substrates because of the variety of metabolic possibilities therein (Agler *et al*., 2011). In the carboxylate platform salts of the carboxylic acids (carboxylates) accumulate, and also, the process occurs at relatively high temperatures (40 °C or 55 °C), thus the process conditions inhibit or kill members of the microbial community that are not "pre-adapted". We hypothesized that microbial assemblages that evolved under conditions similar to those present in platform (high salt and/or high temperature) should be more efficient at biomass conversion and carboxylic acid production (Hollister *et al.,* 2010b; Forrest *et al.,* 2010). To optimize this process, naturally occurring microbial communities from high-salt and/or high-temperature environments were collected from across the United States and Puerto Rico (Figure 1) and screened for platform efficacy using laboratory-scale fermentations.

In addition to optimizing the process through the use of "pre-adapted" microbial assemblages, we set forth to thoroughly understand the bacterial community compositions responsible for proficient performance. Previous studies showed that the marine bacterial communities used in the process are dynamic and respond rapidly to changes in temperatures and substrates (Hollister *et al.*, 2010b; Hollister *et al.,* 2011). In

a study evaluating the microbial dynamics in a demonstration plant employing the MixAlco™ process, cellulose- and xylose-degrading bacteria appeared to dominate the fermentation despite a more diverse marine inoculum (Hollister *et al.*, 2011).

The objective of this study was to characterize multiple bacterial communities before and after undergoing the carboxylate platform laboratory screen. We aimed to evaluate which soil communities were best suited to convert biomass, and also, whether the best-performing communities resembled each other after selection in the fermentation screen. In total, 559 sediment samples from 78 distinct geographic locations were analyzed for process performance after incubation at 55 ºC for 30 days. Conversion was chosen to be the measure to rank fermentation performance. Conversion is the ratio of the amount of volatile solids (combustible materials) that were digested to that which was added. Therefore, it measures the amount of biomass that is converted in the fermentation process into all possible products by the microbial community. These products include carboxylic acids and other products not measured (e.g., hydrogen, carbon dioxide, ethanol, formic acid).

While maximizing geographic diversity, 19 samples from the top 10% of conversion values (0.28-0.46) as well as one sample within the top 15% of conversion values (0.27) (Great Salt Plains NWR, OK) were chosen for analysis (Appendix D). Employing tag-encoded pyrosequencing of partial 16s rRNA gene sequences from whole-community DNA preparations, a large library was constructed from these soils, along with their resulting fermentation communities. Characterization of the communities to evaluate the dominant organisms and compare the community structures

in the context of process performance metrics, allowed us to identify patterns associated with community composition and acids produced. The information gained from this study helps us to refine our attempts to optimize the efficiency and productivity of the carboxylate platform.

Materials and Methods

Sampling Procedure

Sites across the United States and Puerto Rico that were thermal and/or highly saline were chosen based on information from the Geo-Heat Center State Geothermal Databases, as well as internet based searches for national lands also meeting those criteria (Geo-Heat Center, Klamath Falls, OR). For all sites, we received the appropriate authorization (e.g., written or verbal permission, or permits) prior to sampling. For each sample, standard field statistics such as date, GPS coordinates, soil temperature, and a brief description of the site features and geochemistry were recorded on site. In most cases, we collected approximately 1.5 L of sediment or soil for each sample. Specifically, we used a standard stainless steel bulb planter (10-12 cm deep) to pull three adjacent cores, which were placed in independent zip-top bags. Subsequently, the zip-top bag was placed into a vacuum seal bag and the air removed using a Foodsaver™ vacuum sealer (Sunbeam Products, Boca Raton, FL). Each of the three cores was handled differently to accommodate different types of processing in the laboratory at Texas A&M (DNA extraction, soil analysis, and screening for fermentation performance). To insure high-quality nucleic acid extraction, we placed the first core on

dry ice as immediately as possible. We maintained the other two cores in an insulated cooler, such that they acclimated slowly to ambient temperature. Depending on distance to the sampling site and the length of time planned for the sampling trip, samples were either transported by the collection team or shipped to Texas A&M via Federal Express overnight, whichever method was faster and more feasible. Upon receipt, the frozen soil cores were placed at -80 °C immediately. Fermentations were established on the day the samples arrived. We placed all the remaining material at 4°C until further use for additional culturing or soil analysis. The two non-frozen samples were used for the screening process for the carboxylate platform performed in collaboration with Dr. Mark Holtzapple's laboratory at Texas A&M University and soil chemistry analysis performed with the Soil, Water and Forage Testing Laboratory at Texas A&M University. Any remaining samples were stored in vacuum-sealed bags at 4 °C.

Laboratory Fermentation Screen

The following methods for the MixAlco™ fermentation screen were based on methods described in Fu and Holtzapple (2010c) and Forrest *et al.* (2010) with some modifications. Autoclavable centrifuge bottles were used as reactor vessels in either 1 L or 250 mL volumes. The culture conditions consisted of 0.7% yeast extract, 20 g L^{-1} carboxylate salts (calcium acetate, calcium butyrate, calcium propionate), 0.13% urea, 1% calcium carbonate to buffer, with 6% shredded office paper as the cellulosic biomass in 600 or 150 mL of distilled water. Sediment (10 g wet weight) was added to the vessel and the solution was incubated at 55 °C in a rotary incubator for 30 days at 200 rpm. Production of methane gas (CH_3) reduces yield in this platform, so 40 μL of iodoform

(20 g L^{-1} ethanol solution stored at -20 °C) was added as an inhibitor of methanogens every 2 days (Hollister *et al*., 2010b; Forrest *et al.,* 2010). After 30 days of incubation, fermentation solids and broth were collected for carboxylic acid determination, volatile solid analysis, and storage for DNA extraction as well as inocula for future screens.

Soil Physical and Chemical Analysis

Sediment and soil samples were put into an incubator at 75 °C until all moisture was evaporated. Moisture content was taken by weighing the soil before and after drying. The dried samples were then ground with a porcelain mortar and pestle. Samples were sieved to 2 mm and submitted to the Soil, Water, and Forage Testing Laboratory at Texas A&M University for pH (Schofield and Taylor, 1955), detailed salinity (Rhoades and Clark, 1978), and electrical conductivity (Rhoades, 1982).Total carbon, organic carbon, and total nitrogen analysis was also performed (McGeehan and Naylor, 1988). The results of these analyses for all samples collected and screened in the carboxylate platform are listed in Appendix B.

Fermentation Analytical Methods

The following analytical methods are described in Forrest *et al.* (2010). Briefly, the concentration of carboxylic acids was measured by analyzing the fermentation broth by gas chromatography using an Agilent 6890 gas chromatograph with a flame ionization detector (FID), a 7683 series injector, and a 30 m fused-silica capillary column (J&W Scientific Model 123-3232). After 30 days of incubation, each fermentation vessel was centrifuged at 20 °C and 3297 × g for 30 minutes using a Beckman J-6B centrifuge (Beckman Coulter, Inc., Brea, CA, USA) to separate broth

from the solids. An aliquot of the supernatant was collected to analyze carboxylic acid composition. The supernatant collected was mixed with equal volumes of an internal standard (4-methyl-*n*-valeric acid) and 3 M H_3PO_4. The fermentation broth contains both carboxylic acids and salts. By adding acid to the broth, all salts are converted to their corresponding acids. The calibration standard was provided by Matreya, LLC. A portion of the solids was used to determine the amount of undigested volatile solids. Volatile solids (combustible components) in the initial substrate and solid fermentation residues were calculated by drying the material at 105 °C via NREL procedure No. 001, then ashing the material at 575 °C via NREL procedure No. 005 (NREL, 1996). Conversion values are obtained by dividing the amount of volatile solids digested by the amount of initial volatile solids.

Soil and Fermentation Community DNA Extraction

Whole genomic DNA was extracted according to the protocols in Hollister *et al.* (2011). The DNA was extracted using PowerMax Soil DNA Isolation Kits (Mo Bio Laboratories, Inc.) with the following modifications. A 15 g sediment sample plus 15 mL of bead solution was added to each bead beating tube. After 5 minutes of bead beating, lysozyme was added to a final concentration of 1 mg mL^{-1} and samples were incubated at 37°C for 1 h. The manufacturer's solution C1 was then added and the samples were incubated at 65 °C for 1 h. The manufacturer's protocol was followed thereafter. Following elution, the DNA was re-suspended in 10 mM Tris (pH 8.0). DNA concentration was determined using a NanoDrop™ spectrophotometer (NanoDrop

Technologies, Wilmington, DE), concentrated to at least 25 ng μL^{-1} and stored at -20 °C until further analysis.

Fermentation community DNA was extracted using DNeasy Blood and Tissue Kits (Qiagen, Valencia, CA). Prior to extraction, 2.5 mL of fermentation fluid and an equal volume of fermentation solids were placed in a 15 mL centrifuge tube and vortexed at max speed for 5 min. The sample was then centrifuged at 1000 × g for 2 min. The resulting supernatant was then centrifuged in 1.5 or 2 mL tubes at 5000 × g for 10 min until all supernatant was processed. The manufacturer's protocol for Gram-positive bacteria was then followed with the following modification: 200 μL of the elution buffer (10 mM Tris) was added slowly onto the membrane and allowed to incubate at room temperature for 3 min to allow more time for the DNA to bind to the elution buffer. DNA concentration was determined using a ND-1000 spectrophotometer (NanoDrop Technologies, Wilmington, DE) and concentrated to at least 25 ng μL^{-1} in an Eppendorf Vacufuge™ (Eppendorf, Hauppauge, NY), and stored at -20 °C until further analysis.

16S rRNA Gene Amplification and Sequencing

A total of 200 ng (25 ng μL^{-1} in 10 mM Tris pH 8.0) of purified whole community DNA was sent to the Research and Testing Laboratory (RTL, Lubbock, Texas) for tag encoded pyrosequencing. Prior to submission, community DNA was quality ensured by performing 25 μL PCR reactions using the universal bacterial primers 27F (5'-AGA GTT TGA TCC TGG CTC AG-3') and 1492R (5'-CGG TTA CCT TGT TAC GAC TT-3') (Lane, 1991), which amplify the entire 16S rRNA gene region. Each 25 μL reaction contained 100 ng of purified DNA, 1× reaction buffer (10× stock: 500

mM KCl, 300 mM Tris pH 8.3, 15 mM $MgCl_2$), 2.5 U *Taq* polymerase, forward and reverse primers at a final concentration of 0.4 μM each, 1 μM $MgCl_2$, 0.1 mM dNTP mix, and 1 mg mL^{-1} bovine serum albumin. Based on methods within Hollister (2008), thermocycling was conducted using a GeneAmp® PCR System 9700 (Applied Biosystems, Foster City, CA) under the following conditions: initial denaturation at 95 °C for 1 min; 30 cycles of denaturation at 94 °C for 1 min, annealing at 55 °C for 1 min, and extension at 72 °C for 1 min 30; and a final extension at 72 °C for 10 min. The 16S rRNA gene PCR products were confirmed by ultra-violet visualization on a 250 mL 1% agarose gel with 1× TAE (40 mM Tris-acetate, 1 mM EDTA) and a total of 50 ng ethidium bromide. After submission, tag encoded universal bacterial primers 27F and 519R (5'-GWA TTA CCG CGG CKG CTG-3') were used to generate amplicons using Roche 454 Titanium Chemistry (Lane, 1991; Dowd *et al.*, 2008). Sequences were quality checked by RTL according to Acosta-Martinez *et al*. (2008). An average read length of 400 bp was generated. Pyrosequencing reads were submitted to NCBI Short Read Archive under the accession number SRA039014.1.

Bacterial Community Characterization and Comparisons

Based on methods described by Hollister *et al*. (2011), all sequences were checked for quality, trimmed to similar lengths (>350 bp), and subsequently aligned using the Ribosomal Database Project (RDP) Release 10 Aligner tool (Cole *et al.,* 2007, 2009; Wang, Q. *et al.*, 2007) (accessed 27 May 2011). Taxonomic assignment and visualization tools were implemented using the Visualization and Analysis of Microbial Population Structures website maintained by the Josephine Bay Paul Center by

normalizing the library to the maximum number of sequences in all 40 sites (7,798) (Sogin *et al.*, 2011; http://vamps.mbl.edu/index.php) (accessed 28 May 2011). Sequence libraries were screened for potential chimeras using the chimera.slayer function in MOTHUR release 1.19 and the Silva.gold bacterial alignment template file accessed 10 May 2011 from the MOTHUR Wiki website (Schloss *et al.,* 2009; www.MOTHUR.org/wiki/ Silva_reference_files) All potential chimeras identified by MOTHUR were subsequently removed from the dataset. Distance matrices were then constructed using the RDP MOTHUR: column distance matrix function in the pyrosequencing pipeline tools. MOTHUR release 1.17 was then used to cluster operational taxonomic units (OTU, at 97% similarity). To have equal sample sizes for cross community comparisons, the entire library was normalized to the smallest number of site sequences in all 40 samples (1,317) using the normalize.shared function in MOTHUR version 1.19 (Schloss *et al.*, 2009). The Yue-Clayton (θyc) similarity measure was then produced for the normalized data set to determine the similarity in community structure between communities. This metric measures the distribution of OTUs between communities and their relative abundances (Yue and Clayton, 2005). The Jaccard index was also produced from the normalized data set to compare the similarity in community membership between communities. The Jaccard index measures the number of shared OTUs in a community to the total number of OTUs in the two communities being compared (Schloss *et al.,* 2009). Diversity indices such as Shannon's diversity index and Chao I richness estimates, as well as Yue-Clayton (θyc) similarity estimations between sites were also performed with MOTHUR release 1.19. Nearest-neighbor named

sequences to the most abundant OTUs were obtained from the chimera-checked GreenGenes NAST aligned database (Accessed 1 June 2011; DeSantis *et al*., 2006). Maximum parsimony phylogenetic trees with 1,000 bootstraps were constructed using nearest-neighbor named sequences and representative OTU (at 97% similarity) FASTA sequences in MEGA 5 (Tamura *et al.*, 2007). Non-metric multidimensional scaling (NMDS) was used to analyze the visual patterns of OTU compositions (at 97% similarity) with the Bray-Curtis similarity measure as implemented using the PAST software program (Hammer, *et al.,* 2001).

In an effort to link community composition with fermentation performance, the fermentation community composition and the amounts of acetic (C_2), propionic (C_3), butyric (C_4), and valeric (C_5) acids, as well as conversion, for each site were analyzed. The expected frequencies of bacterial classes obtained from actual counts were chi-square transformed. The acid data in g L^{-1} was square-root transformed and the conversions were arcsine square-root transformed and centered. This was to make the data more normally distributed for analysis and allowed analysis of 0 values (Legendre and Gallagher, 2001; Peres-Neto *et al*., 2006). Additional scaling of the acid data to 2 and the conversion data to 1 was performed on the principal coordinates. The resulting scaled principal components of the community classes and the fermentation data were then used to perform two block partial least squares regression (PLS regression) in Microsoft Excel 2008. Briefly PLS regression entails the community and the fermentation data matrices being multiplied and then undergoing singular value decomposition (SVD) using PopTools version 3.2.3. add-in for Microsoft Excel (Hood,

2010). The complete rows of the community composition matrix were then shuffled multiple times to obtain random values, which were also analyzed using SVD. The sum of the singular decomposition values from the original community principal components and the randomly generated principal components underwent Monte Carlo simulation with 10,000 replicates also using PopTools in Microsoft Excel 2008. The Monte Carlo generated p-values of <0.05 were considered significant. This simulation determines how many times the randomly generated singular decomposition value sums equal or exceed those produced by the original data. The same procedure was followed for the analysis of both the soil community classes and fermentation classes to the fermentation performance data, as well as the comparison of the soil classes to the fermentation classes. San Francisco Bay 20, CA was excluded from the performance analysis due to no data for acid products, but was included in the community analyses because it exhibited good conversion performance.

Results

Soil and Sediment Characteristics

Physical and chemical characteristics of each sample are listed in Table 1 and in Appendix B. The sites ranged in pH from acidic (2.30) to basic (9.59), with the majority of soils exhibiting a neutral pH range. The sites also ranged in salinity, as shown by electrical conductivity, from limited (0.14 S m^{-1}) to extreme (15.37 S m^{-1}). The average EC of seawater is between 3.5-5.0 S m^{-1} (Tables of physical and chemical constants, www.kayelaby.npl.co.uk, accessed 5 August 2009). There was also a range in sample

temperature from 9 to 64 °C. The sites can thus be separated into two groups based upon salinity and temperature. One group has salinities ranging from seawater to extreme salinity and the other has virtually no salinity and temperatures that are approximately 30 °C or above. One exception is Owens Lake, CA, which is both extremely saline and thermal, but for the purposes of this study is considered to be in the saline group. Another exception is Laguna Boquerón, PR, which had a very low EC level and was not a thermal feature. Also, Muleshoe Lake and Brazoria NWR 6 samples were 28.8 °C and 29 °C respectively, but are considered saline because of their high EC.

Performance in Fermentations

All 20 samples had high rates of biomass conversion (0.27-0.46), but each differed with respect to other performance metrics (Table 2 and Appendix D). Carboxylic acids are the desired fermentation products for this platform, and the type and quantity of those acids are also a measure of performance. The total amount of any individual acid produced ranged from 0.01 to 9.14 g L^{-1}. Although the amounts of particular acids varied from sample to sample, acetic (C_2) and butyric (C_4) acids represented the highest percentages of all carboxylic acids produced, averaging 72.90 % ± 3.49 and 20.39 % ± 3.14 respectively. Smaller amounts of propionic (C_3) and valeric (C_5) acid were produced, and the communities did not produce any appreciable higher carbon chain carboxylic acids.

Bacterial Community Composition and Cross Community Comparisons

After short, ambiguous, low-quality, and potentially chimeric sequences were removed, the entire library consisted of 185,756 partial 16S rRNA gene sequences.

There were 70,575 soil and 115,181 fermentation bacterial sequences. Each site was analyzed for its community alpha (within a community) diversity using MOTHUR software (Table 3). Among all samples, there were a total of 20,952 OTUs identified (97% similarity cutoff). The soil communities were far more diverse than their resulting fermentation communities as shown by higher Shannon (H') index values for each and the larger number of OTUs for each site. The soil communities comprised 91% of the observed OTUs. By all diversity metrics analyzed, the fermentation communities were less diverse than their soil communities.

Many bacterial phyla are represented in the soil library, although the phylum composition and relative abundance in each soil differ (Figure 3). The fermentation communities were dominated by the phylum *Firmicutes* (72% to 100%), which was never more than 1% of any soil community. There were two dominant classes observed within this phylum, *Clostridia* and *Bacilli*, with the relative proportion of each varying across fermentation communities (Figure 3). Other phyla observed in much fewer numbers in the fermentation communities were *Acidobacteria*, *Actinobacteria*, *Bacteriodetes*, *Planctomycetes*, *Proteobacteria*, and *Thermotogae*. The top 20 soil shared OTUs (occurring in five or more sampling points) were all classified as *Proteobacteria, Chloroflexi, Acidobacteria, Bacteriodetes,* and *Verrumicrobia* (Figure 4). The top fermentation shared OTUs (occurring in 10 or more sampling points) were *Firmicutes*, more specifically in the *Clostridia* or *Bacilli* classes (Figure 5). The most common genera observed in the fermentation communities were *Tepidimicrobium* (21%), *Ureibacillus* (19%), *Geobacillus* (17%), and *Bacillus* (14%), in that order. There

were a substantial number of sequences with unknown classification in both libraries, 16% of the total sequences (VAMPS, accessed 28 May 2011).

As seen in the θ*yc* and Jaccard index similarity dendrograms (Figures 6 and 7), the soil samples (squares in both figures) were more similar to each other than to the fermentation samples (triangles in both figures), and vice versa. One exception was the sample from Sufutara Trail, Yellowstone National Park (NP), WY, which groups with fermentation communities, albeit as a basal branch to the clade, on both dendrograms. Not surprisingly, samples that were taken closer to each other geographically (i.e., the same refuge) tended to be more similar to each other. Overall, the soil samples were very dissimilar from each other with many similarity values being below 1% (data not shown). This was because of the high diversity in each soil sample, indicated by both the diversity metrics and the taxa composition of each.

The fermentation samples tended to be more similar to each other than their initial inoculum. The θ*yc* values were all completely dissimilar for the comparison between the soil samples and the corresponding fermentation communities. Also, less than 1% of the sequences and OTUs observed were shared among the soils and the fermentations. Those OTUs that were shared were in the classes *Bacilli* and *Clostridia*, as well as, classes in the phylum *Proteobacteria*. Even though these classes dominated the fermentations they were not well represented in the soil library. Additionally, eight of the 20 sites in this study had no shared sequences with the corresponding fermentation communities.

Using the abundance of all OTUs at 97% similarity, non-metric multidimensional scaling (NMDS) was performed to further analyze the similarity of cross-community comparisons. Again, the sites grouped into soil communities and fermentation communities (Figure 8). As with the dendrograms, samples that were closer geographically tended to group together. All samples tended to group within the soil or fermentation group classification according to temperature of the original soil sample. The Puerto Rico (BWR1) sample grouped within thermal samples even though it was not thermal but was similar to them in salinity (Table 1). Therefore, all samples tended to group together within the soil or fermentation sets to a large extent based upon salinity and temperature.

Bacterial Classes Correlating with Fermentation Performance

All fermentations were dominated by *Firmicutes* but varied in their relative proportions of *Clostridia* and *Bacilli* (Figure 3). The relative proportions of acetic and butyric acid also varied across samples (Table 2). To test whether composition of bacterial classes within a fermentation affected the amount and types of acids produced, we first performed a principle component analysis (PCA) on bacterial class (the chi-square transformed relative abundance of each). The first principal component accounted for 55% of the variability and consisted of the loading of *Bacilli* and *Clostridia* classes (data not shown). The second and third principal component accounted for the rest of the variability, which were the loadings of *Gammaproteobacteria* and *Thermotogae*. In general, as *Bacilli* members increase the other classes decrease, and as *Gammaproteobacteria* members increase the *Thermotogae* decrease.

The fermentation acid data and conversion also underwent PCA (data not shown). The first principal component accounted for 90% of the variation and included all four types of acids. The next component accounted for 9% of variation and included the tradeoff between propionic acid and valeric acid. Overall, all acids increased together. However, the more valeric acid produced would decrease the amount of the others. Also, as acetic acid and propionic acid increase, butyric and valeric acid decreased.

Next, PLS regression and SVD were performed with each of the following: the principal components from the community classes, the principal components scaled to 2 from the acid data, and the scaled to 1 transformed and centered conversion values. The sum of those values was 1.71. The community matrix was then shuffled several times to obtain randomly generated fermentation community compositions. A Monte Carlo simulation with 10,000 replicates was performed to compare the experimentally derived SVD sum with one that was randomly generated. The randomly generated value was observed 159 times out of 10,000. This resulted in a *p*-value of 0.0159, which was significant. The first singular vector pair, which accounted for 83% of the variation, indicated that when there are more members of the class *Bacilli* present, *Clostridia* members decrease and the amounts of all acids decreases, whereas conversion improves slightly. The second singular vector pair, accounting for 15% of the variation, indicated that as the numbers of *Gammaproteobacteria* increase both the amounts of acids produced and the conversion levels decrease. Therefore, the experimentally observed

community composition significantly correlated with both the amounts and types of acids produced and the level of conversion (Figure 9).

PCA was also performed on the soil class composition treated the same as the fermentation classes above. The first principal coordinate accounted for 55% of variation and consisted of equal loadings of all bacterial classes in the soil (data not shown). The first four principal coordinates were chosen to perform PLS regression and SVD with the same acid and conversion values as above. After Monte Carlo simulation, the randomly generated soil community composition produced a singular decomposition value sum that equaled or exceeded the experimental value 4,992 times out of 10,000. This produced a non-significant *p*-value of 0.4992. Therefore, the soil community composition was not an indicator of the resulting fermentation performances.

A similar procedure of PLS regression and SVD was also performed for the principal components of the soil classes and the fermentation classes to evaluate if the composition of the soil community could predict the fermentation community (data not shown). After Monte Carlo simulation, the randomly generated soil community composition was observed 6,658 times out of 10,000 replicates. This produced a *p*-value of 0.6658, which was not significant. Therefore, the class composition of the soil communities was not seen to be a significant predictor of the class compositions within the fermentations.

Discussion

There was a large amount of diversity associated within the studied soils. Each

soil sample contained sequences that included representatives of many bacterial phyla (Figure 3). This is commonly seen among environmental soil and sediment samples (Hollister *et al.*, 2010a; Lozupone and Knight, 2007; Fierer and Jackson, 2006). Environmental parameters such as pH, moisture content, salinity, and temperature influence bacterial community composition (Hollister *et al.,* 2010a; Fierer and Jackson, 2006; Ikenaga *et al.,* 2010). The NMDS showed the bacterial communities within the soils were more similar to other soils based upon salinity and temperature (Figure 8). The fermentation communities also seemed to be more similar based on these soil factors between fermentation samples. The soil communities were all more similar to each other than the fermentation communities, and vice versa, as measured by a variety of tests.

The selective pressures imposed during the carboxylate screen selected for a narrow range of organisms despite high diversity of the inocula. Phylum *Firmicutes* dominates the fermentation communities, even though these groups of organisms are a minority component of the sediment communities (<1% of the total soil library). Further, the dominant classes seen are *Clostridia* and *Bacilli.* Both classes are known to have members that degrade lignocellulose and cellulose, and are frequently isolated or detected in association with composting and/or other biofuel projects (Watanabe *et al.,* 2010; Tamaru *et al.,* 2010; Izquierdo *et al*., 2010). For example, the genera *Geobacillus* and *Ureibacillus* in the Class *Bacilli* (both dominant genera in the fermentations), are widely distributed genera associated with hot springs and livestock manure composts respectively (Wang, C. *et al.*, 2007; Al-Qodah, 2006; Weon *et al.*, 2007). *G.*

stearothermophilus is highly desirable for forming heat-stable α-amylases that degrade starch and agricultural wastes to supplement animal feed (Al-Qodah, 2006; Ugwuanyi *et al.,* 2008). The selection of these cellulose-degrading organisms is not surprising given that cellulose is the primary carbon source in the screen.

The experimentally observed fermentation community composition was significantly correlated with the increase of both the amount and types of acids produced, and the level of conversion. The community ordination plot of the Singular Vector Pair 1 (fermentation community SA1 and acid SA1) from the SVD showed that as the number of *Clostridia* increases in a community the total amounts and types of acids also increase (Figure 9). However, conversion increased with the proportion of *Bacilli*. As the proportion of *Bacilli* declined in a community, being replaced by a more diverse assemblage including *Clostridia*, *Gammaproteobacteria,* and *Thermotogae* classes, the total amount of acids increased. This was shown by the larger amount of higher molecular weight carboxylic acids produced in these more diverse communities than in those dominated by *Bacilli*.

The trade-off between *Bacilli* and *Clostridia* classes in the fermentations warrants further study. It is not known precisely what parameter in the screen favors one over the other. The soil community composition was not an indicator of the resulting fermentation performances, nor did it predict the class composition of the fermentations. The screen was designed to be reduced in complexity relative to industrial applications employing the carboxylate platform, so there are limited ecological niches available to exploit. However, oxygenation levels of the samples during the screening process could

have influenced the community compositions. Iodoform addition every two days to inhibit methanogens could have introduced varying levels of oxygenation during the 30-day screening process between the samples. *Bacilli* organisms are facultative anaerobes and *Clostridia* are strict anaerobes (Vos *et al.*, 2009); however, some *Clostridia* organisms possess mechanisms to be fairly aerotolerant, such as superoxide dismutase (Hillman, *et al*., 2008).

Although some studies of the bacterial community dynamics in the carboxylate platform have been performed, this study is the first attempt to compare the diversity of a wide range of inocula from different ecologies to the fermentation communities. This direct comparison of the communities in the soil inocula, collected from a wide variety of sites geographically, with the fermentation material allowed us to determine the extent to which the same organisms are favored under screen conditions. More specifically, we determined that these communities with the best performances based on conversion tend to achieve that performance with similar community structures. Using this information, those organisms responsible for efficient conversion of biomass can be selectively targeted in the future for inoculum development and/or enzyme discovery. We have begun to elucidate the organisms that tend to be present, and thus, prescribe the components necessary to optimize the fermentation process, specifically efficient conversion.

CHAPTER III

BACTERIAL COMMUNITY COMPOSITION IN MIXALCO™ FERMENTATIONS AT BOTH LABORATORY AND DEMONSTRATION PLANT SCALES

Introduction

In 2010, fossil fuels accounted for 83% of the total energy consumption in the United States and renewable sources accounted for 7% (U. S. Department of Energy, 2009). In 2008, the United States consumed 378 million gallons/day in gasoline alone. In response to the need to reduce our need for foreign oil, the Renewable Fuel Standard of the United States Energy Independence and Security Act (EISA), mandated in 2007 that 36 billion gallons of biofuels are to be produced annually by 2022. Of that, 16 billion gallons are expected to come from lignocellulosic biomass.

In the spring of 2009, Terrabon, Inc.'s Advanced Biofuels Research Facility (MixAlco™ demonstration plant) located in Bryan, Texas opened to test the MixAlco™ process at a semi-industrial scale. This demonstration plant holds 400 tons of dry biomass, which, after being inoculated with a mixed community of microorganisms, is converted to carboxylate salts (Hollister *et al.*, 2011). These salts are then collected and transformed into a wide array of chemical products (ketones, aldehydes, etc.) and liquid fuels (gasoline, diesel, jet fuel).

This process employs the use of multiple types of feedstocks and a mixed-microbial community able to hydrolyze and ferment the substrate in a single step (Fu and Holtzapple, 2010b). Dedicated agricultural crops and residues can be utilized as well

as non-traditional cellulosic biomass like municipal wastes and animal manures (Aiello-Mazzarri, 2005). The utilization of such waste products significantly benefits the environment by saving such materials from landfills and possible groundwater contamination, and also, lowers costs associated with acquiring suitable biomass. Another major advantage to this platform is the production of fuels suitable for use in current vehicles and transportability using existing infrastructure. This technology has proven useful at both pilot-plant and semi-industrial scales (Hollister *et al.,* 2011).

The mixed-microbial community used to inoculate the demonstration plant originated from Port Arthur, Texas. An investigation of the microbial community composition and dynamics at the plant by Hollister *et al.* (2011) provided insights into the dominant populations in this facility. The bacterial community was quite dynamic and adaptable to changing conditions during the course of 80 days. The community, which was originally quite diverse in the marine sediment, became dominated by *Clostridia* and *Bacteriodetes*-like organisms. *Firmicutes* also dominate in studies of the process using an established laboratory screening protocol (Chapter II; Hollister *et al.,* 2010b; Golub *et al.,* 2011). This similarity in community structures between the demonstration plant at Day 30 and the laboratory screen studies prompted evaluation of the extent to which the laboratory screen predicts outcomes at the demonstration-plant scale when employing the same inoculum community.

The aim of this work is to assess the scalability of the laboratory-scale screen used to evaluate naturally occurring bacterial communities for process efficacy. Tag-encoded pyrosequencing of partial 16s rRNA gene sequences were used to compare the

community compositions of the inoculum (common to all treatments, derived from marine sediment), the demonstration plant at Day 30, a laboratory screen at Day 30 maintained at 40 °C, and a laboratory screen at Day 30 maintained at 55 °C.

This study evaluated whether screening protocol currently in use (Chapter II) was an effective method to predict outcomes in the bacterial community structure and carboxylic acid profiles at a larger scale, specifically, the demonstration plant. Because all laboratory screens are performed for 30 days, it also revealed which screen temperature best reflects the community composition in the plant after a similar amount of time. Knowledge of which cellulose-degrading organisms were enriched in laboratory-scale fermentations during screening and in the biofuels research facility could prove useful in efforts to develop inocula for future demonstration plant inoculations and other biofuel research. This information will also help to improve screening techniques employed in the future.

Materials and Methods

Demonstration Plant Conditions

The following methods are based on Hollister, *et al.* (2011). Terrabon Inc's Advanced Biofuels Research Facility (Bryan, TX), as described by Granda *et al.* (2009), was designed to implement the MixAlco™ platform at a semi-industrial scale. In the summer of 2009, the facility was loaded with 286 dry tons of chipped, pretreated sorghum (*Sorghum bicolor* (L.) Moench) in a slurry volume of 1.3 million liters. The sorghum was pretreated with lime ($Ca(OH)_2$) and maintained at ambient temperature as

described in Kim and Holtzapple (2005). Iodoform (CH_3I) was added to the slurry to inhibit methanogens. The pretreated sorghum slurry was inoculated with marine sand dredgings obtained near Port Arthur, TX. After inoculation, the system was closed and allowed to reach an anaerobic state while maintaining a temperature of approximately 40 °C.

Sample Collection

An aliquot of the Port Arthur marine sediment was collected at the time of demonstration plant inoculation and a fermentation sample was collected after 30 days. Collection procedures are described in Hollister, *et al*. (2011). Approximately 1 L of the marine inocula and 30-day material was collected. The slurried samples were placed in 1 L bottles, sealed, and placed on ice until arrival at Texas A&M University. The samples were then centrifuged (3000 × g, 30 min) to concentrate the solid materials and subsequently stored at -80 °C until DNA extraction (October 2009). DNA extraction of all thawed solids from the demonstration plant and the Port Arthur sediment were performed in October 2009 using PowerMax Soil DNA extraction kits as described in Chapter II (Mo Bio Laboratories, Inc., Carlsbad, CA, USA).

Laboratory Screening of Port Arthur Inoculum

Laboratory screening, using shredded paper as the biomass, was performed as described in Chapter II with the following additions. Port Arthur sediment collected at the time of plant inoculation (Summer 2009) was stored in sealed 1 L bottles in a dark container at 4°C until screen inoculation (November 2009). Port Arthur sediment (10 g) was used to inoculate 1 L fermentation bottles with three replicates at 40 °C and 55 °C.

Fermentation Performance Analysis

The fermentation metrics for the laboratory screens used in this study were conversion and carboxylic acid concentrations (C_2-C_7) (g L^{-1}) determined as described in Chapter II. Carboxylic acid and total acid data was analyzed by gas chromatography and obtained from Terrabon, Inc for the demonstration plant sample. Comparisons of the laboratory screen acid concentrations (three replicates each) were performed using a paired, student's *t* tests and *p* values of <0.05 were considered to represent significant differences. A comparison was also made between the screen acid data relative to that of the demonstration plant by subtracting the average acid value from each screen from that in the demonstration plant.

Bacterial Community Analysis

Post laboratory screen material was collected after 30 days (December 2009) and stored at -80 °C until DNA extraction using DNeasy Blood and Tissue Kits (Qiagen, Valencia, CA). The sample from each replicated laboratory screen with the highest fermentation conversion was chosen to be tag encoded pyrosequenced as described in Chapter II. Nearest-neighbor named sequences to the most abundant OTUs from the screens and demonstration plant, which represented 1% or more of the total sequences, were obtained from the chimera-checked GreenGenes NAST aligned database (Accessed 30 May 2011; DeSantis *et al*., 2006). Neighbor-joining phylogenetic trees using the Jukes and Cantor substitution model with 1,000 bootstraps were constructed using nearest-neighbor named sequences and representative OTU (at 97% similarity) FASTA

sequences in MEGA 5 (Tamura *et al.*, 2007). All other analyses were as described in Chapter II.

Pyrosequencing reads were submitted to NCBI Short Read Archive under the accession number SRA039017.1.

Results

Laboratory Screen Performance

Acetic acid (C_2) was the most abundant acid produced in all fermentation samples (Table 5). The fermentations produced all carboxylic acids ranging from C_2-C_7. The difference between the replicated screen samples acid signatures were tested by paired, Student's t-tests. The 55 °C screen produced significantly more acetic acid than the 40°C screen, $p<0.05$. However, the 40 °C screen produced more higher chain carboxylic acids than the 55 °C screen as seen by higher levels of valeric (C_5) and heptanoic (C_7) acids, however, this difference was not significant ($p<0.10$).
All fermentation samples were collected at 30 days post inoculation using the Port Arthur microbial community. Relative to both screens, the demonstration plant sample (performed at 40 °C) produced less total acid per liter (Table 5). Similar to the 40 °C screen, the demonstration plant also produced more higher-chain carboxylic acids than the 55 °C screen (Figure 10).

Bacterial Community Composition and Cross Community Comparisons

Sequence analysis of the Port Arthur inoculum sample, obtained at the time of demonstration plant inoculation, produced 5,560 16S rRNA gene sequences. According

to OTU analysis at 97% similarity, the inoculum consisted of 2,310 OTUs. The dominant classes in the sample were *Flavobacteria* and *Gammaproteobacteria*. In comparison with the fermentation samples, the sediment community was more diverse, as shown by the higher Shannon (H') index value of 7.10 and 70% of observed OTUs (Table 6).

The demonstration plant was less diverse than the inoculum. There were 608 OTUs observed whereas the number of sequences was 7,332. The diversity of the laboratory screens was even more limited than the demonstration plant (Table 6, Figure 11). Both screens had relatively low Shannon (H') similarity index values and much-reduced OTU numbers. The number of OTUs in the inoculum was 47% of the number of sequences whereas both screens had approximately 5% of the number of sequences cluster into OTUs. A few bacterial classes dominating all fermentation samples reflect the lowered diversity of the fermentations. The dominant class in the demonstration plant was *Bacteriodia*. *Clostridia* organisms dominated both screens and also comprised a large portion of the demonstration plant sequences (Figure 11). Analysis of the dominant OTUs revealed that the fermentation samples shared sample-dominating organisms related to *Clostridium butyricum*, *Clostridium cellulosi*, *Prevotella ruminicola*, *Ralstonia mannitolilytica*, *Bacillus circulans*, and *Fibrobacter succinogenes* (Figure 12).

All of the fermentation samples shared more OTUs between each other than the inoculum (Figure 13). Both of the laboratory screens did not share any OTUs with the inoculum. However, the demonstration plant did share six out of 608 OTUs (~1%) with

the Port Arthur sample. The laboratory screens shared approximately 15% of both screens' OTUs with each other. Therefore, the laboratory screens were more similar to each other than to either the inoculum or the demonstration plant samples. This is also shown in the dendrograms based on similarity in community membership and community structure (Figures 14 and 15). Both dendrograms show that although the demonstration plant was more similar in community membership and structure to the other fermentations, it was more similar to the inoculum sample than the others. Some variation between the inoculum community and the screens could have resulted from a change in the inoculum community between the time it was sequenced (October 2009) and the time it was used as inoculum (December 2009). It is not known how much change in inoculum community composition, if any, may have occurred during storage.

Using the abundance of all OTUs at 97% similarity, NMDS of all the samples based on Bray Curtis similarity index was performed to further analyze the similarity between samples. NMDS also shows a similar trend as the both the similarity in community membership and structure dendrograms which was that the laboratory screens were most similar to each other and all fermentations were dissimilar to their inocula (Figure 16).

Discussion

In agreement with the conclusions supported in Chapter II, across all scales, the fermentation community diversity was less complex than the originally diverse inoculum. We have shown that all of the fermentations were quite different than their

inoculum. Also, the two laboratory screens were more similar to each other than the demonstration plant. No shared OTUs between all of the samples were observed. However, there were shared OTUs between the demonstration plant and the inocula and the laboratory screens.

In a comparison with a thermophilic (55 °C) fermentation community, a mesophilic (40 °C) community employing the carboxylate platform produced significantly different amounts of certain higher molecular weight carboxylic acids and was more productive, even though they converted similar amounts of biomass (Hollister *et al.,* 2010b). There were also significant differences in the acid profiles of the two screens here. The 55 °C screen produced significantly more acetic (C_2) acid, which was also the dominant acid produced in all samples, than the 40 °C screen, $p<0.05$. At the 90% confidence level, the amounts of valeric acid (C_5) and heptanoic acid (C_7) also significantly differed between the screens. The 55 °C screen samples produced the most total acid and the demonstration plant produced less total acid per liter than the screens.

The 40 °C screen supported a more diverse community than the 55 °C derived community. The lower temperature seemed to favor more phylotypes to be metabolically active, and therefore sequenced, than the highly selective elevated temperature. The Port Arthur inoculum was derived from a mesophilic environment (marine sand) and as expected, should harbor a community best suited for such temperatures. Also, the more diverse community of this screen could produce a wider range of carboxylic acids. The 55 °C communities produced much less caproic and no heptanoic acid.

In a previous study of the MixAlco™ demonstration plant, it was found that the Day 30 community was comprised of both *Bacteriodetes* and *Clostridia* organisms (Hollister *et al*., 2011). This was also seen here. *Bacteriodetes* are known degrade both xylose and xylan and *Clostridia* has many known cellulose-degrading organisms (Chassard *et al.,* 2008; Izquierdo *et al*., 2010). The co-occurrence of these organisms serves to digest complex biomass.

Compared to the demonstration plant, both screens had a more narrow community. The community structure observed herein was similar to those of fermentation communities in Chapter II. They were dominated by *Bacilli* and *Clostridia*, albeit in different ratios. The more limited communities, compared to that of the demonstration plant, could be due to the much less complex biomass of the screens. The demonstration plant employed pretreated sorghum and the screens were constructed with paper (primarily cellulose). A more diverse assemblage of organisms is supported with the sorghum, where there are many substrates, besides cellulose available to exploit, such as lignin, hemi-cellulose, and xylose. Indeed, a comparison of marine inocula degrading sorghum at these two temperatures found similar results (Hollister *et al.,* 2010b). Based upon this, the consortium of *Bacilli* and *Clostridia* organisms found within the many screen fermentation communities are well suited and selected in the screen to efficiently degrade cellulose in the form of paper. In the future, a more appropriate screening technique would be to employ the degradation of a more complex substrate, such as sorghum. This would more accurately predict the community

responses in an industrial application where the degradation of a more complex substrate would be necessary.

CHAPTER IV

COMPARISON OF INOCULUM STORAGE CONDITIONS: EXAMINING THE EFFECTS ON BACTERIAL COMMUNITY DIVERSITY, COMPLEXITY, AND COMPOSITION

Introduction

It takes great effort, time, and resources to gather environmental samples, transport them, and screen them for traits of interest. Therefore, a storage method that maintains the diversity and species composition of the original sample is advantageous. A literature review shows that there are many methods to maintain the viability of microbial cells. Freeze-drying (lyophilization) bacterial cells maintains cell viability for many months and results in an easily maintained and rehydrated product (Costa *et al.*, 2002; Devaldez *et al.,* 1985). Freezing samples is also a widely accepted method of bacterial storage. The addition of a cryoprotectant such as glycerol is shown to increase cell viability during storage at sub-zero temperatures (Felthman *et al,* 1978; Sambrook and Russell, 2006).

Currently, four storage methods are used routinely to maintain the collection of communities from the fermentation screens described throughout this dissertation: freeze drying, frozen at -20 ^{o}C with or without 20% glycerol, and refrigeration at 4 ^{o}C.
In our community-screening project, after the original 30-day laboratory screen, communities with high conversion values are characterized in more elaborate screens, such as continuous particle distribution modeling or countercurrent trains (Fu and

Holtzapple, 2010a, 2010b, and 2010c). These screens are more labor intensive and can take many months to complete. Original fermentation materials maintained at -20 °C in glycerol are used to inoculate a culture of the community in the same conditions as the original screen (up culture) and a portion of the up culture is used to inoculate the subsequent screens. The goal of this study was to sequence communities grown from each of these storage conditions to elucidate the method that best maintains the community structure produced during the original screen, in order to use the adapted original community as an inoculum for accurate downstream applications.

This study is based on an experiment wherein four communities were grown from each of the four storage conditions in media identical to that used in the original screen. These small cultures were allowed to grow for 96 hours to capture logarithmic growth of viable organisms and to ensure that those lineages within the community that survive the storage condition were the most represented. Analyses of the resulting sequences revealed which storage method(s) most accurately maintained the original community and were, therefore, the optimal method(s) to use both as potential inoculum and long-term storage.

Materials and Methods

Four storage methods were employed to save fermentation material from the original screen of environmental samples (Chapter II). The methods were as follows: 1 to 15 mL of material at 4 °C in a dark container, 2 mL of material at -20 °C in cryogenic tubes, 2 mL at -20 °C with 20% sterile glycerol in cryogenic tubes, and approximately

20 mL of freeze-dried (lyophilized) material kept inside air-evacuated sealed bags in dark containers at 4 °C. The use of each of these methods was based on a literature review of maintaining the viability of microbial cells (Costa *et al.*, 2002; Devaldez *et al.,* 1985; Felthman *et al.*, 1978; Sambrook and Russell, 2006).

Fermentation materials from four sites stored via the four methods were used as the inoculum in a scaled-down version of the laboratory screen on October 17, 2009. Four previously studied communities involved in multiple screens were chosen: Great Salt Plains NWR 8, OK (E08; stored November 13, 2008), Brazoria NWR 2, TX (F02; stored November 25, 2008), Bitter Lake 8, NM (G08; stored December 19, 2008), and San Francisco Bay NWR 1, CA (H01; stored March 14, 2009). The storage times, relative to the start of this experiment, for each of the chosen sites were as follows: 11 months 5 days (339 days), 10 months 23 days (327), 9 months 29 days (303 days), and 7 months 4 days (218 days), respectively. The constituents of the screen media are described in Chapter II. The calcium salts, yeast extract, calcium carbonate buffer and water were combined in the appropriate concentrations for twenty 10 mL screens and autoclaved. Iodoform (25 μL) was added to each tube to inhibit methanogens. The final volume in each vessel was 10 mL. Each stored material was vortexed briefly to homogenize the samples and 100 μL of each sample (4 °C, -20 °C, and -20 °C with 20% glycerol) was added to the experimental medium prepared in 50 mL centrifuge tubes as inoculum. In addition, 1/20 of the total amount of lyophilized material was reconstituted to 1 mL using sterile filtered distilled water and 100 μL of this was used as inoculum. The cultures were assembled in a 50 mL centrifuge tube with 0.9 g of autoclaved and

shredded paper placed inside. The headspace of each tube was purged with nitrogen gas, capped, and the rack containing the tubes placed inside a sealed nitrogen-filled heat-sealed bag. To mimic conditions of the original screening for 96 h, the bag was placed inside a dark rotary shaker and incubated at 55 °C at 200 rpm. Each tube was then vortexed at maximum speed for 5 min and placed in -80 °C until DNA extraction. Half of the fermented material was used for whole-community DNA extraction using DNeasy Blood and Tissue Kits (Qiagen, Valencia, CA) as described in Chapter II.

The original fermentation communities were sequenced and studied in Chapter II and are also a part of this chapter. Bacterial community analysis was performed also as described in Chapter II.

Pyrosequencing reads were submitted to NCBI Short Read Archive under the accession number SRA039013.2.

Results

In all storage sets, the original fermentation community was more diverse than the stored samples as shown by both higher Shannon (H') similarity index values and more OTUs at 97% similarity (Table 7). Bacteria in the phylum *Firmicutes*, the organisms that dominated fermentation samples in Chapter II and Chapter III, also dominated all samples in this study, although the relative proportions of the classes *Bacilli* and *Clostridia* varied both between storage sets and within a storage set (Figure 17). However, the dominant genera within these classes varied between storage conditions within each sample set (Figure 18).

Within each set, there were storage samples that were quite different phylogenetically relative to the corresponding original sample. For example, the original fermentation sample from Bitter Lake was comprised of *Bacilli* and *Clostridia*, 27% and 72% respectively, whereas the refrigerated sample from this was dominated 99% by *Bacilli*. A similar event took place in the Brazoria NWR storage set where the sample had 20% *Bacilli* and 69% *Clostridia* in the original fermentation but the frozen sample with glycerol was dominated by 89% *Bacilli* and the refrigerated sample 99% *Clostridia*.

The fermentation samples from Great Salt Plains and Brazoria NWR both had a portion of sequences in the *Thermotogae* phylum that were not evident in their storage samples. Similarly, all original fermentation samples had unknown sequences that were not found in their storage communities. This indicates that both *Thermotogae* and some unclassified organisms were lost during the course of storage. Both *Bacilli* and *Clostridia* classes were present in varying proportions within each storage method.

We detected no consistent effects of storage method on the amount of diversity preserved in a sample or the dominant class of organisms. The storage method with the most diversity was different for each sample set (Table 7). The ranking of storage methods with respect to the numbers of OTUs shared with the original community was different across sample sets (Table 8). Many of the shared OTUs between the original fermentation community and the storage methods comprised a small number of the dominant OTUs within the original sample. There was a general trend for the lyophilized sample to share the fewest numbers of OTUs with the original sample. Furthermore, similarity indices indicated that there was a trend for the original fermentation to be

more similar in community membership and structure with one of the frozen samples, either the "gl" or "20" or samples (frozen with or without glycerol respectively) (Table 8).

Discussion

Although still differing from the original community, the frozen samples, either with or without glycerol, were the most similar to the original fermentation screen community. This is a reasonable outcome considering storage at freezing temperatures slow down microbial metabolism and the addition of glycerol decreases the amount of ice crystal formation in the sample, which increases the survival of microorganisms in sub-zero temperatures (Feltham *et al.,* 1978).

Over extended periods of time, each of these storage methods maintained organisms, *Bacilli* and *Clostridia*, which have been shown to be important in fermentation performance in Chapters II and III. Both *Bacilli* and *Clostridia* classes were present in varying proportions within each storage method so it could be concluded that no storage method seemed to have a negative or positive impact on the preservation of either class. In addition, neither storage time or storage method seemed to affect the preservation of these dominating classes. However, many of the shared OTUs between the original fermentation community and the storage methods are a small number of the dominant OTUs within the original sample. It is not known how the loss of *Thermotogae* and unclassified organisms in storage would affect future fermentation performances.

The original sediment communities were studied in Chapter II. Before this experiment occurred, the original sediment communities underwent a number of bottlenecks. They were transported to Texas A&M University, screened for efficacy in the carboxylate platform, and the resulting fermentation communities stored in cold conditions. It is possible that by further growing the stored materials prior to DNA extraction imposed another selection that resulted in the change in community compositions without regard to storage condition. However, growing the stored material was necessary because of the limited amount of stored materials available and the need to evaluate viable cells within the material. Ideally, a pre-adapted community should be maintained in a large continuous culture, which could then be added to the biomass periodically to increase production. However, there still remains the need to effectively store inoculum for long-term purposes or transport.

CHAPTER V

LONGITUDINAL STUDY OF BACTERIAL COMMUNITIES FROM BRAZORIA NATIONAL WILDLIFE REFUGE SEDIMENTS

Introduction

Microbial communities are complex and dynamic systems influenced by both physical and chemical factors in the environment (Torsvik *et al.*, 2002; Litchfield and Gillevet, 2002). Temperature and moisture content change from season to season, and those seasonal changes play a large role in determining the microbial community composition. For example, the moisture content of the soil can change the salt content by dilution and it can also influence the amount of oxygen available (Hollister *et al.*, 2010a; Ventosa *et al.,* 1998). Studies of solar salterns found that microbial diversity within salt ponds have extensive seasonal variability that correlate with seasonal rainfall (Litchfield *et al.,* 2005; 2009).

To further demonstrate the dynamic nature of microbial communities in saline sediments and to understand how the soil communities sampled for our screening of natural microbial communities might change over time, we conducted a longitudinal study of four sampling points within the Brazoria National Wildlife Refuge (NWR). Brazoria NWR is located near Freeport, Texas on the Texas Gulf Coast. It is composed of various ponds, sloughs, and prairies, as well as salt and freshwater marshes that extend into the Intercoastal Waterway. Throughout the course of one year, samples were taken and screened for carboxylate platform performance. Each site within the refuge

was initially chosen based on differences in ecology, specifically soil composition and aquatic characteristics (salt lake, salt marsh, freshwater marsh, and prairie; Figure 19).

On October 23, 2008, the initial sediment samples were collected from nine independent points within the site. Based on higher conversion rate performance within the carboxylate platform screen, we chose four of the nine sampling points to be the basis of this study. We evaluated bacterial diversity (species richness and evenness) and compared the diversity within and between locales from the site throughout four sampling dates over the period of one year. The hypothesis was that there would be seasonal influences (i.e., temperature, moisture content, pH, salt content) on the species composition and abundance within the site. This study increases our knowledge of the dynamic nature of bacterial communities in different ecological niches. Uncovering what physiochemical factors influence the bacterial community diversity of sample inocula will give rationale behind site selections in the future. The information gained from the sediments studied here will also serve as rationale for the continued conservation of this unique refuge.

Materials and Methods

Sampling

Samples from each of four ecologically different locales within the refuge were obtained on October 23, 2008, February 9, 2009, June 18, 2009, and October 27, 2009. Each sampling point was re-sampled as near as possible to the original GPS coordinates

and time of day. Each sample was then screened for efficacy in the carboxylate platform as described in Chapter II.

16S rRNA Gene Analysis

Community 16S rRNA genes were sequenced and analyzed also as described in Chapter II. All samples were normalized to the largest number of sequences in all 16 samples (9,009) and taxonomic assignment and visualization tools were implemented using the Visualization and Analysis of Microbial Population Structures website maintained by the Josephine Bay Paul Center (VAMPS, http://vamps.mbl.edu/index.php) (accessed 28 May 2011). Cross-community comparisons were performed using sequences normalized to the smallest number of sequences within the data set comprised of all 16 samples (4,354).

Pyrosequencing reads were submitted to NCBI Short Read Archive under the accession number SRA039015.1.

Correlation of Community Compositions with Environmental and Geographic Variables

A one-way analysis of variance (ANOVA) was performed to investigate differences in physical and chemical parameters between each of the four sample points with each sample across seasons as replications within a sampling locale using Microsoft Excel 2007 and the PopTools version 3.2.3. add-in (Hood, 2010). To test whether there was an effect of time on the environmental variables, a multivariate analysis of variance (MANOVA) was performed on the samples ordered by season using the repeated-

measures function in JMP Pro Version 9 with (JMP Pro Version 9, SAS Institute Inc., Cary, NC).

To analyze the correlation between community composition and environmental variables, Mantel tests were performed (Hollister *et al.,* 2010a). To quantify the distance between OTUs (97% similarity), Bray-Curtis index of similarity was calculated using the PAST software program (Hammer, *et al.,* 2001). This index is the ratio of unique species between two samples over the total number of species in two samples (Bray and Curtis, 1957). Here "species" were considered to be OTUs at 97% similarity. Euclidean distance was used to quantify the environmental variable structures for each sample (Fierer and Jackson, 2006). Euclidean distance is the measure of the distance between two points as measured by the length of a line connecting them. The Mantel test was performed with the two distance matrices described above as implemented in the PAST software program using 5,000 iterations

To identify any correlation between geographic distance and community composition, a Mantel test was performed. Bray Curtis-similarity index was again used to calculate the "species" distance between samples. The physical distance measured in kilometers between samples was calculated as the distance between each GPS location, taken at the time of sampling, using the Movable Type Scripts web-based tool to calculate the distance between two latitude/longitude points (Accessed 1 June 2011) (http://www.movable-type.co.uk/scripts/latlong.html; Vaness, 2010). These physical distances were then used to calculate Euclidean distance between samples in PAST. The two matrices were used to perform a Mantel test with 5,000 iterations also using PAST.

Results

All samples taken within Brazoria NWR varied in soil physiochemistry (Table 9 and Appendix B). The four samples from the first sampling date, October 23, 2008, had higher water content than the subsequent samples. These first samples also had the highest total nitrogen percentages. The other environmental parameters varied both within and between locales. ANOVA was performed to test for variation in environmental characteristics across the site (Table 10). Water content, electrical conductivity, sodium and magnesium ion content, and total nitrogen, carbon and organic carbon percentages all varied significantly across the samples, $p<0.05$. At the 90% confidence level, pH also varied significantly across samples. The MANOVA indicated that there was a significant effect of time on the environmental variables, $p<0.05$. The soil physical and chemical constituents varied over time within the sampling points.

There was a total of 95,247 partial 16S rRNA gene sequences analyzed in this study. These sequences grouped into 37,684 OTUs at the 97% similarity level. Overall, the samples were quite diverse as demonstrated by the high Shannon (H') index values and the large number of OTUs associated with each sample (Table 11). Most samples had approximately a third to half of their sequences group into OTUs at the 97% similarity level. The bacterial community within the 16 evaluated samples varied over time both within and between locales (Figure 20). The dominant phylum in all communities was *Proteobacteria,* comprising 33% of all observed sequences. Also, there were large percentages of unclassified organisms in the samples, 39% of total library sequences.

In general the samples tended to be more similar in community structure and community membership within a locale than across locales within the refuge (Figure 21). Two exceptions to this were Brazoria 24, which was more similar to samples in Brazoria 9 and Brazoria 63, which was most similar to Brazoria 5 samples. All samples shared more OTUs within a locale than they did across locales at the refuge (Figure 22).

The Mantel test revealed that water content, pH, total nitrogen, carbon, and organic carbon percentages all significantly correlated with the community compositions, $p<0.05$ (Table 12). Even though electrical conductivity also varied between locales, both it and the individual salt ions (alone and together) did not correlate with the community composition. Temperature also varied over the seasons and was not a significant determinant of community composition.

Each locale within the refuge was chosen because each had distinctly different ecological characteristics. They also varied in distances apart (Table 13 and Appendix C). The distances between locales ranged from 0.30 to 3.85 km. There was a significant effect of geographical distance on the bacterial community compositions of the sites, $p<0.05$. NMDS of community similarity based on Bray-Curtis similarity index shows that the samples were generally more similar to samples within their site than to the other sites (Figure 23). The samples also grouped according to water content, total nitrogen, carbon and organic carbon percentages. This complements the results obtained by the Mantel tests, which showed each of these factors to influence bacterial community composition.

Discussion

Soils and sediments are dynamic and heterogeneous environments that harbor a diverse array of microbial communities (Hollister *et al.,* 2010a; Lozupone and Knight, 2007). Those microbial communities are also dynamic and change as influenced by physical and chemical factors in their environment (Torsvik *et al.,* 2002; Litchfield and Gillevet, 2002). The sediments studied herein are no exception. Each sampling point had very diverse communities that differed both within and across locales throughout the year. Certain physiochemical characteristics of the sediments were seen to significantly correlate with this change. The sample communities were significantly correlated with water content, pH, total nitrogen, carbon, and organic carbon percentages. They not only tended to be more similar to others within the same locale, but also to samples that were similar in water content, total nitrogen, carbon, and organic carbon percentages (Figure 23). The NMDS and the Mantel tests showed the importance of soil chemistry as it related to bacterial community composition in this site. Similar findings are observed in other microbial ecology studies. Soil pH is a major determining factor for microbial communities as found in a study of 98 sites across North and South America (Fierer and Jackson, 2006). According to that study diversity is higher in neutral soils and lower in acidic soils.

Microorganisms also vary in distribution and diversity across a range of spatial scales and microbial community composition is non-random (Martiny *et al.,* 2006). Both environmental factors (pH, salt ion concentration, etc.) and geographic distance influence bacterial community composition (Pagaling *et al.,* 2006). A significant

correlation between the geographic proximity of the samples to each other and their genetic distance from each other was observed. Samples that were taken from within the same locale were more similar to each other than to those more taken from a greater distance.

In a study of bacterioplankton communities in the Mid-Atlantic Bight, Nelson *et al.* (2008), concluded that seasonal patterns are also an important influence upon community composition. In addition to environmental factors and geographic proximity significantly influencing the microbial communities within this site, temporal patterns also played an important role. The samples varied, as measured by both phylogeny and OTU compositions, within the same locale throughout the year. This, along with the MANOVA test, supports the influence of time as an important determinant of bacterial community composition.

This study represents the first attempt to characterize bacterial communities within Brazoria NWR. This refuge is a unique assemblage of very different ecotones existing in close proximity. A central goal of microbial ecology is to understand the relationship microorganisms have with their environment and how this occurs at a range of scales and over time. Owing to the dynamic nature of bacterial communities, both time and environmental factors influenced community composition within this refuge. In addition, there exists the future possibility of uncovering many novel organisms important in shaping these ecotones and their functions because many sequences that were generated here were taxonomically unclassified. The information gleaned here

provides rationale for the further protection and management of this and other national wildlife refuges as environments harboring unique microbial assemblages.

CHAPTER VI

ANALYSIS OF FERMENTATION BACTERIAL COMMUNITIES DERIVED FROM THE BRAZORIA NWR INOCULA

Introduction

Based on differences in conversion, product spectra, and carboxylic acid yields demonstrated across the variety of sites selected for screening in Brazoria NWR, sediment community structure and composition were investigated to determine if they influenced fermentation screen outcomes. To further understand these influences, the sediment communities collected from Brazoria NWR were evaluated at each of the four time points in Chapter V to determine if they changed after selective pressures induced by the carboxylate screen. In addition to the original screening of the four locales in October 2008, each subsequent sample was subjected to process screening. The sediment inocula from the first collection date (October 2008) resulted in high conversion. All of the locales chosen for intensive study are represented in the top 5% of fermentation screen performances based on those October 2008 data (Chapter II; Appendix D). However, subsequent screening from the other three sample dates (February 2009, June 2009, and October 2009) resulted in less remarkable conversion performances (Figure 24).

Chapter V describes the changes in bacterial community composition that occur in each sampling point within this refuge during the year. These changes were correlated both with certain environmental variables and geographic distance. Thus, a reasonable

hypothesis is that the differences in process performances reflect the changes in sediment communities throughout the year.

This study, along with the detailed analysis of the other pre- and post-fermentation communities detailed in Chapters II and III, elucidates the extent to which sediment bacterial community dynamics influence biomass degradation in the process screen. By evaluating the screen bacterial community composition in the context of data measuring variation in performance, we found that inocula from the same site collected at different time points does not result in similar process performances and community structures.

Materials and Methods

Samples from each of four ecologically different locales within the refuge that were obtained and analyzed as described in Chapter V were screened for efficacy in the carboxylate platform as described in Chapter II. Community DNA was extracted from the fermentation materials and 16S rRNA genes were sequenced also as described in Chapter II. Because of the large number of sequences analyzed in this chapter (185,636), a few modifications were made in the data analysis pipeline established in Chapter II. After potentially chimeric sequences were removed, a distance matrix was constructed using the MOTHUR release 1.17 dist.seqs function (Schloss, 2009). MOTHUR 1.17 was also used to cluster operational taxonomic units (OTU, at 97% similarity) and produce alpha (Shannon, ChaoI) and beta (θyc, Jaccard) diversity measures after the entire library was normalized to the smallest number of site sequences in all 32 samples (2,862) using

the normalize.shared function. Subsequent analyses were performed as described in Chapter II. All samples were normalized to the largest number of site sequences in all 16 fermentation samples (9,139) and taxonomic assignment and visualization tools were implemented using the Visualization and Analysis of Microbial Population Structures website maintained by the Josephine Bay Paul Center (VAMPS, http://vamps.mbl.edu/index.php) (accessed 28 May 2011).

A one-way analysis of variance (ANOVA) was performed to investigate differences in fermentation performance parameters between each season using all four samples collected in a locale for a season using Microsoft Excel 2007 and the PopTools version 3.2.3. add-in (Hood, 2010). To test whether there was an effect of time on the fermentation performance variables, a multivariate analysis of variance (MANOVA) was performed on the samples also ordered by season using the repeated-measures function in JMP Pro Version 9 (JMP Pro Version 9, SAS Institute Inc., Cary, NC).

In an effort to link sediment community composition with fermentation performances, for each sample, conversion, the fermentation community compositions, (genera and class levels) and acid compositions (i.e., amounts of acetic (C_2), propionic (C_3), butyric (C_4), and valeric (C_5) acids) were analyzed, as described in Chapter II using PCA, PLS regression, SVD, and Monte Carlo simulations. Monte Carlo-generated *p* values of <0.05 were considered significant. The same procedure was followed to analyze the soil community classes to the fermentation data, and to compare soil classes with fermentation classes to see if they could predict the composition of the fermentation communities.

Pyrosequencing reads were submitted to NCBI Short Read Archive under the accession number SRA039016.1.

Results

A total of 185,636 partial 16S rRNA gene sequences were analyzed in the soil and fermentation communities (Table 14). The total number of OTUs observed in the entire library was 46,476 (OTUs at 97% similarity). The sediment communities comprised 86% of these. The number of OTUs and diversity according to the Shannon (H') index varied over time and across sampling points for both the sediment and fermentation communities. However, the fermentation communities were far less diverse than the inocula communities as shown by fewer OTUs and lower Shannon values. Fermentation communities were more similar to each other in community structure and membership than the sediment communities and were also more similar to samples from the same sampling date than to other samples from within locales (Figures 25, 26). In contrast, the sediment communities tended to be more similar in both community structure and membership to samples within sampling points, except for Brazoria 23, 24, and 94, which were more similar to samples from other locales based upon the Jaccard and θ*yc* similarity indices.

The class composition and relative abundance of each class within the soil samples were visibly different both within and between sampling points as was also described previously in Chapter V (Figures 20, 27). In contrast to the soil communities, the fermentation communities were dominated by the phylum *Firmicutes*. There were

two dominant classes observed within this phylum, *Clostridia* and *Bacilli*, with the relative proportions varying among samples. Although there were visual differences in class composition of the fermentations within a site, these differences could not be correlated to the sediment community compositions using PLS regression, SVD, and Monte Carlo simulation analysis (Table 15).

Although the amounts of particular acids varied from sample to sample, acetic (C_2) and butyric (C_4) acid represented the highest percentages of all carboxylic acids produced (Figure 28). Much smaller percentages of propionic (C_3) and valeric (C_5) acid were also produced. There was no appreciable amount of higher molecular weight carboxylic acids detected in any of the samples. Within each sampling point, there was an effect of time on the fermentation performance, $p<0.05$ (Table 16). ANOVA revealed that all four sampling points within a season showed variation in conversion and valeric acid (C_5) production. Additionally, at the 90% confidence level, the samples within a season varied in butyric acid (C_4) and total acid production.

To complement analysis performed in Chapter II that linked sediment or fermentation community composition with performance, PCA, PLS regression, SVD, and Monte Carlo simulation was performed on the microbial compositions and the transformed and scaled performance metrics. The comparison of the principal components of the transformed fermentation community genera and classes to the scaled principal components of the transformed performance metrics were both significant, *p*-value <0.05 (Table 15). The Singular Vector Pair 1 (community SA1 and acid SA1) from the SVD showed that as *Bacilli* decreases and the proportion of *Clostridia* and

organisms within unknown classes in *Firmicutes* increases, the amounts of all acids also increase (Figure 29). Conversion positively increased with the proportion of *Clostridia.* As the proportion of *Bacilli* declined in a community -being replaced by more diverse assemblages including *Clostridia*, *Bacteriodia* and *Thermotogae* classes- the total amount of acids increased. A similar correlation was observed in the genera-level analysis of the fermentation communities (Figure 30). Here, the genera *Tepidimicrobium* and *Symbiobacterium* within *Clostridia*, as well as the genus *Petrotoga* within the class *Thermotogae,* were associated with increased total acid production and conversion. Furthermore, the genus *Ureibacillus,* within the class *Bacilli*, was also positively correlated with the performance metrics. The soil community composition was not an indicator of the resulting fermentation performances or the class composition.

Discussion

This study is the first attempt to evaluate the bacterial community compositions in the carboxylate platform from the same sources of inocula over time. The analysis of the sediment and fermentation communities obtained within Brazoria NWR draws many similarities to the findings in Chapter II. Both data sets showed that despite diverse inocula, *Bacilli* and *Clostridia* organisms dominated the fermentation communities. Organisms within the class *Clostridia* were also correlated with both the amounts and types of acids produced. This effect could be due to the abundance of *Clostridia* organisms in the first sampling period which were more limited in the subsequent samplings. This study does take the findings in Chapter II one step further by defining

the genera within classes that were correlated with increases of fermentation performance. In addition to *Clostridia* abundance being an important factor in fermentation performance, the genera *Petrotoga* (within the class *Thermotogae*) and *Ureibacillus* (within the class *Bacilli*) also significantly correlated with the amounts and types of acids produced and increased conversion.

In Chapter II, the increase of *Bacilli* slightly increased conversion; however, this study showed that the increase in conversion was mostly attributable to the increase of *Clostridia* genera. In addition to *Clostridia* genera correlating with this performance metric, *Ureibacillus* (in the class *Bacilli*) and *Petrotoga* (in the class *Thermotogae*) also significantly contributed to increased levels of fermentation performance. Likely, a more in-depth study of the genera within the sites studied in Chapter II would reveal these genera to also be important in performance therein.

Both *Tepidimicrobium* and *Ureibacillus* were dominant OTUs shared among many fermentation communities in Chapter II (Figure 5). Both genera have been associated with thermophilic anaerobic digestions and composts (Niu, *et al.,* 2009; Gagne, *et al.,* 2001). Organisms within the *Petrotoga* genus are thermophilic xylanolytic anaerobes that have been commonly isolated from oil wells (Miranda-Tello *et al.,* 2004). There are also species within this genus that are moderately halophilic, such as *Petrotoga halophila* (Miranda-Tello *et al.,* 2007). Given that the environment along the Texas Gulf coast is a marine ecosystem and has a lot of oil-related activity nearby, it is not surprising to have sampled these organisms from Brazoria NWR.

It was not possible to show that the dynamic bacterial communities within each sampling point determined the fermentation community composition or performance. Returning to the same location from which a community with good performance was derived did not predict future performances in the screen. This result further underscores the need to develop effective means for microbial community storage to permit further study and application development as described in Chapter IV. This study also expands upon the understanding of which organisms tend to be responsible for efficient fermentation performance in other chapters, by specifically naming associated genera, and it increases our abilities to optimize the carboxylate platform fermentation process, specifically efficient conversion.

CHAPTER VII

ANALYSIS OF SEDIMENT BACTERIAL COMMUNITIES FROM SIX GEOGRAPHICALLY DISTRUBUTED SALINE SITES

Introduction

Compared to aquatic saline systems, saline soils and sediments tend to be heterogeneous in salt content because of periods of dilution resulting from rains (Ventosa *et al.,* 1998). This heterogeneity in physical and chemical content creates a stratified environment that supports diverse assemblages of microbes. Indeed, community structure varies along salinity gradients (Hollister *et al.*, 2010a; Swan *et al.,* 2010; Rahakova *et al.*, 2009). Given this trend, the ways bacterial community structure varied across six geographically distinct saline sites was evaluated. The degree to which geographic proximity vs. environmental characteristics (e.g., salinity) could predict community compositions was determined.

A recent study along a hypersaline gradient at La Sal del Rey, Texas, highlighted the correlations soil physiochemistry has on community diversity (Hollister *et al.*, 2010a). A high amount of community variation was detected between each of the studied transect samples. The samples were more diverse than expected and exhibited a wide variety of taxa, some of which were previously not described as being associated with hypersaline soil. The differences observed therein in community diversity and phylogeny is attributed to the soil heterogeneity resulting from physical stratification, water content, and chemical gradients.

To evaluate the bacterial diversity associated with saline sediments, communities were surveyed from saline sites from the western United States and Puerto Rico that were used for carboxylate platform screening. Detailed analysis was performed on communities sampled from saline environments with distinct ecologies, including hypersaline lakes, areas with a history of salt production, and brackish marshlands. Two samples from each of the following locations were chosen: Mono Lake, CA, Owens Lake, CA, Great Salt Lake, UT, San Francisco Bay NWR, CA, Cabo Rojo NWR, Puerto Rico, and Stillwater NWR, Nevada.

These 12 samples were chosen because they exhibited varying amounts of salt ions (Na, K, Mg, Ca) based on physiochemical analysis (see Chapter II and Appendix B). Each of the sites selected for this project had a salinity value that is above that of seawater (3.5 to 5 S m^{-1}), ranging from 6 to 20 S m^{-1} (Table 17) (Kaye and Laby, 2005). This chapter will show whether community member organization varied within each selected site based upon the salinity of the sample and/or other sediment variables.

In a supplement to the previous study along a hypersaline gradient mentioned above and using the rationale that salt ion concentration and electrical conductivity of the soil effects bacterial diversity, the bacterial diversity within and between these saline sites was evaluated. The hypothesis was that these communities would differ in their community member composition and that this difference would correlate with the difference in environmental variables, because these factors affect diversity. Understanding the bacterial community diversity of these saline sites would not only increase our knowledge of these extreme environments, it would also serve as rationale

to protect and further manage these unique ecosystems. It also serves as rationale for future site selection for samples to be screened in the carboxylate platform.

Materials and Methods

Two samples were obtained from San Francisco Bay NWR, CA (February 9, 2009), Great Salt Lake, UT (May 1, 2009), Cabo Rojo NWR, Puerto Rico (June 1, 2009), Stillwater NWR, Nevada (August 6, 2009), Mono Lake, CA (August 7, 2009), and Owens Lake, CA (August 7, 2009). Each sample underwent physical and chemical analysis as described in Chapter II. Community 16S rRNA genes were sequenced and analyzed also as described in Chapter II. All samples were normalized to the largest number of site sequences in all 12 samples (8,390) and taxonomic assignment and visualization tools were implemented using the Visualization and Analysis of Microbial Population Structures website maintained by the Josephine Bay Paul Center (VAMPS, http://vamps.mbl.edu/index.php) (accessed 28 May 2011). Cross-community comparisons were performed using the entire library normalized to the smallest number of sequences within all 12 samples (2,213).

Mantel tests were performed to analyze the correlation between community compositions with environmental variables or geographic distance as described in Chapter V.

Pyrosequencing reads were submitted to NCBI Short Read Archive under the accession number SRA039018.1.

Results

All of the samples within the six chosen sites ranged in salinity (6.17 to 20.20 S m^{-1}) and pH (7.60 to 10.17) (Table 17). The sites were initially chosen based upon having salinities higher than that of seawater (3 to 4 S m^{-1}). Each sample varied in their amounts of the different ions tested; however, in all samples, the dominant ion was sodium.

A total of 63,302 partial 16S rRNA gene sequences were analyzed from the 12 samples. The most abundant phyla were *Proteobacteria* and *Firmicutes* at 33% and 8%, respectively (Figure 31). Unknown organisms also comprised a substantial portion (44%) of the total sequences. Compared with the phylogenetic analysis, bacterial community analysis based on OTU composition at 97% similarity also showed that the diversity of the samples varied both within and between sites (Table 18).

In comparing community structure and community membership, Mono Lake Island, Great Salt Lake, and Owens Lake samples were all more similar to samples from within their sites than to others. In contrast, Cabo Rojo, San Francisco Bay, and Stillwater samples were more similar to samples from distant sites (Figures 32, 33). The distance between sites ranged from 0.002 to 5,474 km. To evaluate the effect geographic distance had on the bacterial community assemblages, a Mantel test was performed using Euclidean distance between each of the sites calculated from the physical distance between each site (Table 19). The physical distance between the sites did not significantly correlate with the bacterial communities.

To test if environmental variables correlated with community composition, Mantel tests were performed using each measured soil physical and chemical parameters (Table 20). The pH and the magnesium ion content of the sediments were the only variables that significantly correlated with community compositions, *p*-values less than 0.10 and 0.05, respectively. All salt ions together did not correlate with the community and, contrary to the results in Chapter V, water content and the total nitrogen, carbon, and organic carbon also did not correlate with the community structures. These environmental effects upon the community were also seen in the NMDS of the communities based on Bray-Curtis similarity index performed with the abundance of all OTUs (Figure 34). The communities were more similar to other communities based on similar pH and magnesium ion content of the sediments.

Discussion

Hypersaline sediments represent extreme environments. Despite extremely selective conditions, they harbor a diverse assemblage of bacterial life (Litchfield *et al.,* 2006; Hollister *et al.,* 2010a; Oren, 2002). The sediments studied herein were quite diverse. They varied in phylotype composition both within and between sites. Unclassified organisms comprised the majority of the generated sequences (44%). This suggests that there are many organisms evolved in saline environments that are yet to be fully characterized and the potential for the discovery of novel organisms in these environments is quite high. Similar to many other types of sediment, *Proteobacteria* and *Firmicutes* were the dominant classified phyla (Hollister *et al.,* 2010a; Fierer *et al.,*

2007; Chapters II, V). Bacteria within these phyla are known to be important in nitrogen fixation and nutrient cycling within the environment (Fierer *et al*., 2007; Lozupone and Knight, 2007).

Similar to other microbial ecology studies, environmental parameters were major determinants of bacterial community composition (Litchfield *et al.,* 1998; Torsvik *et al.,* 2002; Litchfield and Gillevet, 2002; Hollister et al, 2010a; Lozupone and Knight, 2007; Fierer and Jackson, 2006; Chapter V). The sediments varied in pH (7.60 to 10.17) and this was seen to trend toward a correlation with the communities, $p < 0.10$. Samples were more similar to others that were in similar pH range, either below 9 or above. Magnesium ion contents significantly correlated with community compositions, $p<0.05$. Interestingly, the samples with neutral pHs also had magnesium ion contents above 100 mg kg^{-1} and the converse was true for sediments that were highly alkaline. The rest of the ions did not influence community composition in this study. This could result from the extreme salinity (much higher than sea water) of all samples evaluated.

Mono Lake Island, Great Salt Lake, and Owens Lake samples were all more similar to samples from within their sites than to others. This is interesting given that each of these lakes were originally part of an ancient contiguous body of water in the Great Basin (Thorp and Rogers, 2011). These pluvial lakes (landlocked basins) were formed after a period of increased rainfall after the last glaciation event in North-America which occurred in the late Pleistocene period (Goebel *et al.,* 2011). Having no sources of renewal like rivers, the lakes slowly accumulated large amounts of salts as they evaporated.

Unlike the sediments studied in Chapter V, the sediments studied here did not exhibit any correlations between geographic distance and bacterial community composition. Based upon this, extreme salinity from the dominant sodium ions, differences in magnesium ion content, and pH was more significantly correlated to community composition than geographic proximity. Evaluations of these sediments to those from non-saline environments would help to evaluate this conclusion further.

Two communities herein were also evaluated in Chapter II because they occurred in the top 10% of performances in the screen based on conversion (San Francisco Bay NWR 20 and Owens Lake 1, CA). In the fermentation community resulting from screening, *Firmicutes* dominated the community and were responsible for high amounts of acids produced and efficient conversion (Chapters II, III, and VI). The sediments studied here have the largest numbers of *Firmicutes* present in the sediment community of all the sediments we have studied thus far (8% of total library here, compared to less than 1% in others). The biomass conversion of these fermentations ranged from 0.02 to 0.36, with a median of 0.13 (Appendix D). The percentage of *Firmicutes* in the soil varied between samples, from less than 1% to 24% and did not show any patterns of correlation with conversion values. The highest conversion samples (San Francisco Bay NWR 20 and Owens Lake 1), both with 0.36 conversions, had 0.3% and 4% *Firmicutes* organisms, respectively. Further evaluation of these and other sediments with a large number of organisms in the phylum *Firmicutes* will uncover whether inoculation with a large number of these specific organisms plays a role in determining performance in the carboxylate screen fermentations.

CHAPTER VIII

SUMMARY

Soils and sediments are diverse in both physiochemical characteristics and the microbial communities they contain. Over time, they vary in environmental parameters such as water content, pH, salinity, and nutrient availabilities. This variation influences bacterial community composition (Chapters V and VII). Geographic distance also significantly correlates to bacterial community structures. Bacterial communities that are closer in proximity tend to be more similar to each other, although the environmental parameters of a location can exert more of an influence upon the community. The study of the sampling points within Brazoria NWR shows the dynamic nature of sediment communities and that a sediment community that performs well initially cannot necessarily be re-sampled and expected to produce the same carboxylate process performances. Furthermore, along with the samples from Brazoria NWR, the saline communities studied in Chapter VII have shown the extent to which environmental variables play upon bacterial communities selected as inocula.

The carboxylate process screen is a harsh artificial environment with high temperatures, accumulation of carboxylates, and limited nutrient sources. All initially diverse inocula sediment communities were severely bottlenecked in this screen. A more narrow community, comprised of organisms primarily in the *Firmicutes* phylum, specifically *Bacilli* and *Clostridia* classes, came to dominate every screen. It was revealed herein that genera within these classes (*Tepidimicrobium* and *Ureibacillus*)

were responsible for a significant portion of the carboxylic acids made and the efficient conversion of biomass.

In concert with other studies of the carboxylate platform, we also discovered that a more diverse assemblage of organisms, and therefore a larger spectrum of carboxylic acids made, results from fermentations at 40 °C (Hollister *et al.,* 2010b). The higher temperature used (55 °C) in the screens, and the limited substrate (paper) selected for cellulose-degrading organisms and the resulting dominance of *Bacilli* and *Clostridia*. More complex substrates (e.g., sorghum) harbor more diverse communities (Hollister *et al.,* 2010b; Forrest *et al.,* 2010; Chapter III). These more complex substrates will continue be used in industrial settings employing this process (Holtzapple *et al*., 1999; Granda *et al.,* 2009). More diverse communities also make a wider spectrum of carboxylic acids, which are the desired product of this process.

The central hypothesis was that communities, having evolved to withstand similar selection pressures in the carboxylate platform, would perform more efficiently and with higher rates of biomass conversion than previously used inocula. Results show that these environmental parameters are a good indicator of efficient fermentation communities and this rationale should continue to be employed in future site selections. Compared to the marine community, some of the communities collected and screened from thermal and saline environments could convert up to 3 times more biomass to acids in laboratory-scale screens. A correlation between soil bacterial communities and the resultant fermentation community was not able to be established. However, fermentation communities were more similar to other communities within the same site than to others

suggesting that inocula composition affected their membership since similar patterns were also seen in the sediments. Despite diverse inocula, all communities tend to convert biomass to acids using similar community structures. From the information provided herein, the MixAlco™ process can be further optimized by selectively targeting these organisms, or groups of organisms, responsible for efficient performance. In the future, carboxylate process screening should use more complex substrates (e.g., sorghum) and maintain a temperature of 40 °C to produce more diverse fermentation communities that can produce more diverse and larger amounts of carboxylic acids and to more accurately reflect the conditions employed at industrial scales.

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APPENDIX A

Table 1 Soil physical and chemical characteristics for 20 samples with high rates of conversion.

Site Name	*Sample ID*	*Fermentation ID*	*Soil Characteristics*						
			Textural Class Name	*pH*	*EC ($S\ m^{-1}$)*	*Temperature (℃)[a]*	*Sample Date*	*Latitude (N)*	*Longitude (W)*
Muleshoe Lake NWR, TX	MPL6	pD18	Loamy Sand	7.90	4.85	28.80	10/04/2008	33.98347	102.7191433
Great Salt Plains NWR, OK	GSP8	pE08	Sand	7.40	3.71	19.10	10/09/2008	36.79999	98.2495064
Brazoria NWR 1, TX	Bra1	pF01	Loam	5.58	3.93	20.30	10/23/2008	30.6165	96.33872
Brazoria NWR 2, TX	Bra2	pF02	Clay Loam	6.10	3.15	20.80	10/23/2008	29.0673	95.26022
Brazoria NWR 5, TX	Bra5	pF05	Loam	7.70	5.10	22.30	10/23/2008	29.06083	95.24095
Brazoria NWR 6, TX	Bra6	pF06	Loam	8.10	5.83	29.00	10/23/2008	29.06145	95.23797
Brazoria NWR 9, TX	Bra9	pF09	Sandy Clay	6.90	2.98	21.90	10/23/2008	29.03787	95.26693
Bitter Lake, NM	BL8	pG08	Sandy Loam	7.20	6.19	9.17	11/15/2008	33.47665	104.4106
San Francisco Bay NWR 1, CA	SFB1	pH01	Sandy Loam	7.40	3.85	11.28	02/09/2009	37.49897	122.12807
San Francisco Bay NWR 20, CA	SFB20	pH20	Loam	7.10	7.42	10.00	02/09/2009	37.53262	122.08481
Big Bend NP 4, TX	Big4	pJ04	Sandy Clay	7.30	0.24	31.00	03/17/2009	29.17961	102.99555
Big Bend NP 11, TX	Big11	pJ11	Sandy Loam	7.20	0.14	37.10	03/17/2009	29.18209	102.99237
Big Bend NP 18, TX	Big18	pJ18	Sandy Loam	7.40	0.21	30.40	03/17/2009	29.14979	103.00346
Big Bend NP 19, TX	Big19	pJ19	Sandy Loam	7.30	0.17	31.00	03/17/2009	29.14979	103.00346
Big Bend NP 20, TX	Big20	pJ20	Sandy Loam	7.30	0.29	27.80	03/17/2009	29.14979	103.00346
Baker Hot Springs, UT	BHS5	pK49	N/A	N/A	N/A	47.40	04/27/2009	39.6111	112.729430
Laguna Boquerón NWR, PR	BWR1	pP01	Clay Loam	7.10	0.15	N/A	06/01/2009	18.0095	67.170925
Firehole Drive-Yellowstone NP, WY	FHYS5	pS44	Loamy Sand	6.60	0.29	59.60	07/28/2009	44.53279	110.79746
Sufutara Trail- Yellowstone NP, WY	STYS3	pS48	N/A	2.30	0.34	64.20	07/28/2009	44.79937	110.72836
Owens Lake, CA	OLCA1	pU22	Too Salty	9.59	15.37	33.10	08/06/2009	36.40028	117.95216

Abbreviations: EC, electrical conductivity
[a]Soil temperature at time of collection

Table 2 Performance of 20 fermentation communities. All samples in this study were in the top 10% (0.27-0.46) of conversions from the 559 samples tested in the screen of environmental samples.

			Fermentation Performance Metrics			*Relative Abundance of Acid Products (%)*				
Site Name	*Sample ID*	*Fermentation ID*	*Conversion*[a]	*Selectivity*[b]	*Yield*[c]	*Total Acid Produced g L^{-1}*	*Acetic*	*Propionic*	*Butyric*	*Valeric*
Muleshoe Lake NWR, TX	MPL6	pD18	0.32	0.06	0.02	1.82	69.28	5.99	23.51	1.22
Great Salt Plains NWR, OK	GSP8	pE08	0.27	0.19	0.05	4.62	69.82	6.22	22.50	1.46
Brazoria NWR 1, TX	Bra1	pF01	0.34	0.11	0.04	3.44	69.53	6.69	21.74	2.04
Brazoria NWR 2, TX	Bra2	pF02	0.38	0.12	0.05	4.33	69.96	4.58	24.22	1.24
Brazoria NWR 5, TX	Bra5	pF05	0.36	0.04	0.01	1.15	72.25	5.04	21.42	1.29
Brazoria NWR 6, TX	Bra6	pF06	0.35	0.16	0.06	5.03	70.86	4.93	22.33	1.88
Brazoria NWR 9, TX	Bra9	pF09	0.40	0.13	0.05	4.83	72.33	4.65	21.88	1.14
Bitter Lake, NM	BL8	pG08	0.36	0.28	0.10	9.14	67.03	4.41	27.31	1.25
San Francisco Bay NWR 1, CA	SFB1	pH01	0.37	0.08	0.03	0.71	72.74	7.06	19.48	0.72
San Francisco Bay NWR 20, CA	SFB20	pH20	0.36	N/D	N/D	N/D	N/D	N/D	N/D	N/D
Big Bend NP 4, TX	Big4	pJ04	0.36	0.16	0.06	1.30	71.36	6.02	22.62	0.00
Big Bend NP 11, TX	Big11	pJ11	0.38	0.21	0.08	1.78	77.44	5.99	16.57	0.00
Big Bend NP 18, TX	Big18	pJ18	0.35	0.15	0.05	1.15	78.01	5.50	16.49	0.00
Big Bend NP 19, TX	Big19	pJ19	0.36	0.02	0.01	0.12	77.70	5.65	16.64	0.00
Big Bend NP 20, TX	Big20	pJ20	0.35	0.00	0.00	0.01	74.63	6.14	19.23	0.00
Baker Hot Springs, UT	BHS5	pK49	0.33	0.05	0.01	0.88	68.88	10.10	21.02	0.00
Laguna Boquerón NWR, PR	BWR1	pP01	0.28	0.17	0.05	2.79	76.98	5.93	15.92	1.18
Firehole Drive-Yellowstone NP, WY	FHYS5	pS44	0.41	0.01	0.00	0.17	72.96	6.82	19.96	0.26
Sufutara Trail- Yellowstone NP, WY	STYS3	pS48	0.46	0.05	0.02	1.61	77.51	5.82	16.50	0.17
Owens Lake, CA	OLCA1	pU22	0.36	0.25	0.09	5.56	75.75	6.26	17.99	0.00
		Mean ± St. Dev.	0.36 ± 0.04	0.12 ± 0.08	0.04 ± 0.03	21.6 ± 3.10	72.9 ± 3.49	5.99 ± 1.25	20.4 ± 3.14	0.73 ± 0.72

Values represent the initial screen metrics
[a]Conversion is the ratio of volatile solids digested to the biomass that was originally added
[b]Selectivity is the proportion of digested material that resulted in carboxylic acid production
[c]Yield is the ratio of total carboxylic acids produced to the biomass that was originally added
N/D refers to metrics that were not determined

Table 3 Twenty pairs of sediment and fermentation community characteristics based on OTU analysis (97% similarity). The soil communities were far more diverse than their corresponding fermentation communities.

			Soil Community Characteristics				*Fermentation Community Characteristics*			
Site Name	*Sample ID*	*Fermentation ID*	*Sequence library size*	*Number of OTUs*	*Shannon (H')*	*Chao I Richness Estimate*	*Sequence library size*	*Number of OTUs*	*Shannon (H')*	*Chao I Richness Estimate*
Muleshoe Lake NWR, TX	MPL6	pD18	4148	899	6.17	2370	5395	225	4.14	318
Great Salt Plains NWR, OK	GSP8	pE08	1652	700	6.00	1322	5457	124	3.13	175
Brazoria NWR 1, TX	Bra1	pF01	4438	1242	6.69	4577	6122	113	2.15	185
Brazoria NWR 2, TX	Bra2	pF02	5745	1689	7.17	7914	4728	169	3.55	215
Brazoria NWR 5, TX	Bra5	pF05	4877	1542	6.97	6267	7249	100	2.65	150
Brazoria NWR 6, TX	Bra6	pF06	4660	1100	6.29	4241	4563	106	3.24	130
Brazoria NWR 9, TX	Bra9	pF09	4723	1804	7.30	10140	5060	110	2.99	145
Bitter Lake, NM	BL8	pG08	4721	1158	6.05	4982	7368	77	2.02	119
San Francisco Bay NWR 1, CA	SFB1	pH01	1822	817	6.28	1545	4995	121	3.01	168
San Francisco Bay NWR 20, CA	SFB20	pH20	5410	1514	6.98	6117	7706	45	1.72	75
Big Bend NP 4, TX	Big4	pJ04	1420	744	6.13	1823	5489	59	2.28	76
Big Bend NP 11, TX	Big11	pJ11	1320	598	5.83	1224	4945	51	2.41	58
Big Bend NP 18, TX	Big18	pJ18	1317	602	5.93	1181	5599	65	2.73	70
Big Bend NP 19, TX	Big19	pJ19	2048	486	5.17	975	4803	72	2.93	95
Big Bend NP 20, TX	Big20	pJ20	1659	609	5.76	1244	6883	64	2.32	103
Baker Hot Springs, UT	BHS5	pK49	3444	550	5.44	1435	7797	60	2.17	177
Laguna Boquerón NWR, PR	BWR1	pP01	6739	1998	7.50	9282	3628	120	2.89	160
Firehole Drive-Yellowstone NP, WY	FHYS5	pS44	3785	354	4.43	1107	6665	132	3.38	254
Sufutara Trail- Yellowstone NP, WY	STYS3	pS48	2781	143	2.44	195	5161	46	1.84	63
Owens Lake, CA	OLCA1	pU22	3866	462	4.86	1253	5568	82	2.83	165
Totals			70,575	19,011	-	-	11,5181	1,941	-	-

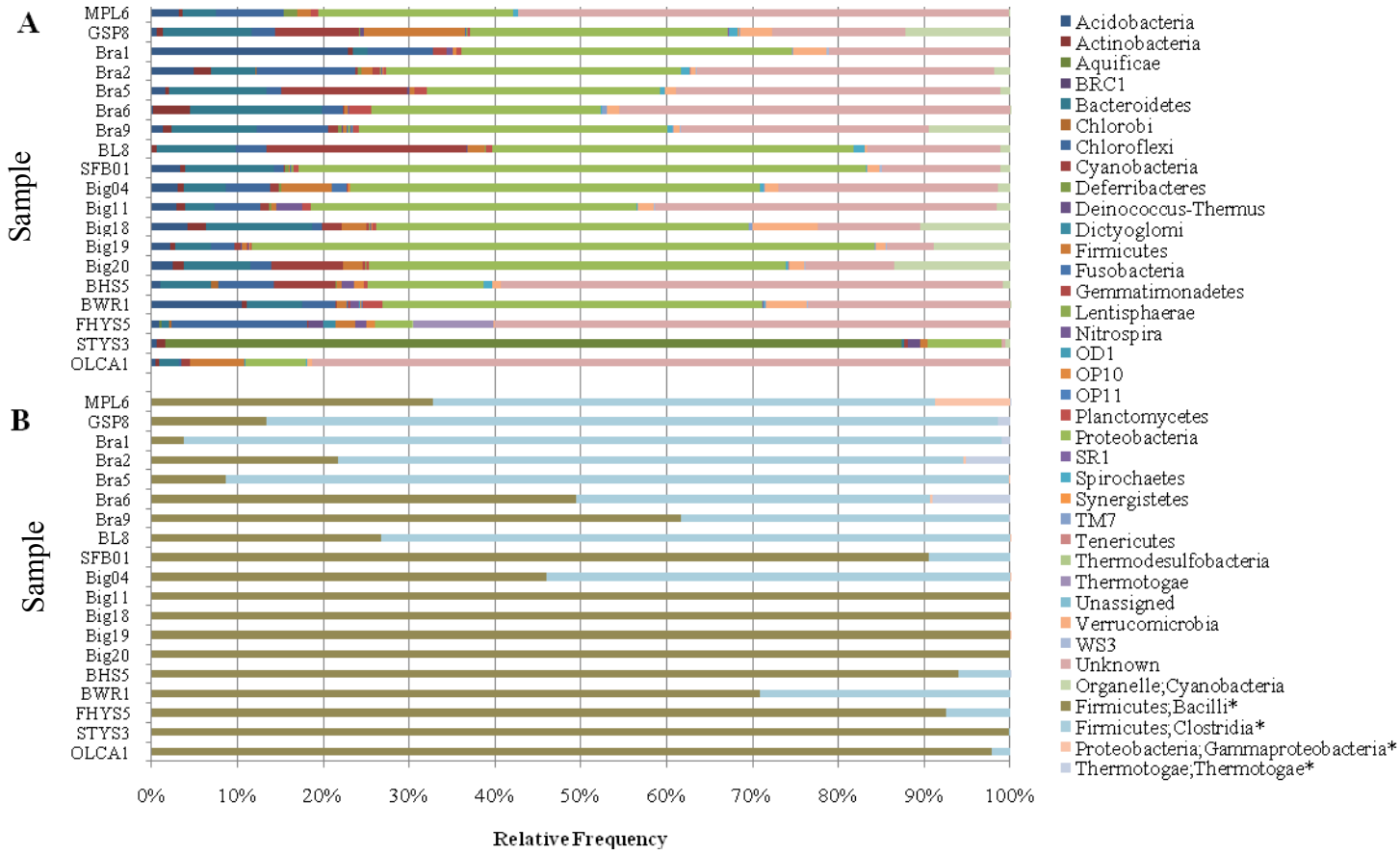

Figure 3 Sediment and fermentation community compositions as measured by pyrosequencing efforts. **(a)** Bacterial phyla represented in the soil community libraries. **(b)** Bacterial classes in the fermentation community libraries. Phyla with 1% of total sequences are shown. All sites were normalized to the maximum number of sequences (7,798). (Key: *Phylum;Class)

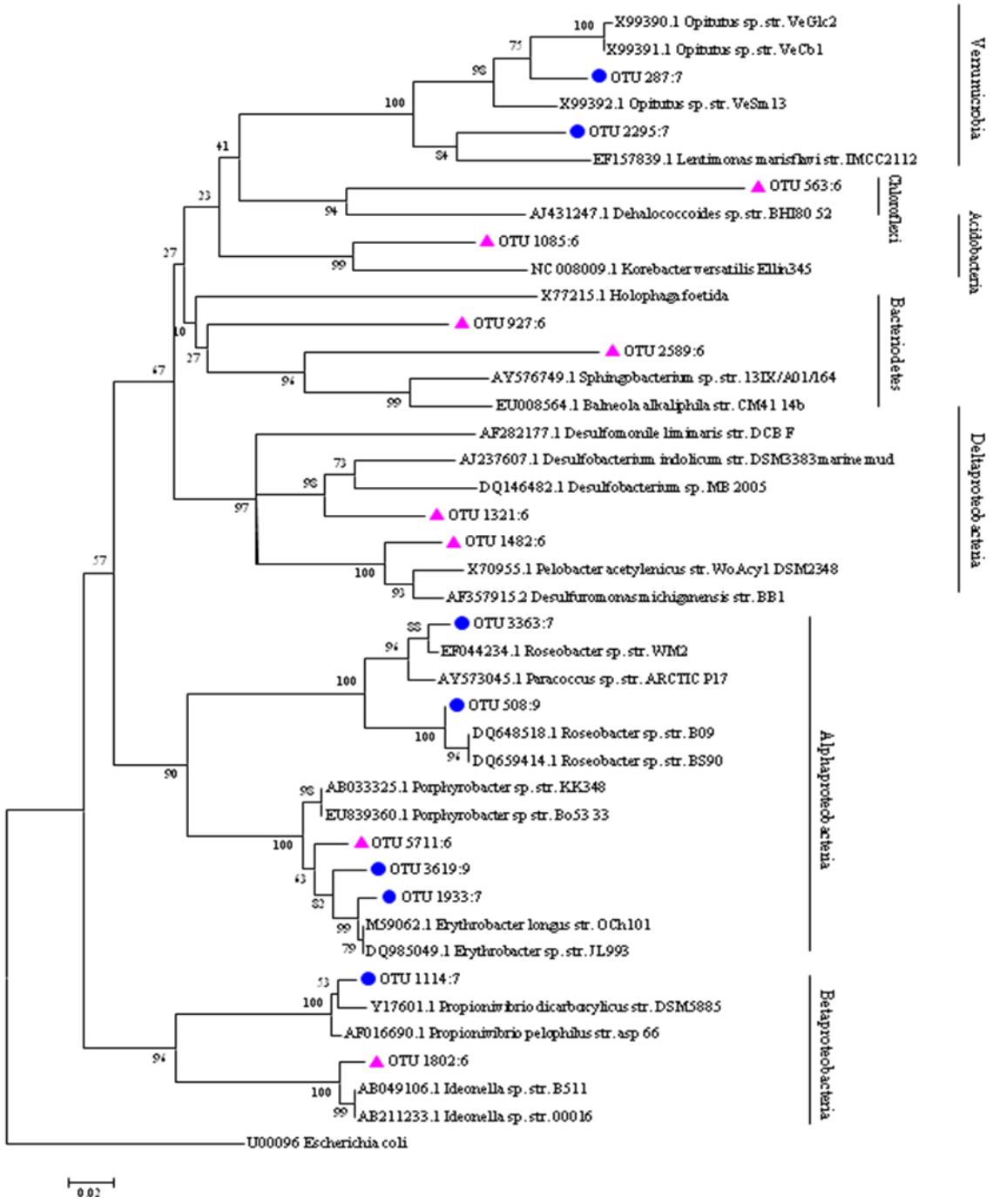

Figure 4 Top shared OTUs in the sediment communities (97% similarity). Accession numbers precede the named isolates. (Labeled as OTU #: # of shared sites; Blue circle, >6 sites; Pink triangle, <6 sites)

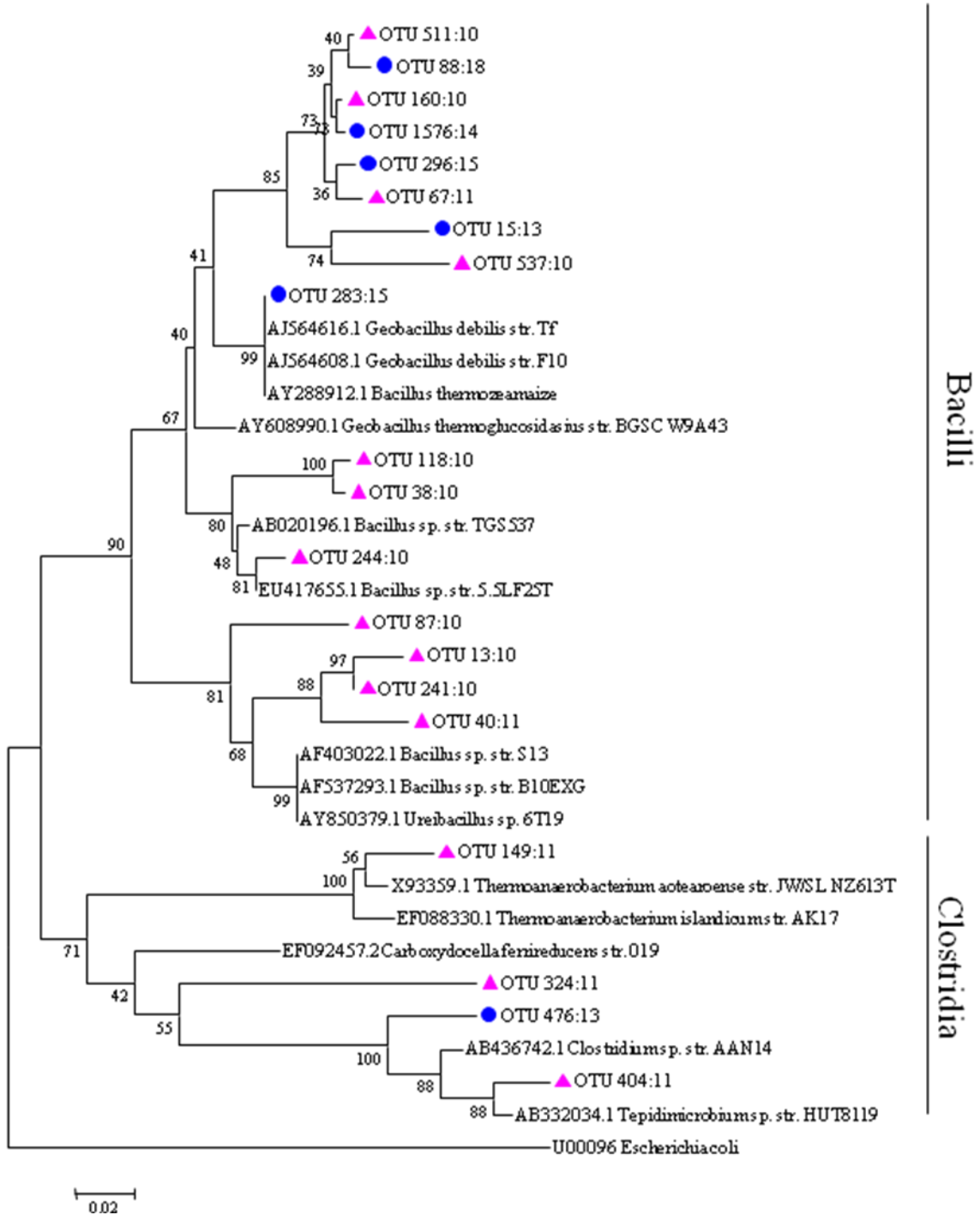

Figure 5 Top shared OTUs in the fermentation communities (97% similarity). Accession numbers precede the named isolates. (Labeled as OTU #: # of shared sites; Blue circle, >11 sites; Pink triangle, <11 sites)

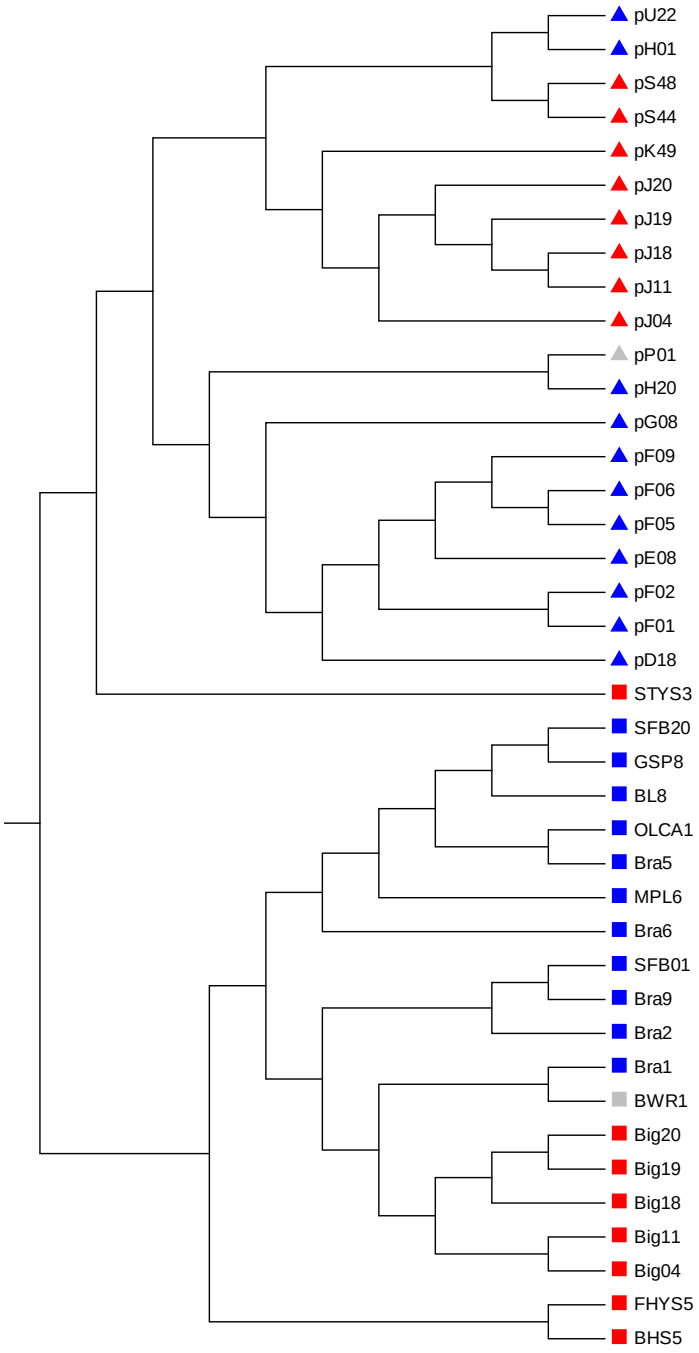

Figure 6 Sediment and fermentation similarity in community structure. This dendrogram is based on θ*yc* similarity values. The soil communities (squares) were more closely related to each other than the fermentation communities (triangles) and vice versa. (Blue, saline sites; Red, thermal sites; Grey, neither thermal or saline)

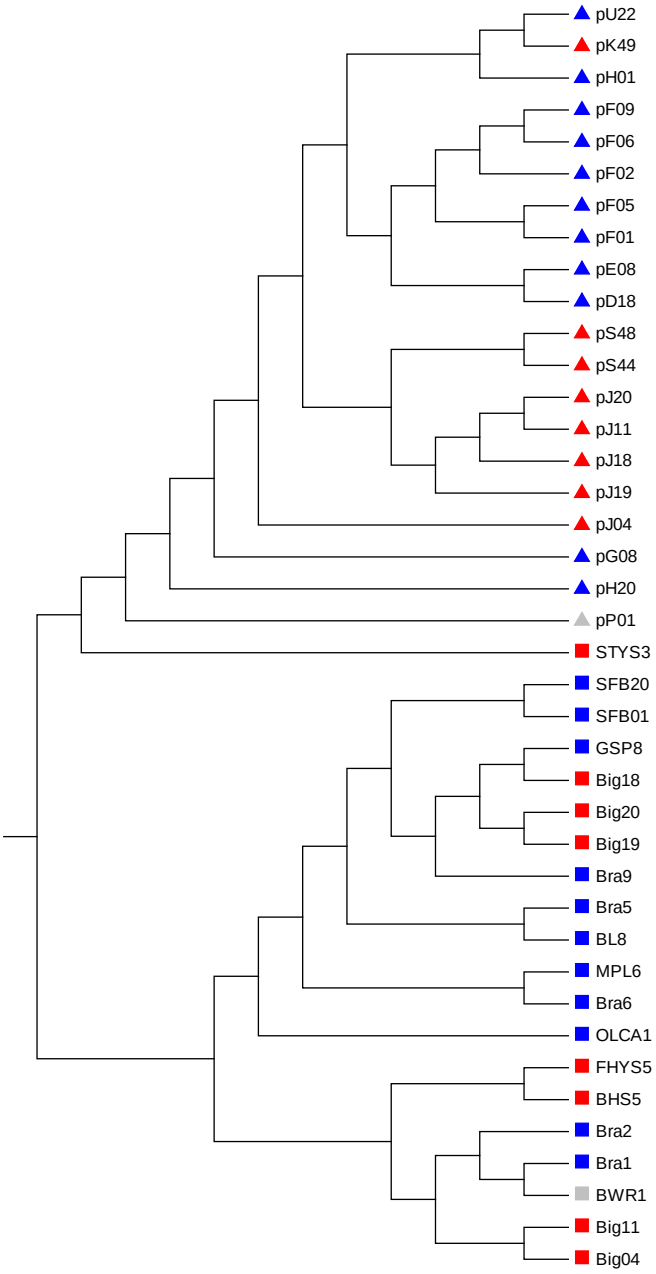

Figure 7 Sediment and fermentation similarity in community membership. Dendrogram representing similarity between soil and fermentor communities based on Jaccard similarity values. The soil communities (squares) were more closely related to each other than the fermentation communities (triangles) and vice versa. (Blue, saline sites; Red, thermal sites; Grey, neither thermal or saline)

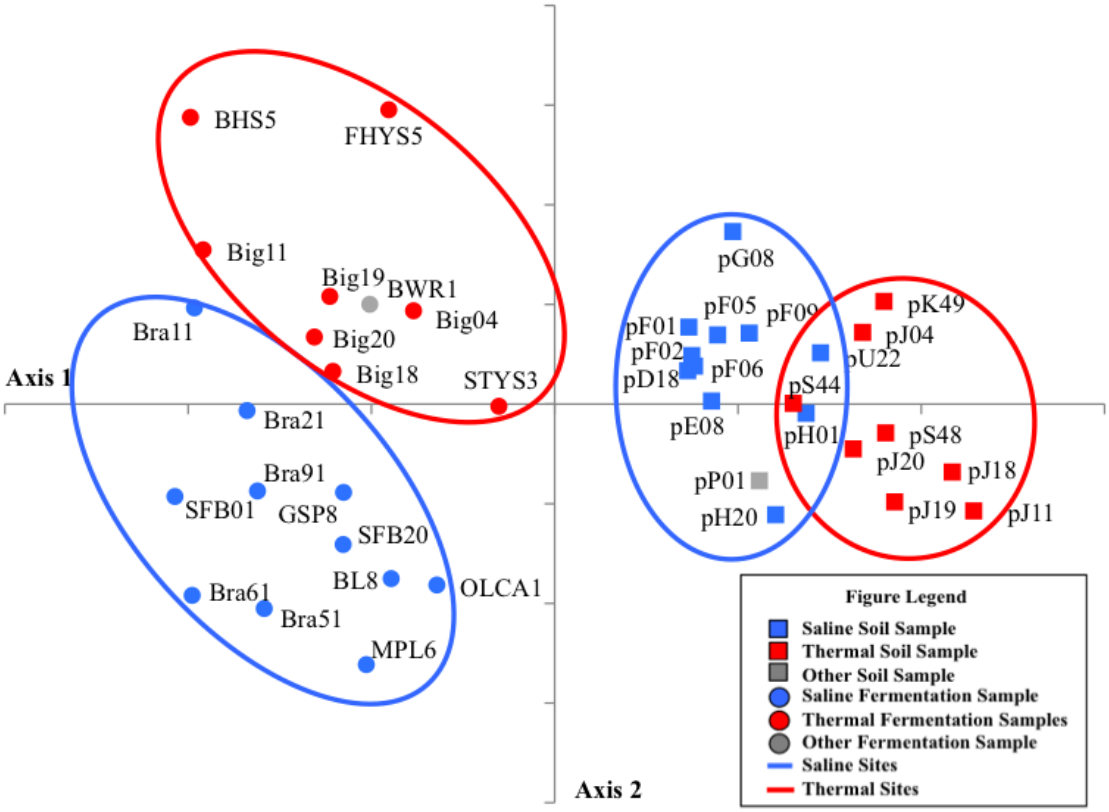

Figure 8 Sediment and fermentation community non-metric multidimensional scaling (NMDS) based on OTU composition (97% similarity). Bray-Curtis similarity measure was used to ordinate samples based on OTU composition at 97% similarity. Soil communities (circles) and fermentation communities (squares) were more similar within the group than to the other. Furthermore, the within each of the community types samples clustered based on the salinity (blue) and temperature (red) of the original sample.

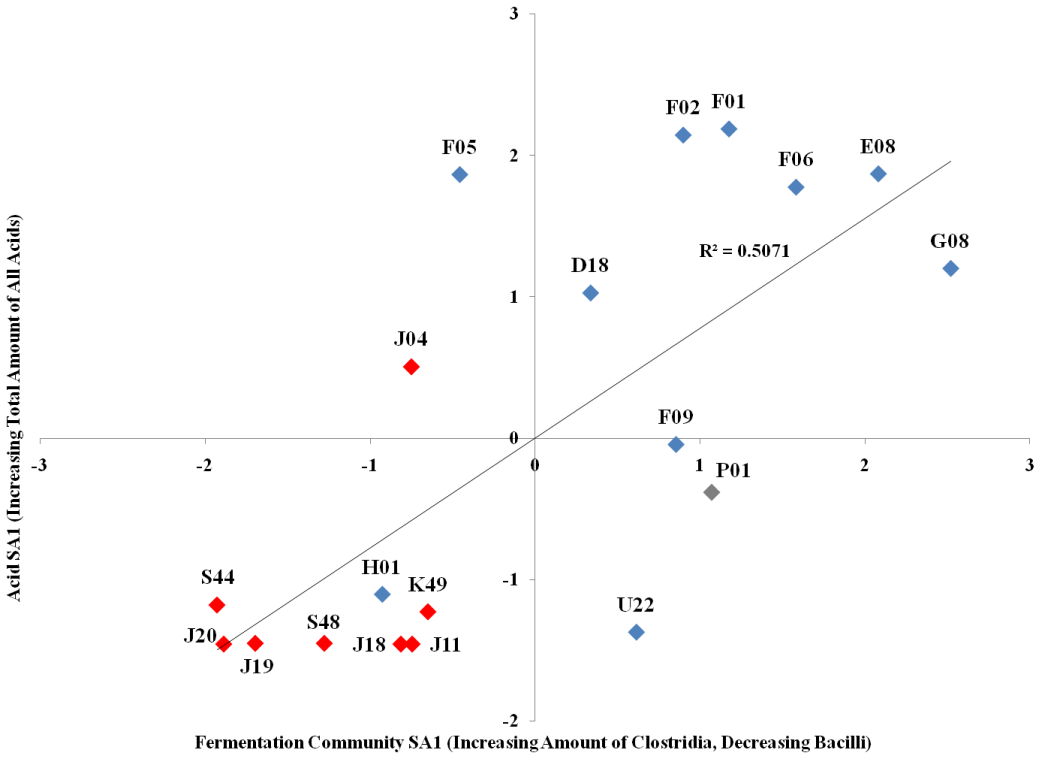

Figure 9 Community ordination plot of the most significant SVD results. The community ordination plot of the Singular Vector Pair 1 (fermentation community SA1 and acid SA1) from the SVD. (Blue, saline sites; Red, thermal sites; Gray, neither saline or thermal)

Table 4 Singular value decomposition (SVD) sums and Monte Carlo simulation results for the 20 samples with good conversion. The *p*-values for comparisons of the principal components of the transformed fermentation community classes to the scaled principal components of the transformed performance metrics are provided.

	Singular Value Decomposition Sums and Monte Carlo Simulation								
Test	*Experimental SVD Sum*	*Random SVD Sum*	*Mean*	*Variance*	*Lower CL*	*Upper CL*	*>Original SVD Sum*	*Valid Iterations*	*p value*
Fermentation Class and Performance Metrics	1.703143	1.173892	1.0984	0.073089	0.607457	1.657682	159	10000	0.0159
Soil Classes and Performance Metrics	2.5882	4.713677	2.701167	0.910328	1.186187	4.851062	4992	10000	0.4992
Soil Classes and Fermentation Classes	2.407194	5.334307	3.070971	1.359371	1.18335	5.447576	6658	10000	0.6658

Abbreviations: SVD: singular value decomposition; CL: confidence limit

Table 5 Laboratory screening and demonstration plant acid concentrations.

Acids Produced	*Carboxylic Acid Concentrations (g L^{-1})*					
	Laboratory Screen 40°C	*Laboratory Screen 55°C*	*t-test p value*[c]	*Demonstration Plant (30 days)*	*Demonstration Plant Relative to 40°C*	*Demonstration Plant Relative to 55°C*
Acetic (C_2)	2.65±0.37	7.06±1.29	0.047	2.59	-0.06	-4.47
Propionic (C_3)	0.67±0.23	0.19±0.13	0.253	1.36	0.70	1.26
Butyric[b] (C_4)	1.74±0.60	3.13±1.87	0.604	0.66	-1.07	-2.47
Valeric[c] (C_5)	0.86±0.09	0.25±0.13	0.081	0.36	-0.50	0.10
Caproic (C_6)	2.39±0.85	0.06±0.04	0.103	0.20	-2.19	0.14
Heptanoic (C_7)	0.17±0.05	0	0.089	0.10	-0.07	0.10
Total Acid Concentration	8.47±1.56	10.57±2.88	0.633	5.27	-3.20	-5.30

[a]Laboratory Screen values represent the mean of three replicates ± SEM. Paired, two-tailed Student's *t* tests were used to generate *p* values.
[b]Sum of C_4 and IC_4 isomers
[c]Sum of C_5 and IC_5 isomers

Table 6 Inoculum and fermentation community characteristics based on OTU analysis.

Sample Description	*Sample ID*	*Community Characteristics*			
		Sequence library size	*Number of OTUs*	*Shannon (H')*	*Chao I Richness Estimate*
Port Arthur, TX Inoculum	PA	5560	2310	7.10	5677
Demonstration Plant 30 days	Dem30	7332	608	4.05	1105
Laboratory Paper Screen 40 °C	PA340	4792	188	2.93	267
Laboratory Paper Screen 55 °C	PA155	3549	176	2.39	362
	Totals	21,233	3,282	-	-

[a]OTUs defined at 97% similarity level

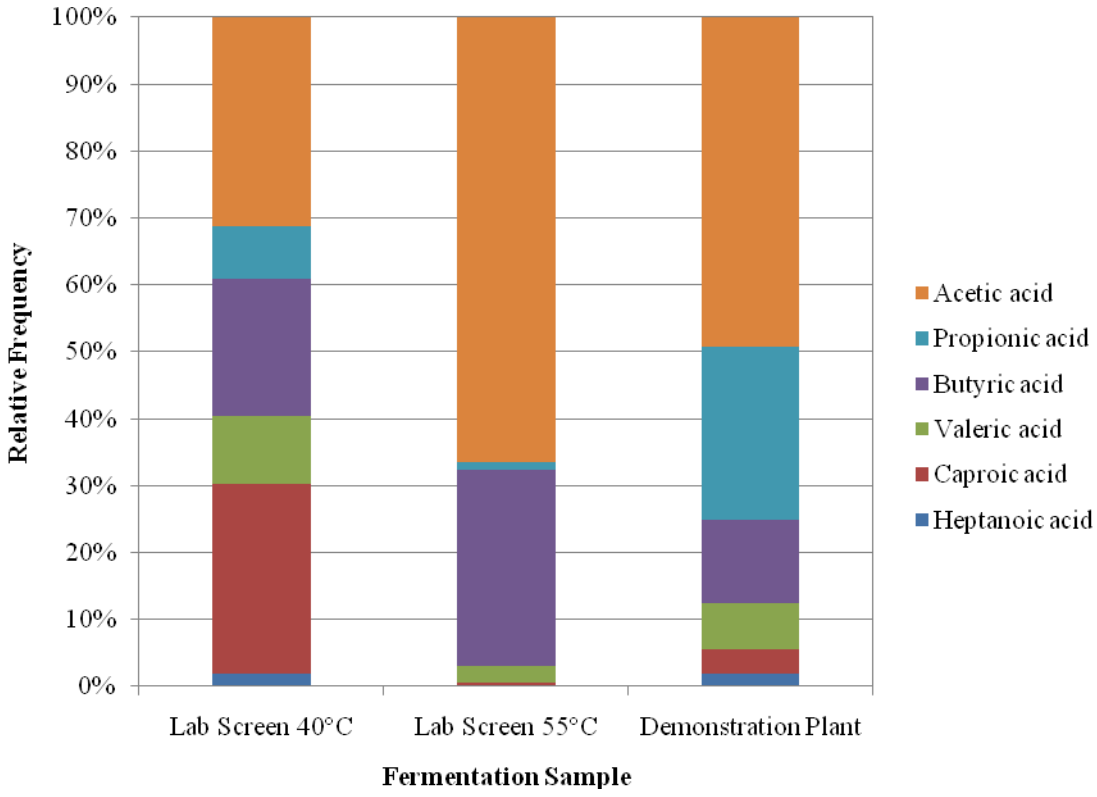

Figure 10 Laboratory screening and demonstration plant acid concentrations. Each sample varied in the relative frequency of acids produced. The 40°C screen and the demonstration plant (also at 40 °C) show a larger amount of high molecular weight acids (C_3-C_7) than the 55°C screen. In all samples, acetic acid (C_2) was the most abundant acid produced.

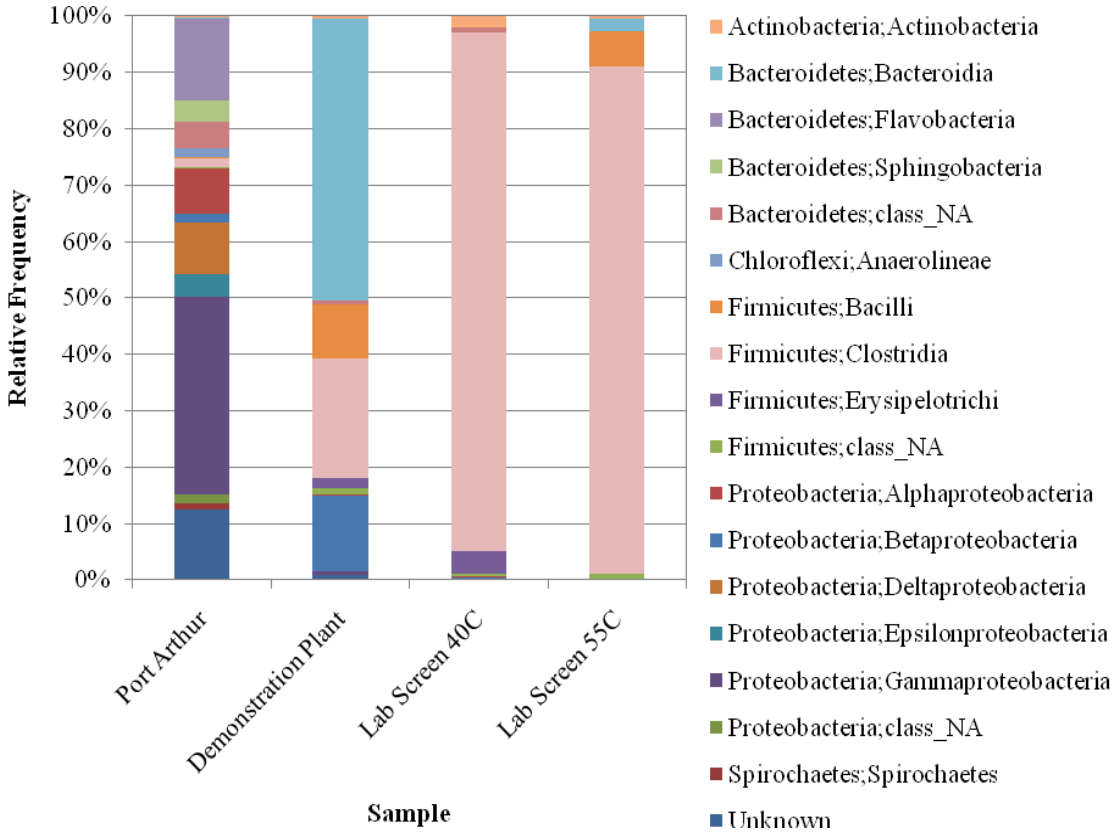

Figure 11 Inoculum and fermentation community compositions as measured by pyrosequencing efforts. The phylum composition and relative abundance within the marine sediment, the demonstration plant and the laboratory screens (VAMPS, accessed 28 May 2011). All sites were normalized to the maximum number of sequences (7,332). (Phylum;Class)

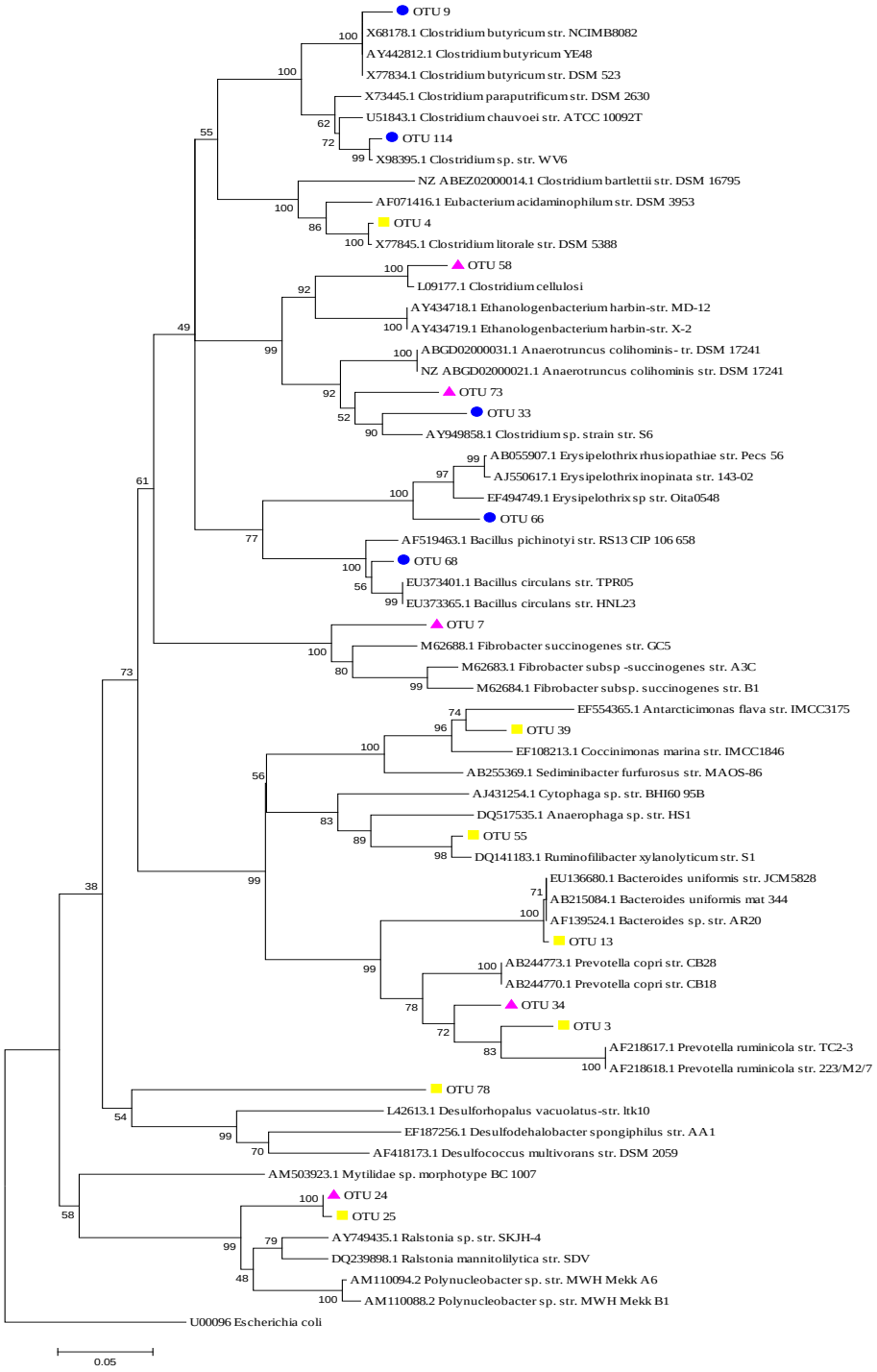

Figure 12 Abundant OTUs in laboratory screens and the demonstration plant. Neighbor-joining phylogenetic tree of abundant OTUs in the laboratory screens and demonstration plant and the OTUs' nearest neighbor isolates from the Greengenes database. Bootstrap values are from 1,000 replicates. GenBank accession numbers are preceding each entry. (Blue circle, shared between 3 sites; Pink triangle, shared between 2 sites; Yellow square, appears in one site)

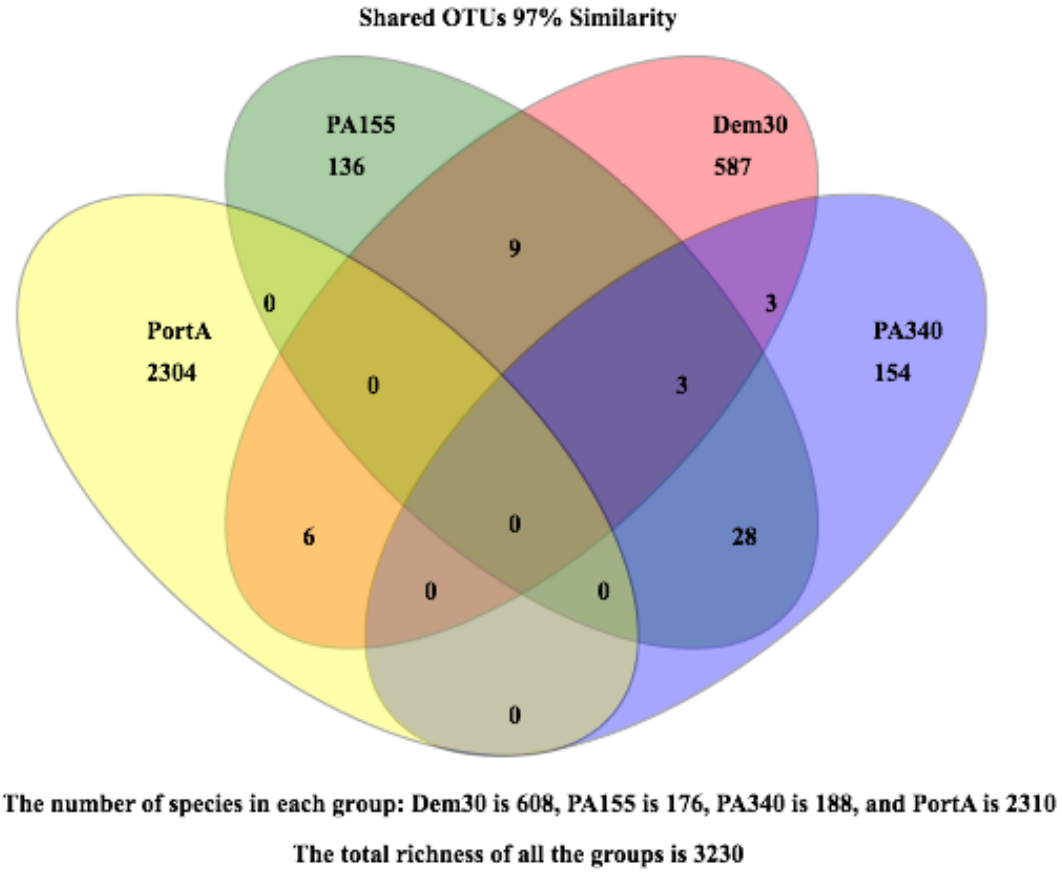

Figure 13 Shared OTUs between the fermentation samples and their inoculum. Venn diagram of shared OTUs at 97% similarity level. Each sample was normalized to the smallest number of sequences in the data set (3,549). (Abbreviations: Dem30, Demonstration Plant 30-day; PA155, Laboratory Screen 55 °C; PA340, Laboratory Screen 40 °C; PortA, Port Arthur Inoculum)

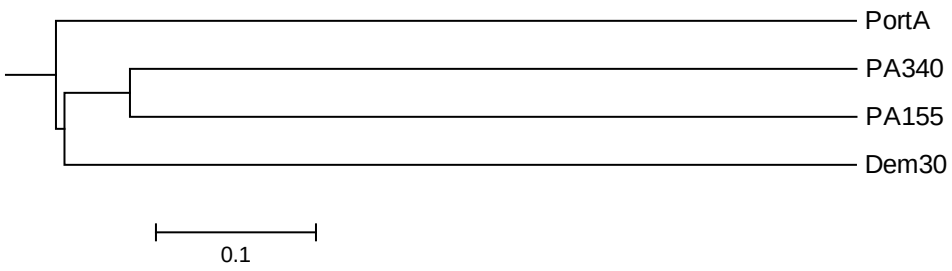

Figure 14 Inoculum and fermentation similarity in community membership. The dendrogram is based on Jaccard index values. (Abbreviations: Dem30, Demonstration Plant 30-day; PA155, Laboratory Screen 55 °C; PA340, Laboratory Screen 40 °C; PortA, Port Arthur Inoculum)

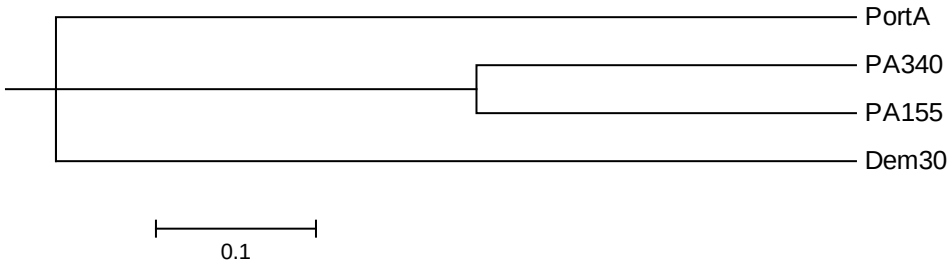

Figure 15 Inoculum and fermentation similarity in community structure. The dendrogram is based on θ*yc* values. (Abbreviations: Dem30, Demonstration Plant 30-day; PA155, Laboratory Screen 55 °C; PA340, Laboratory Screen 40 °C; PortA, Port Arthur Inoculum)

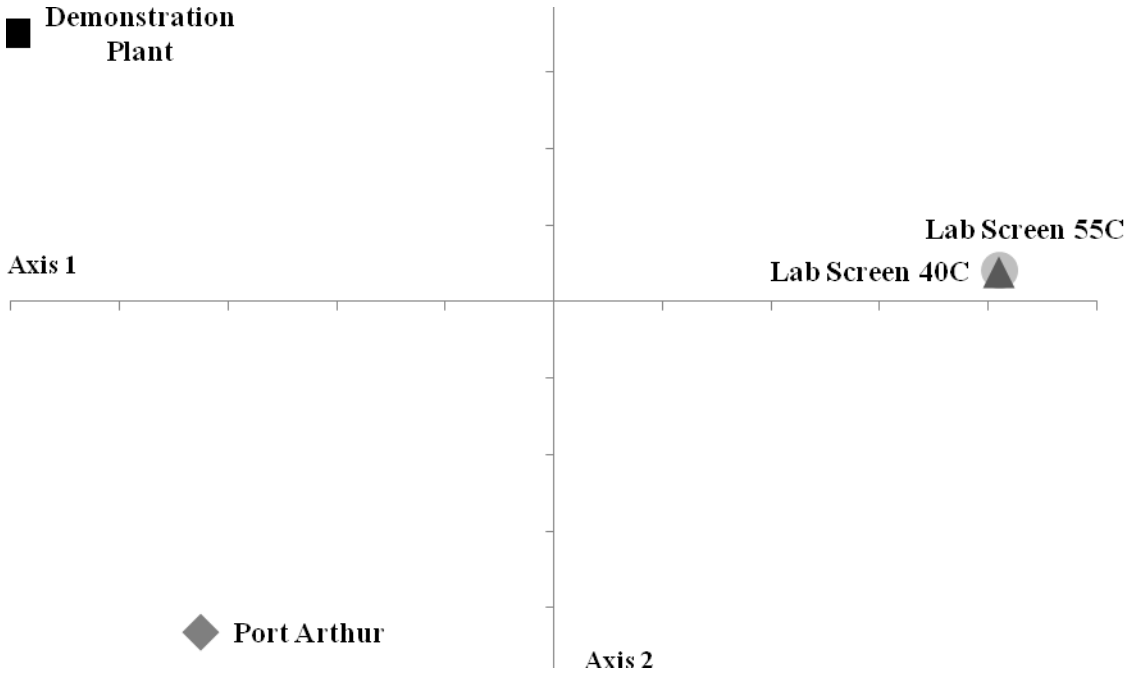

Figure 16 Non-metric multidimensional scaling (NMDS) of the inoculum and fermentation communities based on OTU composition (97% similarity). Bray Curtis similarity index was used to ordinate each sample based on genetic distance to each other.

Table 7 Storage and original fermentation community characteristics based on OTU analysis (97% similarity). There were 109,790 16S rRNA gene sequences analyzed.

		Community Characteristics			
Sample Description	*Sample Id*	*Sequence library size*	*Number of OTUs*	*Shannon (H')*	*Chao I Richness Estimate*
Great Salt Plains NWR, OK					
Original Fermentation	pE08	5542	230	3.65	376
Lyophilized Aliquot	E08lo	4675	63	1.80	88
Refrigerated Sample	E084C	8582	203	3.27	238
Frozen Sample With 10% Glycerol	E08gl	7626	215	3.19	322
Frozen Sample Without Glycerol	E0820	7375	176	3.08	269
Brazoria NWR, TX					
Original Fermentation	pF02	4766	233	3.56	366
Lyophilized Aliquot	F02lo	5932	97	1.83	179
Refrigerated Sample	F024C	5883	88	1.74	150
Frozen Sample With 10% Glycerol	F02gl	5924	56	2.17	98
Frozen Sample Without Glycerol	F0220	3922	350	2.64	548
Bitter Lake, NM					
Original Fermentation	pG08	7364	66	1.81	83.5
Lyophilized Aliquot	G08lo	4622	21	0.95	26
Refrigerated Sample	G084C	3007	25	0.35	42
Frozen Sample With 10% Glycerol	G08gl	6452	37	1.38	47
Frozen Sample Without Glycerol	G0820	5867	34	0.89	52
San Francisco Bay NWR, CA					
Original Fermentation	pH01	4984	208	3.45	360
Lyophilized Aliquot	H01lo	5368	43	1.64	56
Refrigerated Sample	H014C	3697	123	2.30	201
Frozen Sample With 10% Glycerol	H01gl	5368	129	2.71	243
Frozen Sample Without Glycerol	H0120	3928	117	2.77	145

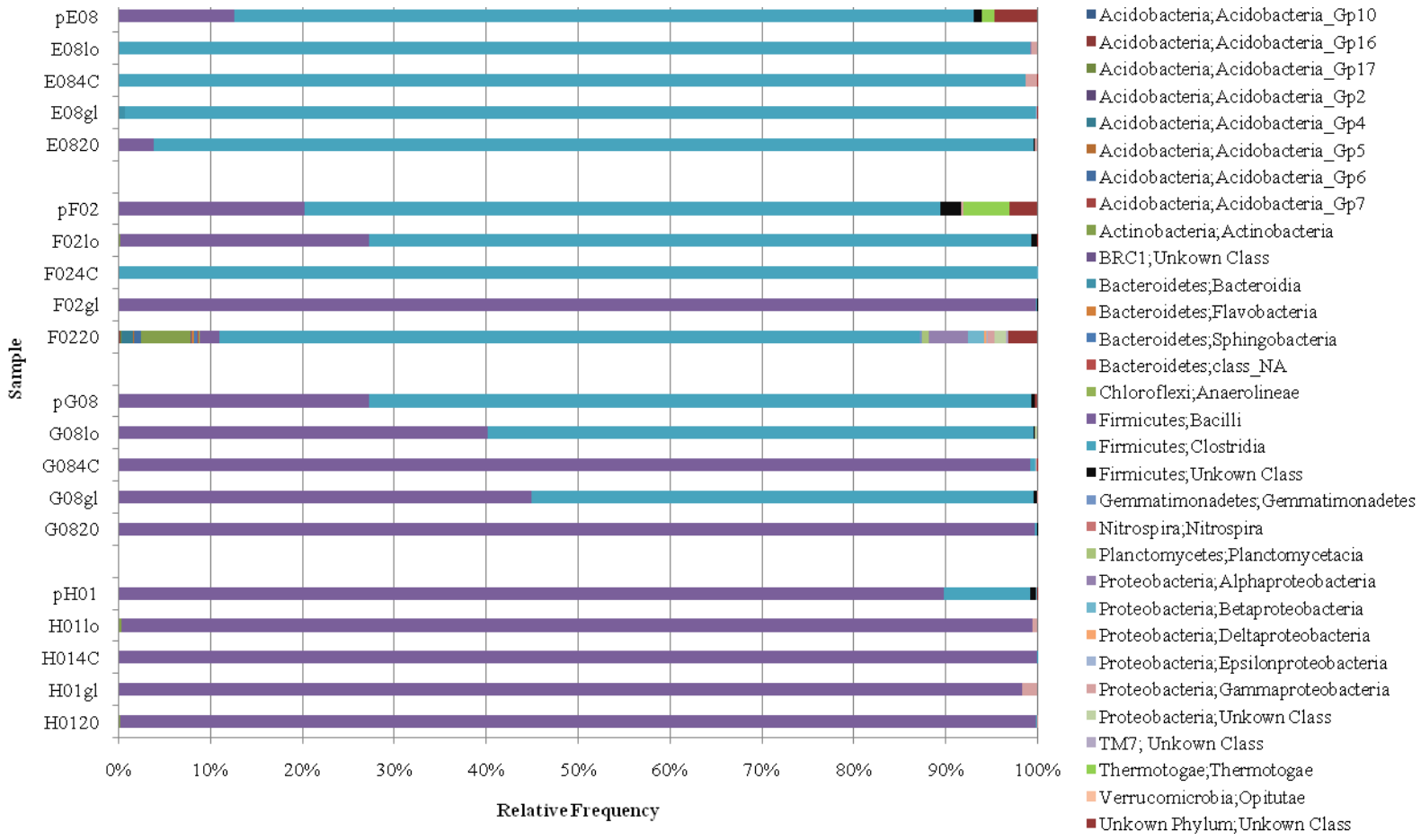

Figure 17 Storage and original fermentation community compositions as measured by pyrosequencing efforts. All sites were normalized to the maximum number of sequences in each site data set. (Sample Key: p, the original fermentation community; lo, lyophilized; 4C, refrigerated; gl, frozen with 20% glycerol; 20, frozen without glycerol) (Phylum;Class)

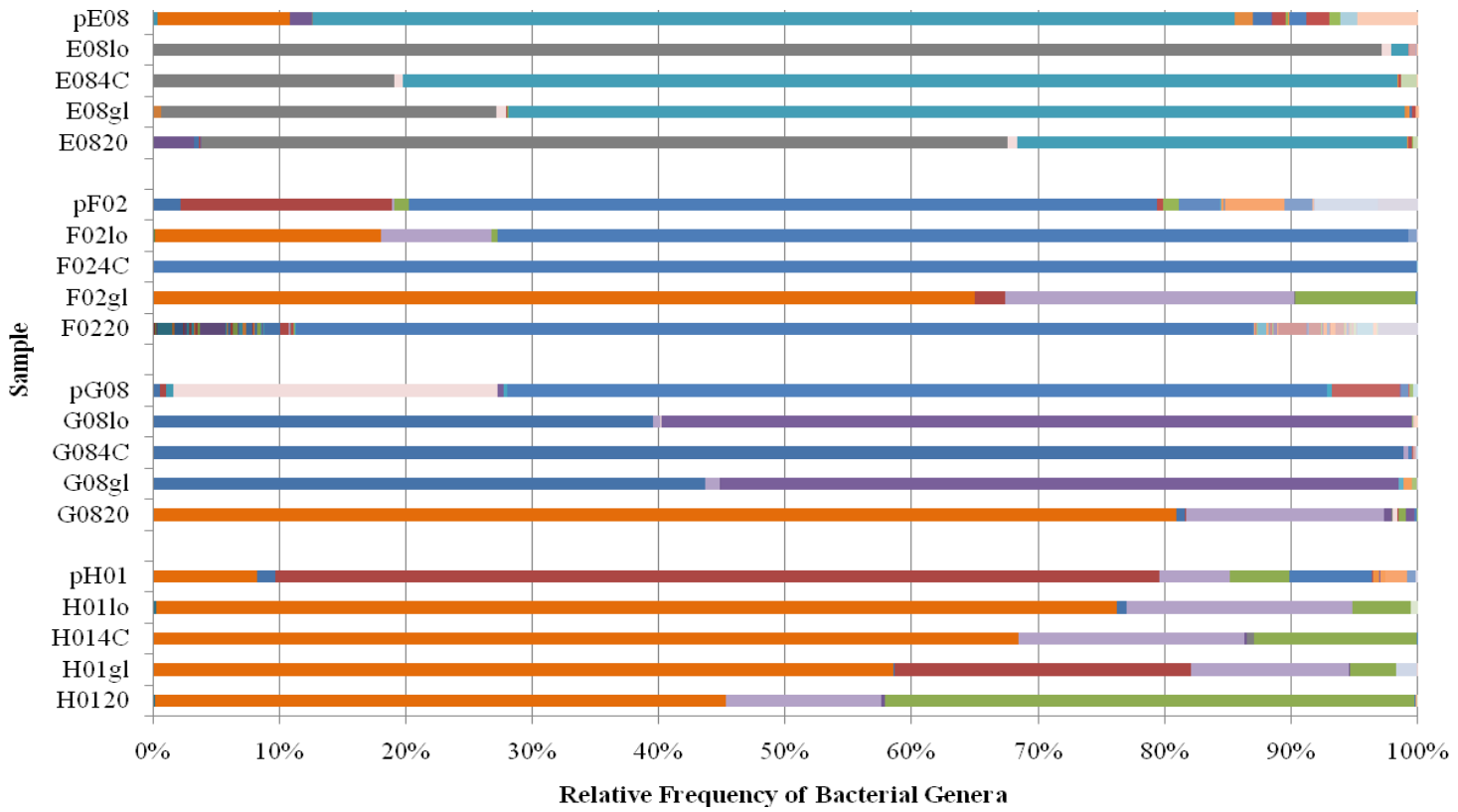

Figure 18 Storage and original inoculum relative frequency of bacterial genera. There were 148 named and unknown genera associated with the fermentations and the storage materials as shown by different colors representing different genera. The dominant genera within sets varied between storage conditions. (Genera key omitted for clarity of the figure)
(Sample Key: p, the original fermentation community; lo, lyophilized; 4C, refrigerated; gl, frozen with 10% glycerol; 20, frozen without glycerol)

Table 8 Storage and original fermentation cross community comparisons based on OTU analysis (97% similarity). The most similar storage community to the original fermentation community varied among sample sets. (Sample Key: p, the original fermentation community; lo, lyophilized; 4C, refrigerated; gl, frozen with 20% glycerol; 20, frozen without glycerol)

		Cross Community Comparisons				
Comparison		*Total OTUs*	*Shared OTUs*	*Shared OTU % of Original Sample*	*Jaccard*	*θyc*
pE08	E08lo	63	12	5%	0.042705	0.000597
pE08	E084C	203	40	17%	0.101781*	0.038247*
pE08	E08gl	215	41	18%	0.101485	0.037554
pE08	E0820	176	28	12%	0.074074	0.013313
pF02	F02lo	97	10	4%	0.03125	0.00156
pF02	F024C	88	20	9%	0.066445*	0.00011
pF02	F02gl	56	4	2%	0.014035	0.00011
pF02	F0220	350	36	15%	0.065814	0.020466*
pG08	G08lo	21	4	6%	0.048193	0.005163*
pG08	G084C	25	7	11%	0.083333	0.001296
pG08	G08gl	37	5	8%	0.05102	0.005154
pG08	G0820	34	9	14%	0.098901*	0.001788
pH01	H01lo	43	20	10%	0.08658	0.065493
pH01	H014C	123	44	21%	0.215331	0.072426
pH01	H01gl	129	71	34%	0.266917*	0.210144*
pH01	H0120	117	48	23%	0.173285	0.0852

*Storage method most similar to original fermentation community

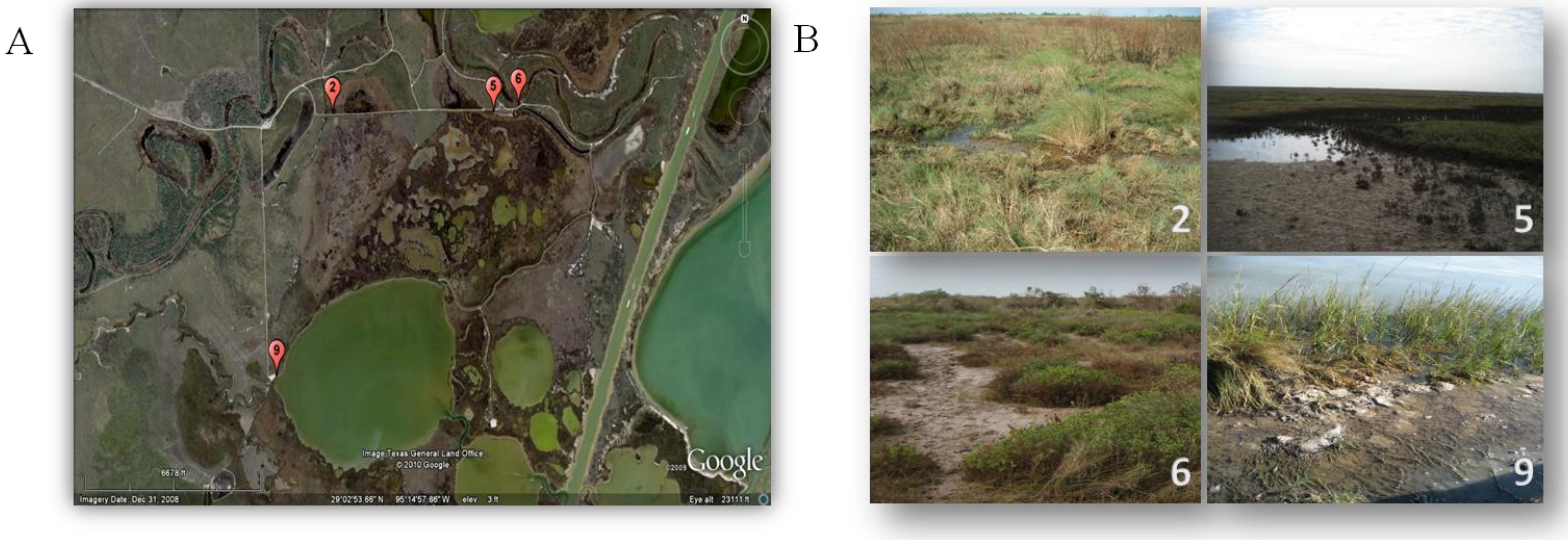

Figure 19 Brazoria NWR sampling point locations. **(a)** The satellite image obtained from Google Earth™ (12-31-2008) shows the location of each sample locale within the refuge. **(b)** The selected locales within the refuge were representative of the refuge's different habitats: freshwater marsh, saltwater marsh, prairie, and salt lake.

Table 9 Brazoria NWR soil physical and chemical characteristics. Samples are labeled according to locale and season.

			Soil Characteristics														
Sample	*Date*	*Sample ID*	*H_2O %*	*Sand %*	*Silt %*	*Clay %*	*Textural Class Names*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Total N, %*	*Total C, %*	*Organic C, %*	*Temp °C[a]*
Fall	10/23/2008	Bra21	46.58	37	26	37	Clay Loam	6.10	3.15	7742.12	492.62	883.37	1360.14	0.4896	4.40576	4.239667	20.8
Winter	02/9/2009	Bra22	43.71	41	22	37	Clay Loam	6.42	2.97	7462.06	228.69	525.11	1018.60	0.3600	4.35117	4.381399	17.7
Summer	06/18/2009	Bra23	35.82	29	28	43	Clay	6.14	2.19	4688.54	179.24	463.92	737.19	0.3330	3.70796	3.836705	29.6
Fall	10/27/2009	Bra24	31.84	34	37	29	Clay Loam	7.71	0.43	901.53	37.54	121.64	98.13	0.2227	2.83564	2.082839	20.6
Fall	10/23/2008	Bra51	21.43	47	44	9	Loam	7.70	5.01	12696.90	573.44	418.68	1951.33	0.1474	0.78377	0.718888	22.3
Winter	02/9/2009	Bra52	15.77	41	50	9	Silt Loam	7.53	8.32	24527.70	477.34	1314.75	3701.25	0.0805	0.46909	0.461561	19.8
Summer	06/18/2009	Bra53	12.75	45	48	7	Loam	7.42	7.77	24600.10	471.88	1448.69	3424.05	0.0739	0.51608	0.525776	50.2
Fall	10/27/2009	Bra54	21.12	42	33	25	Loam	7.52	5.59	15183.90	236.79	699.03	2283.38	0.1335	0.78131	0.608319	21.4
Fall	10/23/2008	Bra61	21.90	41	36	23	Loam	8.10	5.83	20891.70	548.77	215.55	924.53	0.1227	1.01777	1.055112	29
Winter	02/9/2009	Bra62	11.54	37	46	17	Loam	7.74	3.68	9401.73	157.93	806.67	579.00	0.1235	1.6327	1.050358	19.6
Summer	06/18/2009	Bra63	4.15	42	43	15	Loam	7.83	5.63	18174.50	278.50	1289.72	664.98	0.0763	1.01023	1.153274	37
Fall	10/27/2009	Bra64	16.79	32	37	31	Clay Loam	8.81	2.81	8037.14	102.32	150.29	168.59	0.0816	1.3157	0.941969	21.5
Fall	10/23/2008	Bra91	46.88	52	19	29	Sandy Clay Loam	6.90	2.98	9811.72	638.33	459.77	1241.31	0.3091	3.01169	2.787337	21.9
Winter	02/9/2009	Bra92	28.82	35	34	31	Clay Loam	7.04	4.16	10865.20	393.31	621.95	1385.67	0.2837	2.90971	3.046823	20.4
Summer	06/18/2009	Bra93	37.68	36	37	27	Loam	4.59	5.05	13319.00	625.31	855.79	2133.10	0.2838	4.23787	4.206034	36.7
Fall	10/27/2009	Bra94	36.13	30	35	35	Clay Loam	7.79	2.71	6738.41	234.74	362.91	784.05	0.1999	2.67231	2.392583	22.5

[a]Soil temperature taken at time of sampling
Abbreviations: EC, electrical conductivity

Table 10 Brazoria NWR site physical and chemical characteristics within and across locales.

		Site Variation	
	Variable Tested	*Exact F*	*p value*
Within Site Variation			
Repeated Measures-MANOVA	Time	2328.44	<0.0001
Across Site Variation			
ANOVA	% H_2O	15.90921	0.000175
	pH	3.346066	0.055712
	EC S m^{-1}	7.410828	0.004549
	Na mg kg^{-1}	5.874776	0.01046
	K mg kg^{-1}	1.692259	0.221467
	Ca mg kg^{-1}	1.03897	0.410454
	Mg mg kg^{-1}	11.57797	0.000742
	Total N, %	14.88655	0.000239
	Total C, %	32.70258	<0.0001
	Organic C, %	20.66817	<0.0001
	Temp °C	0.313614	0.815276

Repeated Measures-MANOVA implemented in JMP 9 Pro
ANOVA implemented in Microsoft Excel 2007 using PopTools

Table 11 Brazoria NWR bacterial community characteristics based on OTU analysis (97% similarity**).**

	Community Characteristics			
Sample Name	*Sequence Library Size*	*Number of OTUs*	*Shannon (H')*	*Chao I Richness Estimate*
Bra21	5735	2775	7.44	7015
Bra22	6754	2066	6.86	4058
Bra23	4354	1049	6.04	1821
Bra24	5128	2448	7.42	5528
Bra51	4867	2229	6.98	5842
Bra52	6620	2678	7.24	6039
Bra53	7020	2551	7.22	5732
Bra54	4789	1833	6.36	4122
Bra61	4661	1559	6.24	3675
Bra62	9009	2594	7.00	13889
Bra63	8348	2605	7.18	8810
Bra64	4985	1521	6.06	3313
Bra91	4713	2776	7.53	8324
Bra92	6105	2799	7.47	5861
Bra93	7200	3543	7.88	10917
Bra94	4959	2658	7.49	6777
Totals	95,247	37,684		

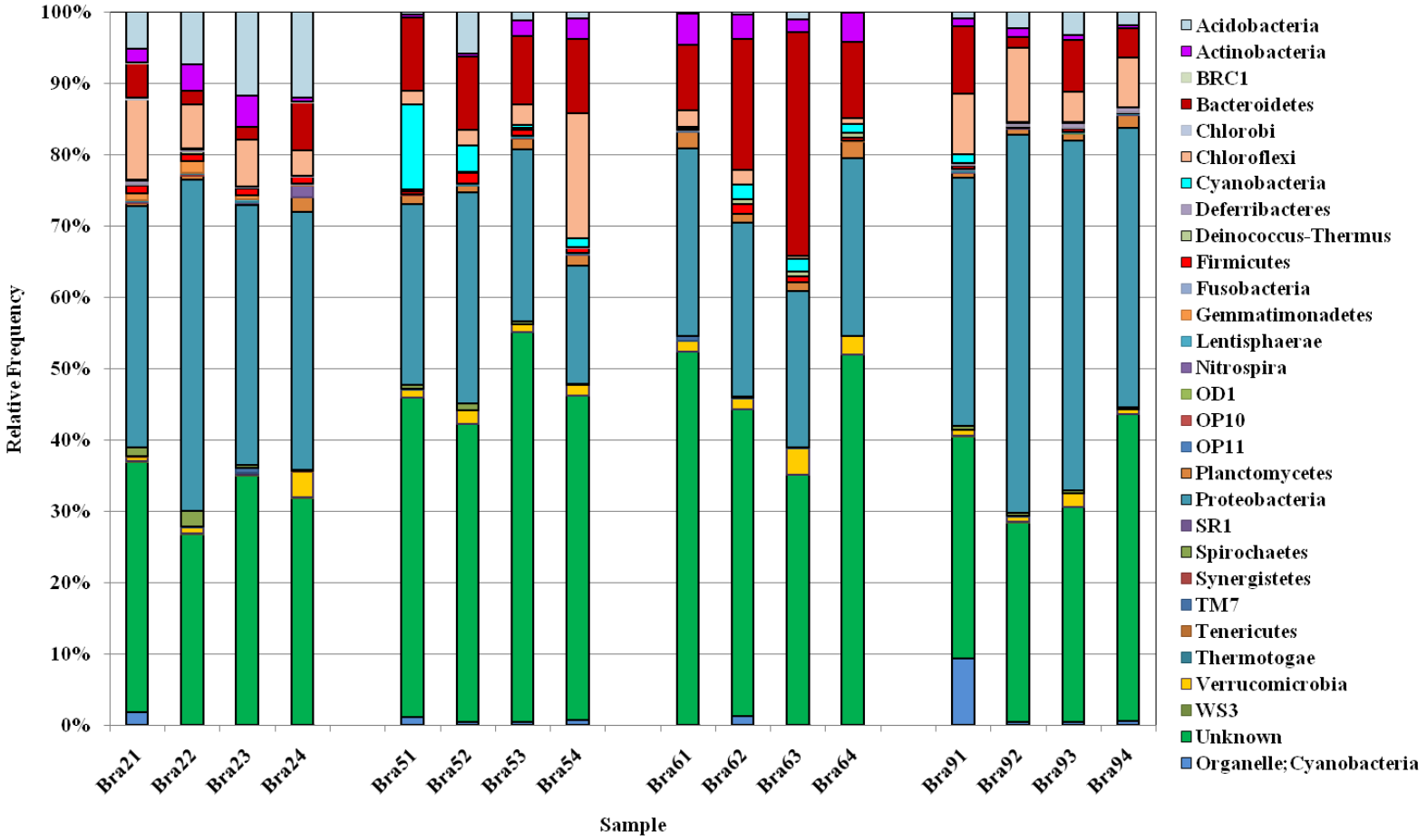

Figure 20 Brazoria NWR bacterial community compositions as measured by pyrosequencing efforts. Samples are labeled according to locale and season. All sites were normalized to the maximum number of sequences in all 16 sites (9,009). (Key: Phylum)

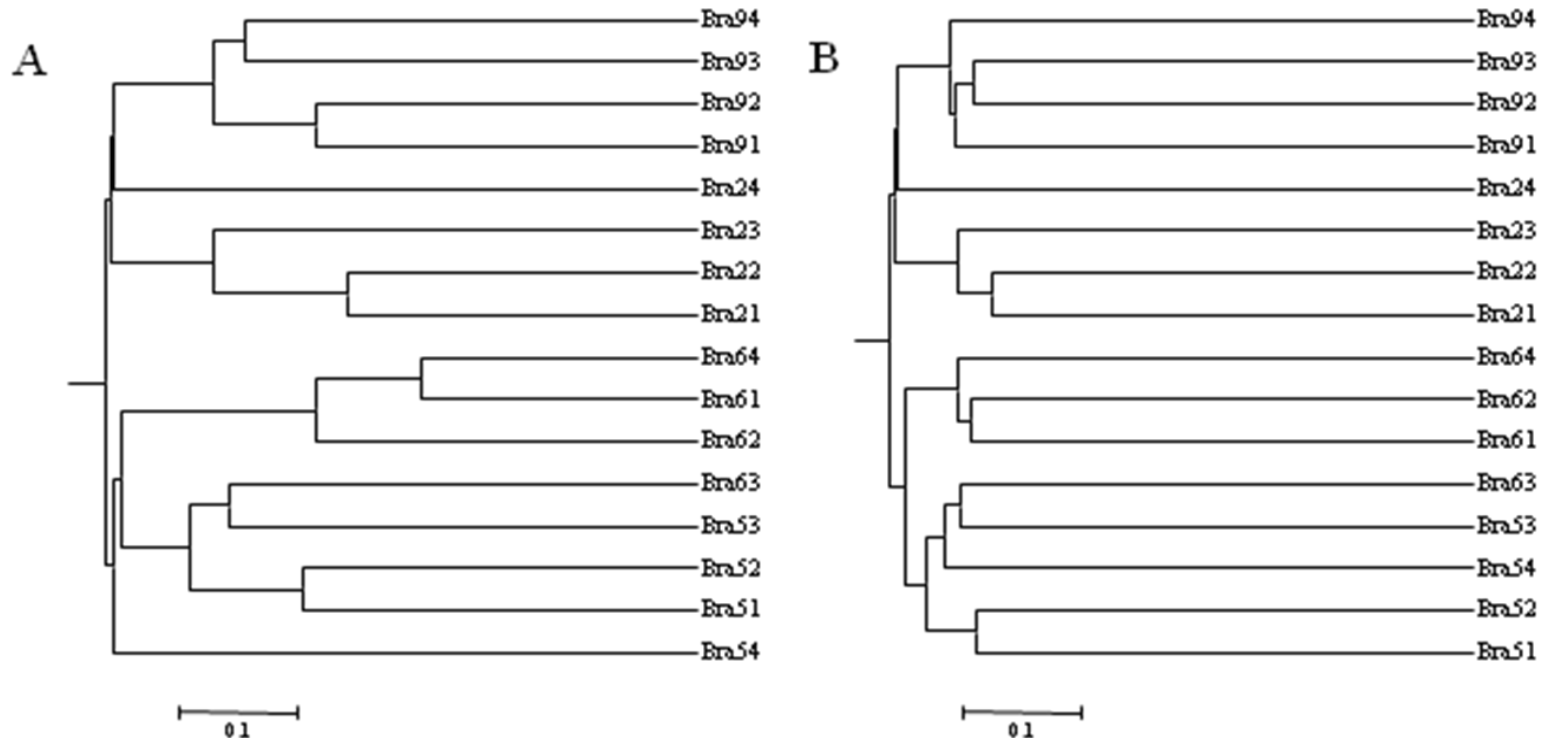

Figure 21 Brazoria NWR community similarities based on OTU analysis (97% similarity). **(a)** Similarity in community structures based on θ*yc* values. **(b)** Similarity in community membership based on Jaccard index values.

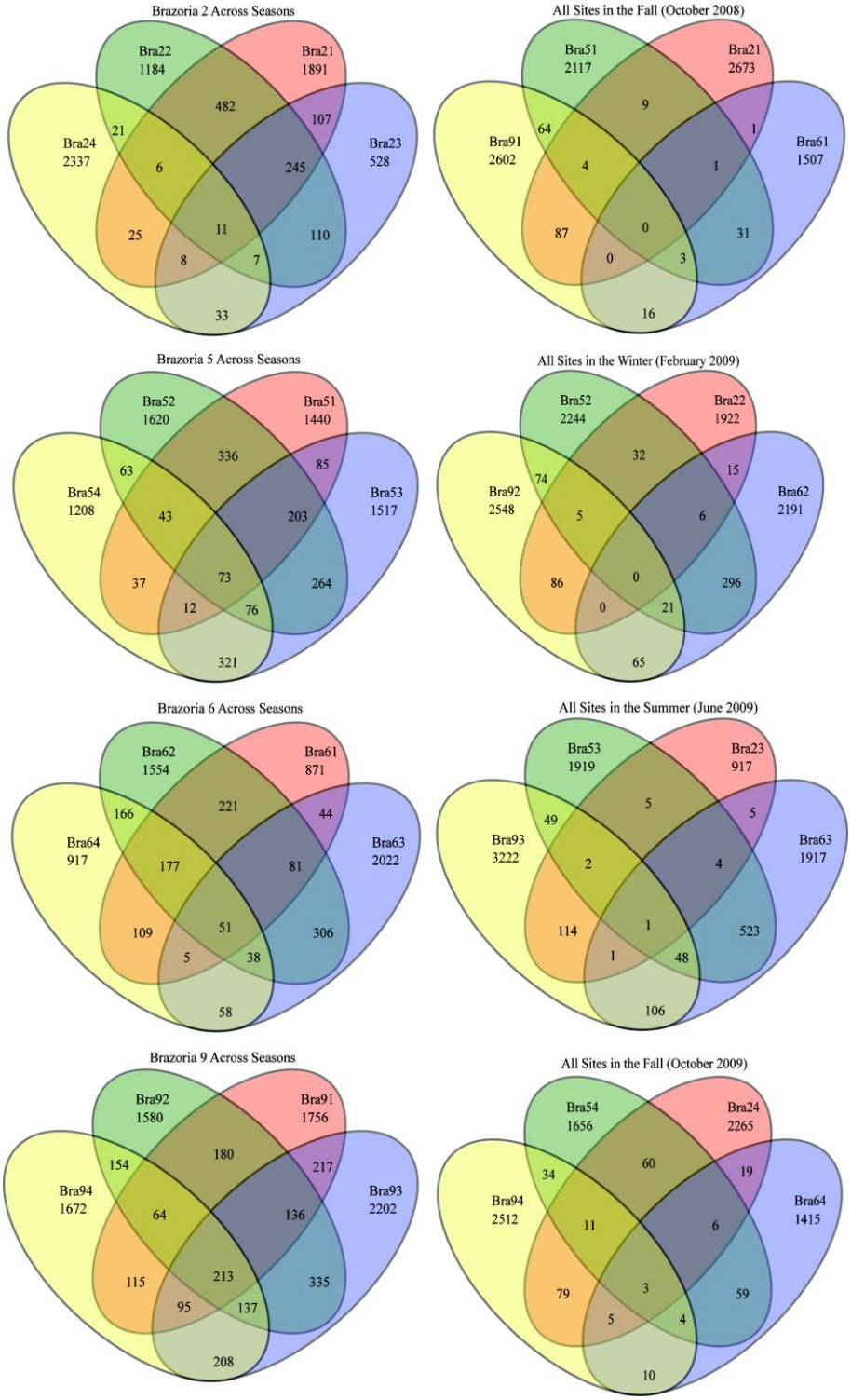

Figure 22 VENN diagrams of shared OTUs for all locales over time and across locales (97% similarity).

Table 12 Brazoria NWR soil physical and chemical characteristics correlate to bacterial community composition.

	Mantel Test	
Variable Tested	*Mantel score (r):*	*p (uncorrelated;onetailed):*
% H_2O	0.1463	0
pH	0.07245	0.028
EC S m^{-1}	-0.05	0.9478
Na mg kg^{-1}	-0.0003	0.469
K mg kg^{-1}	-0.0296	0.8668
Ca mg kg^{-1}	-0.0537	0.972
Mg mg kg^{-1}	-0.0552	0.965
Total N, %	0.2739	0
Totsl C, %	0.2082	0
Organic C, %	0.2921	0
Temp °C	0.042	0.1046
All Ions	-0.0018	0.4876

Bray-Curtis similarity index was used to calculate genetic distance between communities based on OTU compositions (97% similarity)
Euclidean distance was used to calculate the distance between sites based on soil physical and chemical data
Mantel test performed with 5,000 permutations

Table 13 Brazoria NWR geographic characteristics. A Mantel test reveals that there was a significant correlation between site location and community composition for each site and over time.

Geographic Information

Physical Locations

	Latitude (N)	*Longitude (W)*
Bra2	29.06073	95.26022
Bra5	29.06083	95.24095
Bra6	29.06145	95.23797
Bra9	29.03787	95.26693

Distance Between Locales (km)

	Bra2	Bra5	Bra6	Bra9
Bra2	-			
Bra5	1.873	-		
Bra6	2.164	0.2977	-	
Bra9	3.337	3.591	3.847	-

Correlation Between Locale Location and Bacterial Community Composition

	Mantel score (r):	*p* (uncorrelated;onetailed):
Mantel Test	0.3653	0

Mantel test performed with 5,000 permutations

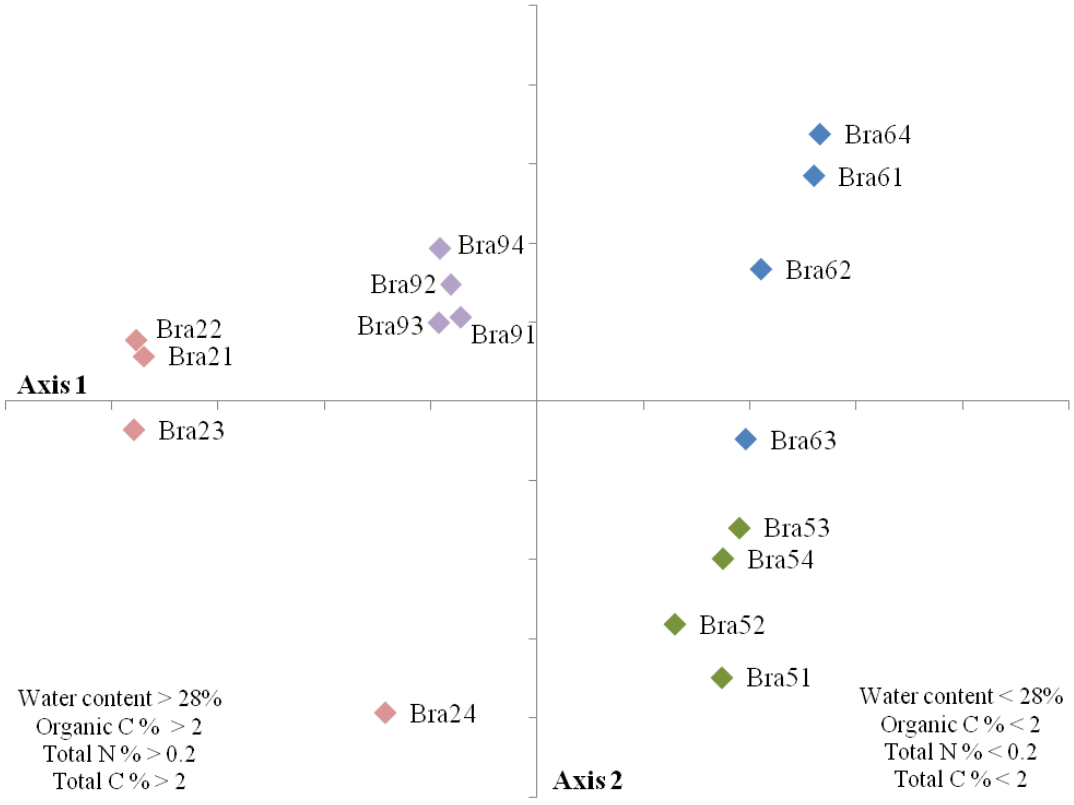

Figure 23 Non-metric multidimensional scaling (NMDS) of Brazoria NWR community similarities based on OTU analysis (97% similarity). Community similarity based on Bray-Curtis similarity index. Samples with similar colors were sampled from within the same locale. The samples are also grouped to the left or right of the vertical axis by the environmental parameters labeled on the chart.

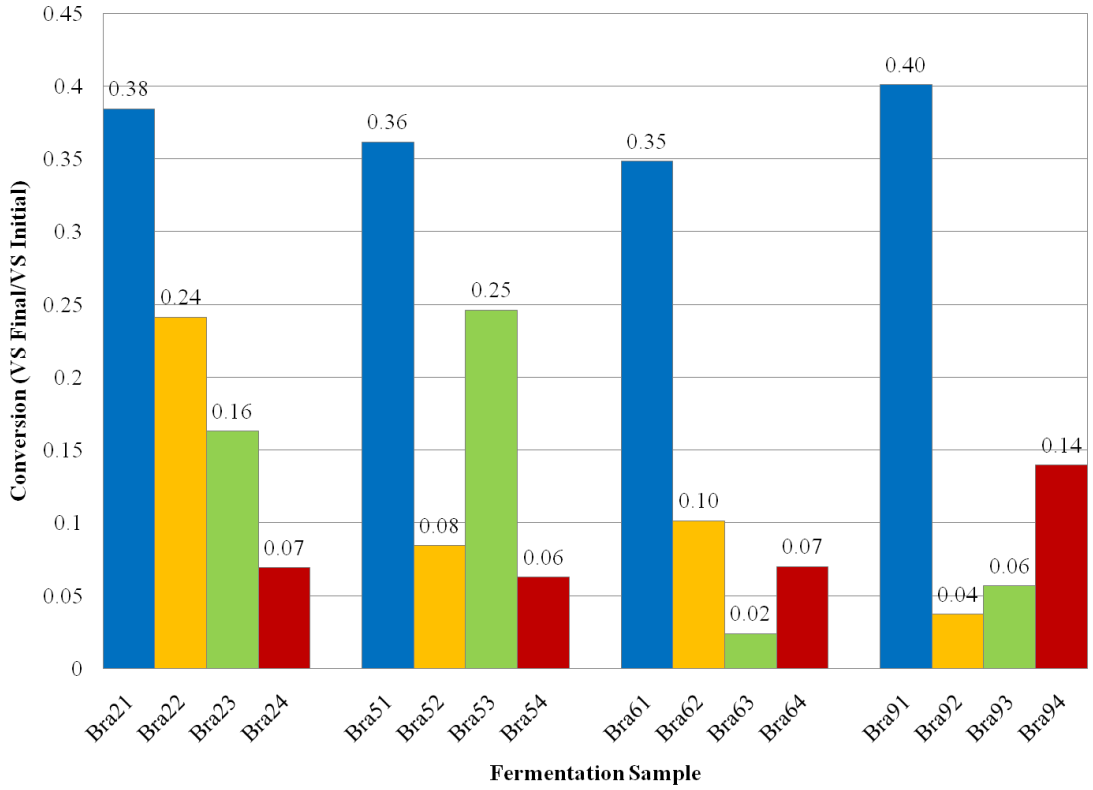

Figure 24 Fermentation performances of all Brazoria NWR samples based on conversion. Samples that are similar in color were sampled in the same season (VS, volatile solids; October 2008, blue; February 2009, orange; June 2009, green; October 2009, maroon)

Table 14 Brazoria NWR sediment and fermentation community characteristics based on OTU analysis (97% similarity).

	Sediment Community Characteristics				*Fermentation Community Characteristics*			
Sample Name	*Sequence Library Size*	*Number of OTUs*	*Shannon (H')*	*Chao I Richness Estimate*	*Sequence Library Size*	*Number of OTUs*	*Shannon (H')*	*Chao I Richness Estimate*
Bra21	5735	2909	7.42	8052	4771	529	4.58	878
Bra22	6754	2189	6.80	4712	7266	496	3.79	979
Bra23	4354	1138	6.14	2025	4568	445	3.95	802
Bra24	5128	2538	7.42	5892	5062	447	4.27	905
					6929	370		
Bra51	4867	2361	7.06	6331			3.53	579
Bra52	6620	2815	7.18	6826	5736	455	3.87	882
Bra53	7020	2737	7.22	6256	3066	349	3.41	672
Bra54	4789	1952	6.52	4754	4778	288	3.10	476
					7890	349		
Bra61	4661	1699	6.49	4101			4.23	528
Bra62	9009	2785	6.92	6106	7319	375	2.32	691
Bra63	8348	2794	7.11	6145	9139	361	3.51	564
Bra64	4985	1645	6.24	3787	8769	348	3.45	591
					2862	461		
Bra91	4713	2902	7.62	9104			4.52	795
Bra92	6105	3045	7.53	7461	4142	165	4.29	910
Bra93	7200	3671	7.80	8925	4495	475	3.97	888
Bra94	4959	2772	7.52	7419	3597	311	4.00	617
Totals	95,247	39,952			90,389	6,524		

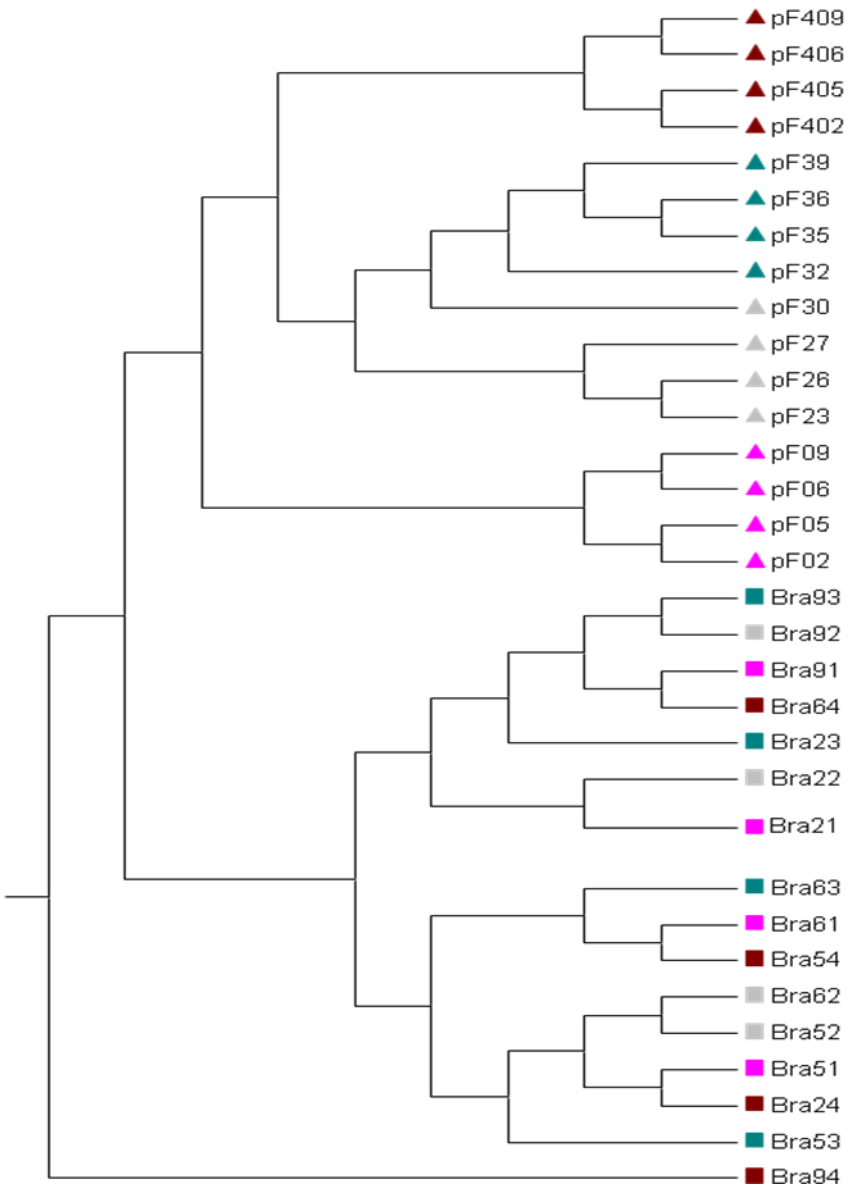

Figure 25 Brazoria NWR sediment and fermentation similarity in community structure. Dendrogram based on θ*yc* values. (Sediment samples, squares; Fermentation samples, triangles; October 2008, pink; February 2009, grey; June 2009, teal; October 2009, maroon)

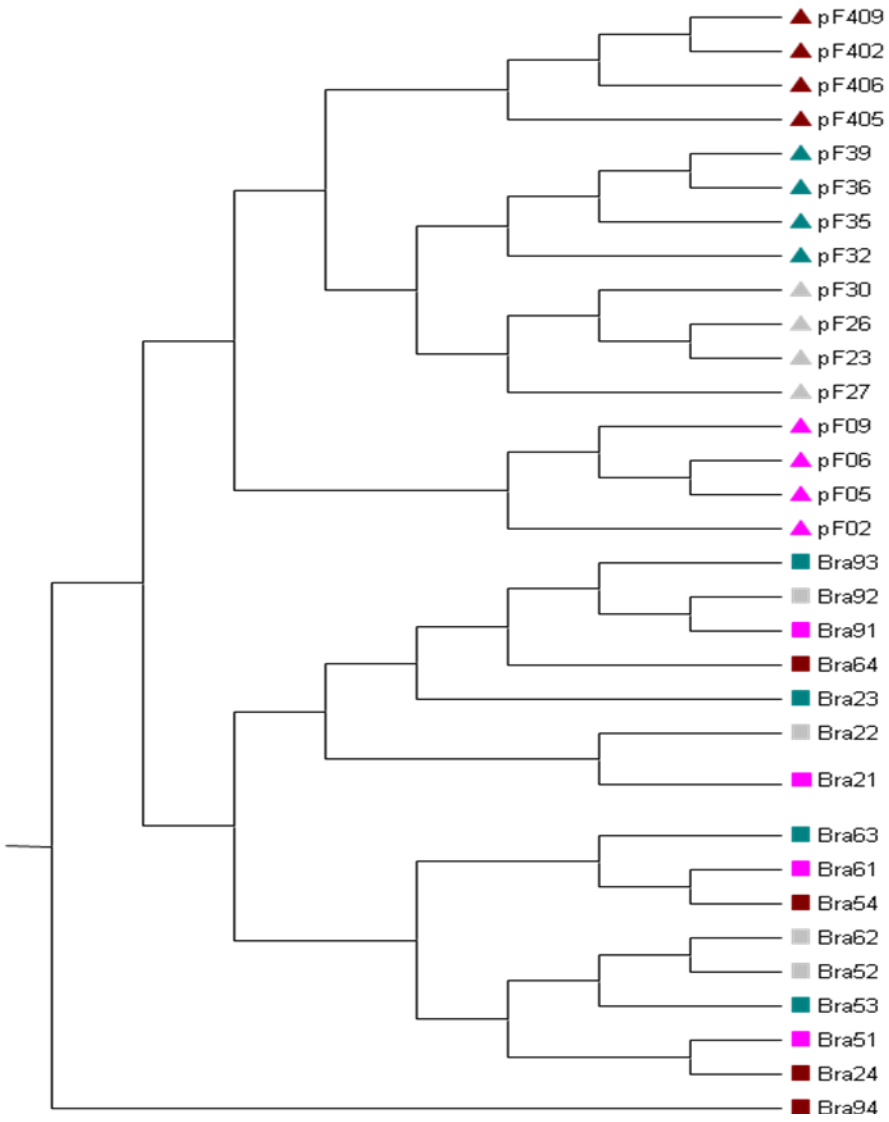

Figure 26 Brazoria NWR sediment and fermentation similarity in community membership. Dendrogram based on Jaccard index values. (Sediment samples, squares; Fermentation samples, triangles; October 2008, pink; February 2009, grey; June 2009, teal; October 2009, maroon)

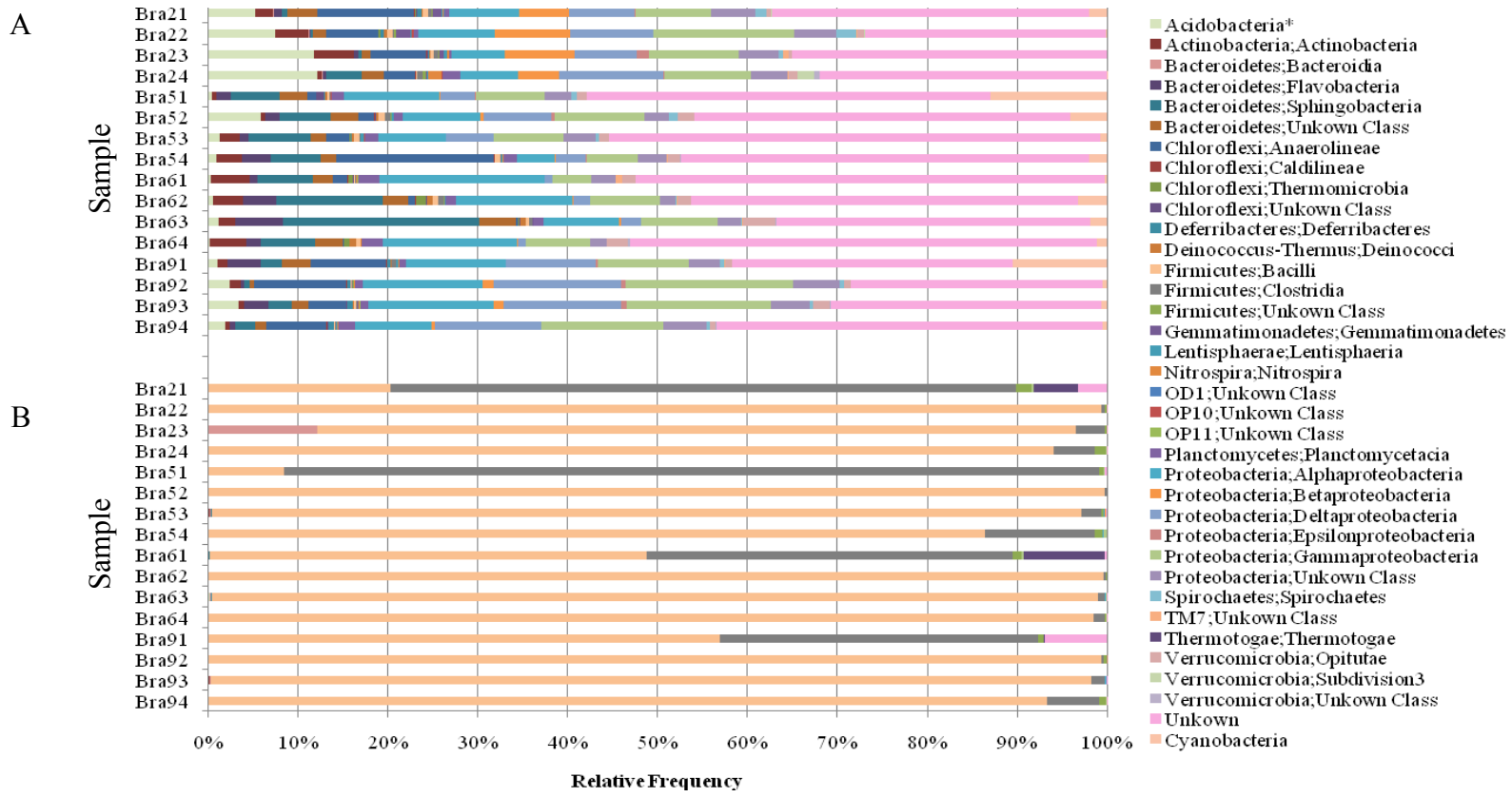

Figure 27 Brazoria NWR sediment and fermentation community compositions as measured by pyrosequencing efforts. **(a)** Bacterial classes represented in the soil community libraries (VAMPS, accessed 28 May 2011) **(b)** Bacterial classes in the fermentation community libraries. All sites were normalized to the maximum number of sequences in the library (9,139). (Key: Phylum;Class, *Phylum only)

Table 15 Singular value decomposition (SVD) sums and Monte Carlo simulation results for Brazoria NWR samples.

	Singular Value Decomposition Sums and Monte Carlo Simulation								
Test	*Experimental SVD Sum*	*Random SVD Sum*	*Mean*	*Variance*	*Lower CL*	*Upper CL*	*>Original SVD Sum*	*Valid Iterations*	*p value*
Fermentation Genera and Performance Metrics	4.226206	2.887169	2.487379	0.126517	1.856534	3.248	0	10000	0
Fermentation Class and Performance Metrics	2.721949	1.447922	1.552157	0.082736	1.044322	2.185987	3	10000	0.0003
Soil Classes and Performance Metrics	3.111385	3.28893	3.369389	0.176863	2.633489	4.265985	7155	10000	0.7155
Soil Classes and Fermentation Classes	6.468258	5.542414	6.079985	0.416497	4.89234	7.404733	5386	20000	0.2693

Abbreviations: SVD: singular value decomposition; CL: confidence limit

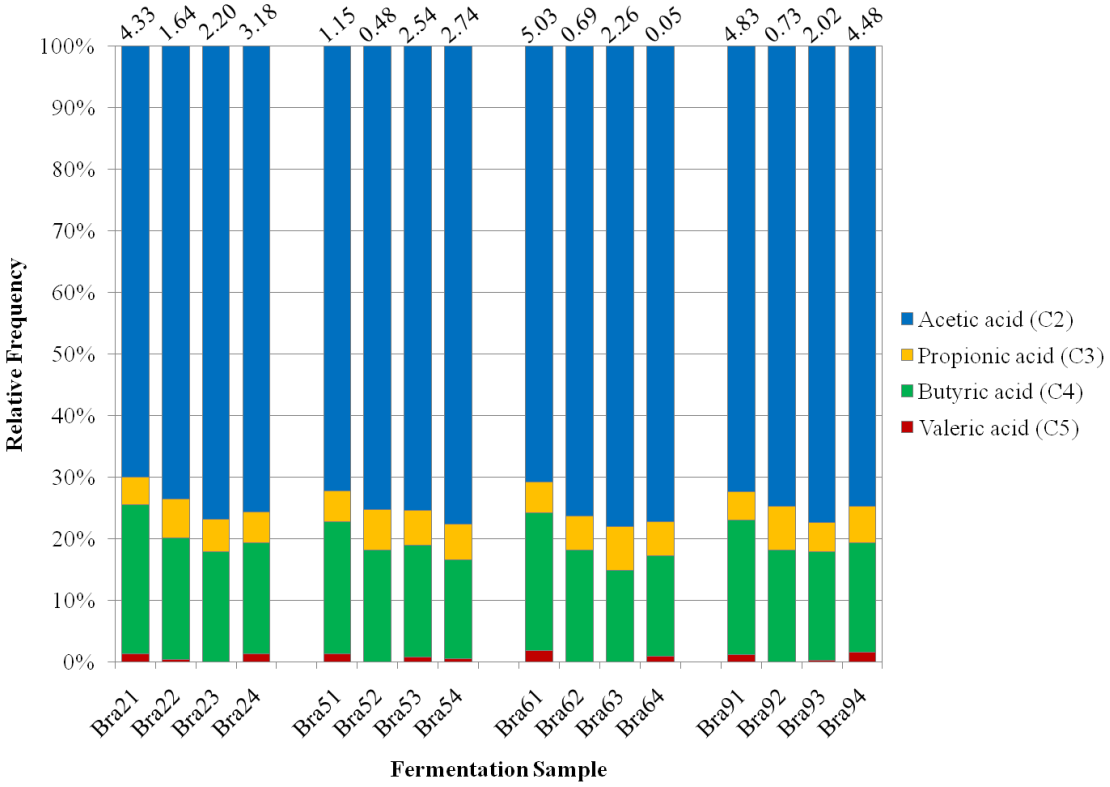

Figure 28 Carboxylic acids produced by the Brazoria NWR samples.
The relative frequency (%) for each type of carboxylic acids is shown and the total amount of all carboxylic acids produced for each sample (g L^{-1}) is listed above the chart.

Table 16 Variation in Brazoria NWR fermentation performances over time.

		Site Variation	
	Variable Tested	*Exact F*	*p value*
Within Site Variation			
Repeated Measures-MANOVA	Time	32.89	<0.0001
Seasonal Variation			
ANOVA	Conversion	9.432646	0.001764
	Acetic acid (C_2)	2.287349	0.130666
	Propionic acid (C_3)	1.605519	0.239875
	Butyric acid (C_4)	3.237997	0.060488
	Valeric acid (C_5)	6.178415	0.008791
	Total Acid	3.336245	0.056128

Repeated Measures-MANOVA implemented in JMP 9 Pro
ANOVA implemented in Microsoft Excel 2007 using PopTools

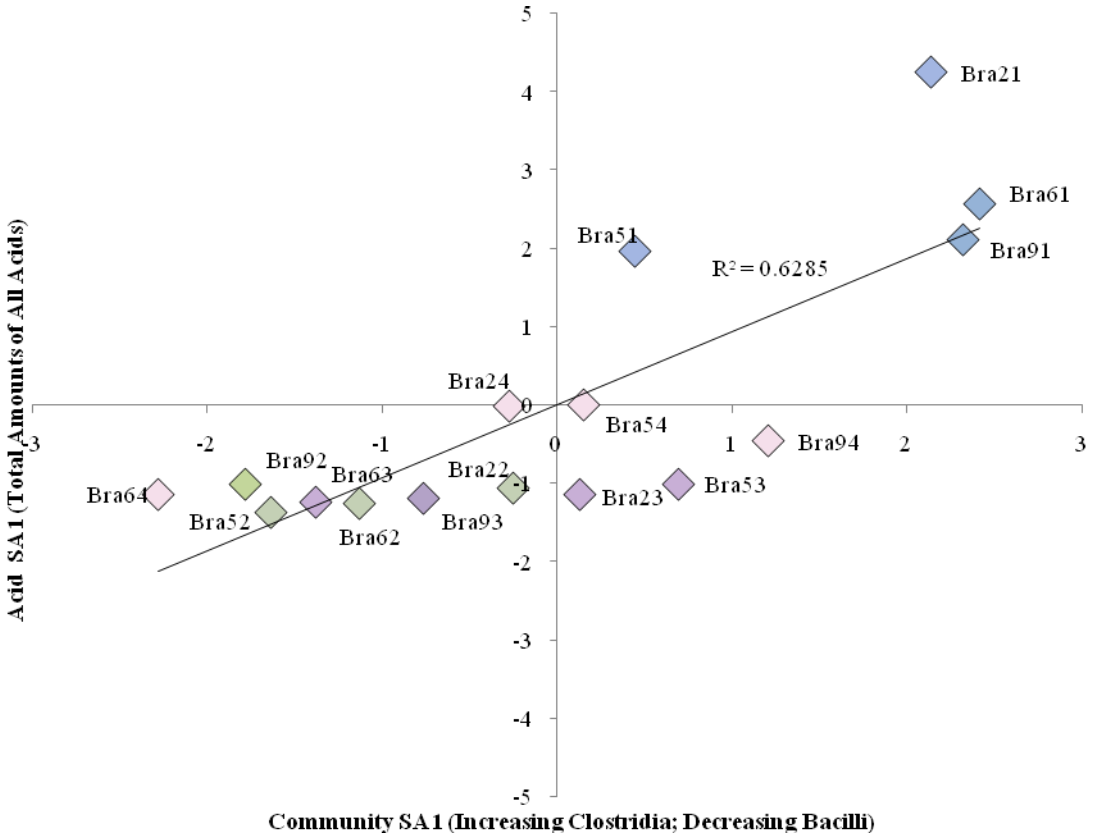

Figure 29 Brazoria NWR fermentation community class composition correlates with fermentation performance. Samples with similar colors were sampled at the same time.

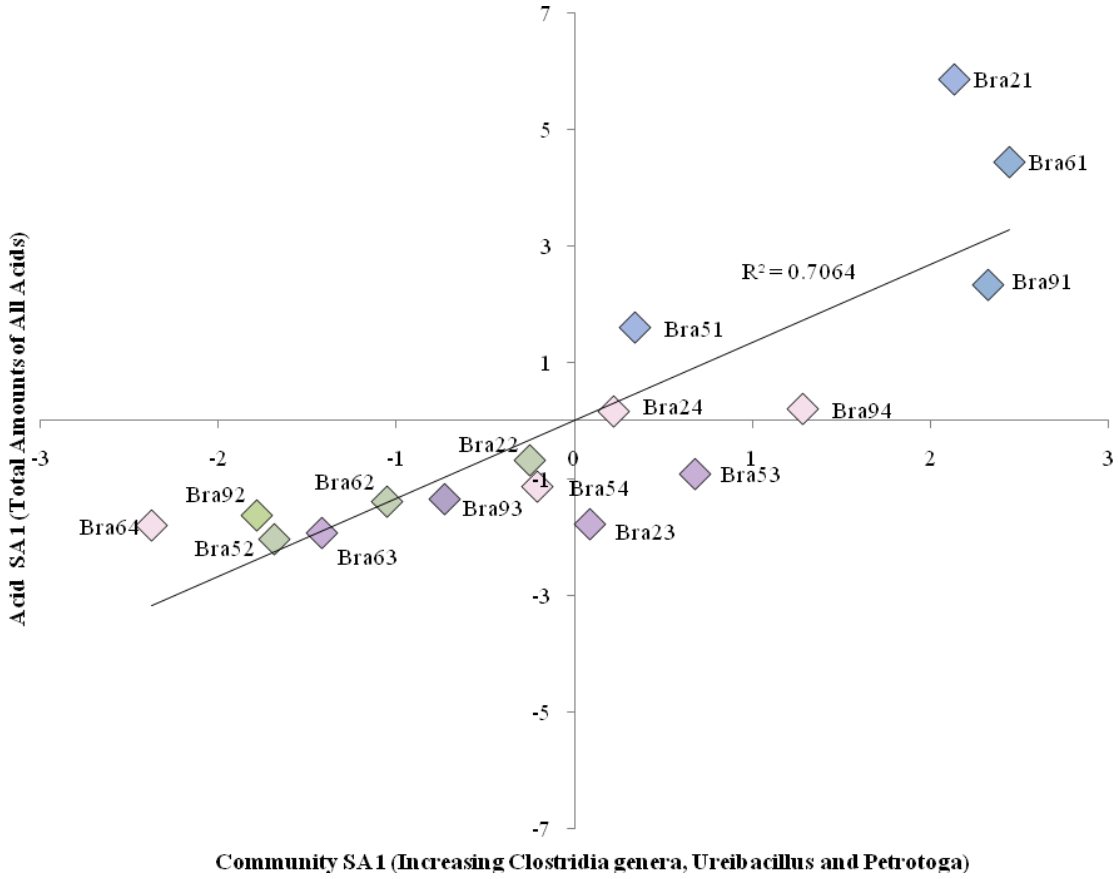

Figure 30 Brazoria NWR fermentation community genera composition correlates with screen performance. Samples with similar colors were sampled at the same time.

Table 17 Saline soil and sediment physical and chemical characteristics. The sites in this study ranged in salinity (6.17 to 20.20 S $m^{-1)}$ and pH (7.60 to 10.17). All sites had electrical conductivity (EC) greater than seawater (>3.5 S m^{-1}).

		Soil Characteristics													
Sample Name	*Sample ID*	*H_2O %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Temp °C[a]*	*Total N, %*	*Total C, %*	*Organic C, %*	*Sample Date*	*Latitude (N)*	*Longitude (W)*
Cabo Rojo NWR 5, PR	CRR 5	47.94	8.14	20.20	88934.50	2316.73	3205.39	12311.9	N/A	0.437	9.5034	5.046	6/1/09	40.6957	111.9491
Cabo Rojo NWR 8, PR	CRR8	40.15	8.04	11.13	43248.40	2307.33	2382.02	5178.86	N/A	0.2307	3.3908	3.3189	6/1/09	40.7485	112.1861
Great Salt Lake 1, UT	GSL1	22.69	7.60	7.68	24033.50	2369.68	2099.78	1084.05	17.7	0.1521	7.3605	2.2595	5/1/09	17.9521	67.1964
Great Salt Lake 3, UT	GSL3	30.09	8.50	6.17	34600.90	992.73	360.68	94.72	17.3	0.2319	7.0296	2.4994	5/1/09	17.9521	67.1964
Mono Lake Island 1, CA	MLIS 1	37.46	10.2	7.06	33625.80	872.70	30.43	26.62	53.7	0.0911	0.7693	0.7924	8/7/09	36.4003	117.9522
Mono Lake Island 2, CA	MLIS 2	43.93	10.1	11.26	72700.20	2362.35	17.98	17.45	46.8	0.1543	1.3518	1.1493	8/7/09	36.3757	117.9773
Owens Lake 1, CA	OLCA 1	52.92	9.59	15.37	164045.0	9973.73	37.48	31.58	33.1	0.1911	5.2237	4.9632	8/7/09	37.5326	122.0848
Owens Lake 2, CA	OLCA 2	35.27	9.80	15.53	106453.0	5475.12	9.90	32.20	44.0	0.1286	4.4134	3.5279	8/7/09	37.4391	121.9618
San Francisco Bay NWR 20, CA	SFB20	57.47	7.10	7.42	1862.20	1291.80	1302.80	2312.80	10.0	0.6079	6.6941	6.7089	2/9/09	39.6025	118.4092
San Francisco Bay NWR 34, CA	SFB34	36.91	7.60	11.60	30151.00	1628.11	1273.38	3963.97	12.9	0.7279	6.4565	6.3225	2/9/09	39.6025	118.3992
Stillwater NWR 2, NV	SWRN2	32.05	7.98	17.30	77678.60	1391.24	979.77	145.72	31.7	0.1267	0.819	0.8528	8/6/09	37.9937	119.0237
Stillwater NWR 3, NV	SWRN3	34.28	7.28	17.35	79470.50	1632.26	656.51	131.13	30.8	0.1127	1.596	1.3964	8/6/09	37.9937	119.0237

[a]Soil temperature taken at time of sampling
Abbreviations: EC, electrical conductivity

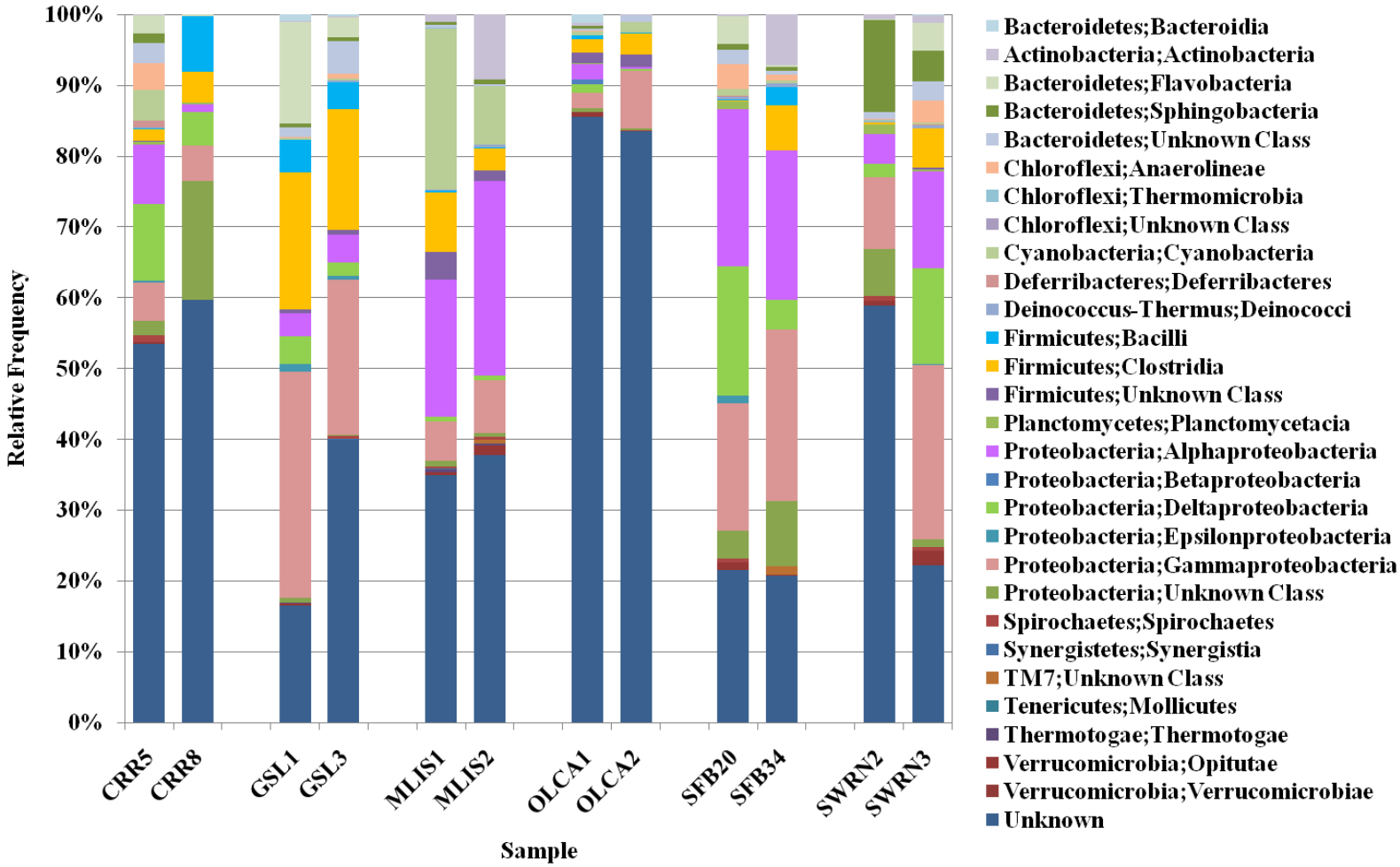

Figure 31 Saline sediment community compositions as measured by pyrosequencing efforts. All sites were normalized to the maximum number of sequences in all 12 sites (8,390). (Key: Phylum; Class)

Table 18 Saline sediment community characteristics based on OTU analysis (97% similarity). There was a total of 63,302 partial 16S rRNA gene sequences analyzed. The sites had varying levels of diversity as shown by the varying OTUs and ChaoI richness estimates. There were a total of 11,902 OTUs at 97% similarity.

		Community Characteristics			
Sample Name	*Sample ID*	*Sequence Library Size*	*Number of OTUs*	*Shannon (H')*	*Chao I Richness Estimate*
Cabo Rojo NWR 5, PR	CRR5	6978	2179	7.19	10410
Cabo Rojo NWR 8, PR	CRR8	2213	95	3.21	112
Great Salt Lake 1, UT	GSL1	5351	1127	6.04	4715
Great Salt Lake 3, UT	GSL3	3138	713	5.30	1400
Mono Lake Island 1, CA	MLIS1	6388	1086	5.65	3982
Mono Lake Island 2, CA	MLIS2	7767	849	5.27	2726
Owens Lake 1, CA	OLCA1	3865	672	5.22	1125
Owens Lake 2, CA	OLCA2	5313	814	5.44	3122
San Francisco Bay NWR 20, CA	SFB20	5410	1989	7.16	9594
San Francisco Bay NWR 34, CA	SFB34	4035	374	4.94	556
Stillwater NWR 2, NV	SWRN2	8390	1031	5.51	3502
Stillwater NWR 3, NV	SWRN3	4454	973	5.78	3214
Totals		63,302	11,902		

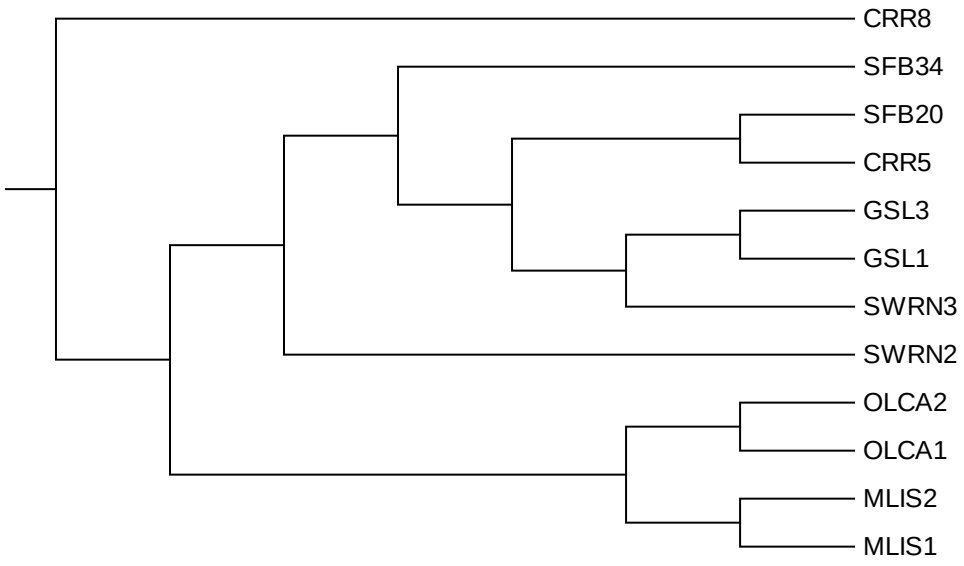

Figure 32 Saline samples similarity in community structure. This dendrogram is based on θ*yc* similarity values.

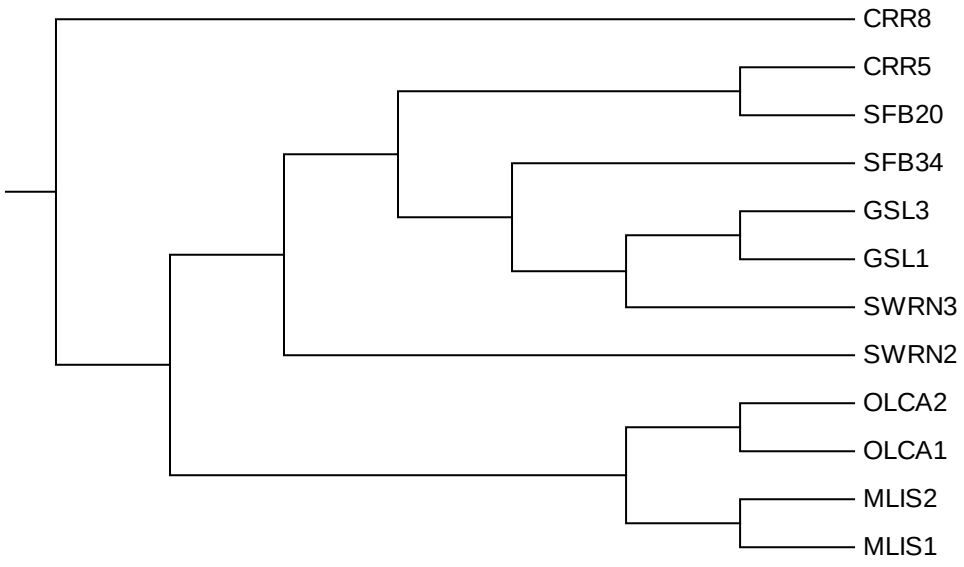

Figure 33 Saline samples similarity in community membership. This dendrogram represents similarity between samples and sites as shown by Jaccard similarity values.

Table 19 Geographic distance between sites does not correlate with saline sediment bacterial community composition. The distance between sites ranged from 0.002 km to 5,474 km.

Geographic Information

Distance Between Sites (km)

	CRR5	CRR 8	GSL1	GSL3	MLIS 1	MLIS 2	OLCA 1	OLCA 2	SFB20	SFB34	SWRN2	SWRN3
CRR5	-											
CRR 8	0	-										
GSL1	4949	4949	-									
GSL3	4970	4970	20.82	-								
MLIS 1	5474	5474	678.2	662.5	-							
MLIS 2	5474	5474	678.2	662.5	0.00239	-						
OLCA 1	5353	5353	707.2	696.1	201	201	-					
OLCA 2	5392	5392	710.8	699.7	202.4	202.4	3.541	-				
SFB20	5733	5733	941.8	924.9	273.9	273.9	388.1	387	-			
SFB34	5721	5721	936.5	919.7	265.7	265.7	374.7	373.4	15.03	-		
SWRN2	5452	5452	562.2	543.7	186.7	186.7	358.3	360.8	393.8	391.6	-	
SWRN3	5451	5451	561.4	542.9	186.9	186.9	358.2	360.7	394.5	392.3	0.8499	-

Correlation Between Site Location and Bacterial Community Composition

	Mantel score (r):	*p* (uncorrelated;onetailed):
Mantel Test (one tailed)	0.03414	0.2448

Mantel test performed with 5,000 permutations

Table 20 Saline soil physical and chemical characteristics correlate with bacterial community composition.

	Mantel Test	
Variable Tested	*Mantel score (r):*	*p (uncorrelated;onetailed):*
% H_2O	-0.0228	0.659
pH	0.05678	0.0614
EC S m-1	0.01278	0.3606
Na mg kg^{-1}	-0.0974	0.9926
K mg kg^{-1}	-0.0722	0.9542
Ca mg kg^{-1}	0.02401	0.2682
Mg mg kg^{-1}	0.1	0.0064
Total N, %	0.01647	0.3146
Totsl C, %	0.02401	0.2682
Organic C, %	-0.0173	0.6772
All Ions	-0.0976	0.9928

Bray-Curtis similarity index was used to calculate genetic distance between communities based on OTU compositions (97% similarity)
Euclidean distance was used to calculate the distance between sites based on soil physical and chemical data
Mantel test performed with 5,000 permutations

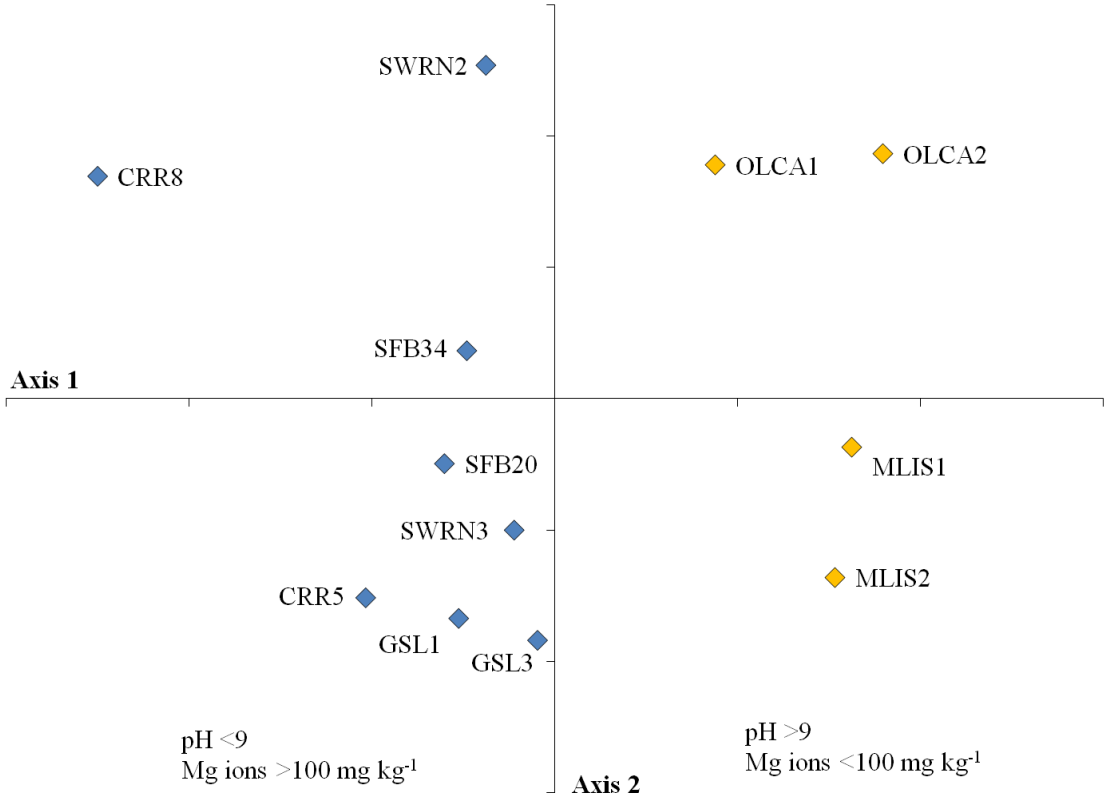

Figure 34 Non-metric multidimensional scaling (NMDS) of saline sediment bacterial community similarities based on OTU analysis (97% similarity). Community comparisons were made using Bray-Curtis similarity index. The samples grouped to either side of the vertical axis based on pH and magnesium ion content (listed in chart). (Yellow, pHs above 9; Blue, pHs below 9)

APPENDIX B

Table 21 Soil physical and chemical data for all samples collected and screened in the carboxylate platform. Analyses were performed by the Soil, Water, and Forage Testing Laboratory at Texas A&M University. The table shows pH (Shofield and Taylor, 1955), detailed salinity (Rhoades and Clark, 1978) (Na, K, Ca, Mg), and electrical conductivity (EC) (Rhoades, 1982). Total carbon, organic carbon, and total nitrogen analysis was also performed (McGeehan and Naylor, 1988). Fermentation data is listed in Appendix D: Table 23 and gps coordinates with sampling dates are listed in Appendix C: Table 22.

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp ^{0}C*
LSDR T1-0	La Sal del Rey	TX	A02	0.82	88	5	7	7.6	0.18	393	13	115	16	0.39	0.1	0.4	33
LSDR T1-65	La Sal del Rey	TX	A03	16.71	88	5	7	7.6	N/D	N/D	N/D	N/D	N/D	0.22	0.12	0.23	34
LSDR T1-130	La Sal del Rey	TX	A04	16.16	84	3	13	7.6	N/D	N/D	N/D	N/D	N/D	0.29	0.08	0.29	35
LSDR T1-195	La Sal del Rey	TX	A05	16.65	84	7	9	7.9	4.3	18990	180	207	942	0.33	0.09	0.34	34
LSDR T1-260	La Sal del Rey	TX	A06	26.54	62	21	17	7.6	10.85	45297	461	769	1200	0.88	0.14	0.91	35
LSDR T1-325	La Sal del Rey	TX	A07	25.19	73	14	13	7.5	9.6	40553	528	1254	1551	0.68	0.1	0.67	34
LSDR T1-390	La Sal del Rey	TX	A08	16.36	79	8	13	7.8	7.5	37404	372	428	1318	0.22	0.13	0.24	34
LSDR T1-455	La Sal del Rey	TX	A09	42.67	47	26	27	7.1	14.45	78163	1419	619	4568	0.94	0.16	0.95	34
LSDR T1-520	La Sal del Rey	TX	A10	43.38	19	12	69	6.8	14.97	100168	2195	440	10107	0.69	0.13	0.69	32
LSDR T1-585	La Sal del Rey	TX	A11	50.89	21	30	49	7	15.16	84186	2134	464	8423	1.07	0.17	1.08	32
LSDR T2-0	La Sal del Rey	TX	A12	2.89	83	6	11	7.8	0.34	720	53	158	49	2.21	0.27	2.1	32
LSDR T2-65	La Sal del Rey	TX	A13	1.08	91	6	3	8.7	0.19	461	42	35	16	0.59	0.12	0.61	33
LSDR T2-130	La Sal del Rey	TX	A14	20.26	71	8	21	8.5	4.52	16863	360	219	350	0.75	0.12	0.79	37
LSDR T2-95	La Sal del Rey	TX	A15	19.95	65	20	15	7.9	8.21	36090	547	1343	954	0.91	0.09	0.93	37
LSDR T2-260	La Sal del Rey	TX	A16	21.99	69	16	15	7.4	15.42	82865	753	594	1789	0.9	0.14	0.91	37
LSDR T2-325	La Sal del Rey	TX	A17	23.84	75	4	21	7.4	14.45	76402	1125	551	3586	0.59	0.14	0.59	34
LSDR T2-390	La Sal del Rey	TX	A18	16.93	75	3	22	7.5	11.95	57633	880	440	3293	0.29	0.09	0.29	34
LSDR T2-455	La Sal del Rey	TX	A19	16.04	45	28	27	7.5	16.7	105057	1427	619	6059	0.29	0.1	0.28	33

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
LSDR T3-0	La Sal del Rey	TX	A20	9.04	70	12	18	8.1	3.42	12025	117	770	701	1.44	0.22	1.43	38
LSDR T3-65	La Sal del Rey	TX	A21	10.11	86	2	12	8	4.03	16435	115	387	744	0.13	0.12	0.15	44
LSDR T3-130	La Sal del Rey	TX	A22	19.56	66	20	14	8.3	7.42	35922	241	810	1891	0.27	0.16	0.26	43
LSDR T3-195	La Sal del Rey	TX	A23	19.16	78	6	16	8	6.28	26752	266	613	1216	0.5	0.09	0.64	43
LSDR T3-260	La Sal del Rey	TX	A24	19.86	81	9	10	8.4	3.86	14434	166	521	493	0.26	0.13	0.27	44
LSDR T3-325	La Sal del Rey	TX	A25	19.5	71	15	14	8.4	6.18	26963	237	803	525	0.77	0.15	0.74	45
LSDR T3-390	La Sal del Rey	TX	A26	25.49	71	19	10	7.9	9.41	43330	498	536	1598	0.46	0.13	0.46	43
LSDR T3-455	La Sal del Rey	TX	A27	30.64	73	13	14	7.4	12.3	67930	889	639	3099	0.64	0.09	0.65	42
GR1	Grulla Lake	NM	D01	30.72	81	11	8	8.2	1.32	2881	494	780	492	1.12	0.13	1.16	21
GR2	Grulla Lake	NM	D02	23.84	75	17	8	8.3	2.04	4505	1191	609	808	1.22	0.17	1.31	21
GR3	Grulla Lake	NM	D03	20.29	67	23	10	8.1	1.92	4945	884	501	889	1.48	0.1	1.52	21
GR4	Grulla Lake	NM	D04	32.82	65	17	18	8.2	1.33	3120	496	308	509	1.41	0.09	1.36	21
GR5	Grulla Lake	NM	D05	27.62	79	17	4	8.3	1.93	4583	983	266	860	0.69	0.1	0.69	21
GR6	Grulla Lake	NM	D06	12.56	71	21	8	8.1	2.53	7127	1396	540	1246	0.9	0.15	1.1	21
GR7	Grulla Lake	NM	D07	10.46	59	21	20	8.2	3.86	10613	1954	575	2344	1.57	0.11	1.56	21
GR8	Grulla Lake	NM	D08	16.59	57	27	16	8.4	3.44	8436	1732	828	2133	0.56	0.1	0.58	21
GR9	Grulla Lake	NM	D09	19.98	75	15	10	8.2	3.56	9636	2042	770	2097	1.05	0.11	0.95	20
GR10	Grulla Lake	NM	D10	14.4	61	23	16	8	4.7	12822	2784	521	2427	1.78	0.12	1.75	21
GR11	Grulla Lake	NM	D11	17.44	71	19	10	8.1	5.06	14095	1906	610	3099	1.25	0.18	1.22	24
GR12	Grulla Lake	NM	D12	19.8	67	23	10	8	5.97	15494	2949	733	3676	1.06	0.11	1.06	25
MPL1 R	Muleshoe Pauls Lake	NM	D13	10.86	65	25	10	8.3	3.96	13828	599	521	985	2.35	0.25	2.76	27
MPL2 R	Muleshoe Pauls Lake	NM	D14	12.21	65	15	20	8	1.97	5745	252	198	401	2.12	0.23	2.12	25
MPL3 R	Muleshoe Pauls Lake	NM	D15	25.83	69	25	6	8.5	2.82	8275	327	302	830	0.55	0.13	0.55	27

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
MPL4 R	Muleshoe Pauls Lake	NM	D16	23.39	81	7	12	8	4.5	16508	524	730	2289	1.16	0.13	1.54	27
MPL5 R	Muleshoe Pauls Lake	NM	D17	18.35	63	11	26	7.9	3.11	9346	397	635	1301	0.86	0.09	2.53	30
MPL6 R	Muleshoe Pauls Lake	NM	D18	32.9	80	16	4	7.9	4.85	14558	639	873	2461	0.8	0.11	0.94	29
MPL7 R	Muleshoe Pauls Lake	NM	D19	37.84	74	18	8	8.1	8.01	29004	1192	826	4556	1.05	0.14	1.09	29
MPL8 R	Muleshoe Pauls Lake	NM	D20	50.79	85	9	6	8	2.01	5059	240	661	1132	1.45	0.28	2.74	22
MPL9 L	Muleshoe Pauls Lake	NM	D21	15.85	53	19	28	7.8	1.89	5070	261	583	1213	3.47	0.35	3.58	20
MWL1 R	Muleshoe White Lake	NM	D22	44.42	65	7	28	8.4	5.6	25044	958	480	1269	1.61	0.16	1.89	30
MWL 2 R	Muleshoe White Lake	NM	D23	52.86	51	19	30	8.3	5.99	23587	942	454	1963	2.13	0.21	2.3	27
MWL3 R	Muleshoe White Lake	NM	D24	22.92	31	35	34	7.9	1.96	6080	224	318	244	0.92	0.27	1.24	26
MWL4 R	Muleshoe White Lake	NM	D25	26.98	79	7	14	8	1.89	5493	202	321	228	2.65	0.19	3.22	20
MGL1 R	Muleshoe Goose Lake	NM	D26	25.65	40	30	30	8.5	6.27	29295	810	637	1890	2.59	0.1	2.75	26
MGL2 R	Muleshoe Goose Lake	NM	D27	19.59	43	23	34	8.6	7.13	28341	694	664	2619	2.43	0.12	2.73	22
MGL3 R	Muleshoe Goose Lake	NM	D28	22.98	77	17	6	8.3	4.16	13346	789	510	1064	1.25	0.07	1.36	22
MGL4 R	Muleshoe Goose Lake	NM	D29	38.42	43	15	42	8.5	2.31	7666	272	276	418	2.64	0.1	2.8	21
MGL5 L	Muleshoe Goose Lake	NM	D30	75.67	41	45	14	8.7	3.85	14505	432	408	1942	3.67	0.27	3.98	25
GSP1	Great Salt Plains NWR	OK	E01	11.71	62	21	17	6.7	0	0	61	278	200	0.07	0.08	0.07	20
GSP2	Great Salt Plains NWR	OK	E02	15.78	76	19	5	9.5	0.12	547	6	13	6	0.1	0.07	0.1	16
GSP3	Great Salt Plains NWR	OK	E03	17.8	88	7	5	7.2	0.04	87	23	11	23	0.28	0.1	0.28	18
GSP4	Great Salt Plains NWR	OK	E04	17.85	92	3	5	7.5	0.72	1546	37	116	44	0.28	0.08	0.49	19
GSP5	Great Salt Plains NWR	OK	E05	24.32	68	7	25	8	1.85	4552	43	97	72	0.7	0.11	0.78	19
GSP6	Great Salt Plains NWR	OK	E06	22.2	96	1	5	7.3	5.03	26483	168	1033	361	0.61	0.09	0.7	21
GSP7	Great Salt Plains NWR	OK	E07	27.26	90	5	5	6.8	3.25	13136	400	1038	236	0.88	0.15	1.87	19

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
GSP8	Great Salt Plains NWR	OK	E08	19.75	93	0	7	7.4	3.71	15534	111	724	208	0.4	0.08	0.61	19
GSP9	Great Salt Plains NWR	OK	E09	14.69	89	4	7	7.5	0.9	1957	74	347	40	1.33	0.12	1.42	22
GSP10	Great Salt Plains NWR	OK	E10	38.27	N/D	N/D	N/D	7.52	0.26	207	14	307	65	5.94	0.61	6.75	18
GSP11	Great Salt Plains NWR	OK	E11	50.48	69	18	13	8.1	0.19	217	23	179	55	5.97	0.61	6.07	18
Bra11	Brazoria NWR	TX	F01	63.3	52	31	17	5.58	3.93	7581	285	1205	1253	12.7	0.99	13.03	20
Bra21	Brazoria NWR	TX	F02	46.58	37	26	37	6.1	3.15	7742	493	883	1360	4.24	0.49	4.41	21
Bra31	Brazoria NWR	TX	F03	26.38	41	24	35	7.6	1.94	4802	283	257	462	1.81	0.18	2.46	22
Bra41	Brazoria NWR	TX	F04	44.84	43	44	13	7.5	2.4	5707	363	443	754	4.67	0.45	5	21
Bra51	Brazoria NWR	TX	F05	21.43	47	44	9	7.7	5.01	12697	573	419	1951	0.72	0.15	0.78	22
Bra61	Brazoria NWR	TX	F06	21.9	41	36	23	8.1	5.83	20892	549	216	925	1.06	0.12	1.02	29
Bra71	Brazoria NWR	TX	F07	48.16	35	30	35	7.4	4.52	10671	507	697	158	3.67	0.34	3.6	22
Bra81	Brazoria NWR	TX	F08	25.22	50	29	21	7.4	4.51	10541	583	477	1588	1.96	0.24	1.92	24
Bra91	Brazoria NWR	TX	F09	46.88	52	19	29	6.9	2.98	9812	638	460	1241	2.79	0.31	3.01	22
Bra12	Brazoria NWR	TX	F22	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	18
Bra22	Brazoria NWR	TX	F23	43.71	41	22	37	6.42	2.97	7462	229	525	1019	4.38	0.36	4.35	18
Bra32	Brazoria NWR	TX	F24	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	20
Bra42	Brazoria NWR	TX	F25	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	18
Bra52	Brazoria NWR	TX	F26	15.77	41	50	9	7.53	8.32	24528	477	1315	3701	0.46	0.08	0.47	20
Bra62	Brazoria NWR	TX	F27	11.54	37	46	17	7.74	3.68	9402	158	807	579	1.05	0.12	1.63	20
Bra72	Brazoria NWR	TX	F28	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	18
Bra82	Brazoria NWR	TX	F29	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	21
Bra92	Brazoria NWR	TX	F30	28.82	35	34	31	7.04	4.16	10865	393	622	1386	3.05	0.28	2.91	20
Bra13	Brazoria NWR	TX	F31	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	31

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
Bra23	Brazoria NWR	TX	F32	35.82	29	28	43	6.14	2.19	4689	179	464	737	3.84	0.33	3.71	30
Bra33	Brazoria NWR	TX	F33	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	34
Bra43	Brazoria NWR	TX	F34	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	29
Bra53	Brazoria NWR	TX	F35	12.75	45	48	7	7.42	7.77	24600	472	1449	3424	0.53	0.07	0.52	50
Bra63	Brazoria NWR	TX	F36	4.15	42	43	15	7.83	5.63	18175	279	1290	665	1.15	0.08	1.01	37
Bra73	Brazoria NWR	TX	F37	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	29
Bra83	Brazoria NWR	TX	F38	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	38
Bra93	Brazoria NWR	TX	F39	37.68	36	37	27	4.59	5.05	13319	625	856	2133	4.21	0.28	4.24	37
Bra14	Brazoria NWR	TX	F401	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	21
Bra24	Brazoria NWR	TX	F402	31.84	34	37	29	7.71	0.43	902	38	122	98	2.08	0.22	2.84	21
Bra34	Brazoria NWR	TX	F403	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	21
Bra44	Brazoria NWR	TX	F404	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	21
Bra54	Brazoria NWR	TX	F405	21.12	42	33	25	7.52	5.59	15184	237	699	2283	0.61	0.13	0.78	21
Bra64	Brazoria NWR	TX	F406	16.79	32	37	31	8.81	2.81	8037	102	150	169	0.94	0.08	1.32	22
Bra74	Brazoria NWR	TX	F407	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	21
Bra84	Brazoria NWR	TX	F408	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	23
Bra94	Brazoria NWR	TX	F409	36.13	30	35	35	7.79	2.71	6738	235	363	784	2.39	0.2	2.67	23
BL1	Bitter Lake NWR	NM	G01	45.27	65	26	9	7.6	5.29	27826	162	542	4377	2.22	0.27	2.2	11
BL2	Bitter Lake NWR	NM	G02	37.21	71	20	9	7.3	5.68	3232	151	542	6015	1.63	0.22	1.55	10
BL3	Bitter Lake NWR	NM	G03	36.18	69	20	11	7.5	5.55	45630	196	536	8069	1.32	0.18	1.45	9
BL4	Bitter Lake NWR	NM	G04	32.21	69	18	13	7.2	8.04	55834	185	510	9623	1.47	0.18	1.47	9
BL5	Bitter Lake NWR	NM	G05	33.29	63	24	13	7.4	7.6	58308	221	543	8464	3.19	0.43	3.3	10
BL7	Bitter Lake NWR	NM	G07	34.03	63	32	5	7.2	3.01	10714	106	544	1336	2.01	0.25	2.45	10

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
BL8	Bitter Lake NWR	NM	G08	43.83	71	18	11	7.2	6.19	37623	228	542	6829	2.26	0.31	2.23	9
BL9	Bitter Lake NWR	NM	G09	30.42	63	28	9	7.5	7.32	46461	189	538	8654	1.53	0.22	1.71	9
BL10	Bitter Lake NWR	NM	G10	60	52	26	22	6.9	8	59520	187	503	10354	4.06	0.5	4.35	11
BL11	Bitter Lake NWR	NM	G11	39.75	82	8	10	7.4	6.13	38244	173	503	6167	1.39	0.22	1.42	10
BL12	Bitter Lake NWR	NM	G12	16.05	78	16	6	8	5.6	34517	139	502	4424	0.98	0.1	1.49	11
BL13	Bitter Lake NWR	NM	G13	27.52	74	16	10	7.3	4.51	18741	100	504	2323	1.23	0.16	1.62	11
BL14	Bitter Lake NWR	NM	G14	40.62	66	26	8	6.9	2.6	8921	177	504	1549	1.63	0.27	2.24	11
BL15	Bitter Lake NWR	NM	G15	46.04	48	48	4	7.8	1.84	4990	60	504	481	2.23	0.28	2.93	10
BL16	Bitter Lake NWR	NM	G16	36.37	45	48	7	7.5	6.47	42404	142	503	5343	2.35	0.22	2.8	11
BL17	Bitter Lake NWR	NM	G17	29.31	61	34	5	7.4	3	12747	73	503	498	1.16	0.16	2.34	10
BL18	Bitter Lake NWR	NM	G18	44.52	57	26	17	7.5	8.7	64274	198	441	4599	2.42	0.25	2.87	12
BL19	Bitter Lake NWR	NM	G19	28.47	73	22	5	7.4	1.85	5946	63	502	346	0.8	0.1	1.02	12
BL20	Bitter Lake NWR	NM	G20	40.9	53	38	9	7.3	3.9	17173	117	502	1316	1.77	0.21	2.57	10
BL21	Bitter Lake NWR	NM	G21	34.72	47	40	13	7.7	5.82	41223	113	402	2944	2.26	0.25	2.62	11
LL1	Bottomless Lake State Park; Lazy Lagoon	NM	G22	33.05	53	40	7	7.1	5.03	26667	644	1696	5217	1.97	0.28	2.13	12
LL2	Bottomless Lake State Park; Lazy Lagoon	NM	G23	31.91	47	48	5	7.4	3.17	10017	287	1203	1861	2.02	0.21	2.57	14
LL3	Bottomless Lake State Park; Lazy Lagoon	NM	G24	39.75	63	30	7	7.2	3.6	12181	341	1502	2119	2.23	0.24	2.78	15
LL4	Bottomless Lake State Park; Lazy Lagoon	NM	G25	25.07	57	36	7	7.8	7.35	45630	196	536	8069	1.32	0.14	1.51	14
Lea1	Bottomless Lake State Park; Lea Lake	NM	G26	18.15	65	28	7	7.2	1.73	590	50	542	254	0.73	0.1	1.39	12
BLM1	Bureau of Land Management; William Sink	NM	G27	14.39	83	8	9	8.2	7.41	16987	2772	1656	1345	0.33	0.06	0.37	7

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
BLM2	Bureau of Land Management; William Sink	NM	G28	15.88	73	14	13	7.4	17.45	66373	7243	1257	3637	0.76	0.08	0.86	8
BLM3	Bureau of Land Management; William Sink	NM	G29	14.58	88	5	7	6.4	10.19	26528	4423	1211	1934	0.36	0.06	0.42	7
BLM4	Bureau of Land Management; William Sink	NM	G30	15.71	66	25	9	7.6	10.65	31096	5143	948	2459	1.58	0.11	1.76	7
BLM5	Bureau of Land Management; Laguna Tuston	NM	G31	17.65	62	5	33	7.5	21.3	65067	18887	885	3858	1.63	0.12	5.34	8
BLM6	Bureau of Land Management; Laguna Tuston	NM	G32	28.44	34	19	47	7.4	21.5	59561	23208	1050	5073	1.73	0.12	2.1	N/D
BLM7	Bureau of Land Management; Laguna Tuston	NM	G33	33.59	41	34	25	7.7	16.13	41380	16551	1078	3096	2.23	0.12	2.8	N/D
BLM8	Bureau of Land Management; Laguna Tuston	NM	G34	38.87	31	26	43	7.3	21.4	79920	29952	1286	7443	2.38	0.22	2.58	N/D
BLM9	Bureau of Land Management; Laguna Plata	NM	G35	20.38	87	0	13	7.3	13.3	33730	10216	976	2975	0.82	0.11	0.98	10
BLM10	Bureau of Land Management; Laguna Plata	NM	G36	8.35	89	8	3	7.9	3.59	8023	746	402	712	0.55	0.06	0.89	14
BLM11	Bureau of Land Management; Laguna Plata	NM	G37	17.81	75	11	14	7.3	8.67	24423	3290	480	2676	0.25	0.07	0.18	14
BLM12	Bureau of Land Management; Laguna Plata	NM	G38	17.62	69	17	14	7.3	10.41	30292	3457	496	1893	0.22	0.09	0.23	13
BLM13	Bureau of Land Management; Laguna Plata	NM	G39	18.76	77	9	14	7.2	14.85	49086	4909	296	1945	1.08	0.12	1.11	13
BLM14	Bureau of Land Management; Laguna Plata	NM	G40	15.28	79	11	10	7.7	11.09	31399	3748	433	1508	0.74	0.09	0.81	12
BLM15	Bureau of Land Management; Laguna Plata	NM	G41	23.17	55	27	18	7.4	15.72	52152	4806	364	1729	1.15	0.11	1.26	9

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
BLM16	Bureau of Land Management; Laguna Plata	NM	G42	9.61	43	21	36	7.5	2.41	4652	479	1244	440	1.8	0.17	1.97	10
BLM17	Bureau of Land Management; Laguna Tonto	NM	G43	12.27	87	5	8	7.3	9.06	23301	3021	347	6576	0.18	0.07	0.15	17
BLM18	Bureau of Land Management; Laguna Tonto	NM	G44	13.68	81	8	11	7.4	10.89	30989	3923	294	5655	0.19	0.09	0.17	18
BLM19	Bureau of Land Management; Laguna Tonto	NM	G45	13.96	83	4	13	7.4	11.56	34609	4112	271	7056	0.24	0.08	0.2	14
BLM20	Bureau of Land Management; Laguna Tonto	NM	G46	14.62	81	6	13	7.3	12.5	47545	5532	366	8848	0.24	0.1	0.24	14
BLM21	Bureau of Land Management; Laguna Gatuna	NM	G47	12.73	84	4	12	7.8	7.71	19110	958	211	1730	0.31	0.09	0.44	18
BLM22	Bureau of Land Management; Laguna Gatuna	NM	G48	13.6	72	16	12	7.7	6.69	16578	889	267	1773	0.6	0.08	0.57	16
BLM23	Bureau of Land Management; Laguna Gatuna	NM	G49	13.77	70	18	12	7.4	11.71	33358	1200	599	2561	0.41	0.08	0.42	13
BLM24	Bureau of Land Management; Laguna Quatro	NM	G50	16.52	68	20	12	7.6	16.25	45198	9725	675	3639	1.39	0.17	1.53	N/D
BLM25	Bureau of Land Management; Laguna Quatro	NM	G51	19.6	12	2	86	7.8	21.4	149756	29400	833	5571	0.37	0.09	0.51	N/D
BLM26	Bureau of Land Management; Laguna Walden	NM	G52	23.38	74	8	18	7.9	16.54	54077	13961	903	4076	0.5	0.11	0.57	N/D
BLM27	Bureau of Land Management; Laguna Uno	NM	G53	44.93	11	22	67	7.4	21	79053	16097	632	3864	1.23	0.08	1.29	N/D
SFB1	San Francisco Bay NWR	CA	H01	56.03	30	33	37	7.4	3.85	8258	739	530	1108	3.01	0.38	3.1	11
SFB2	San Francisco Bay NWR	CA	H02	14.93	70	11	19	7.8	3.49	7328	493	580	893	0.71	0.14	2.12	10
SFB3	San Francisco Bay NWR	CA	H03	17.08	72	13	15	7.4	3.59	7613	559	732	955	1.07	0.15	1.62	11
SFB4	San Francisco Bay NWR	CA	H04	45.29	28	27	45	7.2	2.32	4880	390	258	585	2.25	0.31	2.39	8

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
SFB5	San Francisco Bay NWR	CA	H05	44.43	28	61	11	4.1	5.87	12874	951	910	2104	2.23	0.27	2.05	11
SFB6	San Francisco Bay NWR	CA	H06	45.65	44	15	41	7.3	2.63	5532	366	281	691	3.71	0.41	3.54	8
SFB7	San Francisco Bay NWR	CA	H07	48.34	48	17	35	7.4	2.62	5294	407	277	656	4.3	0.5	4.6	10
SFB8	San Francisco Bay NWR	CA	H08	33.5	59	8	33	7.9	2.5	5359	352	256	615	1.85	0.24	1.86	9
SFB9	San Francisco Bay NWR	CA	H09	60.66	38	21	41	7.2	3.4	7254	474	408	928	6.36	0.77	7.77	8
SFB10	San Francisco Bay NWR	CA	H10	58.5	24	21	55	6.8	3.05	6648	1325	269	788	4.91	0.51	5.36	8
SFB11	San Francisco Bay NWR	CA	H11	46.93	26	19	55	6.6	2.73	5652	410	231	658	2.91	0.3	2.53	9
SFB12	San Francisco Bay NWR	CA	H12	60.23	32	23	45	6.7	2.91	6293	506	446	853	5.3	0.59	5.79	11
SFB13	San Francisco Bay NWR	CA	H13	30.13	60	28	12	7.6	11.61	34999	3000	1440	4859	1.04	0.15	1.09	10
SFB14	San Francisco Bay NWR	CA	H14	30.47	68	14	18	7.5	13.19	32969	2305	1268	4008	0.76	0.09	0.64	15
SFB15	San Francisco Bay NWR	CA	H15	41.82	46	32	22	7.3	14.38	43032	3354	1579	5302	1.34	0.25	1.7	15
SFB16	San Francisco Bay NWR	CA	H16	51.61	32	38	30	7.2	3.92	10392	706	984	1366	2.34	0.21	1.86	11
SFB17	San Francisco Bay NWR	CA	H17	39.73	44	28	28	6.3	2.51	5790	406	314	737	2.14	0.29	2.51	9
SFB18	San Francisco Bay NWR	CA	H18	41.65	50	40	10	7.4	4.84	11685	778	1237	1396	3.37	0.38	4.71	12
SFB19	San Francisco Bay NWR	CA	H19	50.77	54	36	10	7.2	6.37	14811	1053	1208	1678	5.94	0.53	5.58	12
SFB20	San Francisco Bay NWR	CA	H20	57.47	46	40	14	7.1	7.42	18262	1292	1303	2313	6.71	0.61	6.69	10
SFB21	San Francisco Bay NWR	CA	H21	21.44	49	29	22	8.2	0.17	382	11	14	9	0.6	0.16	0.71	12
SFB22	San Francisco Bay NWR	CA	H22	27.4	29	41	30	6.7	0.06	127	16	9	13	1.92	0.27	1.87	10
SFB23	San Francisco Bay NWR	CA	H23	28.38	49	33	18	6.7	0.07	153	16	13	12	2.75	0.35	2.63	10
SFB24	San Francisco Bay NWR	CA	H24	16.71	37	33	30	6.6	1.38	2709	135	375	478	2.1	0.24	1.85	11
SFB25	San Francisco Bay NWR	CA	H25	27.56	55	39	6	7.6	0.49	769	81	442	125	1.52	0.19	1.51	14
SFB26	San Francisco Bay NWR	CA	H26	33.25	61	31	8	7.9	5.7	12868	1041	1466	1447	1.91	0.24	1.72	12

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
SFB27	San Francisco Bay NWR	CA	H27	27.65	49	31	20	7.3	0.39	429	67	468	264	2.05	0.23	2.31	16
SFB28	San Francisco Bay NWR	CA	H28	26.29	69	22	9	7.4	1.31	2213	209	976	420	1.6	0.25	1.64	11
SFB29	San Francisco Bay NWR	CA	H29	19.72	75	16	9	7.6	4.76	11791	634	1172	2261	0.97	0.16	1.08	11
SFB30	San Francisco Bay NWR	CA	H30	29.04	62	21	17	8	9.43	24024	1215	1313	2660	1.57	0.23	1.62	11
SFB31	San Francisco Bay NWR	CA	H31	51.34	41	42	17	6.8	10.96	27568	1493	984	4032	4.98	0.6	4.62	14
SFB32	San Francisco Bay NWR	CA	H32	51.57	37	46	17	6.7	9.25	22474	1228	865	4087	5.39	0.72	5.45	13
SFB33	San Francisco Bay NWR	CA	H33	43.71	28	37	35	6.2	6.78	18256	990	1265	3066	5.96	0.62	5.84	12
SFB34	San Francisco Bay NWR	CA	H34	36.91	51	32	17	7.6	11.6	30151	1628	1273	3964	6.32	0.73	6.46	13
Big1	Big Bend NP	TX	J01	27.8	74	13	13	7.9	0.12	110	14	153	28	0.37	0.07	1.97	35
Big2	Big Bend NP	TX	J02	29.75	5	79	16	7.9	0.1	161	17	69	11	0.98	0.15	3.25	23
Big3	Big Bend NP	TX	J03	6.62	87	5	8	7.6	0.11	105	13	139	17	0.25	0.07	2.13	41
Big4	Big Bend NP	TX	J04	12.76	55	25	20	7.3	0.24	181	34	502	71	0.77	0.14	2.92	31
Big5	Big Bend NP	TX	J05	13.24	78	15	7	8	0.08	99	14	52	11	0.31	0.08	2.1	21
Big6	Big Bend NP	TX	J06	9.72	75	15	10	7.7	0.08	107	17	54	10	0.27	0.1	2.15	20
Big7	Big Bend NP	TX	J07	6.82	76	14	10	7.8	0.07	83	13	46	6	0.26	0.08	2.06	41
Big8	Big Bend NP	TX	J08	9.57	93	1	6	7.7	0.11	113	10	128	20	0.28	0.09	1.88	40
Big9	Big Bend NP	TX	J09	8.19	93	3	4	8	0.06	71	7	39	8	0.21	0.09	1.82	41
Big10	Big Bend NP	TX	J10	8.02	87	5	8	7.6	0.12	98	13	173	24	0.27	0.09	1.94	40
Big11	Big Bend NP	TX	J11	15.88	79	9	12	7.2	0.14	134	17	214	31	0.41	0.1	2.13	37
Big12	Big Bend NP	TX	J12	10.02	85	7	8	7.3	0.08	95	11	59	13	0.34	0.1	2.01	37
Big13	Big Bend NP	TX	J13	24.96	71	13	16	6.9	0.16	126	21	287	48	1.17	0.14	2.92	36
Big14	Big Bend NP	TX	J14	25.42	53	27	20	6.8	0.17	133	22	324	54	1.16	0.18	3.12	35
Big15	Big Bend NP	TX	J15	11.49	82	10	8	7.2	0.13	91	12	123	21	0.47	0.12	2.25	36

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
Big16	Big Bend NP	TX	J16	20.23	70	18	12	6.8	0.27	149	23	500	87	0.54	0.17	3.54	36
Big17	Big Bend NP	TX	J17	8.89	48	14	38	7.6	0.96	2296	35	502	50	0.7	0.14	2.1	24
Big18	Big Bend NP	TX	J18	11.34	80	12	8	7.4	0.21	221	22	306	29	0.35	0.16	1.81	30
Big19	Big Bend NP	TX	J19	8.67	66	17	17	7.3	0.17	182	22	273	31	0.38	0.12	1.95	31
Big20	Big Bend NP	TX	J20	8.7	76	13	11	7.3	0.23	205	24	282	55	0.33	0.08	1.74	28
Big21	Big Bend NP	TX	J21	12.25	72	19	9	7.7	0.12	153	15	113	14	0.35	0.1	1.96	25
Big22	Big Bend NP	TX	J22	26.63	78	13	9	7.3	0.26	357	20	384	34	0.28	0.86	16.56	30
Big23	Big Bend NP	TX	J2-1	9.19	83	9	8	8.11	0.1	124	12	85	16	0.25	0.06	2.43	38
Big24	Big Bend NP	TX	J2-2	27.69	81	9	10	7.92	0.13	162	17	125	26	0.34	0.09	2.46	36
Big25	Big Bend NP	TX	J2-3	37.98	47	28	25	7.46	0.48	560	41	826	223	1.03	0.17	4.68	35
Big26	Big Bend NP	TX	J2-4	69.38	21	27	52	7.72	0.12	147	16	117	18	1.14	0.13	2.03	38
Big27	Big Bend NP	TX	J2-5	23.32	69	19	12	7.18	0.34	254	30	647	104	0.55	0.11	2.41	30
OHS1	Ogden Hot Springs	UT	K01	28.89	71	10	19	7.5	1.16	2114	275	387	7	0.9	0.06	2.95	39
OHS2	Ogden Hot Springs	UT	K02	19.05	85	0	15	7.8	0.82	1475	200	204	6	0.35	0.07	0.68	55
OHS3	Ogden Hot Springs	UT	K03	26.2	69	16	15	7.3	1.28	2421	323	425	11	1.84	0.22	2.6	35
OHS4	Ogden Hot Springs	UT	K04	82	N/D	N/D	N/D	7.25	0.17	82	28	190	91	19.6	0.14	0.86	22
WHS1	Wilson Hot Springs	UT	K05	25.54	73	24	3	7.4	2.23	4526	179	969	194	1.84	0.14	8.7	29
WHS2	Wilson Hot Springs	UT	K06	38.38	68	20	12	7.3	2.81	5478	209	946	207	2.22	0.17	9.38	41
WHS3	Wilson Hot Springs	UT	K07	32.34	73	12	15	7.5	1.92	228	147	468	118	1.98	0.15	9.64	24
WHS4	Wilson Hot Springs	UT	K08	49.42	83	7	10	7	3.5	8078	363	1163	275	2.6	0.31	11.59	15
WHS5	Wilson Hot Springs	UT	K09	45.55	67	22	11	7.3	2.2	4855	196	850	172	2.28	0.23	11.24	35
WHS6	Wilson Hot Springs	UT	K10	37.7	65	20	15	7.3	2.16	4748	158	773	126	1.92	0.19	10.17	23
WHS7	Wilson Hot Springs	UT	K11	33.87	72	10	18	7.2	1.99	428	181	1253	120	2.29	0.19	10.42	14

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
WHS8	Wilson Hot Springs	UT	K12	48.42	79	11	10	7.1	2.99	6438	236	1540	193	1.58	0.17	10.99	30
WHS9	Wilson Hot Springs	UT	K13	36.24	80	6	14	7.4	2.51	5409	185	753	191	1.58	0.18	11.03	55
WHS10	Wilson Hot Springs	UT	K14	46.79	79	13	8	7.2	3.05	8567	295	1201	242	1.48	0.2	11.03	48
WHS11	Wilson Hot Springs	UT	K15	41.17	47	38	15	7.3	5.61	15456	653	1436	751	3.44	0.24	6.98	17
WHS12	Wilson Hot Springs	UT	K16	24.06	52	41	7	7.4	7.5	26665	1374	2282	1016	1.82	0.15	2.35	20
WHS13	Wilson Hot Springs	UT	K17	40.32	51	38	11	7.3	3.17	7629	330	1155	542	3.13	0.23	5.59	39
WHS14	Wilson Hot Springs	UT	K18	65.25	N/D	N/D	N/D	7.41	4.53	11212	448	1415	475	9.36	0.79	10.37	41
FS1	Fish Springs NWR	UT	K19	72.82	59	32	9	7.47	0.83	1146	139	666	140	3.96	0.47	11.63	14
FS2	Fish Springs NWR	UT	K20	46.08	52	34	14	7.7	2.27	6267	492	892	367	3.58	0.39	10.66	9
FS3	Fish Springs NWR	UT	K21	34.23	38	49	13	8.1	7.54	36269	2241	727	2275	5.25	0.26	5.73	10
FS4	Fish Springs NWR	UT	K22	64.06	61	26	13	7.7	0.45	760	100	189	48	4.33	0.48	12.22	18
FS5	Fish Springs NWR	UT	K23	45.8	57	33	10	7.7	3.65	9371	1056	1190	582	8.69	0.49	8.86	9
FS6	Fish Springs NWR	UT	K24	62.48	53	35	12	8.1	0.43	672	133	200	88	13	1.02	12.95	9
FS7	Fish Springs NWR	UT	K25	83.27	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	17.7	1.52	17.63	11
FS8	Fish Springs NWR	UT	K26	49.5	38	30	32	7.9	1.47	4003	538	427	357	4.77	0.26	7.39	11
FS9	Fish Springs NWR	UT	K27	41.21	N/D	N/D	N/D	7.9	8.15	9894	900	316	1234	4.68	0.16	7.28	11
FS10	Fish Springs NWR	UT	K28	24.03	42	51	7	8.4	6.22	22782	1776	736	1775	3.15	0.12	4.57	9
FS11	Fish Springs NWR	UT	K29	28.07	N/D	N/D	N/D	8.1	9.15	25592	2248	526	2442	6.04	0.27	8.09	10
FS12	Fish Springs NWR	UT	K30	33.19	N/D	N/D	N/D	8.5	8.14	46328	2627	770	1698	8.14	0.29	9.13	11
FS13	Fish Springs NWR	UT	K31	67.37	N/D	N/D	N/D	8.09	0.43	783	132	224	87	18.1	0.31	3.61	9
FS14	Fish Springs NWR	UT	K32	37.22	18	52	30	7.3	0.42	584	101	392	167	2.15	0.22	5.61	24
FS15	Fish Springs NWR	UT	K33	65.08	47	30	23	7.53	0.76	1027	137	563	213	12.2	0.77	13.48	14
FS16	Fish Springs NWR	UT	K34	45.05	28	34	38	7.3	0.49	883	110	169	141	3.33	0.28	6.83	15

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
FS17	Fish Springs NWR	UT	K35	62.1	55	32	13	7.51	0.67	1092	178	235	151	5.4	0.57	12.8	13
FS18	Fish Springs NWR	UT	K36	64.94	58	28	14	7.3	1.37	2390	271	540	401	8.77	0.57	14.26	17
FS19	Fish Springs NWR	UT	K37	67.4	61	26	13	7.41	1.02	1731	235	468	220	9.39	0.64	13.84	15
FS20	Fish Springs NWR	UT	K38	73.78	51	14	35	7.41	0.5	823	104	235	98	7.63	0.61	13.18	14
Topas 1	West Topas	UT	K39	21.82	N/D	N/D	N/D	7.7	8.17	24593	471	1310	5141	3.41	0.19	5.84	18
AHS1	Abraham Hot Springs	UT	K40	67.22	64	26	10	7.7	0.67	1047	92	565	40	2.93	0.26	7.8	41
AHS2	Abraham Hot Springs	UT	K41	66.92	64	17	19	7.4	0.9	1397	99	630	120	1.89	0.19	9.4	41
AHS3	Abraham Hot Springs	UT	K42	73.58	57	28	15	7.29	0.84	1139	80	585	105	1.42	0.15	8.59	67
AHS4	Abraham Hot Springs	UT	K43	76.82	59	30	11	7.22	1.06	1182	115	766	142	3.58	0.37	10.87	42
AHS5	Abraham Hot Springs	UT	K44	75.53	69	21	10	7.51	0.93	1168	113	840	90	3.79	0.3	10.32	50
BHS1	Baker Hot Springs	UT	K45	57.08	38	51	11	7.4	0.61	847	48	833	6078	2	0.11	6.56	69
BHS2	Baker Hot Springs	UT	K46	33	50	45	5	7.3	0.82	1206	86	735	125	0.82	0.07	7.23	82
BHS3	Baker Hot Springs	UT	K47	79.07	44	52	4	6.81	1.02	1174	111	1255	124	7.99	0.1	7.27	44
BHS4	Baker Hot Springs	UT	K48	53.43	71	20	9	7.28	2.24	4037	404	1291	312	3.88	0.25	5.12	26
BHS5	Baker Hot Springs	UT	K49	89.6	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	3.45	0.43	3.43	47
BHS6	Baker Hot Springs	UT	K50	60.16	64	19	17	7.1	1.21	2080	228	964	149	4.54	0.39	10.85	14
BHS7	Baker Hot Springs	UT	K51	47.86	50	35	15	7.5	0.46	735	50	454	25	1.02	0.08	10.33	49
BHS8	Baker Hot Springs	UT	K52	58.88	72	13	15	7.4	0.79	1178	93	810	36	1.79	0.13	10.86	18
BHS9	Baker Hot Springs	UT	K53	55.68	48	40	12	7.59	0.92	1169	86	855	77	1.26	0.14	9.29	72
BHS10	Baker Hot Springs	UT	K54	50.57	58	31	11	7.4	0.47	766	58	288	43	1.34	0.1	11.06	37
BHS11	Baker Hot Springs	UT	K55	76.03	66	26	8	7.48	0.71	1069	95	727	83	6.2	0.54	13.97	39
AI1	Antelope Island	UT	L01	16.12	N/D	N/D	N/D	8.7	9.67	33063	2764	548	2476	1.37	0.07	9	18
AI2	Antelope Island	UT	L02	17.72	98	0	2	8.6	0.92	1809	163	112	223	1.43	0.07	3.98	18

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
AI3	Antelope Island	UT	L03	64.2	N/D	N/D	N/D	8.1	9.91	37773	3275	1861	2685	9	1.07	13.08	18
AI4	Antelope Island	UT	L04	15.91	88	2	10	7.7	0.9	1615	170	159	210	0.63	0.11	0.74	19
GSL1	Great Salt Lake	UT	L05	22.69	74	16	10	7.6	7.68	24034	2370	2100	1084	2.26	0.15	7.36	18
GSL2	Great Salt Lake	UT	L06	14.58	90	4	6	8.1	4.49	11776	977	1095	529	1.66	0.07	8.68	18
GSL3	Great Salt Lake	UT	L07	30.09	82	6	12	8.5	6.17	34601	993	361	95	2.5	0.23	7.03	17
SHS1	Saratoga Hot Springs	UT	L08	44.26	30	32	38	7.2	0.23	285	44	211	92	5.04	0.42	5.23	13
SHS2	Saratoga Hot Springs	UT	L09	45.75	36	44	20	6.9	0.42	308	59	820	156	2.39	0.26	3.7	38
IHS1	Indian Hot Springs	UT	L10	60.26	81	9	10	6.9	4.38	11652	787	1313	228	3.4	0.41	12.63	15
IHS2	Indian Hot Springs	UT	L11	43.25	75	14	11	7.1	3.13	7436	535	1150	128	3.4	0.27	10.54	14
IHS3	Indian Hot Springs	UT	L12	41.82	56	33	11	7.1	3.7	8524	621	2421	287	2.9	0.17	9.46	31
IHS4	Indian Hot Springs	UT	L13	37.08	71	21	8	6.8	3.11	6697	504	2412	335	4.19	0.2	7.11	38
SCW1	Salt Creek Waterfowl Preserve	UT	L14	55.23	36	30	34	7.5	0.77	1419	143	337	93	4.87	0.41	8.71	11
Knoll1	Knoll Spring	UT	L15	39	76	12	12	7.7	2.19	5304	334	695	209	1.46	0.13	4.24	18
LB1	Lincoln Beach	UT	L16	76.33	N/D	N/D	N/D	7.18	0.6	1041	230	419	176	14	0.8	17.95	13
UL1	Utah Lake	UT	L17	41.3	28	28	44	7.7	0.15	159	46	157	39	4.33	0.33	11.14	14
UL2	Utah Lake	UT	L18	33.48	70	12	18	7.5	0.15	194	69	185	50	2.61	0.29	6.56	9
WS1	Warm Springs	UT	L19	25.09	68	16	16	7	1.04	1481	137	1459	173	1.94	0.15	4.78	38
WS2	Warm Springs	UT	L20	61.86	52	36	12	6.8	1.25	2217	178	1108	196	4.41	0.35	5.78	32
WS3	Warm Springs	UT	L21	57.61	60	28	12	6.8	1.21	2077	152	1025	173	5.39	0.43	7.34	37
WS4	Warm Springs	UT	L22	23.5	40	32	28	6.8	1.56	2941	219	1024	255	1.85	0.17	1.96	39
BRR1	Bear River Reserve	UT	L23	42.58	32	42	26	7.5	0.27	426	76	206	84	2.96	0.28	5.45	12
BRR2	Bear River Reserve	UT	L24	33.47	21	40	39	7.5	1	2335	226	88	112	2.24	0.21	3.87	12
BRR3	Bear River Reserve	UT	L25	37.1	37	38	25	7.2	0.15	236	39	52	36	2	0.23	4.6	12

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
SWR1	Savannah NWR	GA	M01	44.76	28	24	48	3.94	0.26	286	34	183	115	3.63	0.38	3.64	29
SWR2	Savannah NWR	GA	M02	55.95	37	15	48	4.64	0.31	602	32	105	106	4.63	0.47	4.75	27
CR1	Cape Romainee NWR	SC	M03	71.75	87	7	6	5.66	3.36	5865	299	531	1132	14.3	1.01	14.73	22
CR2	Cape Romainee NWR	SC	M04	52.39	88	6	6	4.23	2.56	4699	246	550	1202	4.15	0.4	5.54	24
CR3	Cape Romainee NWR	SC	M05	47.24	86	1	13	5.05	1.54	2814	170	259	565	4.97	0.35	5.04	23
CR4	Cape Romainee NWR	SC	M06	27.58	86	5	9	6.62	3.94	8708	450	769	1186	0.92	0.13	0.97	27
CR5	Cape Romainee NWR	SC	M07	58.13	70	20	10	4.68	6.01	12894	739	907	2145	4.29	0.33	5.32	24
CR6	Cape Romainee NWR	SC	M08	24.53	58	11	31	6.01	1.59	1020	62	44	85	1.53	0.23	1.85	24
CR7	Cape Romainee NWR	SC	M09	33.29	80	5	15	6.14	1.59	3023	140	259	411	0.46	0.11	0.49	25
CR8	Cape Romainee NWR	SC	M10	22.18	100	0	0	5.72	0.08	146	14	13	8	0.81	0.1	0.86	27
CR9	Cape Romainee NWR	SC	M11	32.61	95	2	3	6.37	3.19	6825	345	306	914	1.81	0.19	1.76	25
CR10	Cape Romainee NWR	SC	M12	19.98	98	0	2	6.62	0.88	1178	115	244	275	0.2	0.12	0.75	29
CR11	Cape Romainee NWR	SC	M13	28.57	90	3	7	5.36	2.16	3925	240	644	765	0.92	0.09	2.19	27
CR12	Cape Romainee NWR	SC	M14	25.25	84	3	13	4.62	2.47	4434	280	666	855	0.94	0.1	0.9	27
CR13	Cape Romainee NWR	SC	M15	19.04	85	9	6	6.41	3.46	7041	289	979	1185	0.75	0.13	0.72	30
CR14	Cape Romainee NWR	SC	M16	38.35	80	10	10	6.06	4.9	11330	613	649	1609	1.41	0.18	1.47	25
CR15	Cape Romainee NWR	SC	M17	31.12	97	1	2	6.34	2.91	6128	326	488	888	1.16	0.15	1.14	27
CR16	Cape Romainee NWR	SC	M18	12.38	N/D	N/D	N/D	7.62	0.95	1054	106	111	182	0.08	0.09	0.09	29
CR17	Cape Romainee NWR	SC	M19	14.05	92	0	8	7.95	0.16	290	27	23	16	0.09	0.07	0.11	31
CR18	Cape Romainee NWR	SC	M20	21.04	98	0	2	6.77	0.31	529	38	93	82	1.17	0.13	0.94	23
CR19	Cape Romainee NWR	SC	M21	35.97	N/D	N/D	N/D	6.16	0.37	660	53	78	121	2.96	0.14	0.91	26
CR20	Cape Romainee NWR	SC	M22	64.44	N/D	N/D	N/D	5.9	0.62	1138	88	118	242	11.2	0.72	11.44	27

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
CR21	Cape Romaine NWR	SC	M23	34.46	N/D	N/D	N/D	4.8	0.12	74	23	56	30	2.98	0.3	3.15	26
CR22	Cape Romaine NWR	SC	M24	28.76	N/D	N/D	N/D	3.6	0.1	134	24	17	19	9.9	0.3	9.31	22
CR23	Cape Romaine NWR	SC	M25	24.05	N/D	N/D	N/D	6.66	0.85	982	84	754	197	1.03	0.13	1.51	31
CR24	Cape Romaine NWR	SC	M26	38.26	81	4	15	6.61	3.3	5458	301	493	832	1.61	0.21	1.53	27
CR25	Cape Romaine NWR	SC	M27	40.8	85	1	14	6.6	1.98	2731	172	551	490	1.43	0.19	1.52	28
PI1	Pinkney Island NWR	SC	M28	36.31	85	3	12	3.81	0.07	44	14	33	17	5.99	0.49	5.44	23
PI2	Pinkney Island NWR	SC	M29	22.2	83	13	4	6.61	1.77	3109	229	136	321	0.15	0.08	0.16	25
PI3	Pinkney Island NWR	SC	M30	23.11	67	9	24	6.21	1.9	3021	161	153	386	0.49	0.11	0.43	25
PI4	Pinkney Island NWR	SC	M31	41.26	95	3	2	5.59	1.01	1157	101	108	260	2.98	0.29	3.09	25
PI5	Pinkney Island NWR	SC	M32	28.67	80	6	14	6.08	4.52	7606	346	342	1111	1.28	0.15	1.65	25
PI6	Pinkney Island NWR	SC	M33	29.45	78	9	13	5.72	3.75	6675	271	417	981	1.44	0.16	1.5	26
PI7	Pinkney Island NWR	SC	M34	31.91	95	1	4	4.98	2.45	3678	217	290	628	2.16	0.15	1.7	24
PI8	Pinkney Island NWR	SC	M35	33.8	90	5	5	3.83	3.74	6320	399	553	1100	1.09	0.17	1.2	25
PI9	Pinkney Island NWR	SC	M36	66.85	N/D	N/D	N/D	4.92	0.14	83	40	216	49	24.8	0.76	21.13	23
PI10	Pinkney Island NWR	SC	M37	35.52	92	2	6	5.72	0.06	74	34	42	11	1.91	0.22	2.29	25
PI11	Pinkney Island NWR	SC	M38	68.49	71	18	11	6.44	5.31	11905	672	638	1668	8.49	0.54	8.19	26
PI12	Pinkney Island NWR	SC	M39	28.74	89	5	6	6.82	3.46	7125	358	655	985	0.76	0.12	0.79	26
PI13	Pinkney Island NWR	SC	M40	49.79	62	30	8	6.55	5.71	15062	744	1265	2292	2.31	0.27	2.64	27
PI14	Pinkney Island NWR	SC	M41	30.1	89	2	9	7.22	3.15	6435	438	748	933	1.57	0.15	2.37	27
SI1	Sapelo Island Microbial Observatory	GA	N01	16.89	98	0	2	7.6	2.5	5012	252	283	633	0.11	0.06	0.1	19
SI2	Sapelo Island Microbial Observatory	GA	N02	14.96	98	0	2	7.49	1.6	3154	171	177	383	0.09	0.08	0.11	18

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
SI3	Sapelo Island Microbial Observatory	GA	N03	46.52	54	33	13	6.5	5.31	14447	542	635	2118	2.46	0.29	2.49	20
SI4	Sapelo Island Microbial Observatory	GA	N04	62.64	52	37	11	5.36	6.57	17444	649	878	2778	5.04	0.47	5	19
SI5	Sapelo Island Microbial Observatory	GA	N05	16.25	98	0	2	5.02	0.21	155	26	151	39	5.21	0.23	5.15	20
SI6	Sapelo Island Microbial Observatory	GA	N06	81.53	N/D	N/D	N/D	6.3	4.21	8695	503	401	1186	14.9	0.95	14.63	19
SI7	Sapelo Island Microbial Observatory	GA	N07	53.06	88	1	11	6	2.03	4268	320	254	565	3.67	0.27	3.21	20
SI8	Sapelo Island Microbial Observatory	GA	N08	32.74	81	3	16	6.42	1.98	4169	186	267	557	1.37	0.17	1.2	21
SI9	Sapelo Island Microbial Observatory	GA	N09	18.22	92	3	5	6.88	1.19	2476	137	111	266	0.42	0.11	0.45	20
SI10	Sapelo Island Microbial Observatory	GA	N10	19.05	88	3	9	6.24	1.45	2991	138	118	339	0.41	0.1	0.42	19
SI11	Sapelo Island Microbial Observatory	GA	N11	37.36	90	5	5	5.87	1.63	3535	196	154	436	4.64	0.19	4.53	20
SI12	Sapelo Island Microbial Observatory	GA	N12	54.33	70	11	19	6.01	2.41	5380	308	259	709	0.59	0.54	7.09	19
SI13	Sapelo Island Microbial Observatory	GA	N13	69.31	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	46	0.11	45.33	16
SI14	Sapelo Island Microbial Observatory	GA	N14	70.33	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	46.4	0.23	45.71	17
SI15	Sapelo Island Microbial Observatory	GA	N15	75.95	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	44.9	0.29	45.38	20
SI16	Sapelo Island Microbial Observatory	GA	N16	47.52	N/D	N/D	N/D	4.73	0.34	843	55	41	84	1.11	0.34	11.01	21

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
SI17	Sapelo Island Microbial Observatory	GA	N17	61.07	N/D	N/D	N/D	4.63	0.48	1045	64	48	91	0.63	0.75	40.69	19
SI18	Sapelo Island Microbial Observatory	GA	N18	17.69	90	3	7	7.63	0.06	92	20	9	8	0.35	0.03	0.13	17
SI19	Sapelo Island Microbial Observatory	GA	N19	20.82	94	3	3	6.58	0.03	54	6	13	7	0.73	0.14	0.45	18
SI20	Sapelo Island Microbial Observatory	GA	N20	39.61	90	7	3	5.4	1.61	3077	180	262	573	2.43	0.29	3.43	19
SI21	Sapelo Island Microbial Observatory	GA	N21	39.7	94	3	3	5.7	0.19	296	16	88	83	2.15	0.19	2.03	20
SWR3	Sapelo Island Microbial Observatory	GA	N22	35.18	86	5	9	5.84	0.07	54	11	91	7	0.89	0.13	0.89	17
BWR 1	Laguna Boquerón NWR	PR	P01	58.36	35	27	38	7.1	0.16	86	13	244	56	4.87	0.5	5.02	N/D
BWR 2	Laguna Boquerón NWR	PR	P02	40.52	37	8	55	6.55	1.14	1811	101	659	275	2.56	0.23	2.8	N/D
BWR 3	Laguna Boquerón NWR	PR	P03	52.58	53	13	34	6.84	0.34	308	49	475	136	7.06	0.46	7.57	N/D
BWR 4	Laguna Boquerón NWR	PR	P04	68.33	66	23	11	4.79	7.21	20284	702	1211	4102	7.77	0.36	7.52	N/D
BWR 5	Laguna Boquerón NWR	PR	P05	49.71	62	18	24	6.99	2.06	3623	119	514	637	4.47	0.31	4.82	N/D
BWR 6	Laguna Boquerón NWR	PR	P06	17.21	61	10	29	7.59	3.31	7525	325	525	774	1.24	0.12	1.86	N/D
BWR 7	Laguna Boquerón NWR	PR	P07	51.15	47	46	7	6.25	5.6	1470	555	2759	2778	4.38	0.31	4.52	N/D
CAR 1	Laguna Cartagena NWR	PR	P08	61.15	63	25	12	4.83	0.41	295	32	571	225	7.24	0.79	7.2	N/D
CAR 2	Laguna Cartagena NWR	PR	P09	65.34	N/D	N/D	N/D	5.41	0.37	216	26	574	185	6.63	0.79	6.95	N/D
CAR 3	Laguna Cartagena NWR	PR	P10	53.77	53	43	4	5.09	0.31	136	25	541	163	5.47	0.69	5.72	N/D
CAR 4	Laguna Cartagena NWR	PR	P11	60.19	69	19	12	4.88	0.37	205	39	472	207	10.02	1.03	10.15	N/D
CRR 1	Cabo Rojo NWR	PR	P12	21.93	97	2	1	8.15	2.72	5722	302	443	721	0.69	0.09	9.38	N/D
CRR 10	Cabo Rojo NWR	PR	P13	29.41	99	1	0	8.67	4.17	8996	443	589	1057	1.56	0.11	5.54	N/D

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
CRR 2	Cabo Rojo NWR	PR	P14	29.14	N/D	N/D	N/D	8.3	10.76	34784	1926	2577	3870	0.61	0.09	9.53	N/D
CRR 3	Cabo Rojo NWR	PR	P15	31.01	89	4	7	7.88	5.35	14421	814	770	2052	1.85	0.11	8.11	N/D
CRR 4	Cabo Rojo NWR	PR	P16	32.41	N/D	N/D	N/D	8.34	8.42	28340	1889	1918	4142	2.51	0.24	10.16	N/D
CRR 5	Cabo Rojo NWR	PR	P17	47.94	N/D	N/D	N/D	8.14	20.2	88935	2317	3205	12312	5.05	0.44	9.5	N/D
CRR 6	Cabo Rojo NWR	PR	P18	27.79	N/D	N/D	N/D	8.03	11.69	55483	3410	2261	2166	1.13	0.05	2.34	N/D
CRR 7	Cabo Rojo NWR	PR	P19	37.9	N/D	N/D	N/D	7.82	14.31	94641	6393	4199	10166	1.27	0.11	2.19	N/D
CRR 8	Cabo Rojo NWR	PR	P20	40.15	N/D	N/D	N/D	8.04	11.13	43248	2307	2382	5179	3.32	0.23	3.39	N/D
CRR 9	Cabo Rojo NWR	PR	P21	44.02	77	3	20	7.99	4.2	11800	580	1436	1353	5.44	0.61	10.56	N/D
JBR 1	Jabos Bay Research Reserve	PR	P22	43.51	N/D	N/D	N/D	7.51	15.43	113099	4132	5641	15003	5.56	0.34	5.74	N/D
JBR 2	Jabos Bay Research Reserve	PR	P23	55.18	34	22	44	7.84	1.92	4856	303	544	794	7.97	0.48	8.04	N/D
JBR 3	Jabos Bay Research Reserve	PR	P24	32.88	N/D	N/D	N/D	7.84	10.19	27329	1294	1370	3834	5.1	0.26	5.23	N/D
JBR 4	Jabos Bay Research Reserve	PR	P25	37.49	N/D	N/D	N/D	7.89	7.54	28473	1110	1689	3406	7.36	0.24	6.02	N/D
JBR 5	Jabos Bay Research Reserve	PR	P26	18.05	N/D	N/D	N/D	8.23	8.8	30438	1061	1746	4171	2.01	0.11	2.38	N/D
JBR 6	Jabos Bay Research Reserve	PR	P27	52.17	72	15	13	8.09	7.2	20326	1004	1848	2503	7.62	0.42	12.96	N/D
JBR 7	Jabos Bay Research Reserve	PR	P28	64.82	73	6	21	7.68	11.03	33715	1740	1967	3852	13.7	0.72	15.29	N/D
JBR 8	Jabos Bay Research Reserve	PR	P29	58.01	N/D	N/D	N/D	8.31	12.8	63588	3059	3446	7921	7.35	0.5	12.02	N/D
JBR 9	Jabos Bay Research Reserve	PR	P30	46.52	73	17	10	7.49	4.21	9798	519	1419	1366	3.92	0.21	11.5	N/D
JBR 13	Jabos Bay Research Reserve	PR	P31	30.43	87	1	12	7.33	2.99	6112	476	715	962	1.63	0.12	2.94	N/D
JBR 14	Jabos Bay Research Reserve	PR	P32	43.56	81	8	10	6.91	4.42	10338	595	1212	1444	4.07	0.22	4.23	N/D
JBR 10	Jabos Bay Research Reserve	PR	P33	48.87	80	9	11	7.59	3.79	8141	469	1133	1094	3.17	0.26	11.71	N/D
JBR 11	Jabos Bay Research Reserve	PR	P34	56.56	N/D	N/D	N/D	7.81	4.79	11346	603	10414	1867	11.6	0.54	15.07	N/D
JBR 12	Jabos Bay Research Reserve	PR	P35	77.31	N/D	N/D	N/D	6.46	10.67	29635	1502	1430	4182	21	1.08	20.94	N/D

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
CIP1	Caladesy Island SP	FL	Q01	23.93	97	1	2	7.4	2.97	5888	377	323	796	0.9	0.11	0.97	32
CIP2	Caladesy Island SP	FL	Q02	21.93	98	0	2	7.62	2.78	4821	285	272	643	0.75	0.11	0.82	32
CIP3	Caladesy Island SP	FL	Q03	53.33	92	2	6	6.26	5.71	12454	738	644	1837	5.8	0.39	5.75	32
CIP4	Caladesy Island SP	FL	Q04	16.41	99	0	1	8.08	2.08	3888	170	245	509	0.26	0.07	0.99	32
CIP5	Caladesy Island SP	FL	Q05	15.95	100	0	0	8.58	1.94	4299	220	255	497	0.17	0.09	0.32	34
CIP6	Caladesy Island SP	FL	Q06	81.15	87	3	10	7.3	3.33	6713	376	816	1086	18.5	1.3	17.59	31
CIP7	Caladesy Island SP	FL	Q07	54.87	N/D	N/D	N/D	7.17	2.43	4881	260	550	687	3.38	0.24	4.58	33
HIP1	Honeymoon Island SP	FL	Q08	79.44	N/D	N/D	N/D	6.49	9.9	25880	1567	1084	3280	20.4	2.01	20.58	31
HIP2	Honeymoon Island SP	FL	Q09	29.83	94	1	5	7.59	3.8	7668	427	592	929	1.07	0.09	1.31	34
HIP3	Honeymoon Island SP	FL	Q10	22.84	94	0	6	7.5	2.88	5933	346	429	745	0.64	0.08	0.57	37
HIP4	Honeymoon Island SP	FL	Q11	28.12	95	1	4	7.08	4.14	8999	587	721	1119	1.54	0.15	2.45	33
CHP1	Charlot Harbor SP	FL	Q12	19.23	98	0	2	7.19	2.72	5506	320	269	709	0.23	0.08	0.24	30
CHP2	Charlot Harbor SP	FL	Q13	17.01	94	0	6	8.5	2.02	3918	162	282	479	0.4	0.09	5.27	32
CHP3	Charlot Harbor SP	FL	Q14	27.18	99	1	0	7.63	3.94	8738	518	463	1069	1.63	0.17	4.45	31
CHP4	Charlot Harbor SP	FL	Q15	21.53	96	0	4	7.2	2.9	5718	181	728	836	0.7	0.1	0.66	35
CHP5	Charlot Harbor SP	FL	Q16	34.14	92	0	8	6.2	5.04	10230	403	850	1367	2.32	0.25	2.21	32
CHP6	Charlot Harbor SP	FL	Q17	17.13	97	0	3	6.53	5.46	11387	411	753	1620	0.28	0.07	0.24	34
RBR1	Rookery Bay Reserve	FL	Q18	22.45	96	2	2	7.33	2.82	5695	356	565	676	0.8	0.13	1.22	29
RBR2	Rookery Bay Reserve	FL	Q19	69.13	N/D	N/D	N/D	6.13	9.65	23909	1136	1192	3317	17.6	1.21	16.57	31
RBR3	Rookery Bay Reserve	FL	Q20	17.41	95	0	5	7.49	2.55	4601	229	250	578	0.24	0.06	0.27	29
RBR4	Rookery Bay Reserve	FL	Q21	74.65	48	39	13	7.11	6.55	14321	733	855	1712	18.1	0.88	18.96	31
RBR5	Rookery Bay Reserve	FL	Q22	17.18	87	8	5	7.79	2.35	4524	181	859	561	5.66	0.05	7.23	29
RBR6	Rookery Bay Reserve	FL	Q23	16.99	80	10	10	7.92	1.72	3414	159	491	259	0.55	0.07	7.22	30

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
RBR7	Rookery Bay Reserve	FL	Q24	69.47	77	7	16	7.09	4.25	9714	599	695	1304	14	0.63	15.21	28
RBR8	Rookery Bay Reserve	FL	Q25	83.23	N/D	N/D	N/D	4.79	2.42	4557	243	643	855	33	1.84	32.92	27
RBR9	Rookery Bay Reserve	FL	Q26	32.21	92	2	6	7.63	1.14	2242	117	227	274	2.51	0.24	3.02	28
CSP1	Collier-Seminole SP	FL	Q27	46.15	95	0	5	7.38	1.1	1910	86	398	292	3.04	0.27	3.25	27
TTI1	The Thousands Islands NWR	FL	Q28	57.81	93	2	5	6.31	0.79	1276	67	385	211	7.39	0.5	7.59	30
JSB1	Jemez Spring Baths	NM	R01	31.72	64	26	10	7.83	0.32	605	80	176	13	9.7	0.12	3.03	45
JSB2	Jemez Spring Baths	NM	R02	21.71	88	6	6	7.88	0.2	313	64	158	9	43.3	0.09	1.92	38
JSB3	Jemez Spring Baths	NM	R03	20.39	76	18	6	8.32	0.15	265	35	92	9	0.11	0.08	1.49	45
JSB4	Jemez Spring Baths	NM	R04	39.39	86	12	2	8.44	0.31	602	68	141	9	0.35	0.09	11.99	35
JSB5	Jemez Spring Baths	NM	R05	49.33	54	24	22	7.51	0.47	978	186	196	15	3.81	0.22	8.58	34
NSS1	New Mexico Sulfur Springs	NM	R06	55.26	N/D	N/D	N/D	2.58	0.37	53	41	59	27	2.2	0.23	2.07	59
NSS2	New Mexico Sulfur Springs	NM	R07	43.73	58	18	24	2.82	0.31	69	47	99	39	2.2	0.25	2.09	46
NSS3	New Mexico Sulfur Springs	NM	R08	29.82	80	18	2	1.74	4.19	92	43	120	45	0.61	0.09	0.63	66
NSS4	New Mexico Sulfur Springs	NM	R09	32.61	66	14	20	2.71	0.2	49	23	164	39	0.94	0.15	0.89	35
NSS5	New Mexico Sulfur Springs	NM	R10	26.86	74	20	6	2.19	0.61	75	111	160	49	0.41	0.09	0.41	21
NSS6	New Mexico Sulfur Springs	NM	R11	35.17	60	38	2	2.18	1.52	25	35	37	22	0.49	0.13	0.47	44
NSS7	New Mexico Sulfur Springs	NM	R12	34.04	72	12	16	2.47	0.48	66	96	103	49	1.15	0.1	1.16	27
SLS1	Soda Lake Side	NM	R13	48.86	74	20	6	6.93	0.73	891	221	1290	54	2.57	0.35	2.62	37
SAC1	San Antonio cabin	NM	R14	72.07	68	20	12	7.21	0.15	108	47	87	10	3.33	0.19	8.29	36
CLS1	Caribbean Lake Spring	NM	R15	71.64	N/D	N/D	N/D	4.14	0.08	41	31	75	14	13.1	1.03	13.4	18
NGYS 1	Norris Geyser Yellowstone NP	WY	S01	N/D	97	2	1	2.79	0.12	210	37	27	3	0.12	0.32	0.3	79
NGYS 2	Norris Geyser Yellowstone NP	WY	S02	N/D	85	8	7	6.3	0.24	362	27	36	3	0.08	0.36	0.37	87

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
NGYS 3	Norris Geyser Yellowstone NP	WY	S03	N/D	88	7	5	2.93	0.21	273	39	84	7	0.07	0.43	0.44	80
NGYS 4	Norris Geyser Yellowstone NP	WY	S04	N/D	50	33	17	3.54	0.2	323	88	149	9	0.07	0.44	0.39	83
NGYS 5	Norris Geyser Yellowstone NP	WY	S05	N/D	94	3	3	4.14	0.15	189	48	15	2	0.02	0.09	0.07	93
NGYS 6	Norris Geyser Yellowstone NP	WY	S06	N/D	44	48	8	2.32	0.68	932	217	104	17	0.35	3.76	3.59	51
NGYS 7	Norris Geyser Yellowstone NP	WY	S07	N/D	88	11	1	2.93	0.14	186	32	37	7	0.13	0.79	0.74	29
NGYS 8	Norris Geyser Yellowstone NP	WY	S08	N/D	86	13	1	2.97	0.09	132	16	33	4	0.04	0.47	0.46	91
NGYS 9	Norris Geyser Yellowstone NP	WY	S09	N/D	69	22	9	2.88	0.11	112	12	34	4	0.03	0.15	0.13	88
NGYS 10	Norris Geyser Yellowstone NP	WY	S10	N/D	15	34	51	2.89	0.18	297	42	42	2	0.05	0.12	0.11	77
NGYS 11	Norris Geyser Yellowstone NP	WY	S11	N/D	23	32	45	3.05	0.18	343	51	21	3	0.15	0.8	0.86	29
NGYS 12	Norris Geyser Yellowstone NP	WY	S12	N/D	69	22	9	2.24	0.25	265	46	44	7	0.12	1.2	1.14	64
NGYS 13	Norris Geyser Yellowstone NP	WY	S13	N/D	77	8	15	3.15	0.22	319	62	62	5	0.3	1.5	1.53	46
NGYS 14	Norris Geyser Yellowstone NP	WY	S14	N/D	53	40	7	2.28	0.42	280	60	50	4	0.05	0.15	0.14	78
NGYS 15	Norris Geyser Yellowstone NP	WY	S15	N/D	29	30	41	2.81	0.18	265	72	31	4	0.23	1.82	1.79	38
NGYS 16	Norris Geyser Yellowstone NP	WY	S16	N/D	65	30	5	2.01	2.14	242	76	25	4	0.09	2.62	2.74	82
NGYS 17	Norris Geyser Yellowstone NP	WY	S17	N/D	79	10	11	2.41	0.3	122	22	27	5	0.1	0.76	0.62	93
NGYS 18	Norris Geyser Yellowstone NP	WY	S18	N/D	99	0	1	2.25	0.82	221	46	22	5	0.08	0.36	0.32	65
NGYS 19	Norris Geyser Yellowstone NP	WY	S19	N/D	95	4	1	2.85	0.16	152	41	31	6	0.12	1.09	1.18	28
SMYS 1	Sentinel Meadows Yellowstone NP	WY	S20	N/D	59	28	13	2.55	0.42	410	117	135	23	0.39	4.59	4.96	41
SMYS 2	Sentinel Meadows Yellowstone NP	WY	S21	N/D	59	16	25	4.55	0.21	404	48	52	8	0.47	3.56	3.43	39
SMYS 3	Sentinel Meadows Yellowstone NP	WY	S22	N/D	85	4	11	7.2	0.2	504	17	10	2	0.15	0.8	0.74	56
SMYS 4	Sentinel Meadows Yellowstone NP	WY	S23	N/D	81	8	11	4.16	0.26	573	36	65	5	0.45	5.91	5.84	51
SMYS 5	Sentinel Meadows Yellowstone NP	WY	S24	N/D	45	34	21	7.13	0.14	307	14	6	1	0.18	0.96	0.94	45

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
SMYS 6	Sentinel Meadows Yellowstone NP	WY	S25	N/D	35	40	25	3.12	0.23	487	35	45	10	0.31	4.11	4.01	46
HVYS 1	Hidden Valley Yellowstone NP	WY	S26	N/D	53	46	1	2.22	0.53	141	73	100	39	0.18	0.92	0.93	64
HVYS 2	Hidden Valley Yellowstone NP	WY	S27	N/D	90	5	5	2.24	0.7	84	39	272	34	0.28	2.06	2.14	32
HVYS 3	Hidden Valley Yellowstone NP	WY	S28	N/D	72	17	11	3.02	0.18	105	70	63	30	0.08	0.3	0.29	55
HVYS 4	Hidden Valley Yellowstone NP	WY	S29	N/D	30	21	49	2.54	0.21	24	9	18	9	0.24	1.94	1.95	27
HVYS 5	Hidden Valley Yellowstone NP	WY	S30	N/D	50	49	1	2.11	1.33	52	34	28	10	0.09	0.3	0.28	51
HVYS 6	Hidden Valley Yellowstone NP	WY	S31	N/D	72	11	17	2.41	0.31	85	8	43	25	0.05	0.26	0.25	55
HVYS 7	Hidden Valley Yellowstone NP	WY	S32	N/D	55	18	27	2.25	0.5	135	14	110	38	0.05	0.11	0.11	65
HVYS 8	Hidden Valley Yellowstone NP	WY	S33	N/D	35	37	28	2.24	0.84	40	7	7	8	0.12	0.39	0.4	44
HVYS 9	Hidden Valley Yellowstone NP	WY	S34	N/D	15	55	30	2.17	0.9	43	18	28	9	0.08	0.37	0.37	46
HVYS 10	Hidden Valley Yellowstone NP	WY	S35	N/D	49	46	5	2.34	0.38	335	43	39	9	0.12	0.14	0.13	72
HVYS 11	Hidden Valley Yellowstone NP	WY	S36	N/D				2.04	1.16	65	14	6	7	0.06	0.09	0.08	60
HVYS 12	Hidden Valley Yellowstone NP	WY	S37	N/D	89	4	7	5.54	0.21	359	76	118	11	0.05	0.28	0.28	78
WFYS 1	Whisky Flats Yellowstone NP	WY	S38	N/D	N/D	N/D	N/D	5.56	0.2	335	79	132	13	1.31	9.37	9.25	21
WFYS 2	Whisky Flats Yellowstone NP	WY	S39	N/D	N/D	N/D	N/D	6.42	0.14	184	53	73	2	0.09	0.78	0.84	19
FDYS 1	Firehole drive Yellowstone NP	WY	S40	N/D	83	8	9	6.44	0.15	305	17	20	2	0.48	6.6	6.54	15
FHYS 2	Firehole drive Yellowstone NP	WY	S41	N/D	77	14	9	8.21	0.17	428	30	11	1	0.08	0.63	0.19	79
FHYS 3	Firehole drive Yellowstone NP	WY	S42	N/D	65	30	5	8.07	0.1	196	7	6	1	0.49	3.15	3.16	54
FHYS 4	Firehole drive Yellowstone NP	WY	S43	N/D	69	16	15	8.06	0.33	802	43	22	3	0.35	2.56	2.34	37
FHYS 5	Firehole drive Yellowstone NP	WY	S44	N/D	85	12	3	6.6	0.29	324	67	312	12	0.11	0.47	0.46	60
FHYS 6	Firehole drive Yellowstone NP	WY	S45	N/D	71	26	3	2.25	0.35	84	24	32	6	0.18	1.1	1.15	20
STYS 1	Sulfatara Trail Yellowstone NP	WY	S46	N/D	N/D	N/D	N/D	2.19	0.27	561	35	63	5	0.12	1.6	1.56	66

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
STYS 2	Sulfatara Trail Yellowstone NP	WY	S47	N/D	53	42	5	2.31	0.37	84	6	45	6	0.04	0.8	0.77	83
STYS 3	Sulfatara Trail Yellowstone NP	WY	S48	N/D	N/D	N/D	N/D	2.3	0.34	58	8	48	6	0.14	1.61	1.59	64
SWRN1	Stillwater NWR	NV	T01	45.25	60	22	18	7.29	2	4835	196	587	150	1.68	0.22	2.29	23
SWRN2	Stillwater NWR	NV	T02	32.05	N/D	N/D	N/D	7.98	17.3	77679	1391	980	146	0.85	0.13	0.82	32
SWRN3	Stillwater NWR	NV	T03	34.28	N/D	N/D	N/D	7.28	17.35	79471	1632	657	131	1.4	0.11	1.6	31
GBS 1	Great Boiling Springs	NV	T04	68.5	71	9	20	4.29	1.72	3772	408	854	35	1.45	0.25	1.42	42
GBS 2	Great Boiling Springs	NV	T05	66.27	29	29	42	4.75	1.38	3262	307	679	24	1.31	0.3	1.32	56
GBS 3	Great Boiling Springs	NV	T06	67.51	35	19	46	5.55	1.01	2271	176	180	10	2.42	0.29	2.32	53
GBS 4	Great Boiling Springs	NV	T07	71.34	29	25	46	6.75	1.25	2933	336	441	17	1.1	0.21	1.1	60
GBS 5	Great Boiling Springs	NV	T08	76.82	23	31	46	6.3	1.43	3425	376	632	33	1.02	0.21	0.95	65
GBS 6	Great Boiling Springs	NV	T09	81.19	25	38	37	6.56	1.78	4265	458	692	38	1	0.23	1.06	41
GBS 7	Great Boiling Springs	NV	T10	42.19	23	25	52	8.18	0.56	1270	91	103	9	0.92	0.15	1.05	82
GBS 8	Great Boiling Springs	NV	T11	51.13	43	18	39	6.67	0.78	1940	164	163	5	1.14	0.2	1.14	51
GBS 9	Great Boiling Springs	NV	T12	71.46	43	14	43	7.54	4.22	12788	1057	811	22	6.29	0.47	6.47	22
FRN 1	Fly Ranch	NV	T13	70.86	43	16	41	8.1	0.22	492	27	145	8	5.18	0.44	11.72	22
FRN 2	Fly Ranch	NV	T14	59.56	69	14	17	7.87	0.29	629	26	188	13	1.94	0.21	10.21	72
FRN 3	Fly Ranch	NV	T15	46.93	61	26	13	7.67	0.42	699	57	698	32	1.29	0.13	8.56	43
FRN 4	Fly Ranch	NV	T16	35.97	75	14	11	8.36	0.11	248	16	29	4	0.62	0.14	12.12	48
FRN 5	Fly Ranch	NV	T17	49.04	92	4	4	8.37	0.22	524	43	127	16	1.22	0.18	12.27	46
CBHS 1	Buckeye Hot Spring	CA	U01	11.16	86	8	6	7.01	0.24	258	41	468	48	0.31	0.1	0.28	36
CBHS 2	Buckeye Hot Spring	CA	U02	25.92	92	4	4	6.95	0.52	820	94	1072	82	1.11	0.09	1.4	33
CBHS 3	Buckeye Hot Spring	CA	U03	18.87	72	18	10	7.8	0.14	219	25	168	17	0.44	0.09	4.29	60

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
CBHS 4	Buckeye Hot Spring	CA	U04	76.93	85	8	7	7.49	0.41	944	77	284	33	7.71	0.79	11.15	48
MLNB 1	Mono Lake Navy Beach	CA	U05	39.83	82	8	10	7.63	0.21	270	38	268	78	1.62	0.13	5.31	34
MLNB 2	Mono Lake Navy Beach	CA	U06	49.67	78	18	4	7.59	0.39	542	70	536	180	1.74	0.14	8.24	31
MLNB 3	Mono Lake Navy Beach	CA	U07	55.04	72	14	14	7.67	0.76	1280	97	1117	227	2.91	0.21	8.14	24
MLNB 4	Mono Lake Navy Beach	CA	U08	27.9	79	14	7	7.67	0.32	561	86	226	91	0.97	0.17	3.19	26
MLNB 5	Mono Lake Navy Beach	CA	U09	29.52	91	6	3	7.79	0.27	477	59	207	82	0.63	0.13	1.78	37
MLIS 1	Mono Lake Island Hot Springs (Paoha Island)	CA	U10	37.46	89	6	5	10.17	7.06	33626	873	30	27	0.79	0.09	0.77	54
MLIS 2	Mono Lake Island Hot Springs (Paoha Island)	CA	U11	43.93	N/D	N/D	N/D	10.07	11.26	72700	2362	18	17	1.15	0.15	1.35	47
MLIS 3	Mono Lake Island Hot Springs (Paoha Island)	CA	U12	37.58	63	16	21	9.95	2.28	7778	205	18	5	0.78	0.21	1.06	52
MLIS 4	Mono Lake Island Hot Springs (Paoha Island)	CA	U13	40.07	35	46	19	10	2.57	9819	229	13	5	0.85	0.1	1.01	37
MLIS 5	Mono Lake Island Hot Springs (Paoha Island)	CA	U14	33.84	57	12	31	10.08	1.73	5999	140	5	4	0.47	0.17	0.61	82
MLIS 6	Mono Lake Island Hot Springs (Paoha Island)	CA	U15	40.8	49	32	19	7.87	0.57	812	247	578	332	1.77	0.21	4.51	19
MLIS 7	Mono Lake Island Hot Springs (Paoha Island)	CA	U16	34.99	89	10	1	6.02	0.06	89	16	29	6	0.74	0.14	0.69	19
HCMA 1	Hot Creek at Mammoth	CA	U17	37.3	84	9	7	7.57	0.35	601	50	199	7	0.97	0.15	0.97	47
HCMA 2	Hot Creek at Mammoth	CA	U18	48.6	80	13	7	7.5	0.28	600	52	189	8	1.53	0.14	2.1	56
HCMA 3	Hot Creek at Mammoth	CA	U19	34.25	48	35	17	8.98	0.11	265	13	5	2	0.24	0.1	0.76	73
HCMA 4	Hot Creek at Mammoth	CA	U20	82.5	55	26	19	7.1	0.41	982	58	127	3	2.16	0.32	3.45	52
HCMA 5	Hot Creek at Mammoth	CA	U21	52	46	37	17	7.94	0.25	583	54	117	5	0.64	0.13	1.6	70

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
OLCA 1	Owens Lake (dry lake)	CA	U22	52.92	N/D	N/D	N/D	9.59	15.37	164045	9974	37	32	4.96	0.19	5.22	33
OLCA 2	Owens Lake (dry lake)	CA	U23	35.27	N/D	N/D	N/D	9.8	15.53	106453	5475	10	32	3.53	0.13	4.41	44
OLCA 3	Owens Lake (dry lake)	CA	U24	27.3	N/D	N/D	N/D	9.57	14.72	186457	9145	36	74	2.08	0.09	3.31	41
HBSP1	Hapuna Beach SP	HI	V01	N/D	98	0	2	8.13	2.36	1082	255	431	402	0.04	10.19	0.72	26
HBSP2	Hapuna Beach SP	HI	V02	N/D	98	0	2	8.28	2.12	4740	225	396	359	0.04	10.45	0.82	26
HBSP3	Hapuna Beach SP	HI	V03	N/D	98	0	2	8.45	0.26	510	29	60	33	0.05	10.53	0.79	26
APHW1	Alchiline ponds	HI	V04	N/D	84	2	14	7.43	0.67	873	113	479	360	0.22	2.93	2.26	26
APHW2	Alchiline ponds	HI	V05	N/D	96	0	4	7.33	0.3	432	38	123	62	0.09	1.21	0.95	26
APHW3	Alchiline ponds	HI	V06	N/D	N/D	N/D	N/D	7.14	0.44	577	165	99	91	0.43	4.53	3.65	26
APHW4	Alchiline ponds	HI	V07	N/D	94	0	6	8.04	0.37	613	56	119	61	0.09	7.63	1.06	25
NELH1	Natural Energy Lab Hawaii	HI	V08	N/D	82	6	12	7.56	2.13	4080	306	314	338	0.55	8.31	4	24
NELH2	Natural Energy Lab Hawaii	HI	V09	N/D	94	0	6	7.79	1.02	1953	101	176	131	0.11	5.38	1.14	23
NELH3	Natural Energy Lab Hawaii	HI	V10	N/D	86	6	8	7.53	1.98	3872	167	312	365	0.35	4.71	3.82	23
NELH4	Natural Energy Lab Hawaii	HI	V11	N/D	90	0	10	7.84	0.82	1294	79	206	143	0.11	6.43	1.26	24
KKHW1	Kekahi Kai State Park	HI	V12	N/D	96	2	2	8.07	2.32	5158	230	335	316	0.06	6.38	0.62	24
KKHW2	Kekahi Kai State Park	HI	V13	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	20.29	1.74	21.12	28
KKHW3	Kekahi Kai State Park	HI	V14	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	1.6	19	18.73	27
KKHW4	Kekahi Kai State Park	HI	V15	N/D	N/D	N/D	N/D	7.01	2.6	5353	532	167	509	1.3	17.88	17.83	27
KKHW5	Kekahi Kai State Park	HI	V16	N/D	67	20	13	7.19	2.39	4075	255	369	501	0.49	13.3	5.59	26
ONHW1	Onekahakaha Beach park	HI	V19	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	21.9	1.51	22.85	23
ONHW2	Onekahakaha Beach park	HI	V20	N/D	75	12	13	7.63	3.34	7867	389	470	726	0.37	10.89	4.46	23
ONHW3	Onekahakaha Beach park	HI	V21	N/D	77	8	15	7.66	2.8	5893	290	939	552	0.19	9.93	2.19	24

Table 21 continued

Sample Name	*Site Name*	*State*	*Fermen-tation ID*	*H2O %*	*Sand %*	*Silt %*	*Clay %*	*pH*	*EC S m^{-1}*	*Na mg kg^{-1}*	*K mg kg^{-1}*	*Ca mg kg^{-1}*	*Mg mg kg^{-1}*	*Organic C, %*	*Total N, %*	*Total C, %*	*Temp °C*
ONHW4	Onekahakaha Beach park	HI	V22	N/D	93	0	7	8.14	2.33	5060	269	323	393	0.07	9.21	0.91	24
WRHW1	Wailoa River State Park	HI	V23	N/D	N/D	N/D	N/D	6.33	0.4	626	90	30	60	0.83	8.03	7.9	23
AFHW1	Akaka Falls State Park	HI	V24	N/D	17	16	67	6.12	0.02	39	1	1	1	0.15	1.37	1.34	24
AFHW2	Akaka Falls State Park	HI	V25	N/D	N/D	N/D	N/D	6.06	0.07	53	25	32	16	1.21	20.78	20.45	20
AFHW3	Akaka Falls State Park	HI	V26	N/D	N/D	N/D	N/D	6.32	0.04	24	24	17	5	1.02	16.28	16.28	21
CPHW1	Carlsmith County Park	HI	V27	N/D	N/D	N/D	N/D	6.72	1.02	1335	206	85	239	0.78	7.57	7.55	21
CPHW2	Carlsmith County Park	HI	V28	N/D	99	0	1	7.5	1.19	2650	114	117	151	0.07	0.27	0.25	23
CPHW3	Carlsmith County Park	HI	V29	N/D	N/D	N/D	N/D	6.17	0.62	1056	76	76	176	0.84	8.22	8.15	23
CPHW4	Carlsmith County Park	HI	V30	N/D	81	18	1	3.9	1.09	1408	103	400	1028	0.37	4.38	3.97	24
Galveston	Open Access Beach 8 mile Rd	TX	Control	N/D	97	2	1	7.92	2.60	3999.03	201.80	371.79	410.44	0.36	0.06	0.92	N/D

Abbreviations: EC, electrical conductivity; Na, sodium; K, potassium; Ca, calcium; Mg, magnesium, C, carbon; N, nitrogen; Temp, temperature
Soil Temperature taken at time of sampling
EC, pH, Na, K, Ca, and Mg values based on detailed salinity testing

APPENDIX C

Table 22 Geographic locations of all samples collected and screened in the carboxylate platform (N/D, no data). All samples fermentation data are listed in Appendix D: Table 23 and soil physical and chemical data are listed in Appendix B: Table 21.

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
LSDR T1-0	La Sal del Rey	TX	N/D	N/D	6/23/2008	GSL3	Great Salt Lake	UT	40.74851	112.18609	5/4/2009
LSDR T1-65	La Sal del Rey	TX	26.54056	98.04939	6/23/2008	SHS1	Saratoga Hot Springs	UT	40.35265	111.89934	5/4/2009
LSDR T1-130	La Sal del Rey	TX	26.54054	98.04958	6/23/2008	SHS2	Saratoga Hot Springs	UT	40.35278	111.89959	5/4/2009
LSDR T1-195	La Sal del Rey	TX	26.5405	98.0498	6/23/2008	IHS1	Indian Hot Springs	UT	41.57959	112.2342	5/4/2009
LSDR T1-260	La Sal del Rey	TX	26.54047	98.05001	6/23/2008	IHS2	Indian Hot Springs	UT	41.57601	112.23415	5/4/2009
LSDR T1-325	La Sal del Rey	TX	26.54046	98.05018	6/23/2008	IHS3	Indian Hot Springs	UT	41.57602	112.23391	5/4/2009
LSDR T1-390	La Sal del Rey	TX	26.54042	98.05038	6/23/2008	IHS4	Indian Hot Springs	UT	41.57622	112.23376	5/4/2009
LSDR T1-455	La Sal del Rey	TX	26.5404	98.05057	6/23/2008	SCW1	Salt Creek Waterfowl Preserve	UT	41.63346	112.25749	5/4/2009
LSDR T1-520	La Sal del Rey	TX	26.54037	98.05081	6/23/2008	Knoll1	Knoll Spring	UT	40.70045	112.28488	5/4/2009
LSDR T1-585	La Sal del Rey	TX	26.54034	98.05097	6/23/2008	LB1	Lincoln Beach	UT	40.13836	111.80196	5/4/2009
LSDR T2-0	La Sal del Rey	TX	26.53975	98.06214	6/23/2008	UL1	Utah Lake	UT	40.2627	111.66437	5/4/2009
LSDR T2-65	La Sal del Rey	TX	26.53966	98.06198	6/23/2008	UL2	Utah Lake	UT	40.13743	111.93693	5/4/2009
LSDR T2-130	La Sal del Rey	TX	26.53958	98.06178	6/23/2008	WS1	Warm Springs	UT	40.79135	111.90076	5/4/2009
LSDR T2-95	La Sal del Rey	TX	26.5395	98.06161	6/23/2008	WS2	Warm Springs	UT	40.79131	111.90077	5/4/2009
LSDR T2-260	La Sal del Rey	TX	26.53944	98.06142	6/23/2008	WS3	Warm Springs	UT	40.79122	111.90089	5/4/2009
LSDR T2-325	La Sal del Rey	TX	26.53935	98.06124	6/23/2008	WS4	Warm Springs	UT	40.79089	111.90062	5/4/2009
LSDR T2-390	La Sal del Rey	TX	26.53928	98.06106	6/23/2008	BRR1	Bear River Reserve	UT	41.4815	112.28072	5/4/2009
LSDR T2-455	La Sal del Rey	TX	26.53919	98.06088	6/23/2008	BRR2	Bear River Reserve	UT	41.48371	112.30993	5/4/2009
LSDR T3-0	La Sal del Rey	TX	26.53002	98.06296	6/23/2008	BRR3	Bear River Reserve	UT	41.48128	112.31256	5/4/2009
LSDR T3-65	La Sal del Rey	TX	26.53019	98.06296	6/23/2008	SWR1	Savannah NWR	GA	32.16222	81.11403	5/18/2009
LSDR T3-130	La Sal del Rey	TX	26.5304	98.06291	6/23/2008	SWR2	Savannah NWR	GA	32.16226	81.11399	5/18/2009
LSDR T3-195	La Sal del Rey	TX	26.53055	98.06289	6/23/2008	CR1	Cape Romaine NWR	SC	32.92027	79.59494	5/18/2009
LSDR T3-260	La Sal del Rey	TX	26.53075	98.06286	6/23/2008	CR2	Cape Romaine NWR	SC	32.92033	79.59494	5/18/2009

Table 22 continued

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
LSDR T3-325	La Sal del Rey	TX	26.53092	98.06284	6/23/2008	CR3	Cape Romaine NWR	SC	32.92037	79.59493	5/18/2009
LSDR T3-390	La Sal del Rey	TX	26.53111	98.06279	6/23/2008	CR4	Cape Romaine NWR	SC	32.92635	79.58544	5/18/2009
LSDR T3-455	La Sal del Rey	TX	26.53127	98.06274	6/23/2008	CR5	Cape Romaine NWR	SC	32.92639	79.58557	5/18/2009
GR1	Grulla Lake	NM	34.0974281	103.0546328	10/4/2008	CR6	Cape Romaine NWR	SC	32.9279	79.58293	5/18/2009
GR2	Grulla Lake	NM	34.0966506	103.0567858	10/4/2008	CR7	Cape Romaine NWR	SC	32.92791	79.58291	5/18/2009
GR3	Grulla Lake	NM	34.0963092	103.0579967	10/4/2008	CR8	Cape Romaine NWR	SC	32.92938	79.57901	5/18/2009
GR4	Grulla Lake	NM	34.09624	103.0581825	10/4/2008	CR9	Cape Romaine NWR	SC	32.92678	79.57674	5/18/2009
GR5	Grulla Lake	NM	34.0961811	103.0584547	10/4/2008	CR10	Cape Romaine NWR	SC	32.9181	79.57662	5/18/2009
GR6	Grulla Lake	NM	34.0961125	103.0586839	10/4/2008	CR11	Cape Romaine NWR	SC	32.91934	79.57753	5/18/2009
GR7	Grulla Lake	NM	34.0960536	103.0589453	10/4/2008	CR12	Cape Romaine NWR	SC	32.91778	79.57793	5/18/2009
GR8	Grulla Lake	NM	34.0959761	103.0591856	10/4/2008	CR13	Cape Romaine NWR	SC	32.91788	79.5779	5/18/2009
GR9	Grulla Lake	NM	34.0959256	103.0594036	10/4/2008	CR14	Cape Romaine NWR	SC	32.91233	79.58088	5/18/2009
GR10	Grulla Lake	NM	34.0958303	103.059655	10/4/2008	CR15	Cape Romaine NWR	SC	32.90959	79.58036	5/18/2009
GR11	Grulla Lake	NM	34.0973492	103.0507978	10/4/2008	CR16	Cape Romaine NWR	SC	32.90615	79.58254	5/18/2009
GR12	Grulla Lake	NM	34.09688	103.0513503	10/4/2008	CR17	Cape Romaine NWR	SC	32.90621	79.58259	5/18/2009
MPL1 R	Muleshoe Pauls Lake	NM	33.9841147	102.7184119	10/4/2008	CR18	Cape Romaine NWR	SC	32.90634	79.58264	5/18/2009
MPL2 R	Muleshoe Pauls Lake	NM	33.9840619	102.7184889	10/4/2008	CR19	Cape Romaine NWR	SC	32.91014	79.58323	5/18/2009
MPL3 R	Muleshoe Pauls Lake	NM	33.9838933	102.7186342	10/4/2008	CR20	Cape Romaine NWR	SC	32.90959	79.58672	5/18/2009
MPL4 R	Muleshoe Pauls Lake	NM	33.9837719	102.7188864	10/4/2008	CR21	Cape Romaine NWR	SC	32.90419	79.59888	5/18/2009
MPL5 R	Muleshoe Pauls Lake	NM	33.9835875	102.7191511	10/4/2008	CR22	Cape Romaine NWR	SC	32.90656	79.61488	5/18/2009
MPL6 R	Muleshoe Pauls Lake	NM	33.98347	102.7191433	10/4/2008	CR23	Cape Romaine NWR	SC	32.91298	79.61333	5/18/2009
MPL7 R	Muleshoe Pauls Lake	NM	33.9833878	102.7190806	10/4/2008	CR24	Cape Romaine NWR	SC	32.9399	79.65724	5/18/2009
MPL8 R	Muleshoe Pauls Lake	NM	33.9842019	102.7182581	10/4/2008	CR25	Cape Romaine NWR	SC	32.93987	79.65714	5/18/2009
MPL9 L	Muleshoe Pauls Lake	NM	33.9845414	102.7180864	10/4/2008	PI1	Pinkney Island NWR	SC	32.26295	80.76013	5/18/2009
MWL1 R	Muleshoe White Lake	NM	33.9477722	102.7711614	10/4/2008	PI2	Pinkney Island NWR	SC	32.26214	80.76319	5/18/2009
MWL 2 R	Muleshoe White Lake	NM	33.9478575	102.7708886	10/4/2008	PI3	Pinkney Island NWR	SC	32.26215	80.76318	5/18/2009
MWL3 R	Muleshoe White Lake	NM	33.9477306	102.7708597	10/4/2008	PI4	Pinkney Island NWR	SC	32.25858	80.76606	5/18/2009

Table 22 continued

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
MWL4 R	Muleshoe White Lake	NM	33.9479831	102.7708531	10/4/2008	PI5	Pinkney Island NWR	SC	32.25779	80.76542	5/18/2009
MGL1 R	Muleshoe Goose Lake	NM	33.9572517	102.7495444	10/4/2008	PI6	Pinkney Island NWR	SC	32.25779	80.76543	5/18/2009
MGL2 R	Muleshoe Goose Lake	NM	33.9571886	102.7495461	10/4/2008	PI7	Pinkney Island NWR	SC	32.25421	80.75639	5/18/2009
MGL3 R	Muleshoe Goose Lake	NM	33.9569503	102.7473669	10/4/2008	PI8	Pinkney Island NWR	SC	32.25432	80.75631	5/18/2009
MGL4 R	Muleshoe Goose Lake	NM	33.9571911	102.7472306	10/4/2008	PI9	Pinkney Island NWR	SC	32.24395	80.77541	5/18/2009
MGL5 L	Muleshoe Goose Lake	NM	33.9559233	102.7528364	10/4/2008	PI10	Pinkney Island NWR	SC	32.24204	80.77625	5/18/2009
GSP1	Great Salt Plains NWR	OK	36.711555	98.269889	10/9/2008	PI11	Pinkney Island NWR	SC	32.24071	80.77653	5/18/2009
GSP2	Great Salt Plains NWR	OK	36.712861	98.270667	10/9/2008	PI12	Pinkney Island NWR	SC	32.24076	80.77678	5/18/2009
GSP3	Great Salt Plains NWR	OK	36.7128547	98.2706881	10/9/2008	PI13	Pinkney Island NWR	SC	32.2384	80.77825	5/18/2009
GSP4	Great Salt Plains NWR	OK	36.801394	98.2514769	10/9/2008	PI14	Pinkney Island NWR	SC	32.23866	80.77831	5/18/2009
GSP5	Great Salt Plains NWR	OK	36.8007137	98.2508558	10/9/2008	SI1	Sapelo Island Microbial Observatory	GA	31.39024	81.26427	5/20/2009
GSP6	Great Salt Plains NWR	OK	36.7992279	98.2496708	10/9/2008	SI2	Sapelo Island Microbial Observatory	GA	31.39024	81.26427	5/20/2009
GSP7	Great Salt Plains NWR	OK	36.7992369	98.2496707	10/9/2008	SI3	Sapelo Island Microbial Observatory	GA	31.39187	81.26329	5/20/2009
GSP8	Great Salt Plains NWR	OK	36.799993	98.2495065	10/9/2008	SI4	Sapelo Island Microbial Observatory	GA	31.38953	81.2841	5/20/2009
GSP9	Great Salt Plains NWR	OK	36.8112587	98.192691	10/9/2008	SI5	Sapelo Island Microbial Observatory	GA	31.39017	81.28489	5/20/2009
GSP10	Great Salt Plains NWR	OK	36.811177	98.1927256	10/9/2008	SI6	Sapelo Island Microbial Observatory	GA	31.3902	81.27746	5/20/2009
GSP11	Great Salt Plains NWR	OK	36.811133	98.1927709	10/9/2008	SI7	Sapelo Island Microbial Observatory	GA	31.39273	81.27266	5/20/2009
Bra11	Brazoria NWR	TX	30.6165	96.33872	10/24/2008	SI8	Sapelo Island Microbial Observatory	GA	31.43136	81.28293	5/20/2009
Bra21	Brazoria NWR	TX	29.0673	95.26022	10/24/2008	SI9	Sapelo Island Microbial Observatory	GA	31.43978	81.2778	5/20/2009
Bra31	Brazoria NWR	TX	29.06099	95.24221	10/24/2008	SI10	Sapelo Island Microbial Observatory	GA	31.43978	81.2778	5/20/2009
Bra41	Brazoria NWR	TX	29.06112	95.24279	10/24/2008	SI11	Sapelo Island Microbial Observatory	GA	31.43978	81.2778	5/20/2009
Bra51	Brazoria NWR	TX	29.06083	95.24095	10/24/2008	SI12	Sapelo Island Microbial Observatory	GA	31.45966	81.27784	5/20/2009
Bra61	Brazoria NWR	TX	29.06145	95.23797	10/24/2008	SI13	Sapelo Island Microbial Observatory	GA	31.45947	81.277683	5/20/2009
Bra71	Brazoria NWR	TX	29.05743	95.22941	10/24/2008	SI14	Sapelo Island Microbial Observatory	GA	31.45947	81.277683	5/20/2009

Table 22 continued

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
Bra81	Brazoria NWR	TX	29.03794	95.26758	10/24/2008	SI15	Sapelo Island Microbial Observatory	GA	31.45947	81.277683	5/20/2009
Bra91	Brazoria NWR	TX	29.03787	95.26693	10/24/2008	SI16	Sapelo Island Microbial Observatory	GA	31.45947	81.277683	5/20/2009
Bra12	Brazoria NWR	TX	29.06031	95.26811	2/9/2009	SI17	Sapelo Island Microbial Observatory	GA	31.45951	81.277707	5/20/2009
Bra22	Brazoria NWR	TX	29.06072	95.26024	2/9/2009	SI18	Sapelo Island Microbial Observatory	GA	31.43195	81.23861	5/20/2009
Bra32	Brazoria NWR	TX	29.06099	95.24221	2/9/2009	SI19	Sapelo Island Microbial Observatory	GA	31.43261	81.23948	5/20/2009
Bra42	Brazoria NWR	TX	29.06111	95.24224	2/9/2009	SI20	Sapelo Island Microbial Observatory	GA	31.43471	81.23911	5/20/2009
Bra52	Brazoria NWR	TX	29.06083	95.24095	2/9/2009	SI21	Sapelo Island Microbial Observatory	GA	31.39784	81.27876	5/20/2009
Bra62	Brazoria NWR	TX	29.06145	95.23797	2/9/2009	SWR3	Sapelo Island Microbial Observatory	GA	32.1616	81.11426	5/20/2009
Bra72	Brazoria NWR	TX	29.05743	95.22941	2/9/2009	BWR 1	Laguna Boquerón NWR	PR	18.0095901	67.17092514	6/1/2009
Bra82	Brazoria NWR	TX	29.03794	95.26758	2/9/2009	BWR 2	Laguna Boquerón NWR	PR	N/D	N/D	6/1/2009
Bra92	Brazoria NWR	TX	29.03787	95.26693	2/9/2009	BWR 3	Laguna Boquerón NWR	PR	N/D	N/D	6/1/2009
Bra13	Brazoria NWR	TX	29.06031	95.26809	6/18/2009	BWR 4	Laguna Boquerón NWR	PR	N/D	N/D	6/1/2009
Bra23	Brazoria NWR	TX	29.06071	95.26022	6/18/2009	BWR 5	Laguna Boquerón NWR	PR	N/D	N/D	6/1/2009
Bra33	Brazoria NWR	TX	29.06099	95.24221	6/18/2009	BWR 6	Laguna Boquerón NWR	PR	N/D	N/D	6/1/2009
Bra43	Brazoria NWR	TX	29.06111	95.24221	6/18/2009	BWR 7	Laguna Boquerón NWR	PR	N/D	N/D	6/1/2009
Bra53	Brazoria NWR	TX	29.06083	95.24095	6/18/2009	CAR 1	Laguna Cartagena NWR	PR	18.012365	67.101681	6/1/2009
Bra63	Brazoria NWR	TX	29.06145	95.23797	6/18/2009	CAR 2	Laguna Cartagena NWR	PR	N/D	N/D	6/1/2009
Bra73	Brazoria NWR	TX	29.05743	95.22941	6/18/2009	CAR 3	Laguna Cartagena NWR	PR	N/D	N/D	6/1/2009
Bra83	Brazoria NWR	TX	29.03794	95.26758	6/18/2009	CAR 4	Laguna Cartagena NWR	PR	N/D	N/D	6/1/2009
Bra93	Brazoria NWR	TX	29.03791	95.26693	6/18/2009	CRR 1	Cabo Rojo NWR	PR	17.9615062	67.20611572	6/1/2009
Bra14	Brazoria NWR	TX	29.06024	95.26809	10/27/2009	CRR 10	Cabo Rojo NWR	PR	N/D	N/D	6/1/2009
Bra24	Brazoria NWR	TX	29.06069	95.26022	10/27/2009	CRR 2	Cabo Rojo NWR	PR	N/D	N/D	6/1/2009
Bra34	Brazoria NWR	TX	29.06097	95.24221	10/27/2009	CRR 3	Cabo Rojo NWR	PR	N/D	N/D	6/1/2009
Bra44	Brazoria NWR	TX	29.06111	95.24224	10/27/2009	CRR 4	Cabo Rojo NWR	PR	N/D	N/D	6/1/2009
Bra54	Brazoria NWR	TX	29.06083	95.24095	10/27/2009	CRR 5	Cabo Rojo NWR	PR	17.9521165	67.19641685	6/1/2009
Bra64	Brazoria NWR	TX	29.06145	95.23797	10/27/2009	CRR 6	Cabo Rojo NWR	PR	N/D	N/D	6/1/2009
Bra74	Brazoria NWR	TX	29.05743	95.22941	10/27/2009	CRR 7	Cabo Rojo NWR	PR	N/D	N/D	6/1/2009
Bra84	Brazoria NWR	TX	29.03794	95.26758	10/27/2009	CRR 8	Cabo Rojo NWR	PR	N/D	N/D	6/1/2009
Bra94	Brazoria NWR	TX	29.03787	95.26693	10/27/2009	CRR 9	Cabo Rojo NWR	PR	N/D	N/D	6/1/2009

Table 22 continued

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
BL1	Bitter Lake NWR	NM	33.4767	104.41093	11/15/2008	JBR 1	Jabos Bay Research Reserve	PR	17.9450126	66.23931885	6/1/2009
BL2	Bitter Lake NWR	NM	33.47678	104.41092	11/15/2008	JBR 2	Jabos Bay Research Reserve	PR	N/D	N/D	6/1/2009
BL3	Bitter Lake NWR	NM	33.47675	104.41093	11/15/2008	JBR 3	Jabos Bay Research Reserve	PR	N/D	N/D	6/1/2009
BL4	Bitter Lake NWR	NM	33.47675	104.41083	11/15/2008	JBR 4	Jabos Bay Research Reserve	PR	N/D	N/D	6/1/2009
BL5	Bitter Lake NWR	NM	33.47679	104.41089	11/15/2008	JBR 5	Jabos Bay Research Reserve	PR	17.9330723	66.2528801	6/1/2009
BL7	Bitter Lake NWR	NM	33.47637	104.41084	11/15/2008	JBR 6	Jabos Bay Research Reserve	PR	N/D	N/D	6/1/2009
BL8	Bitter Lake NWR	NM	33.47665	104.4106	11/15/2008	JBR 7	Jabos Bay Research Reserve	PR	N/D	N/D	6/1/2009
BL9	Bitter Lake NWR	NM	33.47645	104.41027	11/15/2008	JBR 8	Jabos Bay Research Reserve	PR	N/D	N/D	6/1/2009
BL10	Bitter Lake NWR	NM	33.47616	104.41001	11/15/2008	JBR 9	Jabos Bay Research Reserve	PR	17.9534229	66.2212944	6/1/2009
BL11	Bitter Lake NWR	NM	33.47608	104.41015	11/15/2008	JBR 13	Jabos Bay Research Reserve	PR	N/D	N/D	6/1/2009
BL12	Bitter Lake NWR	NM	33.47748	104.41156	11/15/2008	JBR 14	Jabos Bay Research Reserve	PR	N/D	N/D	6/1/2009
BL13	Bitter Lake NWR	NM	33.48433	104.41254	11/15/2008	JBR 10	Jabos Bay Research Reserve	PR	N/D	N/D	6/1/2009
BL14	Bitter Lake NWR	NM	33.48438	104.41253	11/15/2008	JBR 11	Jabos Bay Research Reserve	PR	N/D	N/D	6/1/2009
BL15	Bitter Lake NWR	NM	33.4749	104.41996	11/15/2008	JBR 12	Jabos Bay Research Reserve	PR	N/D	N/D	6/1/2009
BL16	Bitter Lake NWR	NM	33.47498	104.41896	11/15/2008	CIP1	Caladesy Island SP	FL	28.03691	82.819287	6/21/2009
BL17	Bitter Lake NWR	NM	33.47568	104.41901	11/15/2008	CIP2	Caladesy Island SP	FL	28.033671	82.818246	6/21/2009
BL18	Bitter Lake NWR	NM	33.4753	104.41959	11/15/2008	CIP3	Caladesy Island SP	FL	28.035404	82.819051	6/21/2009
BL19	Bitter Lake NWR	NM	33.47541	104.42092	11/15/2008	CIP4	Caladesy Island SP	FL	28.03571	82.82124	6/21/2009
BL20	Bitter Lake NWR	NM	33.47548	104.4208	11/15/2008	CIP5	Caladesy Island SP	FL	28.03563	82.82116	6/21/2009
BL21	Bitter Lake NWR	NM	33.47504	104.42078	11/15/2008	CIP6	Caladesy Island SP	FL	28.03563	82.82116	6/21/2009
LL1	Bottomless Lake State Park; Lazy Lagoon	NM	33.35378	104.34125	11/15/2008	CIP7	Caladesy Island SP	FL	28.03563	82.82116	6/21/2009
LL2	Bottomless Lake State Park; Lazy Lagoon	NM	33.25377	104.34126	11/15/2008	HIP1	Honeymoon Island SP	FL	28.06157	82.88411	6/21/2009
LL3	Bottomless Lake State Park; Lazy Lagoon	NM	33.35347	104.34136	11/15/2008	HIP2	Honeymoon Island SP	FL	28.07613	82.83224	6/21/2009
LL4	Bottomless Lake State Park; Lazy Lagoon	NM	33.35347	104.34139	11/15/2008	HIP3	Honeymoon Island SP	FL	28.07841	82.83236	6/21/2009
Lea1	Bottomless Lake State Park; Lea Lake	NM	33.31957	104.33134	11/15/2008	HIP4	Honeymoon Island SP	FL	28.07801	82.83236	6/21/2009
BLM1	Bureau of Land Management; William Sink	NM	33.31943	104.33158	11/15/2008	CHP1	Charlot Harbor SP	FL	27.02194	82.04329	6/21/2009

Table 22 continued

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
BLM2	Bureau of Land Management; William Sink	NM	32.57158	103.81595	11/15/2008	CHP2	Charlot Harbor SP	FL	26.73842	82.06823	6/21/2009
BLM3	Bureau of Land Management; William Sink	NM	32.5719	103.81592	11/15/2008	CHP3	Charlot Harbor SP	FL	26.72683	82.26221	6/21/2009
BLM4	Bureau of Land Management; William Sink	NM	32.57116	103.81534	11/15/2008	CHP4	Charlot Harbor SP	FL	26.84609	82.23879	6/21/2009
BLM5	Bureau of Land Management; Laguna Tuston	NM	32.55714	103.78246	11/15/2008	CHP5	Charlot Harbor SP	FL	26.84939	82.23745	6/21/2009
BLM6	Bureau of Land Management; Laguna Tuston	NM	32.55712	103.7825	11/15/2008	CHP6	Charlot Harbor SP	FL	26.8494	82.23743	6/21/2009
BLM7	Bureau of Land Management; Laguna Tuston	NM	32.55491	103.78332	11/15/2008	RBR1	Rookery Bay Reserve	FL	25.93208	81.65522	6/21/2009
BLM8	Bureau of Land Management; Laguna Tuston	NM	32.5549	103.78331	11/15/2008	RBR2	Rookery Bay Reserve	FL	25.93091	81.67734	6/21/2009
BLM9	Bureau of Land Management; Laguna Plata	NM	32.58537	103.75041	11/15/2008	RBR3	Rookery Bay Reserve	FL	25.93185	81.6774	6/21/2009
BLM10	Bureau of Land Management; Laguna Plata	NM	32.58555	103.75049	11/15/2008	RBR4	Rookery Bay Reserve	FL	25.98402	81.72775	6/21/2009
BLM11	Bureau of Land Management; Laguna Plata	NM	32.58678	103.75097	11/15/2008	RBR5	Rookery Bay Reserve	FL	26.02539	81.7289	6/21/2009
BLM12	Bureau of Land Management; Laguna Plata	NM	32.58637	103.75103	11/15/2008	RBR6	Rookery Bay Reserve	FL	26.02746	81.72796	6/21/2009
BLM13	Bureau of Land Management; Laguna Plata	NM	32.58636	103.75123	11/15/2008	RBR7	Rookery Bay Reserve	FL	26.02759	81.72767	6/21/2009
BLM14	Bureau of Land Management; Laguna Plata	NM	32.5869	103.75131	11/15/2008	RBR8	Rookery Bay Reserve	FL	26.02368	81.70964	6/21/2009
BLM15	Bureau of Land Management; Laguna Plata	NM	32.58716	103.75141	11/15/2008	RBR9	Rookery Bay Reserve	FL	26.05067	81.70126	6/21/2009
BLM16	Bureau of Land Management; Laguna Plata	NM	32.58058	103.74753	11/15/2008	CSP1	Collier-Seminole SP	FL	25.98796	81.59447	6/21/2009
BLM17	Bureau of Land Management; Laguna Tonto	NM	32.61189	103.67965	11/15/2008	TTI1	The Thousands Islands NWR	FL	25.97143	81.55548	6/21/2009

Table 22 continued

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
BLM18	Bureau of Land Management; Laguna Tonto	NM	32.6119	103.67954	11/15/2008	JSB1	Jemez Spring Baths	NM	35.7725478	106.6910517	7/20/2009
BLM19	Bureau of Land Management; Laguna Tonto	NM	32.6119	103.67956	11/15/2008	JSB2	Jemez Spring Baths	NM	35.7720047	106.6912172	7/20/2009
BLM20	Bureau of Land Management; Laguna Tonto	NM	32.61194	103.67937	11/15/2008	JSB3	Jemez Spring Baths	NM	35.7718497	106.6913356	7/20/2009
BLM21	Bureau of Land Management; Laguna Gatuna	NM	32.56469	103.69756	11/15/2008	JSB4	Jemez Spring Baths	NM	35.7720364	106.6908858	7/20/2009
BLM22	Bureau of Land Management; Laguna Gatuna	NM	32.56522	103.69743	11/15/2008	JSB5	Jemez Spring Baths	NM	35.7721553	106.6907667	7/20/2009
BLM23	Bureau of Land Management; Laguna Gatuna	NM	32.56545	103.6974	11/15/2008	NSS1	New Mexico Sulfur Springs	NM	35.9068656	106.6161508	7/20/2009
BLM24	Bureau of Land Management; Laguna Quatro	NM	32.34662	103.96127	11/15/2008	NSS2	New Mexico Sulfur Springs	NM	35.9068572	106.6160953	7/20/2009
BLM25	Bureau of Land Management; Laguna Quatro	NM	32.34661	103.96135	11/15/2008	NSS3	New Mexico Sulfur Springs	NM	35.907205	106.6163683	7/20/2009
BLM26	Bureau of Land Management; Laguna Walden	NM	32.33785	103.98898	11/15/2008	NSS4	New Mexico Sulfur Springs	NM	35.9073433	106.6161494	7/20/2009
BLM27	Bureau of Land Management; Laguna Uno	NM	32.37233	103.94394	11/15/2008	NSS5	New Mexico Sulfur Springs	NM	35.9076514	106.6160339	7/20/2009
SFB1	San Francisco Bay NWR	CA	37.49897	122.12807	2/9/2009	NSS6	New Mexico Sulfur Springs	NM	35.9077081	106.6158356	7/20/2009
SFB2	San Francisco Bay NWR	CA	37.4915	122.13855	2/9/2009	NSS7	New Mexico Sulfur Springs	NM	35.9080264	106.6156203	7/20/2009
SFB3	San Francisco Bay NWR	CA	37.49164	122.13852	2/9/2009	SLS1	Soda Lake Side	NM	35.9070136	106.6891994	7/20/2009
SFB4	San Francisco Bay NWR	CA	37.49031	122.14211	2/9/2009	SAC1	San Antonio cabin	NM	35.9709475	106.5620842	7/20/2009
SFB5	San Francisco Bay NWR	CA	37.49032	122.14176	2/9/2009	CLS1	Caribbean Lake Spring	NM	35.9173156	106.5944425	7/20/2009
SFB6	San Francisco Bay NWR	CA	37.47631	122.12467	2/9/2009	NGYS 1	Norris Geyser Yellowstone NP	WY	44.72662	110.70906	7/28/2009
SFB7	San Francisco Bay NWR	CA	37.47625	122.12459	2/9/2009	NGYS 2	Norris Geyser Yellowstone NP	WY	44.72662	110.70913	7/28/2009
SFB8	San Francisco Bay NWR	CA	37.47487	122.12618	2/9/2009	NGYS 3	Norris Geyser Yellowstone NP	WY	44.72283	110.71014	7/28/2009
SFB9	San Francisco Bay NWR	CA	37.46878	122.12448	2/9/2009	NGYS 4	Norris Geyser Yellowstone NP	WY	44.72792	110.71026	7/28/2009

Table 22 continued

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
SFB10	San Francisco Bay NWR	CA	37.46862	122.12439	2/9/2009	NGYS 5	Norris Geyser Yellowstone NP	WY	44.72792	110.71026	7/28/2009
SFB11	San Francisco Bay NWR	CA	37.46872	122.11977	2/9/2009	NGYS 6	Norris Geyser Yellowstone NP	WY	44.72854	110.71005	7/28/2009
SFB12	San Francisco Bay NWR	CA	37.48298	122.15121	2/9/2009	NGYS 7	Norris Geyser Yellowstone NP	WY	44.72896	110.71194	7/28/2009
SFB13	San Francisco Bay NWR	CA	37.48682	122.17701	2/9/2009	NGYS 8	Norris Geyser Yellowstone NP	WY	44.72866	110.71198	7/28/2009
SFB14	San Francisco Bay NWR	CA	37.4869	122.17385	2/9/2009	NGYS 9	Norris Geyser Yellowstone NP	WY	44.72866	110.71198	7/28/2009
SFB15	San Francisco Bay NWR	CA	37.48697	122.17388	2/9/2009	NGYS 10	Norris Geyser Yellowstone NP	WY	44.72964	110.71204	7/28/2009
SFB16	San Francisco Bay NWR	CA	37.49905	122.12796	2/9/2009	NGYS 11	Norris Geyser Yellowstone NP	WY	44.72973	110.71176	7/28/2009
SFB17	San Francisco Bay NWR	CA	37.52921	122.06172	2/9/2009	NGYS 12	Norris Geyser Yellowstone NP	WY	44.73168	110.71133	7/28/2009
SFB18	San Francisco Bay NWR	CA	37.53267	122.08501	2/9/2009	NGYS 13	Norris Geyser Yellowstone NP	WY	44.73204	110.71116	7/28/2009
SFB19	San Francisco Bay NWR	CA	37.53268	122.085	2/9/2009	NGYS 14	Norris Geyser Yellowstone NP	WY	44.73254	110.7098	7/28/2009
SFB20	San Francisco Bay NWR	CA	37.53262	122.08481	2/9/2009	NGYS 15	Norris Geyser Yellowstone NP	WY	44.73162	110.71006	7/28/2009
SFB21	San Francisco Bay NWR	CA	37.48841	122.97262	2/9/2009	NGYS 16	Norris Geyser Yellowstone NP	WY	44.73326	110.70973	7/28/2009
SFB22	San Francisco Bay NWR	CA	37.48462	121.96939	2/9/2009	NGYS 17	Norris Geyser Yellowstone NP	WY	44.73434	110.70752	7/28/2009
SFB23	San Francisco Bay NWR	CA	37.48465	121.96942	2/9/2009	NGYS 18	Norris Geyser Yellowstone NP	WY	44.73494	11070747	7/28/2009
SFB24	San Francisco Bay NWR	CA	37.4844	121.96524	2/9/2009	NGYS 19	Norris Geyser Yellowstone NP	WY	44.73506	110.70774	7/28/2009
SFB25	San Francisco Bay NWR	CA	37.48201	121.96414	2/9/2009	SMYS 1	Sentinel Meadows Yellowstone NP	WY	44.56115	110.83535	7/28/2009
SFB26	San Francisco Bay NWR	CA	37.48185	121.96413	2/9/2009	SMYS 2	Sentinel Meadows Yellowstone NP	WY	44.56111	110.83546	7/28/2009
SFB27	San Francisco Bay NWR	CA	37.48187	121.9644	2/9/2009	SMYS 3	Sentinel Meadows Yellowstone NP	WY	44.56145	110.8362	7/28/2009
SFB28	San Francisco Bay NWR	CA	37.48145	121.96882	2/9/2009	SMYS 4	Sentinel Meadows Yellowstone NP	WY	44.56166	110.83635	7/28/2009
SFB29	San Francisco Bay NWR	CA	37.48022	121.96863	2/9/2009	SMYS 5	Sentinel Meadows Yellowstone NP	WY	44.56174	110.83642	7/28/2009
SFB30	San Francisco Bay NWR	CA	37.4805	121.96908	2/9/2009	SMYS 6	Sentinel Meadows Yellowstone NP	WY	44.56191	110.83729	7/28/2009
SFB31	San Francisco Bay NWR	CA	37.44041	121.96094	2/9/2009	HVYS 1	Hidden Valley Yellowstone NP	WY	44.65135	110.48046	7/28/2009
SFB32	San Francisco Bay NWR	CA	37.44037	121.96169	2/9/2009	HVYS 2	Hidden Valley Yellowstone NP	WY	44.65135	110.48046	7/28/2009
SFB33	San Francisco Bay NWR	CA	37.43904	121.96181	2/9/2009	HVYS 3	Hidden Valley Yellowstone NP	WY	44.65138	110.4805	7/28/2009

Table 22 continued

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
SFB34	San Francisco Bay NWR	CA	37.43905	121.96183	2/9/2009	HVYS 4	Hidden Valley Yellowstone NP	WY	44.6513	110.48065	7/28/2009
Big1	Big Bend NP	TX	29.19979	102.91743	3/17/2009	HVYS 5	Hidden Valley Yellowstone NP	WY	44.65266	110.47659	7/28/2009
Big2	Big Bend NP	TX	29.20088	102.91495	3/17/2009	HVYS 6	Hidden Valley Yellowstone NP	WY	44.65281	110.48209	7/28/2009
Big3	Big Bend NP	TX	29.17961	102.99555	3/17/2009	HVYS 7	Hidden Valley Yellowstone NP	WY	44.65284	110.48273	7/28/2009
Big4	Big Bend NP	TX	29.17961	102.99555	3/17/2009	HVYS 8	Hidden Valley Yellowstone NP	WY	44.65284	110.48273	7/28/2009
Big5	Big Bend NP	TX	29.17961	102.99555	3/17/2009	HVYS 9	Hidden Valley Yellowstone NP	WY	44.65278	110.48329	7/28/2009
Big6	Big Bend NP	TX	29.17961	102.99555	3/17/2009	HVYS 10	Hidden Valley Yellowstone NP	WY	44.65329	110.48474	7/28/2009
Big7	Big Bend NP	TX	29.17961	102.99555	3/17/2009	HVYS 11	Hidden Valley Yellowstone NP	WY	44.65329	110.48474	7/28/2009
Big8	Big Bend NP	TX	29.18208	102.9924	3/17/2009	HVYS 12	Hidden Valley Yellowstone NP	WY	44.65381	110.47796	7/28/2009
Big9	Big Bend NP	TX	29.18208	102.9924	3/17/2009	WFYS 1	Whisky Flats Yellowstone NP	WY	44.5359	110.82634	7/28/2009
Big10	Big Bend NP	TX	29.18208	102.9924	3/17/2009	WFYS 2	Whisky Flats Yellowstone NP	WY	44.53521	110.82498	7/28/2009
Big11	Big Bend NP	TX	29.18209	102.99237	3/17/2009	FDYS 1	Firehole drive Yellowstone NP	WY	44.5467	110.81074	7/28/2009
Big12	Big Bend NP	TX	29.18213	102.99237	3/17/2009	FHYS 2	Firehole drive Yellowstone NP	WY	44.53413	110.7978	7/28/2009
Big13	Big Bend NP	TX	29.18215	102.99232	3/17/2009	FHYS 3	Firehole drive Yellowstone NP	WY	44.53406	110.79783	7/28/2009
Big14	Big Bend NP	TX	29.18216	102.99236	3/17/2009	FHYS 4	Firehole drive Yellowstone NP	WY	44.53282	110.79742	7/28/2009
Big15	Big Bend NP	TX	29.18218	102.99226	3/17/2009	FHYS 5	Firehole drive Yellowstone NP	WY	44.53279	110.79746	7/28/2009
Big16	Big Bend NP	TX	29.18218	102.9922	3/17/2009	FHYS 6	Firehole drive Yellowstone NP	WY	44.53346	110.79766	7/28/2009
Big17	Big Bend NP	TX	29.17718	103.00127	3/17/2009	STYS 1	Sulfatara Trail Yellowstone NP	WY	44.80024	110.72825	7/28/2009
Big18	Big Bend NP	TX	29.14979	103.00346	3/17/2009	STYS 2	Sulfatara Trail Yellowstone NP	WY	44.79937	110.72836	7/28/2009
Big19	Big Bend NP	TX	29.14979	103.00346	3/17/2009	STYS 3	Sulfatara Trail Yellowstone NP	WY	44.79937	110.72836	7/28/2009
Big20	Big Bend NP	TX	29.14979	103.00346	3/17/2009	SWRN1	Stillwater NWR	NV	39.59249	118.41799	8/6/2009
Big21	Big Bend NP	TX	29.14979	103.00346	3/17/2009	SWRN2	Stillwater NWR	NV	39.602	118.40915	8/6/2009
Big22	Big Bend NP	TX	29.14986	103.00404	3/17/2009	SWRN3	Stillwater NWR	NV	39.60254	118.39923	8/6/2009
Big23	Big Bend NP	TX	29.19839	102.91938	6/20/2009	GBS 1	Great Boiling Springs	NV	40.666261	119.36647	8/6/2009
Big24	Big Bend NP	TX	29.1998	102.91761	6/20/2009	GBS 2	Great Boiling Springs	NV	40.66254	119.36644	8/6/2009
Big25	Big Bend NP	TX	29.17942	102.95332	6/20/2009	GBS 3	Great Boiling Springs	NV	40.66244	119.36645	8/6/2009
Big26	Big Bend NP	TX	29.17955	102.99559	6/20/2009	GBS 4	Great Boiling Springs	NV	40.66136	119.36629	8/6/2009
Big27	Big Bend NP	TX	29.17955	102.99559	6/20/2009	GBS 5	Great Boiling Springs	NV	40.66134	119.36628	8/6/2009
OHS1	Ogden Hot Springs	UT	41.23589	111.924	4/27/2009	GBS 6	Great Boiling Springs	NV	40.66146	119.36621	8/6/2009
OHS2	Ogden Hot Springs	UT	41.23575	111.92481	4/27/2009	GBS 7	Great Boiling Springs	NV	40.66174	119.36606	8/6/2009
OHS3	Ogden Hot Springs	UT	41.23499	111.92708	4/27/2009	GBS 8	Great Boiling Springs	NV	40.66288	119.36649	8/6/2009
OHS4	Ogden Hot Springs	UT	41.23466	111.92745	4/27/2009	GBS 9	Great Boiling Springs	NV	40.66284	119.36681	8/6/2009

Table 22 continued

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
WHS1	Wilson Hot Springs	UT	39.90848	113.42739	4/27/2009	FRN 1	Fly Ranch	NV	40.86139	119.33281	8/6/2009
WHS2	Wilson Hot Springs	UT	39.90848	113.42734	4/27/2009	FRN 2	Fly Ranch	NV	40.86139	119.33281	8/6/2009
WHS3	Wilson Hot Springs	UT	39.90848	113.42734	4/27/2009	FRN 3	Fly Ranch	NV	40.8592	119.33195	8/6/2009
WHS4	Wilson Hot Springs	UT	39.90782	113.42729	4/27/2009	FRN 4	Fly Ranch	NV	40.85928	119.3318	8/6/2009
WHS5	Wilson Hot Springs	UT	39.90784	113.42738	4/27/2009	FRN 5	Fly Ranch	NV	40.85906	119.3337	8/6/2009
WHS6	Wilson Hot Springs	UT	39.90754	113.42929	4/27/2009	CBHS 1	Buckeye Hot Spring	CA	38.23951	119.32615	8/6/2009
WHS7	Wilson Hot Springs	UT	39.9074	113.42937	4/27/2009	CBHS 2	Buckeye Hot Spring	CA	38.23949	119.3262	8/6/2009
WHS8	Wilson Hot Springs	UT	39.90698	113.43097	4/27/2009	CBHS 3	Buckeye Hot Spring	CA	38.2391	119.32531	8/6/2009
WHS9	Wilson Hot Springs	UT	39.90676	113.43084	4/27/2009	CBHS 4	Buckeye Hot Spring	CA	38.2391	119.32531	8/6/2009
WHS10	Wilson Hot Springs	UT	39.90662	113.43079	4/27/2009	MLNB 1	Mono Lake Navy Beach	CA	37.941	119.02295	8/6/2009
WHS11	Wilson Hot Springs	UT	39.9065	113.43108	4/27/2009	MLNB 2	Mono Lake Navy Beach	CA	37.941	119.02295	8/6/2009
WHS12	Wilson Hot Springs	UT	39.90622	113.43146	4/27/2009	MLNB 3	Mono Lake Navy Beach	CA	37.941	119.02295	8/6/2009
WHS13	Wilson Hot Springs	UT	39.90591	113.432	4/27/2009	MLNB 4	Mono Lake Navy Beach	CA	37.94112	119.02205	8/6/2009
WHS14	Wilson Hot Springs	UT	39.90432	113.43264	4/27/2009	MLNB 5	Mono Lake Navy Beach	CA	37.94109	119.02017	8/6/2009
FS1	Fish Springs NWR	UT	39.88738	113.41326	4/27/2009	MLIS 1	Mono Lake Island Hot Springs (Paoha Island)	CA	37.9937	119.02366	8/6/2009
FS2	Fish Springs NWR	UT	39.88738	113.41319	4/27/2009	MLIS 2	Mono Lake Island Hot Springs (Paoha Island)	CA	37.99368	119.02367	8/6/2009
FS3	Fish Springs NWR	UT	39.88726	113.4127	4/27/2009	MLIS 3	Mono Lake Island Hot Springs (Paoha Island)	CA	37.99395	119.02338	8/6/2009
FS4	Fish Springs NWR	UT	39.8872	113.41269	4/27/2009	MLIS 4	Mono Lake Island Hot Springs (Paoha Island)	CA	37.99391	119.02356	8/6/2009
FS5	Fish Springs NWR	UT	39.88767	113.41215	4/27/2009	MLIS 5	Mono Lake Island Hot Springs (Paoha Island)	CA	37.99387	119.02359	8/6/2009
FS6	Fish Springs NWR	UT	39.88186	113.37465	4/27/2009	MLIS 6	Mono Lake Island Hot Springs (Paoha Island)	CA	37.98822	119.02663	8/6/2009
FS7	Fish Springs NWR	UT	39.88233	113.38259	4/27/2009	MLIS 7	Mono Lake Island Hot Springs (Paoha Island)	CA	37.95632	119.05291	8/6/2009
FS8	Fish Springs NWR	UT	39.88233	113.38259	4/27/2009	HCMA 1	Hot Creek at Mammoth	CA	37.66052	118.82903	8/6/2009
FS9	Fish Springs NWR	UT	39.88338	113.38981	4/27/2009	HCMA 2	Hot Creek at Mammoth	CA	37.66096	118.82895	8/6/2009
FS10	Fish Springs NWR	UT	39.88343	113.38999	4/27/2009	HCMA 3	Hot Creek at Mammoth	CA	37.6613	118.82877	8/6/2009
FS11	Fish Springs NWR	UT	39.85957	113.37751	4/27/2009	HCMA 4	Hot Creek at Mammoth	CA	37.6613	118.82876	8/6/2009

Table 22 continued

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
FS12	Fish Springs NWR	UT	39.8594	113.3778	4/27/2009	HCMA 5	Hot Creek at Mammoth	CA	37.66139	118.8286	8/6/2009
FS13	Fish Springs NWR	UT	39.85908	113.37823	4/27/2009	OLCA 1	Owens Lake (dry lake)	CA	36.40028	117.95216	8/6/2009
FS14	Fish Springs NWR	UT	39.84984	113.39555	4/27/2009	OLCA 2	Owens Lake (dry lake)	CA	36.37568	117.97728	8/6/2009
FS15	Fish Springs NWR	UT	39.81984	113.39522	4/27/2009	OLCA 3	Owens Lake (dry lake)	CA	36.35583	117.98262	8/6/2009
FS16	Fish Springs NWR	UT	39.83228	113.39167	4/27/2009	HBSP1	Hapuna Beach SP	HI	19.9908836	155.824769	5/4/2010
FS17	Fish Springs NWR	UT	39.83407	113.3907	4/27/2009	HBSP2	Hapuna Beach SP	HI	19.9916382	155.82614	5/4/2010
FS18	Fish Springs NWR	UT	39.83421	113.38833	4/27/2009	HBSP3	Hapuna Beach SP	HI	19.994819	155.825956	5/4/2010
FS19	Fish Springs NWR	UT	39.8342	113.38831	4/27/2009	APHW1	Alchiline ponds	HI	19.852757	155.9272626	5/4/2010
FS20	Fish Springs NWR	UT	39.84161	113.39196	4/27/2009	APHW2	Alchiline ponds	HI	19.8527848	155.92725	5/4/2010
Topas 1	West Topas	UT	39.4564	112.79061	4/27/2009	APHW3	Alchiline ponds	HI	19.8948557	155.9018	5/4/2010
AHS1	Abraham Hot Springs	UT	39.61189	112.72747	4/27/2009	APHW4	Alchiline ponds	HI	19.8948466	155.9018	5/4/2010
AHS2	Abraham Hot Springs	UT	39.61205	112.72751	4/27/2009	NELH1	Natural Energy Lab Hawaii	HI	19.731411	156.0565463	5/4/2010
AHS3	Abraham Hot Springs	UT	39.61255	112.72929	4/27/2009	NELH2	Natural Energy Lab Hawaii	HI	19.731298	156.056777	5/4/2010
AHS4	Abraham Hot Springs	UT	39.61255	112.7293	4/27/2009	NELH3	Natural Energy Lab Hawaii	HI	19.731298	156.056777	5/4/2010
AHS5	Abraham Hot Springs	UT	39.61255	112.7293	4/27/2009	NELH4	Natural Energy Lab Hawaii	HI	19.73127	156.056777	5/4/2010
BHS1	Baker Hot Springs	UT	39.61139	112.72996	4/27/2009	KKHW1	Kekahi Kai State Park	HI	19.7812468	156.0424609	5/4/2010
BHS2	Baker Hot Springs	UT	39.61136	112.72992	4/27/2009	KKHW2	Kekahi Kai State Park	HI	19.7810034	156.04193	5/4/2010
BHS3	Baker Hot Springs	UT	39.61113	112.72962	4/27/2009	KKHW3	Kekahi Kai State Park	HI	19.7810410	156.042026	5/4/2010
BHS4	Baker Hot Springs	UT	39.6111	112.72944	4/27/2009	KKHW4	Kekahi Kai State Park	HI	19.7811572	156.041957	5/4/2010
BHS5	Baker Hot Springs	UT	39.6111	112.72943	4/27/2009	KKHW5	Kekahi Kai State Park	HI	19.780491	156.0420647	5/4/2010
BHS6	Baker Hot Springs	UT	39.61107	112.72939	4/27/2009	ONHW1	Onekahakaha Beach park	HI	19.7372015	155.0375515	5/11/2010
BHS7	Baker Hot Springs	UT	39.6111	112.72944	4/27/2009	ONHW2	Onekahakaha Beach park	HI	19.7372015	155.0375515	5/11/2010
BHS8	Baker Hot Springs	UT	39.61097	112.72937	4/27/2009	ONHW3	Onekahakaha Beach park	HI	19.7372015	155.0375515	5/11/2010
BHS9	Baker Hot Springs	UT	39.61104	112.7293	4/27/2009	ONHW4	Onekahakaha Beach park	HI	19.7372015	155.0375515	5/11/2010
BHS10	Baker Hot Springs	UT	39.61104	112.7293	4/27/2009	WRHW1	Wailoa River State Park	HI	19.7171918	155.037303	5/11/2010
BHS11	Baker Hot Springs	UT	39.61066	112.73028	4/27/2009	AFHW1	Akaka Falls State Park	HI	19.855835	155.039079	5/11/2010
AI1	Antelope Island	UT	41.05686	112.25206	5/4/2009	AFHW2	Akaka Falls State Park	HI	19.853698	155.0390523	5/11/2010

Table 22 continued

Sample Name	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*	*Sample Name*	*Site Name*	*State*	*Latitude (N)*	*Longitude (W)*	*Trip Date*
AI2	Antelope Island	UT	41.057	112.25059	5/4/2009	AFHW3	Akaka Falls State Park	HI	19.8537278	155.0390526	5/11/2010
AI3	Antelope Island	UT	41.07565	112.22187	5/4/2009	CPHW1	Carlsmith County Park	HI	19.7349488	155.0139037	5/11/2010
AI4	Antelope Island	UT	41.07493	122.22114	5/4/2009	CPHW2	Carlsmith County Park	HI	19.7360199	155.0134403	5/11/2010
GSL1	Great Salt Lake	UT	40.69574	111.9491	5/4/2009	CPHW3	Carlsmith County Park	HI	19.7352555	155.0131349	5/11/2010
GSL2	Great Salt Lake	UT	40.73554	112.21073	5/4/2009	CPHW4	Carlsmith County Park	HI	19.7352278	155.0131918	5/11/2010

APPENDIX D

Table 23 Fermentation performance metrics for all samples screened in the carboxylate platform. Methods listed in Chapter II. Additional sample data is listed in Appendix B: Table 21 and Appendix C: Table 23. Change in acid concentration here is listed as total acid concentration in the text, as well as in the figures and tables in Appendix A.

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
LSDR T1-0	La Sal del Rey	A02	77.26	40.59	14.77	11.77	7.45	0.30	3.77	0.25	0.00	0.00	0.26	0.50	0.13
LSDR T1-65	La Sal del Rey	A03	71.48	27.46	11.15	9.85	7.87	0.30	1.68	0.00	0.00	0.00	0.18	0.61	0.11
LSDR T1-130	La Sal del Rey	A04	75.78	36.89	12.18	10.18	7.31	0.38	2.54	0.00	0.00	0.00	0.22	0.51	0.11
LSDR T1-195	La Sal del Rey	A05	73.19	30.04	14.46	11.34	6.72	0.47	4.15	0.00	0.00	0.00	0.24	0.50	0.12
LSDR T1-260	La Sal del Rey	A06	75.89	36.34	11.74	9.55	6.29	0.44	2.74	0.08	0.00	0.00	0.20	0.53	0.10
LSDR T1-325	La Sal del Rey	A07	75.61	35.56	14.54	11.63	7.31	0.53	3.71	0.08	0.00	0.00	0.18	0.70	0.13
LSDR T1-390	La Sal del Rey	A08	74.14	31.64	12.37	10.28	7.17	0.32	2.78	0.00	0.00	0.00	0.25	0.44	0.11
LSDR T1-455	La Sal del Rey	A09	75.68	37.13	13.92	11.71	8.44	0.40	2.76	0.11	0.00	0.00	0.18	0.73	0.13
LSDR T1-520	La Sal del Rey	A10	75.38	32.31	8.64	7.63	6.11	0.26	1.27	0.00	0.00	0.00	0.14	0.59	0.08
LSDR T1-585	La Sal del Rey	A11	76.94	32.60	11.86	9.85	6.93	0.27	2.56	0.10	0.00	0.00	0.20	0.54	0.11
LSDR T2-0	La Sal del Rey	A12	78.61	42.22	4.91	4.13	2.95	0.16	1.02	0.00	0.00	0.00	0.13	0.35	0.05
LSDR T2-65	La Sal del Rey	A13	76.82	32.14	8.60	7.01	5.40	0.27	1.65	0.00	0.00	0.00	0.10	0.78	0.08
LSDR T2-130	La Sal del Rey	A14	72.33	27.88	9.49	8.17	6.19	0.40	1.48	0.00	0.00	0.09	0.19	0.48	0.09
LSDR T2-95	La Sal del Rey	A15	72.64	31.56	8.60	6.84	4.19	0.37	2.27	0.00	0.00	0.00	0.17	0.45	0.07
LSDR T2-260	La Sal del Rey	A16	68.94	24.49	8.05	6.75	4.82	0.28	1.54	0.11	0.00	0.00	0.10	0.76	0.07
LSDR T2-325	La Sal del Rey	A17	70.50	29.12	8.12	6.82	4.81	0.39	1.61	0.00	0.00	0.00	0.13	0.58	0.07
LSDR T2-390	La Sal del Rey	A18	72.31	24.81	14.47	11.27	6.74	0.69	3.24	0.34	0.00	0.27	0.14	0.87	0.12

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Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
LSDR T2-455	La Sal del Rey	A19	72.67	25.16	11.37	9.25	6.12	0.36	2.72	0.06	0.00	0.00	0.16	0.64	0.10
LSDR T3-0	La Sal del Rey	A20	77.17	37.05	13.28	11.39	8.53	0.48	2.25	0.12	0.00	0.00	0.13	0.97	0.13
LSDR T3-65	La Sal del Rey	A21	73.39	29.08	6.60	5.14	3.22	0.00	1.59	0.08	0.10	0.14	0.13	0.43	0.06
LSDR T3-130	La Sal del Rey	A22	73.91	29.29	11.39	9.70	7.16	0.43	2.03	0.08	0.00	0.00	0.07	1.58	0.11
LSDR T3-195	La Sal del Rey	A23	67.04	20.39	15.92	12.79	8.44	0.48	3.36	0.19	0.00	0.32	0.09	1.65	0.14
LSDR T3-260	La Sal del Rey	A24	73.45	29.76	11.45	9.45	6.45	0.47	2.44	0.09	0.00	0.00	0.05	2.02	0.10
LSDR T3-325	La Sal del Rey	A25	73.14	31.74	14.54	11.98	8.27	0.44	2.95	0.32	0.00	0.00	0.15	0.87	0.13
LSDR T3-390	La Sal del Rey	A26	71.99	28.87	11.45	9.17	5.76	0.44	2.91	0.06	0.00	0.00	0.14	0.72	0.10
LSDR T3-455	La Sal del Rey	A27	77.77	38.36	13.28	11.57	8.93	0.59	1.96	0.08	0.00	0.00	0.14	0.92	0.13
GR1	Grulla Lake	D01	28.87	8.07	5.48	4.69	3.48	0.27	0.85	0.09	0.00	0.00	0.20	0.26	0.05
GR2	Grulla	D02	25.15	6.90	0.10	0.09	0.06	0.01	0.02	0.00	0.00	0.00	0.22	0.00	0.00
GR3	Grulla	D03	24.84	9.90	1.05	0.88	0.63	0.04	0.19	0.01	0.00	0.00	0.19	0.05	0.01
GR4	Grulla	D04	27.90	8.96	5.54	4.62	3.23	0.29	1.04	0.07	0.00	0.00	0.27	0.19	0.05
GR5	Grulla	D05	25.99	6.39	6.66	5.51	3.79	0.29	1.34	0.09	0.00	0.00	0.17	0.36	0.06
GR6	Grulla	D06	25.25	7.00	2.78	2.28	1.55	0.11	0.59	0.04	0.00	0.00	0.22	0.12	0.03
GR7	Grulla	D07	25.51	8.71	4.10	3.43	2.41	0.19	0.77	0.06	0.00	0.00	0.22	0.17	0.04
GR8	Grulla	D08	28.97	4.67	2.36	1.92	1.26	0.10	0.51	0.03	0.01	0.00	0.23	0.09	0.02
GR9	Grulla	D09	28.03	5.96	4.04	3.37	2.38	0.18	0.76	0.05	0.00	0.00	0.24	0.16	0.04
GR10	Grulla	D10	30.66	9.76	-1.55	-1.27	-0.84	-0.07	-0.33	-0.02	-0.01	0.00	0.21	-0.07	-0.01
GR11	Grulla	D11	27.60	7.40	3.35	2.74	1.83	0.16	0.69	0.05	0.01	0.00	0.30	0.10	0.03
GR12	Grulla	D12	23.86	7.70	3.22	2.64	1.77	0.13	0.69	0.04	0.00	0.00	0.23	0.13	0.03
MPL1 R	Muleshoe Pauls Lake	D13	26.77	8.97	4.39	3.64	2.53	0.18	0.87	0.06	0.00	0.00	0.21	0.19	0.04
MPL2 R	Muleshoe Pauls Lake	D14	31.42	8.04	2.88	2.38	1.62	0.13	0.58	0.04	0.00	0.00	0.22	0.12	0.03
MPL3 R	Muleshoe Pauls Lake	D15	16.39	4.19	2.55	2.11	1.46	0.12	0.50	0.04	0.00	0.00	0.22	0.11	0.02
MPL4 R	Muleshoe Pauls Lake	D16	18.34	4.88	3.31	2.73	1.85	0.15	0.68	0.04	0.00	0.00	0.29	0.11	0.03
MPL5 R	Muleshoe Pauls Lake	D17	15.63	4.32	1.69	1.40	0.95	0.08	0.34	0.02	0.00	0.00	0.30	0.05	0.02

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
MPL6 R	Muleshoe Pauls Lake	D18	15.85	3.34	2.18	1.82	1.26	0.11	0.43	0.02	0.00	0.00	0.32	0.06	0.02
MPL7 R	Muleshoe Pauls Lake	D19	18.76	4.63	2.31	1.92	1.33	0.10	0.46	0.03	0.00	0.00	0.28	0.08	0.02
MPL8 R	Muleshoe Pauls Lake	D20	21.46	3.92	1.20	1.00	0.69	0.06	0.23	0.01	0.00	0.00	0.20	0.06	0.01
MPL9 L	Muleshoe Pauls Lake	D21	39.55	9.83	-0.37	-0.31	-0.21	-0.02	-0.07	0.00	0.00	0.00	0.24	-0.01	0.00
MWL1 R	Muleshoe White Lake	D22	21.45	6.04	3.26	2.86	2.25	0.13	0.48	0.01	0.00	0.00	0.30	0.11	0.03
MWL 2 R	Muleshoe White Lake	D23	23.09	6.83	2.47	2.06	1.44	0.11	0.48	0.03	0.00	0.00	0.14	0.17	0.02
MWL3 R	Muleshoe White Lake	D24	13.75	3.15	2.90	2.41	1.68	0.13	0.57	0.04	0.00	0.00	0.18	0.15	0.03
MWL4 R	Muleshoe White Lake	D25	32.55	10.24	2.02	1.68	1.17	0.10	0.39	0.03	0.00	0.00	0.21	0.09	0.02
MGL1 R	Muleshoe Goose Lake	D26	27.35	11.94	4.75	3.96	2.78	0.20	0.91	0.07	0.00	0.00	0.18	0.24	0.04
MGL2 R	Muleshoe Goose Lake	D27	21.32	10.66	3.36	2.80	1.96	0.13	0.68	0.04	0.00	0.00	0.13	0.24	0.03
MGL3 R	Muleshoe Goose Lake	D28	16.80	4.59	2.61	2.16	1.48	0.11	0.53	0.04	0.00	0.00	0.13	0.18	0.02
MGL4 R	Muleshoe Goose Lake	D29	26.98	12.15	3.08	2.53	1.71	0.12	0.66	0.04	0.00	0.00	0.23	0.12	0.03
MGL5 L	Muleshoe Goose Lake	D30	32.38	15.20	2.92	2.43	1.71	0.09	0.59	0.04	0.00	0.00	0.17	0.16	0.03
Galveston	Control	D31	19.50	0.37	6.98	5.88	4.23	0.27	1.30	0.07	0.00	0.00	0.19	0.34	0.07
GSP1	Great Salt Plains	E01	14.72	1.19	5.06	4.32	3.16	0.28	0.86	0.02	0.00	0.00	0.23	0.21	0.05
GSP2	Great Salt Plains	E02	16.14	0.69	0.43	0.36	0.26	0.02	0.08	0.00	0.00	0.00	0.22	0.02	0.00
GSP3	Great Salt Plains	E03	23.30	1.72	2.67	2.21	1.53	0.09	0.55	0.03	0.00	0.00	0.19	0.13	0.02
GSP4	Great Salt Plains	E04	18.88	1.37	0.52	0.44	0.31	0.02	0.11	0.00	0.00	0.00	0.16	0.03	0.00
GSP5	Great Salt Plains	E05	20.91	1.92	2.41	2.05	1.49	0.11	0.43	0.01	0.00	0.00	0.25	0.09	0.02
GSP6	Great Salt Plains	E06	21.67	1.89	4.24	3.58	2.58	0.19	0.77	0.04	0.00	0.00	0.20	0.20	0.04
GSP7	Great Salt Plains	E07	29.45	3.03	5.02	4.25	3.07	0.20	0.97	0.00	0.00	0.00	0.23	0.21	0.05
GSP8	Great Salt Plains	E08	19.39	1.13	5.54	4.62	3.23	0.29	1.04	0.07	0.00	0.00	0.27	0.19	0.05
GSP9	Great Salt Plains	E09	6.78	3.77	2.77	2.34	1.68	0.12	0.52	0.02	0.00	0.00	0.21	0.12	0.03
GSP10	Great Salt Plains	E10	52.47	15.32	4.56	3.84	2.76	0.19	0.83	0.06	0.00	0.00	0.23	0.19	0.04
GSP11	Great Salt Plains	E11	56.38	16.60	1.82	1.54	1.12	0.07	0.34	0.02	0.00	0.00	0.17	0.10	0.02
Galveston	Control	E12	19.50	0.37	-0.22	-0.18	-0.13	-0.01	-0.04	0.00	0.00	0.00	0.20	-0.01	0.00
Bra11	Brazoria NWR	F01	61.99	21.05	4.13	3.44	2.39	0.23	0.75	0.07	0.00	0.00	0.34	0.11	0.04
Bra21	Brazoria NWR	F02	54.97	11.94	5.19	4.33	3.03	0.20	1.05	0.05	0.00	0.00	0.38	0.12	0.05

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
Bra31	Brazoria NWR	F03	30.94	5.94	3.76	3.14	2.20	0.18	0.70	0.06	0.00	0.00	0.29	0.12	0.03
Bra41	Brazoria NWR	F04	39.20	6.25	2.09	1.75	1.25	0.08	0.43	0.00	0.00	0.00	0.32	0.06	0.02
Bra51	Brazoria NWR	F05	25.35	2.48	1.36	1.15	0.83	0.06	0.25	0.01	0.00	0.00	0.36	0.04	0.01
Bra61	Brazoria NWR	F06	21.11	4.14	6.01	5.03	3.56	0.25	1.12	0.09	0.00	0.00	0.35	0.16	0.06
Bra71	Brazoria NWR	F07	52.84	6.82	0.51	0.44	0.32	0.02	0.09	0.00	0.00	0.00	0.28	0.02	0.00
Bra81	Brazoria NWR	F08	27.46	5.75	0.37	0.31	0.22	0.02	0.07	0.01	0.00	0.00	0.30	0.01	0.00
Bra91	Brazoria NWR	F09	47.97	9.54	5.72	4.83	3.49	0.22	1.06	0.06	0.00	0.00	0.40	0.13	0.05
C. therm.	Control	F20	N/D	N/D	1.84	1.20	0.91	0.08	0.21	0.00	0.00	0.00	0.12	0.45	0.05
Galveston	Control	F21	19.50	0.37	2.76	1.77	1.31	0.08	0.37	0.01	0.00	0.00	0.15	0.53	0.08
Bra12	Brazoria NWR	F22	39.11	14.26	1.66	1.07	0.79	0.07	0.20	0.01	0.00	0.00	0.17	0.27	0.05
Bra22	Brazoria NWR	F23	52.65	13.65	2.55	1.64	1.21	0.10	0.33	0.01	0.00	0.00	0.24	0.30	0.07
Bra32	Brazoria NWR	F24	28.69	6.00	1.12	0.73	0.55	0.05	0.13	0.00	0.00	0.00	0.11	0.29	0.03
Bra42	Brazoria NWR	F25	39.13	8.60	0.88	0.57	0.41	0.04	0.12	0.00	0.00	0.00	0.04	0.72	0.03
Bra52	Brazoria NWR	F26	19.07	2.74	0.74	0.48	0.36	0.03	0.09	0.00	0.00	0.00	0.08	0.25	0.02
Bra62	Brazoria NWR	F27	17.50	5.95	1.06	0.69	0.53	0.04	0.13	0.00	0.00	0.00	0.10	0.30	0.03
Bra72	Brazoria NWR	F28	31.31	6.47	2.07	1.34	1.00	0.09	0.25	0.00	0.00	0.00	0.06	0.91	0.06
Bra82	Brazoria NWR	F29	19.25	7.29	2.14	1.39	1.05	0.09	0.23	0.02	0.00	0.00	0.06	0.95	0.06
Bra92	Brazoria NWR	F30	32.16	7.88	1.12	0.73	0.54	0.05	0.13	0.00	0.00	0.00	0.04	0.86	0.03
Bra13	Brazoria NWR	F31	43.88	14.80	2.02	1.31	0.99	0.07	0.24	0.01	0.00	0.00	0.19	0.12	0.02
Bra23	Brazoria NWR	F32	44.07	9.87	3.40	2.20	1.69	0.12	0.39	0.00	0.00	0.00	0.16	0.23	0.04
Bra33	Brazoria NWR	F33	25.78	6.49	3.06	2.00	1.58	0.11	0.31	0.01	0.00	0.00	0.26	0.13	0.03
Bra43	Brazoria NWR	F34	27.39	13.91	2.35	1.53	1.18	0.07	0.27	0.00	0.00	0.00	0.27	0.10	0.03
Bra53	Brazoria NWR	F35	15.08	2.78	3.95	2.54	1.92	0.14	0.46	0.02	0.00	0.00	0.25	0.18	0.04
Bra63	Brazoria NWR	F36	11.31	4.43	3.46	2.26	1.76	0.16	0.34	0.00	0.00	0.00	0.02	1.62	0.04
Bra73	Brazoria NWR	F37	31.26	9.20	2.75	1.79	1.37	0.12	0.30	0.00	0.00	0.00	0.02	1.37	0.03
Bra83	Brazoria NWR	F38	14.19	35.76	3.70	2.42	1.97	0.09	0.37	0.00	0.00	0.00	0.08	0.51	0.04
Bra93	Brazoria NWR	F39	40.90	10.99	3.11	2.02	1.56	0.10	0.35	0.01	0.00	0.00	0.06	0.59	0.03
Galveston	Control	F40	19.50	0.55	2.73	1.77	1.35	0.13	0.29	0.00	0.00	0.00	0.06	0.56	0.03
Bra14	Brazoria NWR	F401	29.79	5.40	1.02	0.85	0.62	0.05	0.17	0.01	0.00	0.00	0.06	0.24	0.01
Bra24	Brazoria NWR	F402	38.42	7.45	3.81	3.18	2.40	0.16	0.57	0.04	0.00	0.00	0.07	0.74	0.05

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
Bra34	Brazoria NWR	F403	32.72	5.50	2.92	2.44	1.93	0.14	0.35	0.02	0.00	0.00	0.05	0.80	0.04
Bra44	Brazoria NWR	F404	21.71	2.85	3.04	2.56	1.87	0.14	0.53	0.01	0.00	0.00	0.07	0.59	0.04
Bra54	Brazoria NWR	F405	29.40	4.52	3.24	2.74	2.12	0.16	0.44	0.02	0.00	0.00	0.06	0.72	0.05
Bra64	Brazoria NWR	F406	20.44	4.29	0.06	0.05	0.04	0.00	0.01	0.00	0.00	0.00	0.07	0.01	0.00
Bra74	Brazoria NWR	F407	31.58	4.52	4.33	3.69	2.78	0.23	0.69	0.00	0.00	0.00	0.08	0.79	0.06
Bra84	Brazoria NWR	F408	20.01	4.06	4.33	3.65	2.81	0.20	0.63	0.00	0.00	0.00	0.09	0.63	0.06
Bra94	Brazoria NWR	F409	43.72	7.59	5.30	4.48	3.35	0.26	0.80	0.07	0.00	0.00	0.14	0.52	0.07
No Inoculum	Control	F41	N/D	N/D	0.04	0.03	0.02	0.00	0.00	0.00	0.00	0.00	0.01	0.06	0.00
Galveston	Control	F410	15.85	0.69	N/D	6.43	4.94	0.36	1.10	0.03	0.00	0.00	0.13	0.81	0.10
No Inoculum	Control	F411	N/D	N/D	N/D	1.09	0.81	0.07	0.21	0.00	0.00	0.00	0.03	0.54	0.02
No Inoculum	Control	F412	N/D	N/D	N/D	1.49	1.15	0.10	0.24	0.00	0.00	0.00	0.04	0.69	0.02
BL1	Bitter Lake NWR	G01	53.71	9.27	3.93	3.33	2.42	0.18	0.70	0.02	0.00	0.01	0.19	0.19	0.04
BL2	Bitter Lake NWR	G02	54.20	11.24	2.76	2.30	1.59	0.15	0.52	0.03	0.00	0.00	0.17	0.15	0.03
BL3	Bitter Lake NWR	G03	52.33	10.22	5.88	4.92	3.48	0.25	1.07	0.12	0.00	0.00	0.18	0.30	0.05
BL4	Bitter Lake NWR	G04	45.17	5.39	3.39	2.86	2.06	0.15	0.59	0.05	0.00	0.00	0.17	0.19	0.03
BL5	Bitter Lake NWR	G05	38.95	6.50	4.15	3.44	2.37	0.21	0.78	0.08	0.00	0.00	0.15	0.25	0.04
Galveston	Control	G06	18.23	1.15	6.35	5.39	3.93	0.30	1.12	0.00	0.00	0.04	0.16	0.37	0.06
BL7	Bitter Lake NWR	G07	46.86	10.52	5.63	4.87	3.72	0.25	0.76	0.14	0.00	0.00	0.33	0.16	0.05
BL8	Bitter Lake NWR	G08	61.88	11.71	11.17	9.14	6.13	0.40	2.50	0.11	0.00	0.00	0.36	0.28	0.10
BL9	Bitter Lake NWR	G09	42.86	8.95	9.93	8.50	6.58	0.48	1.34	0.20	0.00	0.00	0.32	0.30	0.09
BL10	Bitter Lake NWR	G10	62.89	14.51	4.85	4.17	2.91	0.21	0.97	0.00	0.00	0.00	0.25	0.19	0.05
BL11	Bitter Lake NWR	G11	47.28	6.45	3.55	2.93	2.08	0.14	0.65	0.08	0.00	0.00	0.13	0.26	0.03
BL12	Bitter Lake NWR	G12	30.80	6.58	5.64	4.81	3.47	0.32	0.95	0.06	0.00	0.00	0.26	0.20	0.05
BL13	Bitter Lake NWR	G13	40.14	6.69	5.99	4.97	3.41	0.29	1.26	0.01	0.00	0.00	0.36	0.15	0.06
BL14	Bitter Lake NWR	G14	54.96	7.40	5.69	4.77	3.37	0.28	1.04	0.07	0.00	0.00	0.23	0.23	0.05
BL15	Bitter Lake NWR	G15	48.17	10.77	4.12	3.48	2.54	0.16	0.72	0.07	0.00	0.00	0.25	0.15	0.04
BL16	Bitter Lake NWR	G16	42.05	10.72	8.37	6.99	4.92	0.39	1.52	0.16	0.00	0.00	0.19	0.42	0.08

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
BL17	Bitter Lake NWR	G17	36.91	7.76	2.57	2.18	1.60	0.11	0.43	0.04	0.00	0.00	0.26	0.09	0.02
BL18	Bitter Lake NWR	G18	52.01	17.91	3.86	3.23	2.30	0.17	0.68	0.08	0.00	0.00	0.23	0.15	0.04
BL19	Bitter Lake NWR	G19	37.29	5.77	4.66	3.85	2.63	0.19	1.00	0.04	0.00	0.00	0.35	0.12	0.04
BL20	Bitter Lake NWR	G20	52.89	10.40	3.17	2.65	1.87	0.12	0.59	0.06	0.00	0.00	0.24	0.12	0.03
BL21	Bitter Lake NWR	G21	42.99	11.65	2.56	2.09	1.43	0.10	0.47	0.05	0.01	0.04	0.34	0.07	0.02
LL1	Bottomless Lake State Park; Lazy Lagoon	G22	41.36	9.30	7.91	6.65	4.67	0.48	1.46	0.05	0.00	0.00	0.30	0.25	0.07
LL2	Bottomless Lake State Park; Lazy Lagoon	G23	39.42	10.07	10.34	8.46	5.63	0.44	2.36	0.04	0.00	0.00	0.38	0.25	0.09
LL3	Bottomless Lake State Park; Lazy Lagoon	G24	44.56	9.17	7.96	6.61	4.60	0.27	1.65	0.08	0.00	0.00	0.34	0.22	0.07
LL4	Bottomless Lake State Park; Lazy Lagoon	G25	36.32	9.20	3.12	2.60	1.85	0.09	0.60	0.06	0.00	0.00	0.22	0.13	0.03
Lea1	Bottomless Lake State Park; Lea Lake	G26	28.77	5.36	3.68	3.09	2.22	0.15	0.67	0.06	0.00	0.00	0.27	0.12	0.03
BLM1	Bureau of Land Management; William Sink	G27	18.77	2.20	3.71	3.07	2.11	0.18	0.71	0.07	0.00	0.00	0.21	0.16	0.03
BLM2	Bureau of Land Management; William Sink	G28	21.38	5.19	4.90	4.16	3.04	0.19	0.89	0.05	0.00	0.00	0.27	0.17	0.05
BLM3	Bureau of Land Management; William Sink	G29	17.29	2.61	3.79	3.14	2.17	0.18	0.72	0.07	0.00	0.00	0.19	0.18	0.03
BLM4	Bureau of Land Management; William Sink	G30	16.86	6.42	4.48	3.75	2.66	0.17	0.85	0.08	0.00	0.00	0.22	0.19	0.04
BLM5	Bureau of Land Management; Laguna Tuston	G31	20.62	8.11	4.93	4.02	2.69	0.17	1.04	0.10	0.00	0.01	0.14	0.32	0.04
BLM6	Bureau of Land Management; Laguna Tuston	G32	32.39	7.60	3.55	2.97	2.12	0.12	0.68	0.05	0.00	0.00	0.18	0.18	0.03
BLM7	Bureau of Land Management; Laguna Tuston	G33	48.70	12.73	4.08	3.33	2.24	0.17	0.84	0.08	0.00	0.00	0.18	0.20	0.04
BLM8	Bureau of Land Management; Laguna Tuston	G34	16.78	47.90	5.70	4.70	3.22	0.20	1.16	0.11	0.00	0.00	0.29	0.16	0.05
BLM9	Bureau of Land Management; Laguna Plata	G35	6.89	2.87	3.22	2.71	1.94	0.14	0.60	0.04	0.00	0.00	0.18	0.17	0.03

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
BLM10	Bureau of Land Management; Laguna Plata	G36	18.04	3.83	5.08	4.29	3.09	0.24	0.92	0.04	0.00	0.00	0.18	0.27	0.05
BLM11	Bureau of Land Management; Laguna Plata	G37	14.80	1.95	4.02	3.34	2.32	0.18	0.76	0.07	0.00	0.00	0.12	0.31	0.04
BLM12	Bureau of Land Management; Laguna Plata	G38	21.31	2.45	5.29	4.31	2.93	0.19	0.99	0.10	0.03	0.08	0.12	0.40	0.05
BLM13	Bureau of Land Management; Laguna Plata	G39	20.15	4.73	3.31	2.71	1.84	0.13	0.68	0.07	0.00	0.00	0.19	0.16	0.03
BLM14	Bureau of Land Management; Laguna Plata	G40	19.49	3.60	3.75	3.13	2.20	0.16	0.70	0.07	0.00	0.00	0.14	0.26	0.03
BLM15	Bureau of Land Management; Laguna Plata	G41	28.15	5.54	6.37	5.33	3.79	0.25	1.16	0.13	0.00	0.00	0.10	0.58	0.06
BLM16	Bureau of Land Management; Laguna Plata	G42	16.44	9.91	5.58	4.79	3.58	0.23	0.93	0.05	0.00	0.00	0.17	0.31	0.05
BLM17	Bureau of Land Management; Laguna Tonto	G43	12.60	2.31	1.77	1.48	1.04	0.08	0.34	0.02	0.00	0.00	0.20	0.08	0.02
BLM18	Bureau of Land Management; Laguna Tonto	G44	12.81	2.70	2.82	2.36	1.66	0.14	0.50	0.05	0.00	0.00	0.09	0.28	0.03
BLM19	Bureau of Land Management; Laguna Tonto	G45	13.43	2.23	6.02	5.00	3.46	0.28	1.14	0.11	0.00	0.00	0.09	0.59	0.06
BLM20	Bureau of Land Management; Laguna Tonto	G46	15.03	2.83	8.54	7.13	5.10	0.29	1.58	0.03	0.04	0.09	0.34	0.23	0.08
BLM21	Bureau of Land Management; Laguna Gatuna	G47	13.42	1.95	3.20	2.70	1.94	0.12	0.63	0.01	0.00	0.00	0.34	0.09	0.03
BLM22	Bureau of Land Management; Laguna Gatuna	G48	15.43	3.28	5.99	5.00	3.52	0.26	1.14	0.09	0.00	0.00	0.21	0.26	0.06
BLM23	Bureau of Land Management; Laguna Gatuna	G49	23.56	4.75	4.02	3.37	2.41	0.17	0.71	0.08	0.00	0.00	0.28	0.14	0.04
BLM24	Bureau of Land Management; Laguna Quatro	G50	20.45	7.40	3.31	2.80	2.03	0.15	0.56	0.06	0.00	0.00	0.25	0.12	0.03

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
BLM25	Bureau of Land Management; Laguna Quatro	G51	21.78	2.78	3.92	3.30	2.34	0.22	0.68	0.06	0.00	0.00	0.21	0.17	0.04
BLM26	Bureau of Land Management; Laguna Walden	G52	36.56	7.43	3.46	2.86	1.98	0.12	0.71	0.06	0.00	0.00	0.29	0.11	0.03
BLM27	Bureau of Land Management; Laguna Uno	G53	30.05	34.98	5.11	4.25	2.98	0.18	0.98	0.11	0.00	0.00	0.24	0.18	0.04
SFB1	San Francisco Bay NWR	H01	62.91	12.88	0.83	0.71	0.52	0.05	0.14	0.01	0.00	0.00	0.37	0.08	0.03
SFB2	San Francisco Bay NWR	H02	14.25	4.57	0.99	0.85	0.63	0.06	0.16	0.00	0.00	0.00	0.27	0.14	0.04
SFB3	San Francisco Bay NWR	H03	20.62	4.86	0.65	0.55	0.40	0.03	0.11	0.00	0.00	0.00	0.27	0.09	0.02
SFB4	San Francisco Bay NWR	H04	48.55	9.14	1.88	1.62	1.22	0.09	0.30	0.01	0.00	0.00	0.17	0.41	0.07
SFB5	San Francisco Bay NWR	H05	48.19	9.00	2.48	2.17	1.66	0.15	0.35	0.00	0.00	0.00	0.10	0.93	0.10
SFB6	San Francisco Bay NWR	H06	45.41	8.79	0.90	0.78	0.59	0.04	0.15	0.00	0.00	0.00	0.11	0.32	0.03
SFB7	San Francisco Bay NWR	H07	59.98	14.40	2.41	2.06	1.51	0.12	0.39	0.03	0.00	0.00	0.29	0.31	0.09
SFB8	San Francisco Bay NWR	H08	26.11	4.22	2.32	2.01	1.54	0.11	0.35	0.02	0.00	0.00	0.19	0.48	0.09
SFB9	San Francisco Bay NWR	H09	60.61	16.55	0.91	0.79	0.60	0.05	0.13	0.01	0.00	0.00	0.14	0.26	0.03
SFB10	San Francisco Bay NWR	H10	60.11	18.94	1.05	0.90	0.68	0.05	0.16	0.01	0.00	0.00	0.17	0.23	0.04
SFB11	San Francisco Bay NWR	H11	53.19	12.90	1.01	0.87	0.65	0.05	0.17	0.00	0.00	0.00	0.23	0.17	0.04
SFB12	San Francisco Bay NWR	H12	61.57	15.16	0.72	0.62	0.47	0.03	0.11	0.01	0.00	0.00	0.12	0.23	0.03
SFB13	San Francisco Bay NWR	H13	37.33	7.04	1.39	1.19	0.89	0.06	0.23	0.01	0.00	0.00	0.17	0.31	0.05
SFB14	San Francisco Bay NWR	H14	39.66	6.25	1.26	1.09	0.82	0.07	0.19	0.01	0.00	0.00	0.13	0.36	0.05
SFB15	San Francisco Bay NWR	H15	39.15	8.59	0.52	0.45	0.34	0.03	0.08	0.00	0.00	0.00	0.14	0.14	0.02
SFB16	San Francisco Bay NWR	H16	52.62	9.63	1.74	1.52	1.17	0.09	0.24	0.02	0.00	0.00	0.15	0.45	0.07
SFB17	San Francisco Bay NWR	H17	39.04	7.80	1.48	1.29	0.99	0.06	0.22	0.01	0.00	0.00	0.06	0.93	0.06
SFB18	San Francisco Bay NWR	H18	50.47	14.50	0.86	0.74	0.57	0.04	0.13	0.01	0.00	0.00	0.12	0.27	0.03
SFB19	San Francisco Bay NWR	H19	54.61	16.38	3.82	3.25	2.36	0.25	0.59	0.05	0.00	0.00	0.19	0.77	0.14
SFB20	San Francisco Bay NWR	H20	62.54	21.23	N/D	N/D	N/D	N/D	N/D	N/D	N/D	N/D	0.36	N/D	N/D
SFB21	San Francisco Bay NWR	H21	22.51	3.18	0.95	0.82	0.61	0.05	0.15	0.00	0.00	0.00	0.07	0.49	0.04
SFB22	San Francisco Bay NWR	H22	29.92	5.71	1.59	1.37	1.02	0.09	0.26	0.00	0.00	0.00	0.13	0.45	0.06

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
SFB23	San Francisco Bay NWR	H23	24.10	4.44	0.42	0.36	0.27	0.02	0.07	0.00	0.00	0.00	0.07	0.24	0.02
SFB24	San Francisco Bay NWR	H24	19.03	6.23	2.25	1.96	1.49	0.11	0.36	0.00	0.00	0.00	0.09	0.98	0.09
SFB25	San Francisco Bay NWR	H25	30.65	4.34	1.34	1.18	0.91	0.08	0.19	0.00	0.00	0.00	0.15	0.36	0.05
SFB26	San Francisco Bay NWR	H26	38.96	6.01	1.06	0.92	0.70	0.05	0.16	0.01	0.00	0.00	0.17	0.24	0.04
SFB27	San Francisco Bay NWR	H27	32.07	6.49	0.58	0.50	0.38	0.03	0.09	0.00	0.00	0.00	0.02	0.99	0.02
SFB28	San Francisco Bay NWR	H28	34.25	5.72	0.41	0.36	0.28	0.02	0.07	0.00	0.00	0.00	0.15	0.11	0.02
SFB29	San Francisco Bay NWR	H29	27.51	3.78	0.44	0.38	0.29	0.02	0.07	0.00	0.00	0.00	0.14	0.13	0.02
SFB30	San Francisco Bay NWR	H30	36.21	5.46	1.60	1.38	1.05	0.08	0.24	0.01	0.00	0.00	0.17	0.36	0.06
SFB31	San Francisco Bay NWR	H31	54.47	17.84	1.66	1.43	1.07	0.08	0.26	0.02	0.00	0.00	0.14	0.46	0.06
SFB32	San Francisco Bay NWR	H32	52.45	15.52	1.11	0.97	0.75	0.06	0.15	0.01	0.00	0.00	0.19	0.23	0.04
SFB33	San Francisco Bay NWR	H33	45.54	15.92	0.17	0.15	0.11	0.01	0.03	0.00	0.00	0.00	0.13	0.05	0.01
SFB34	San Francisco Bay NWR	H34	57.39	18.87	1.09	0.95	0.73	0.05	0.16	0.01	0.00	0.00	0.13	0.32	0.04
Galveston	Control	H35	19.50	0.37	0.37	0.32	0.25	0.02	0.06	0.00	0.00	0.00	0.15	0.10	0.01
Big1	Big Bend NP	J01	26.74	1.88	0.94	0.82	0.63	0.05	0.14	0.00	0.00	0.00	0.31	0.12	0.04
Big2	Big Bend NP	J02	31.04	5.86	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.30	0.00	0.00
Big3	Big Bend NP	J03	17.77	1.30	1.09	0.93	0.68	0.09	0.16	0.00	0.00	0.00	0.31	0.13	0.04
Big4	Big Bend NP	J04	23.25	3.19	1.54	1.30	0.93	0.08	0.29	0.00	0.00	0.00	0.36	0.16	0.06
Big5	Big Bend NP	J05	19.75	1.52	2.21	1.92	1.47	0.11	0.34	0.00	0.00	0.00	0.32	0.27	0.09
Big6	Big Bend NP	J06	21.10	1.77	3.79	3.30	2.54	0.18	0.58	0.00	0.00	0.00	0.28	0.53	0.15
Big7	Big Bend NP	J07	19.27	1.60	1.89	1.64	1.25	0.10	0.30	0.00	0.00	0.00	0.26	0.28	0.07
Big8	Big Bend NP	J08	21.38	0.38	1.78	1.54	1.13	0.16	0.26	0.00	0.00	0.00	0.30	0.23	0.07
Big9	Big Bend NP	J09	20.35	0.54	0.90	0.78	0.60	0.04	0.14	0.00	0.00	0.00	0.30	0.12	0.04
Big10	Big Bend NP	J10	18.94	0.08	2.91	2.55	1.99	0.15	0.42	0.00	0.00	0.00	0.29	0.39	0.11
Big11	Big Bend NP	J11	22.82	0.57	2.04	1.78	1.38	0.11	0.30	0.00	0.00	0.00	0.38	0.21	0.08
Big12	Big Bend NP	J12	21.87	0.64	2.31	2.01	1.54	0.11	0.36	0.00	0.00	0.00	0.27	0.33	0.09
Big13	Big Bend NP	J13	39.41	2.78	1.51	1.32	1.01	0.07	0.23	0.00	0.00	0.00	0.28	0.21	0.06
Big14	Big Bend NP	J14	33.86	1.36	1.13	0.96	0.70	0.06	0.20	0.00	0.00	0.00	0.31	0.14	0.04
Big15	Big Bend NP	J15	18.44	4.14	1.38	1.18	0.86	0.07	0.24	0.00	0.00	0.00	0.12	0.45	0.05

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
Big16	Big Bend NP	J16	26.88	3.77	3.12	2.75	2.16	0.16	0.43	0.00	0.00	0.00	0.31	0.40	0.12
Big17	Big Bend NP	J17	20.76	4.03	1.78	1.53	1.14	0.09	0.30	0.00	0.00	0.00	0.23	0.30	0.07
Big18	Big Bend NP	J18	20.28	2.80	1.31	1.15	0.90	0.06	0.19	0.00	0.00	0.00	0.35	0.15	0.05
Big19	Big Bend NP	J19	26.37	3.03	0.14	0.12	0.10	0.01	0.02	0.00	0.00	0.00	0.36	0.02	0.01
Big20	Big Bend NP	J20	16.99	2.27	0.02	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.35	0.00	0.00
Big21	Big Bend NP	J21	22.18	2.54	0.36	0.31	0.25	0.02	0.05	0.00	0.00	0.00	0.25	0.06	0.01
Galveston	Control	J23	21.68	0.79	1.19	1.03	0.78	0.06	0.19	0.00	0.00	0.00	0.37	0.12	0.05
C. therm.	Control	J24	N/D	N/D	2.33	1.98	1.44	0.12	0.42	0.00	0.00	0.00	0.29	0.31	0.09
Big22	Big Bend NP	J22	18.36	1.38	0.24	0.21	0.16	0.01	0.04	0.00	0.00	0.00	0.32	0.03	0.01
Big23	Big Bend NP	J2-1	26.32	1.64	1.04	0.90	0.67	0.05	0.18	0.00	0.00	0.00	0.18	0.08	0.02
Big24	Big Bend NP	J2-2	27.84	1.94	2.53	2.15	1.48	0.33	0.35	0.00	0.00	0.00	0.26	0.14	0.04
Big25	Big Bend NP	J2-3	31.89	3.71	3.59	3.07	2.27	0.17	0.60	0.03	0.00	0.00	0.10	0.51	0.05
Big26	Big Bend NP	J2-4	88.59	6.62	0.04	0.03	0.03	0.00	0.00	0.00	0.00	0.00	0.19	0.00	0.00
Big27	Big Bend NP	J2-5	25.04	2.70	3.33	2.81	1.89	0.41	0.50	0.00	0.00	0.00	0.22	0.22	0.05
Galveston	Control	J2-6	19.20	0.23	1.42	1.24	0.96	0.07	0.21	0.00	0.00	0.00	0.23	0.09	0.02
C. therm.	Control	J2-7	N/D	N/D	1.39	1.22	0.94	0.07	0.20	0.00	0.00	0.00	0.16	0.13	0.02
No Inoculum	Control	J2-8	N/D	N/D	0.64	0.55	0.41	0.04	0.10	0.00	0.00	0.00	0.06	0.16	0.01
OHS1	Ogden Hot Springs	K01	22.10	1.68	0.31	0.27	0.20	0.02	0.06	0.00	0.00	0.00	0.08	0.05	0.00
OHS2	Ogden Hot Springs	K02	18.13	1.48	0.80	0.69	0.52	0.04	0.13	0.00	0.00	0.00	0.13	0.09	0.01
OHS3	Ogden Hot Springs	K03	24.05	3.25	2.07	1.81	1.41	0.09	0.31	0.00	0.00	0.00	0.12	0.26	0.03
OHS4	Ogden Hot Springs	K04	86.50	42.37	1.32	1.14	0.85	0.08	0.22	0.00	0.00	0.00	0.10	0.18	0.02
WHS1	Wilson Hot Springs	K05	27.42	6.23	0.93	0.81	0.61	0.05	0.15	0.00	0.00	0.00	0.09	0.15	0.01
WHS2	Wilson Hot Springs	K06	39.77	7.01	2.42	2.10	1.60	0.13	0.36	0.01	0.00	0.00	0.05	0.66	0.04
WHS3	Wilson Hot Springs	K07	34.17	6.00	0.62	0.54	0.41	0.03	0.10	0.00	0.00	0.00	0.12	0.07	0.01
WHS4	Wilson Hot Springs	K08	52.86	7.92	1.84	1.61	1.26	0.09	0.26	0.00	0.00	0.00	0.22	0.12	0.03
WHS5	Wilson Hot Springs	K09	51.18	6.44	1.64	1.41	1.05	0.09	0.27	0.00	0.00	0.00	0.18	0.13	0.02
WHS6	Wilson Hot Springs	K10	37.66	5.87	0.86	0.75	0.56	0.05	0.13	0.00	0.00	0.00	0.07	0.19	0.01
WHS7	Wilson Hot Springs	K11	34.56	6.61	2.89	2.54	1.99	0.13	0.41	0.00	0.00	0.00	0.11	0.37	0.04
WHS8	Wilson Hot Springs	K12	49.24	4.72	0.54	0.48	0.37	0.03	0.08	0.00	0.00	0.00	0.12	0.06	0.01

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
WHS9	Wilson Hot Springs	K13	36.54	4.50	1.37	1.20	0.92	0.08	0.20	0.00	0.00	0.00	0.11	0.18	0.02
WHS10	Wilson Hot Springs	K14	48.53	4.95	0.26	0.22	0.17	0.01	0.04	0.00	0.00	0.00	0.13	0.03	0.00
WHS11	Wilson Hot Springs	K15	48.59	15.87	1.18	1.03	0.80	0.06	0.17	0.00	0.00	0.00	0.13	0.13	0.02
WHS12	Wilson Hot Springs	K16	34.60	8.57	0.47	0.41	0.30	0.05	0.06	0.00	0.00	0.00	0.11	0.06	0.01
WHS13	Wilson Hot Springs	K17	45.88	11.04	0.95	0.82	0.62	0.05	0.14	0.00	0.00	0.00	0.10	0.14	0.01
WHS14	Wilson Hot Springs	K18	67.28	22.49	0.35	0.31	0.24	0.02	0.05	0.00	0.00	0.00	0.13	0.04	0.01
FS1	Fish Springs NWR	K19	73.36	11.36	0.98	0.85	0.65	0.05	0.15	0.00	0.00	0.00	0.15	0.10	0.01
FS2	Fish Springs NWR	K20	47.45	10.41	0.81	0.71	0.55	0.04	0.11	0.00	0.00	0.00	0.15	0.08	0.01
FS3	Fish Springs NWR	K21	40.70	38.04	0.34	0.29	0.21	0.01	0.06	0.00	0.00	0.00	0.10	0.04	0.00
FS4	Fish Springs NWR	K22	63.45	11.39	0.68	0.59	0.45	0.04	0.10	0.00	0.00	0.00	0.06	0.16	0.01
FS5	Fish Springs NWR	K23	50.53	26.84	0.72	0.63	0.48	0.04	0.11	0.00	0.00	0.00	0.12	0.08	0.01
FS6	Fish Springs NWR	K24	62.12	28.05	0.94	0.82	0.64	0.04	0.13	0.01	0.00	0.00	0.10	0.14	0.01
FS7	Fish Springs NWR	K25	83.14	40.06	1.18	1.02	0.77	0.07	0.17	0.01	0.00	0.00	0.10	0.17	0.02
FS8	Fish Springs NWR	K26	26.27	17.82	1.19	1.02	0.75	0.06	0.20	0.01	0.00	0.00	0.10	0.16	0.02
FS9	Fish Springs NWR	K27	43.04	18.53	0.97	0.85	0.65	0.05	0.14	0.00	0.00	0.00	0.02	0.80	0.01
FS10	Fish Springs NWR	K28	29.87	16.26	0.59	0.51	0.38	0.03	0.10	0.00	0.00	0.00	0.16	0.05	0.01
FS11	Fish Springs NWR	K29	33.29	22.19	0.10	0.09	0.07	0.01	0.01	0.00	0.00	0.00	0.16	0.01	0.00
FS12	Fish Springs NWR	K30	35.82	28.65	0.10	0.08	0.06	0.00	0.01	0.00	0.00	0.00	0.10	0.01	0.00
FS13	Fish Springs NWR	K31	68.37	35.56	0.63	0.55	0.42	0.03	0.10	0.00	0.00	0.00	0.17	0.05	0.01
FS14	Fish Springs NWR	K32	39.50	7.65	0.16	0.14	0.11	0.01	0.02	0.00	0.00	0.00	0.08	0.03	0.00
FS15	Fish Springs NWR	K33	68.30	24.82	0.33	0.28	0.21	0.01	0.06	0.00	0.00	0.00	0.15	0.03	0.00
FS16	Fish Springs NWR	K34	45.75	11.06	0.94	0.80	0.59	0.04	0.16	0.01	0.00	0.00	0.08	0.17	0.01
FS17	Fish Springs NWR	K35	62.46	14.90	0.23	0.21	0.16	0.01	0.04	0.00	0.00	0.00	0.16	0.02	0.00
FS18	Fish Springs NWR	K36	64.36	18.33	0.72	0.62	0.46	0.04	0.12	0.00	0.00	0.00	0.09	0.12	0.01
FS19	Fish Springs NWR	K37	67.89	16.77	1.22	1.06	0.80	0.06	0.20	0.00	0.00	0.00	0.29	0.06	0.02
FS20	Fish Springs NWR	K38	76.25	14.76	1.49	1.29	0.98	0.07	0.24	0.00	0.00	0.00	0.24	0.09	0.02
Topas 1	West Topas	K39	24.99	12.96	0.51	0.44	0.33	0.03	0.08	0.00	0.00	0.00	0.17	0.04	0.01
AHS1	Abraham Hot Springs	K40	68.79	8.98	2.46	2.11	1.56	0.12	0.42	0.00	0.00	0.00	0.09	0.39	0.04
AHS2	Abraham Hot Springs	K41	60.54	4.03	0.39	0.33	0.24	0.02	0.07	0.00	0.00	0.00	0.16	0.03	0.01
AHS3	Abraham Hot Springs	K42	69.65	7.00	1.67	1.46	1.12	0.08	0.26	0.00	0.00	0.00	0.20	0.12	0.02
AHS4	Abraham Hot Springs	K43	76.67	12.04	1.03	0.88	0.66	0.05	0.17	0.00	0.00	0.00	0.15	0.10	0.01
AHS5	Abraham Hot Springs	K44	72.23	9.15	0.92	0.85	0.74	0.03	0.08	0.00	0.00	0.00	0.16	0.09	0.01

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
BHS1	Baker Hot Springs	K45	57.53	7.44	2.01	1.72	1.27	0.09	0.36	0.00	0.00	0.00	0.20	0.15	0.03
BHS2	Baker Hot Springs	K46	36.89	5.23	0.96	0.83	0.63	0.05	0.15	0.00	0.00	0.00	0.22	0.06	0.01
BHS3	Baker Hot Springs	K47	81.95	9.13	0.03	0.03	0.02	0.00	0.01	0.00	0.00	0.00	0.13	0.00	0.00
BHS4	Baker Hot Springs	K48	63.27	11.90	1.01	0.88	0.67	0.05	0.16	0.00	0.00	0.00	0.04	0.36	0.01
BHS5	Baker Hot Springs	K49	92.18	10.03	1.05	0.88	0.61	0.09	0.18	0.00	0.00	0.00	0.33	0.05	0.01
BHS6	Baker Hot Springs	K50	56.91	14.11	1.00	0.86	0.64	0.05	0.16	0.00	0.00	0.00	0.10	0.15	0.01
BHS7	Baker Hot Springs	K51	47.16	3.77	1.50	1.31	1.01	0.08	0.22	0.00	0.00	0.00	0.29	0.08	0.02
BHS8	Baker Hot Springs	K52	59.80	5.45	1.03	0.91	0.71	0.05	0.15	0.00	0.00	0.00	0.06	0.26	0.02
BHS9	Baker Hot Springs	K53	57.87	5.28	1.94	1.69	1.29	0.10	0.30	0.00	0.00	0.00	0.23	0.12	0.03
BHS10	Baker Hot Springs	K54	51.03	4.47	0.48	0.41	0.31	0.03	0.08	0.00	0.00	0.00	0.15	0.05	0.01
BHS11	Baker Hot Springs	K55	76.37	15.31	0.87	0.75	0.56	0.04	0.14	0.00	0.00	0.00	0.19	0.07	0.01
Galveston	Control	K56	19.55	2.76	0.33	0.28	0.21	0.02	0.05	0.00	0.00	0.00	0.08	0.06	0.00
C. therm.	Control	K57	N/D	N/D	1.13	0.96	0.70	0.06	0.21	0.00	0.00	0.00	0.05	0.36	0.02
AI1	Antelope Island	L01	16.84	5.66	0.90	0.77	0.56	0.04	0.16	0.00	0.00	0.00	0.05	0.26	0.01
AI2	Antelope Island	L02	17.45	6.39	0.54	0.47	0.37	0.03	0.07	0.00	0.00	0.00	0.14	0.06	0.01
AI3	Antelope Island	L03	61.04	27.81	2.41	2.13	1.69	0.11	0.30	0.03	0.00	0.00	0.12	0.28	0.03
AI4	Antelope Island	L04	14.69	0.28	0.80	0.69	0.53	0.04	0.12	0.00	0.00	0.00	0.09	0.13	0.01
GSL1	Great Salt Lake	L05	22.96	7.02	1.04	0.90	0.67	0.05	0.17	0.00	0.00	0.00	0.10	0.15	0.01
GSL2	Great Salt Lake	L06	14.56	5.07	0.09	0.08	0.06	0.00	0.01	0.00	0.00	0.00	0.15	0.01	0.00
GSL3	Great Salt Lake	L07	29.91	9.14	1.10	0.96	0.74	0.06	0.16	0.00	0.00	0.00	0.07	0.23	0.02
SHS1	Saratoga Hot Springs	L08	44.12	11.45	0.17	0.15	0.12	0.01	0.03	0.00	0.00	0.00	0.24	0.01	0.00
SHS2	Saratoga Hot Springs	L09	46.28	6.07	0.53	0.47	0.36	0.02	0.08	0.00	0.00	0.00	0.16	0.05	0.01
IHS1	Indian Hot Springs	L10	53.49	19.20	0.93	0.80	0.60	0.04	0.15	0.00	0.00	0.00	0.26	0.05	0.01
IHS2	Indian Hot Springs	L11	41.96	10.38	0.14	0.11	0.07	0.01	0.03	0.00	0.00	0.00	0.09	0.02	0.00
IHS3	Indian Hot Springs	L12	42.46	7.38	1.77	1.52	1.13	0.07	0.31	0.01	0.00	0.00	0.15	0.17	0.03
IHS4	Indian Hot Springs	L13	37.07	8.43	0.80	0.70	0.55	0.03	0.11	0.01	0.00	0.00	0.18	0.06	0.01
SCW1	Salt Creek Waterfowl Preserve	L14	55.42	13.26	0.35	0.30	0.24	0.02	0.05	0.00	0.00	0.00	0.13	0.04	0.01
Knoll1	Knoll Spring	L15	42.71	6.49	0.63	0.56	0.43	0.04	0.09	0.00	0.00	0.00	0.11	0.08	0.01
LB1	Lincoln Beach	L16	79.28	33.02	0.83	0.71	0.53	0.03	0.14	0.00	0.00	0.00	0.18	0.06	0.01
UL1	Utah Lake	L17	42.58	9.20	0.68	0.60	0.48	0.03	0.09	0.00	0.00	0.00	0.22	0.05	0.01
UL2	Utah Lake	L18	30.96	9.97	1.10	0.95	0.71	0.06	0.18	0.00	0.00	0.00	0.03	0.45	0.02

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
WS1	Warm Springs	L19	27.59	4.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.00	0.00
WS2	Warm Springs	L20	60.15	10.42	1.50	1.26	0.90	0.06	0.28	0.01	0.00	0.00	0.24	0.09	0.02
WS3	Warm Springs	L21	55.50	10.24	1.92	1.61	1.14	0.07	0.38	0.01	0.00	0.00	0.12	0.22	0.03
WS4	Warm Springs	L22	25.95	3.93	0.98	0.81	0.55	0.04	0.21	0.00	0.00	0.00	0.12	0.11	0.01
BRR1	Bear River Reserve	L23	45.22	9.08	0.99	0.85	0.63	0.05	0.18	0.00	0.00	0.00	0.20	0.07	0.01
BRR2	Bear River Reserve	L24	34.97	9.35	0.43	0.37	0.28	0.02	0.07	0.00	0.00	0.00	0.19	0.03	0.01
BRR3	Bear River Reserve	L25	38.89	6.49	1.00	0.87	0.67	0.06	0.14	0.00	0.00	0.00	0.11	0.13	0.01
Galveston	Control	L26	19.63	0.52	1.10	0.95	0.71	0.06	0.19	0.00	0.00	0.00	0.21	0.08	0.02
C. therm.	Control	L27	N/D	N/D	0.91	0.77	0.54	0.04	0.18	0.00	0.00	0.00	0.18	0.07	0.01
SWR1	Savannah NWR	M01	45.07	13.28	0.03	0.03	0.02	0.00	0.01	0.00	0.00	0.00	0.17	0.00	0.00
SWR2	Savannah NWR	M02	55.06	15.53	0.41	0.35	0.27	0.02	0.06	0.00	0.00	0.00	0.23	0.03	0.01
CR1	Cape Romaine NWR	M03	72.70	35.92	0.95	0.83	0.63	0.05	0.15	0.00	0.00	0.00	0.03	0.42	0.01
CR2	Cape Romaine NWR	M04	51.55	12.86	1.74	1.50	1.13	0.09	0.28	0.00	0.00	0.00	0.09	0.27	0.02
CR3	Cape Romaine NWR	M05	46.74	12.44	0.13	0.11	0.08	0.01	0.02	0.00	0.00	0.00	0.25	0.01	0.00
CR4	Cape Romaine NWR	M06	31.25	4.17	1.06	0.91	0.68	0.05	0.17	0.00	0.00	0.00	0.07	0.23	0.02
CR5	Cape Romaine NWR	M07	58.34	11.78	2.20	1.91	1.44	0.12	0.32	0.02	0.00	0.00	0.15	0.21	0.03
CR6	Cape Romaine NWR	M08	25.59	6.93	0.77	0.67	0.50	0.04	0.12	0.00	0.00	0.00	0.16	0.07	0.01
CR7	Cape Romaine NWR	M09	32.78	2.62	0.64	0.55	0.42	0.03	0.10	0.00	0.00	0.00	0.04	0.21	0.01
CR8	Cape Romaine NWR	M10	23.10	2.04	1.75	1.52	1.17	0.09	0.27	0.00	0.00	0.00	0.12	0.22	0.03
CR9	Cape Romaine NWR	M11	33.10	4.52	0.74	0.64	0.48	0.04	0.12	0.00	0.00	0.00	0.23	0.05	0.01
CR10	Cape Romaine NWR	M12	19.74	0.73	0.49	0.43	0.33	0.02	0.07	0.00	0.00	0.00	0.16	0.05	0.01
CR11	Cape Romaine NWR	M13	40.37	0.31	0.43	0.38	0.30	0.02	0.06	0.00	0.00	0.00	0.22	0.03	0.01
CR12	Cape Romaine NWR	M14	25.69	2.83	1.28	1.13	0.88	0.07	0.18	0.00	0.00	0.00	0.13	0.15	0.02
CR13	Cape Romaine NWR	M15	25.98	2.83	2.71	2.37	1.83	0.16	0.38	0.00	0.00	0.00	0.08	0.48	0.04
CR14	Cape Romaine NWR	M16	42.05	6.02	0.28	0.24	0.18	0.01	0.05	0.00	0.00	0.00	0.14	0.03	0.00
CR15	Cape Romaine NWR	M17	12.98	0.35	0.93	0.80	0.60	0.05	0.14	0.01	0.00	0.00	0.11	0.13	0.01
CR16	Cape Romaine NWR	M18	33.12	3.95	3.68	3.16	2.36	0.17	0.62	0.00	0.00	0.01	0.09	0.60	0.05
CR17	Cape Romaine NWR	M19	13.80	0.39	0.07	0.06	0.05	0.00	0.01	0.00	0.00	0.00	0.18	0.01	0.00
CR18	Cape Romaine NWR	M20	28.02	3.11	2.49	2.15	1.63	0.13	0.38	0.00	0.00	0.01	0.24	0.15	0.04
CR19	Cape Romaine NWR	M21	37.39	7.78	1.03	0.89	0.66	0.07	0.16	0.00	0.00	0.00	0.14	0.11	0.01
CR20	Cape Romaine NWR	M22	65.44	26.23	1.44	1.25	0.96	0.08	0.21	0.00	0.00	0.00	0.12	0.18	0.02
CR21	Cape Romaine NWR	M23	33.64	6.96	0.30	0.27	0.21	0.02	0.05	0.00	0.00	0.00	0.18	0.03	0.00

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
CR22	Cape Romaine NWR	M24	29.60	27.99	0.72	0.62	0.47	0.04	0.12	0.00	0.00	0.00	0.27	0.04	0.01
CR23	Cape Romaine NWR	M25	24.89	2.99	0.47	0.41	0.31	0.03	0.07	0.00	0.00	0.00	0.20	0.03	0.01
CR24	Cape Romaine NWR	M26	38.59	5.28	0.92	0.80	0.61	0.05	0.15	0.00	0.00	0.00	0.11	0.12	0.01
CR25	Cape Romaine NWR	M27	41.76	5.16	0.88	0.77	0.59	0.05	0.13	0.00	0.00	0.00	0.11	0.12	0.01
PI1	Pinkney Island NWR	M28	37.81	12.29	1.93	1.69	1.31	0.10	0.27	0.01	0.00	0.00	0.04	0.77	0.03
PI2	Pinkney Island NWR	M29	23.74	2.84	0.44	0.38	0.28	0.03	0.06	0.00	0.00	0.00	0.14	0.05	0.01
PI3	Pinkney Island NWR	M30	23.19	1.53	1.87	1.63	1.26	0.10	0.26	0.00	0.00	0.01	0.09	0.31	0.03
PI4	Pinkney Island NWR	M31	42.26	7.80	0.81	0.70	0.53	0.05	0.12	0.00	0.00	0.00	0.15	0.08	0.01
PI5	Pinkney Island NWR	M32	28.81	4.51	0.28	0.24	0.18	0.01	0.05	0.00	0.00	0.00	0.04	0.11	0.00
PI6	Pinkney Island NWR	M33	30.36	4.82	1.94	1.67	1.24	0.12	0.29	0.02	0.00	0.00	0.10	0.29	0.03
PI7	Pinkney Island NWR	M34	32.34	5.08	1.21	1.06	0.81	0.06	0.18	0.00	0.00	0.00	0.10	0.18	0.02
PI8	Pinkney Island NWR	M35	35.98	4.05	1.16	0.99	0.73	0.06	0.20	0.00	0.00	0.00	0.21	0.08	0.02
PI9	Pinkney Island NWR	M36	69.96	42.86	2.21	1.89	1.39	0.10	0.40	0.00	0.00	0.00	0.12	0.26	0.03
PI10	Pinkney Island NWR	M37	37.91	7.59	1.79	1.56	1.19	0.10	0.26	0.01	0.00	0.00	0.15	0.18	0.03
PI11	Pinkney Island NWR	M38	70.14	19.56	1.48	1.27	0.95	0.07	0.25	0.00	0.00	0.00	0.09	0.23	0.02
PI12	Pinkney Island NWR	M39	31.24	3.05	1.28	1.12	0.86	0.08	0.18	0.00	0.00	0.00	0.17	0.11	0.02
PI13	Pinkney Island NWR	M40	49.98	8.21	0.38	0.33	0.25	0.02	0.06	0.00	0.00	0.00	0.07	0.08	0.01
PI14	Pinkney Island NWR	M41	40.32	4.71	0.85	0.74	0.57	0.05	0.12	0.00	0.00	0.00	0.17	0.07	0.01
Galveston	Control	M42	19.77	1.02	1.05	0.91	0.69	0.05	0.17	0.00	0.00	0.00	0.09	0.16	0.02
C. therm.	Control	M43	N/D	N/D	2.00	1.76	1.38	0.10	0.29	0.00	0.00	0.00	0.14	0.21	0.03
SI1	Sapelo Island Microbial Observatory	N01	16.39	0.30	1.26	1.10	0.86	0.07	0.17	0.01	0.00	0.00	0.06	0.29	0.02
SI2	Sapelo Island Microbial Observatory	N02	18.13	0.41	1.09	0.95	0.74	0.07	0.15	0.00	0.00	0.00	0.09	0.17	0.02
SI3	Sapelo Island Microbial Observatory	N03	46.02	10.66	2.68	2.29	1.65	0.20	0.42	0.01	0.00	0.00	0.08	0.45	0.04
SI4	Sapelo Island Microbial Observatory	N04	63.83	18.51	1.29	1.14	0.89	0.06	0.18	0.00	0.00	0.00	0.16	0.12	0.02
SI5	Sapelo Island Microbial Observatory	N05	14.78	11.09	2.45	2.13	1.62	0.12	0.37	0.01	0.00	0.00	0.06	0.64	0.04
SI6	Sapelo Island Microbial Observatory	N06	82.43	35.92	2.14	1.77	1.19	0.18	0.38	0.02	0.00	0.00	0.04	0.68	0.03
SI7	Sapelo Island Microbial Observatory	N07	52.94	9.31	1.67	1.43	1.05	0.08	0.28	0.02	0.00	0.00	0.08	0.29	0.02
SI8	Sapelo Island Microbial Observatory	N08	34.17	4.49	1.17	1.03	0.81	0.05	0.16	0.00	0.00	0.00	0.08	0.21	0.02

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
SI9	Sapelo Island Microbial Observatory	N09	17.56	1.39	1.49	1.30	1.00	0.06	0.22	0.01	0.00	0.00	0.20	0.11	0.02
SI10	Sapelo Island Microbial Observatory	N10	19.16	1.66	2.45	2.10	1.58	0.10	0.41	0.01	0.00	0.00	0.11	0.32	0.03
SI11	Sapelo Island Microbial Observatory	N11	43.77	12.60	3.57	3.06	2.29	0.16	0.57	0.05	0.00	0.00	0.17	0.30	0.05
SI12	Sapelo Island Microbial Observatory	N12	54.03	17.20	2.24	1.93	1.42	0.18	0.31	0.02	0.00	0.00	0.08	0.40	0.03
SI13	Sapelo Island Microbial Observatory	N13	71.48	97.65	1.86	1.57	1.07	0.26	0.24	0.00	0.00	0.00	0.14	0.18	0.03
SI14	Sapelo Island Microbial Observatory	N14	71.66	97.97	1.48	1.27	0.94	0.07	0.25	0.01	0.00	0.00	0.11	0.20	0.02
SI15	Sapelo Island Microbial Observatory	N15	77.23	95.07	0.72	0.62	0.45	0.04	0.13	0.00	0.00	0.00	0.01	0.77	0.01
SI16	Sapelo Island Microbial Observatory	N16	49.19	22.69	2.27	1.88	1.29	0.13	0.43	0.03	0.00	0.00	0.10	0.31	0.03
SI17	Sapelo Island Microbial Observatory	N17	38.40	86.82	2.84	2.41	1.75	0.17	0.46	0.03	0.00	0.01	0.11	0.38	0.04
SI18	Sapelo Island Microbial Observatory	N18	18.91	0.39	0.28	0.25	0.19	0.02	0.04	0.00	0.00	0.00	0.17	0.02	0.00
SI19	Sapelo Island Microbial Observatory	N19	20.75	0.67	0.15	0.12	0.08	0.01	0.03	0.00	0.00	0.00	0.17	0.01	0.00
SI20	Sapelo Island Microbial Observatory	N20	38.53	7.89	0.97	0.83	0.61	0.05	0.15	0.02	0.00	0.00	0.19	0.07	0.01
SI21	Sapelo Island Microbial Observatory	N21	35.99	7.04	5.73	4.89	3.58	0.35	0.90	0.04	0.00	0.02	0.12	0.70	0.08
SWR3	Sapelo Island Microbial Observatory	N22	28.81	2.72	1.79	1.55	1.18	0.09	0.26	0.01	0.00	0.00	0.14	0.18	0.03
Galveston	Control	N23	18.72	0.11	1.45	1.23	0.90	0.07	0.24	0.02	0.00	0.00	0.29	0.07	0.02
C. therm.	Control	N24	N/D	N/D	0.23	0.19	0.14	0.01	0.04	0.00	0.00	0.00	0.21	0.02	0.00
BWR 1	Laguna Boquerón NWR	P01	58.61	16.79	3.20	2.79	2.15	0.17	0.44	0.03	0.00	0.00	0.28	0.17	0.05
BWR 2	Laguna Boquerón NWR	P02	41.02	10.53	1.33	1.15	0.86	0.07	0.21	0.01	0.00	0.00	0.12	0.16	0.02
BWR 3	Laguna Boquerón NWR	P03	56.13	21.08	2.40	2.08	1.57	0.19	0.30	0.02	0.00	0.00	0.27	0.13	0.03
BWR 4	Laguna Boquerón NWR	P04	63.19	21.60	1.02	0.90	0.71	0.05	0.13	0.00	0.00	0.00	0.15	0.10	0.01
BWR 5	Laguna Boquerón NWR	P05	51.06	11.99	0.72	0.62	0.46	0.04	0.13	0.00	0.00	0.00	0.14	0.08	0.01
BWR 6	Laguna Boquerón NWR	P06	28.69	5.65	2.02	1.76	1.35	0.10	0.31	0.00	0.00	0.00	0.24	0.12	0.03
BWR 7	Laguna Boquerón NWR	P07	51.36	13.17	1.20	1.02	0.75	0.05	0.21	0.01	0.00	0.00	0.16	0.11	0.02
CAR 1	Laguna Cartagena NWR	P08	50.68	15.86	1.16	1.01	0.78	0.05	0.17	0.00	0.00	0.00	0.16	0.10	0.02
CAR 2	Laguna Cartagena NWR	P09	57.25	22.46	1.48	1.28	0.99	0.07	0.21	0.01	0.00	0.00	0.20	0.11	0.02
CAR 3	Laguna Cartagena NWR	P10	60.58	20.22	2.15	1.86	1.43	0.10	0.32	0.02	0.00	0.00	0.14	0.23	0.03

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
CAR 4	Laguna Cartagena NWR	P11	63.29	25.52	2.73	2.37	1.82	0.11	0.40	0.04	0.00	0.00	0.20	0.19	0.04
CRR 1	Cabo Rojo NWR	P12	22.45	2.24	0.19	0.16	0.12	0.01	0.03	0.00	0.00	0.00	0.03	0.10	0.00
CRR 10	Cabo Rojo NWR	P13	23.74	2.07	2.07	1.82	1.43	0.09	0.28	0.02	0.00	0.00	0.13	0.24	0.03
CRR 2	Cabo Rojo NWR	P14	19.70	18.15	1.59	1.38	1.05	0.07	0.24	0.01	0.00	0.00	0.11	0.20	0.02
CRR 3	Cabo Rojo NWR	P15	40.72	7.02	1.37	1.19	0.92	0.06	0.20	0.01	0.00	0.00	0.20	0.10	0.02
CRR 4	Cabo Rojo NWR	P16	60.40	14.11	3.08	2.58	1.84	0.15	0.54	0.06	0.00	0.00	0.11	0.37	0.04
CRR 5	Cabo Rojo NWR	P17	14.90	7.74	1.52	1.29	0.94	0.07	0.25	0.02	0.00	0.01	0.13	0.17	0.02
CRR 6	Cabo Rojo NWR	P18	26.37	8.55	1.15	0.99	0.74	0.06	0.18	0.01	0.00	0.00	0.16	0.10	0.02
CRR 7	Cabo Rojo NWR	P19	36.47	13.91	0.81	0.71	0.54	0.04	0.12	0.00	0.00	0.00	0.11	0.11	0.01
CRR 8	Cabo Rojo NWR	P20	47.59	14.41	1.36	1.18	0.89	0.06	0.21	0.01	0.00	0.00	0.13	0.15	0.02
CRR 9	Cabo Rojo NWR	P21	33.46	5.91	1.79	1.57	1.23	0.07	0.25	0.02	0.00	0.00	0.22	0.12	0.03
JBR 1	Jabos Bay Research Reserve	P22	43.55	16.09	1.50	1.29	0.96	0.09	0.23	0.01	0.00	0.00	0.09	0.24	0.02
JBR 2	Jabos Bay Research Reserve	P23	54.75	16.37	1.34	1.15	0.87	0.07	0.21	0.01	0.00	0.00	0.17	0.11	0.02
JBR 3	Jabos Bay Research Reserve	P24	42.23	17.64	0.80	0.70	0.55	0.04	0.11	0.01	0.00	0.00	0.14	0.08	0.01
JBR 4	Jabos Bay Research Reserve	P25	41.03	18.20	1.34	1.16	0.88	0.06	0.21	0.01	0.00	0.00	0.11	0.18	0.02
JBR 5	Jabos Bay Research Reserve	P26	21.38	9.50	1.24	1.08	0.83	0.05	0.19	0.01	0.00	0.00	0.16	0.11	0.02
JBR 6	Jabos Bay Research Reserve	P27	53.39	13.81	2.77	2.36	1.73	0.13	0.47	0.02	0.00	0.00	0.11	0.37	0.04
JBR 7	Jabos Bay Research Reserve	P28	65.96	22.21	2.61	2.27	1.75	0.13	0.36	0.03	0.00	0.00	0.15	0.26	0.04
JBR 8	Jabos Bay Research Reserve	P29	49.13	16.32	2.31	2.03	1.60	0.12	0.29	0.03	0.00	0.00	0.11	0.31	0.03
JBR 9	Jabos Bay Research Reserve	P30	48.06	7.93	0.65	0.56	0.42	0.04	0.11	0.00	0.00	0.00	0.14	0.07	0.01
JBR 13	Jabos Bay Research Reserve	P31	31.99	5.14	1.02	0.88	0.66	0.06	0.15	0.01	0.00	0.00	0.21	0.07	0.01
JBR 14	Jabos Bay Research Reserve	P32	36.33	9.19	1.74	1.45	1.00	0.10	0.34	0.01	0.00	0.00	0.12	0.19	0.02
JBR 10	Jabos Bay Research Reserve	P33	48.55	7.89	0.87	0.73	0.53	0.04	0.16	0.00	0.00	0.00	0.11	0.11	0.01
JBR 11	Jabos Bay Research Reserve	P34	61.20	20.19	2.45	2.14	1.63	0.17	0.32	0.02	0.00	0.00	0.14	0.25	0.04
JBR 12	Jabos Bay Research Reserve	P35	78.50	42.02	1.72	1.49	1.14	0.06	0.27	0.01	0.00	0.00	0.16	0.15	0.02
Galveston	Control	P36	19.70	0.97	1.39	1.23	0.99	0.07	0.18	0.00	0.00	0.00	0.12	0.18	0.02

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
C. therm.	Control	P37	N/D	N/D	0.31	0.27	0.20	0.03	0.04	0.00	0.00	0.00	0.19	0.02	0.00
CIP1	Caladesy Island SP	Q01	36.87	3.60	1.57	1.39	1.10	0.07	0.21	0.00	0.00	0.00	0.09	0.26	0.02
CIP2	Caladesy Island SP	Q02	21.96	2.59	1.72	1.52	1.19	0.08	0.25	0.00	0.00	0.00	0.06	0.42	0.02
CIP3	Caladesy Island SP	Q03	43.87	9.81	1.54	1.35	1.05	0.07	0.22	0.00	0.00	0.00	0.11	0.20	0.02
CIP4	Caladesy Island SP	Q04	16.51	0.85	0.13	0.12	0.09	0.01	0.02	0.00	0.00	0.00	0.09	0.02	0.00
CIP5	Caladesy Island SP	Q05	16.31	0.71	0.40	0.34	0.26	0.02	0.06	0.00	0.00	0.00	0.09	0.06	0.01
CIP6	Caladesy Island SP	Q06	82.26	51.32	1.85	1.62	1.26	0.11	0.24	0.02	0.00	0.00	0.08	0.33	0.03
CIP7	Caladesy Island SP	Q07	47.39	8.35	0.97	0.84	0.64	0.05	0.15	0.00	0.00	0.00	0.12	0.11	0.01
HIP1	Honeymoon Island SP	Q08	79.69	20.76	0.91	0.80	0.62	0.05	0.13	0.00	0.00	0.00	0.15	0.09	0.01
HIP2	Honeymoon Island SP	Q09	28.54	3.48	1.69	1.48	1.15	0.09	0.24	0.01	0.00	0.00	0.13	0.19	0.02
HIP3	Honeymoon Island SP	Q10	25.14	32.89	0.74	0.65	0.50	0.03	0.12	0.00	0.00	0.00	0.15	0.06	0.01
HIP4	Honeymoon Island SP	Q11	32.68	5.12	0.85	0.73	0.54	0.05	0.14	0.00	0.00	0.00	0.09	0.14	0.01
CHP1	Charlot Harbor SP	Q12	21.29	1.65	2.02	1.77	1.37	0.11	0.29	0.00	0.00	0.00	0.06	0.46	0.03
CHP2	Charlot Harbor SP	Q13	16.50	1.63	0.36	0.31	0.23	0.04	0.04	0.00	0.00	0.00	0.16	0.03	0.01
CHP3	Charlot Harbor SP	Q14	25.52	4.07	0.51	0.44	0.34	0.03	0.08	0.00	0.00	0.00	0.11	0.07	0.01
CHP4	Charlot Harbor SP	Q15	22.20	4.09	1.65	1.44	1.12	0.07	0.25	0.00	0.00	0.00	0.16	0.15	0.02
CHP5	Charlot Harbor SP	Q16	38.41	7.45	1.39	1.19	0.88	0.07	0.24	0.00	0.00	0.00	0.09	0.21	0.02
CHP6	Charlot Harbor SP	Q17	16.67	41.10	0.47	0.41	0.31	0.03	0.07	0.00	0.00	0.00	0.15	0.04	0.01
RBR1	Rookery Bay Reserve	Q18	20.08	40.28	1.76	1.53	1.17	0.09	0.27	0.00	0.00	0.00	0.17	0.13	0.02
RBR2	Rookery Bay Reserve	Q19	66.96	25.67	1.69	1.48	1.14	0.08	0.24	0.01	0.00	0.00	0.11	0.21	0.02
RBR3	Rookery Bay Reserve	Q20	17.66	0.70	2.48	2.20	1.74	0.12	0.33	0.00	0.00	0.01	0.09	0.40	0.04
RBR4	Rookery Bay Reserve	Q21	74.39	30.68	1.81	1.57	1.19	0.11	0.26	0.00	0.00	0.00	0.05	0.50	0.03
RBR5	Rookery Bay Reserve	Q22	18.81	2.52	1.18	1.02	0.76	0.06	0.19	0.00	0.00	0.00	0.13	0.13	0.02
RBR6	Rookery Bay Reserve	Q23	16.94	3.21	0.52	0.46	0.35	0.03	0.07	0.00	0.00	0.00	0.15	0.05	0.01
RBR7	Rookery Bay Reserve	Q24	68.60	25.89	1.19	1.03	0.78	0.05	0.20	0.00	0.00	0.00	0.12	0.14	0.02
RBR8	Rookery Bay Reserve	Q25	83.24	52.40	2.23	1.96	1.53	0.10	0.32	0.01	0.00	0.00	0.13	0.24	0.03
RBR9	Rookery Bay Reserve	Q26	31.04	5.53	1.68	1.47	1.14	0.09	0.24	0.00	0.00	0.00	0.17	0.14	0.02
CSP1	Collier-Seminole SP	Q27	37.48	5.78	0.73	0.64	0.50	0.04	0.10	0.00	0.00	0.00	0.18	0.06	0.01
TTI1	The Thousands Islands NWR	Q28	59.38	15.38	0.79	0.69	0.52	0.04	0.12	0.00	0.00	0.00	0.09	0.13	0.01
Galveston	Control	Q29	19.49	1.36	1.39	1.19	0.86	0.14	0.19	0.00	0.00	0.00	0.13	0.15	0.02
C. therm.	Control	Q30	N/D	N/D	1.59	1.41	1.11	0.08	0.22	0.00	0.00	0.00	0.09	0.26	0.02

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
No Inoculum	Control	Q31	N/D	N/D	0.28	0.24	0.17	0.01	0.05	0.00	0.00	0.00	0.08	0.05	0.00
JSB1	Jemez Spring Baths	R01	32.56	3.77	2.11	1.83	1.40	0.12	0.31	0.00	0.00	0.00	0.23	0.14	0.03
JSB2	Jemez Spring Baths	R02	74.72	1.55	0.53	0.46	0.34	0.03	0.08	0.00	0.00	0.00	0.12	0.07	0.01
JSB3	Jemez Spring Baths	R03	20.65	31.17	0.37	0.32	0.25	0.02	0.05	0.00	0.00	0.00	0.14	0.04	0.01
JSB4	Jemez Spring Baths	R04	36.97	1.29	2.37	2.08	1.63	0.09	0.36	0.00	0.00	0.00	0.14	0.24	0.03
JSB5	Jemez Spring Baths	R05	50.62	7.28	0.13	0.12	0.09	0.01	0.02	0.00	0.00	0.00	0.20	0.01	0.00
NSS1	New Mexico Sulfur Springs	R06	58.28	71.80	1.18	1.03	0.78	0.07	0.17	0.00	0.00	0.00	0.07	0.24	0.02
NSS2	New Mexico Sulfur Springs	R07	41.43	15.52	3.76	3.26	2.49	0.18	0.60	0.00	0.00	0.00	0.13	0.42	0.05
NSS3	New Mexico Sulfur Springs	R08	31.25	4.72	0.87	0.76	0.58	0.05	0.13	0.00	0.00	0.00	0.11	0.11	0.01
NSS4	New Mexico Sulfur Springs	R09	32.87	5.18	2.16	1.88	1.43	0.13	0.32	0.00	0.00	0.00	0.13	0.24	0.03
NSS5	New Mexico Sulfur Springs	R10	28.16	2.31	1.14	0.98	0.72	0.10	0.15	0.00	0.00	0.00	0.07	0.21	0.02
NSS6	New Mexico Sulfur Springs	R11	28.34	41.42	2.75	2.37	1.78	0.14	0.45	0.00	0.00	0.00	0.07	0.59	0.04
NSS7	New Mexico Sulfur Springs	R12	32.16	11.59	1.27	1.12	0.88	0.07	0.17	0.00	0.00	0.00	0.05	0.38	0.02
SLS1	Soda Lake Side	R13	48.36	4.28	2.06	1.74	1.24	0.11	0.39	0.00	0.00	0.00	0.08	0.36	0.03
SAC1	San Antonio cabin	R14	65.18	6.54	0.50	0.44	0.34	0.03	0.07	0.00	0.00	0.00	0.05	0.14	0.01
CLS1	Caribbean Lake Spring	R15	75.19	34.33	3.05	2.68	2.09	0.14	0.43	0.01	0.00	0.00	0.07	0.64	0.04
BHS 7	Baker Hot Springs	R16	48.59	4.45	1.21	1.05	0.80	0.07	0.18	0.00	0.00	0.00	0.12	0.14	0.02
SHS 1	Saratoga Hot Springs	R17	43.89	12.45	1.08	0.95	0.73	0.07	0.15	0.00	0.00	0.00	0.12	0.13	0.01
IHS 1	Indian Hot Springs	R18	52.23	10.33	0.83	0.71	0.53	0.04	0.13	0.01	0.00	0.00	0.11	0.10	0.01
FS 19	Fish Springs NWR	R19	64.92	17.18	1.68	1.44	1.05	0.08	0.29	0.00	0.00	0.00	0.05	0.47	0.02
FS 20	Fish Springs NWR	R20	72.58	16.14	3.10	2.68	2.02	0.20	0.45	0.01	0.00	0.00	0.07	0.69	0.05
Galveston	Control	R21	20.04	0.82	3.15	2.74	2.08	0.17	0.47	0.01	0.00	0.00	0.11	0.43	0.05
C. therm.	Control	R22	N/D	N/D	0.49	0.43	0.34	0.03	0.07	0.00	0.00	0.00	0.07	0.11	0.01
No Inoculum	Control	R23	N/D	N/D	0.09	0.08	0.06	0.01	0.01	0.00	0.00	0.00	0.02	0.05	0.00
NGYS 1	Norris Geyser Yellowstone NP	S01	31.84	3.37	1.07	0.92	0.69	0.05	0.17	0.01	0.00	0.00	0.03	0.42	0.01
NGYS 2	Norris Geyser Yellowstone NP	S02	53.46	7.26	1.26	1.07	0.78	0.06	0.22	0.01	0.00	0.00	0.03	0.68	0.02
NGYS 3	Norris Geyser Yellowstone NP	S03	22.74	12.28	2.43	2.10	1.60	0.13	0.35	0.03	0.00	0.00	0.16	0.21	0.03

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
NGYS 4	Norris Geyser Yellowstone NP	S04	28.24	5.90	1.39	1.20	0.92	0.06	0.21	0.01	0.00	0.00	0.05	0.39	0.02
NGYS 5	Norris Geyser Yellowstone NP	S05	29.96	1.06	0.94	0.82	0.63	0.05	0.14	0.00	0.00	0.00	0.10	0.13	0.01
NGYS 6	Norris Geyser Yellowstone NP	S06	52.61	9.34	0.32	0.28	0.21	0.02	0.05	0.00	0.00	0.00	0.11	0.04	0.00
NGYS 7	Norris Geyser Yellowstone NP	S07	65.87	10.48	1.19	1.02	0.78	0.05	0.19	0.01	0.00	0.00	0.14	0.12	0.02
NGYS 8	Norris Geyser Yellowstone NP	S08	20.71	3.50	0.61	0.53	0.40	0.04	0.09	0.00	0.00	0.00	0.11	0.08	0.01
NGYS 9	Norris Geyser Yellowstone NP	S09	18.91	3.49	1.00	0.86	0.66	0.05	0.16	0.00	0.00	0.00	0.07	0.19	0.01
NGYS 10	Norris Geyser Yellowstone NP	S10	32.98	6.30	1.24	1.08	0.83	0.07	0.17	0.01	0.00	0.00	0.08	0.21	0.02
NGYS 11	Norris Geyser Yellowstone NP	S11	51.43	10.88	2.34	1.95	1.36	0.10	0.49	0.00	0.00	0.00	0.05	0.65	0.03
NGYS 12	Norris Geyser Yellowstone NP	S12	29.78	5.47	0.85	0.74	0.56	0.05	0.12	0.00	0.00	0.00	0.05	0.21	0.01
NGYS 13	Norris Geyser Yellowstone NP	S13	53.36	9.53	0.05	0.05	0.03	0.00	0.01	0.00	0.00	0.00	0.04	0.02	0.00
NGYS 14	Norris Geyser Yellowstone NP	S14	21.94	38.73	3.12	2.69	2.01	0.15	0.51	0.01	0.00	0.00	0.10	0.42	0.04
NGYS 15	Norris Geyser Yellowstone NP	S15	49.07	7.03	1.72	1.49	1.14	0.07	0.28	0.00	0.00	0.00	0.04	0.56	0.02
NGYS 16	Norris Geyser Yellowstone NP	S16	47.15	20.94	1.43	1.25	0.97	0.06	0.22	0.00	0.00	0.00	0.04	0.51	0.02
NGYS 17	Norris Geyser Yellowstone NP	S17	28.73	3.69	2.02	1.74	1.30	0.09	0.33	0.01	0.00	0.00	0.11	0.26	0.03
NGYS 18	Norris Geyser Yellowstone NP	S18	14.34	3.47	1.64	1.42	1.07	0.09	0.25	0.01	0.00	0.00	0.05	0.39	0.02
NGYS 19	Norris Geyser Yellowstone NP	S19	26.79	3.87	0.61	0.52	0.38	0.03	0.11	0.00	0.00	0.00	0.04	0.23	0.01
SMYS 1	Sentinel Meadows Yellowstone NP	S20	71.23	18.93	2.12	1.80	1.30	0.10	0.39	0.00	0.00	0.00	0.14	0.23	0.03
SMYS 2	Sentinel Meadows Yellowstone NP	S21	63.99	9.90	1.55	1.32	0.96	0.07	0.28	0.00	0.00	0.00	0.03	0.74	0.02
SMYS 3	Sentinel Meadows Yellowstone NP	S22	44.62	6.13	0.81	0.70	0.53	0.04	0.12	0.00	0.00	0.00	0.08	0.14	0.01
SMYS 4	Sentinel Meadows Yellowstone NP	S23	74.68	12.63	1.69	1.47	1.14	0.08	0.25	0.01	0.00	0.00	0.05	0.45	0.02
SMYS 5	Sentinel Meadows Yellowstone NP	S24	58.17	6.95	0.75	0.65	0.50	0.05	0.10	0.00	0.00	0.00	0.06	0.18	0.01
SMYS 6	Sentinel Meadows Yellowstone NP	S25	61.77	10.53	0.67	0.57	0.42	0.04	0.11	0.00	0.00	0.00	0.07	0.13	0.01

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
HVYS 1	Hidden Valley Yellowstone NP	S26	57.32	9.82	1.19	1.03	0.79	0.06	0.17	0.01	0.00	0.00	0.07	0.26	0.02
HVYS 2	Hidden Valley Yellowstone NP	S27	36.53	7.25	2.37	2.01	1.46	0.11	0.43	0.00	0.00	0.00	0.12	0.29	0.03
HVYS 3	Hidden Valley Yellowstone NP	S28	18.09	2.27	0.99	0.86	0.66	0.06	0.14	0.01	0.00	0.00	0.06	0.27	0.02
HVYS 4	Hidden Valley Yellowstone NP	S29	28.16	3.85	1.28	1.11	0.83	0.05	0.21	0.01	0.00	0.00	0.02	0.84	0.02
HVYS 5	Hidden Valley Yellowstone NP	S30	51.38	6.14	1.29	1.11	0.82	0.08	0.21	0.01	0.00	0.00	0.03	0.67	0.02
HVYS 6	Hidden Valley Yellowstone NP	S31	40.69	50.61	0.85	0.74	0.55	0.06	0.13	0.00	0.00	0.00	0.16	0.07	0.01
HVYS 7	Hidden Valley Yellowstone NP	S32	34.63	6.44	1.50	1.31	1.00	0.07	0.22	0.01	0.00	0.00	0.05	0.47	0.02
HVYS 8	Hidden Valley Yellowstone NP	S33	33.92	12.58	2.64	2.31	1.79	0.13	0.36	0.02	0.00	0.00	0.10	0.37	0.04
HVYS 9	Hidden Valley Yellowstone NP	S34	41.73	40.58	1.18	1.02	0.75	0.08	0.19	0.00	0.00	0.00	0.09	0.17	0.02
HVYS 10	Hidden Valley Yellowstone NP	S35	30.26	14.11	1.47	1.28	0.97	0.10	0.21	0.00	0.00	0.00	0.14	0.14	0.02
HVYS 11	Hidden Valley Yellowstone NP	S36	35.51	3.62	1.98	1.67	1.18	0.12	0.38	0.00	0.00	0.00	0.04	0.66	0.02
HVYS 12	Hidden Valley Yellowstone NP	S37	42.15	70.62	0.88	0.78	0.61	0.05	0.12	0.00	0.00	0.00	0.14	0.08	0.01
WFYS 1	Whisky Flats Yellowstone NP	S38	34.19	3.30	1.42	1.24	0.96	0.07	0.21	0.01	0.00	0.00	0.08	0.26	0.02
WFYS 2	Whisky Flats Yellowstone NP	S39	92.04	19.90	0.79	0.67	0.48	0.05	0.14	0.00	0.00	0.00	0.09	0.12	0.01
FDYS 1	Firehole drive Yellowstone NP	S40	69.34	19.42	0.87	0.74	0.54	0.05	0.15	0.00	0.00	0.00	0.03	0.40	0.01
FHYS 2	Firehole drive Yellowstone NP	S41	59.41	7.89	1.04	0.91	0.71	0.05	0.15	0.00	0.00	0.00	0.12	0.12	0.01
FHYS 3	Firehole drive Yellowstone NP	S42	79.11	9.84	0.57	0.49	0.37	0.03	0.09	0.00	0.00	0.00	0.03	0.23	0.01
FHYS 4	Firehole drive Yellowstone NP	S43	67.53	10.92	1.68	1.43	1.04	0.09	0.29	0.00	0.00	0.00	0.06	0.38	0.02
FHYS 5	Firehole drive Yellowstone NP	S44	50.22	4.98	0.19	0.17	0.12	0.01	0.03	0.00	0.00	0.00	0.41	0.01	0.00
FHYS 6	Firehole drive Yellowstone NP	S45	38.39	5.21	1.15	0.99	0.75	0.06	0.18	0.01	0.00	0.00	0.03	0.50	0.02
STYS 1	Sulfatara Trail Yellowstone NP	S46	34.12	22.41	1.45	1.27	0.98	0.08	0.21	0.00	0.00	0.00	0.07	0.29	0.02
STYS 2	Sulfatara Trail Yellowstone NP	S47	20.06	1.48	2.58	2.23	1.70	0.11	0.41	0.02	0.00	0.00	0.09	0.42	0.04
STYS 3	Sulfatara Trail Yellowstone NP	S48	36.33	23.25	1.84	1.61	1.25	0.09	0.27	0.00	0.00	0.00	0.46	0.05	0.02

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
Galveston	Control	S49	18.89	0.78	1.43	1.23	0.92	0.08	0.23	0.01	0.00	0.00	0.10	0.21	0.02
C. therm.	Control	S50	N/D	N/D	2.08	1.76	1.27	0.14	0.34	0.01	0.00	0.00	0.04	0.86	0.03
No Inoculum	Control	S51	N/D	N/D	0.16	0.14	0.11	0.01	0.02	0.00	0.00	0.00	0.02	0.11	0.00
SWRN1	Stillwater NWR	T01	47.10	5.68	0.88	0.75	0.55	0.04	0.15	0.00	0.00	0.00	0.07	0.19	0.01
SWRN2	Stillwater NWR	T02	30.97	6.20	2.44	2.13	1.64	0.12	0.36	0.01	0.00	0.00	0.08	0.44	0.04
SWRN3	Stillwater NWR	T03	34.31	6.74	1.54	1.34	1.03	0.07	0.24	0.00	0.00	0.00	0.02	0.93	0.02
GBS 1	Great Boiling Springs	T04	65.18	5.09	2.13	1.80	1.30	0.10	0.40	0.01	0.00	0.00	0.07	0.41	0.03
GBS 2	Great Boiling Springs	T05	64.55	6.08	1.60	1.37	1.01	0.08	0.28	0.00	0.00	0.00	0.05	0.47	0.02
GBS 3	Great Boiling Springs	T06	69.65	7.35	1.66	1.43	1.07	0.09	0.27	0.01	0.00	0.00	0.05	0.44	0.02
GBS 4	Great Boiling Springs	T07	73.16	4.98	0.99	0.85	0.62	0.05	0.18	0.00	0.00	0.00	0.05	0.28	0.01
GBS 5	Great Boiling Springs	T08	78.22	3.69	0.37	0.32	0.23	0.02	0.07	0.00	0.00	0.00	0.04	0.14	0.01
GBS 6	Great Boiling Springs	T09	80.84	3.91	1.51	1.29	0.96	0.07	0.25	0.01	0.00	0.00	0.06	0.36	0.02
GBS 7	Great Boiling Springs	T10	37.30	3.32	0.51	0.45	0.35	0.02	0.07	0.00	0.00	0.00	0.05	0.15	0.01
GBS 8	Great Boiling Springs	T11	50.58	3.96	0.09	0.07	0.05	0.00	0.01	0.00	0.00	0.00	0.03	0.04	0.00
GBS 9	Great Boiling Springs	T12	70.90	15.31	0.34	0.29	0.21	0.02	0.06	0.00	0.00	0.00	0.05	0.10	0.00
FRN 1	Fly Ranch	T13	66.55	10.01	1.57	1.34	0.96	0.11	0.26	0.01	0.00	0.00	0.06	0.37	0.02
FRN 2	Fly Ranch	T14	57.53	3.89	1.33	1.16	0.90	0.05	0.20	0.01	0.00	0.00	0.06	0.31	0.02
FRN 3	Fly Ranch	T15	43.97	3.16	1.36	1.18	0.91	0.06	0.20	0.01	0.00	0.00	0.03	0.61	0.02
FRN 4	Fly Ranch	T16	33.72	1.68	1.37	1.19	0.92	0.07	0.20	0.00	0.00	0.00	0.06	0.35	0.02
FRN 5	Fly Ranch	T17	45.42	2.77	1.83	1.61	1.25	0.10	0.26	0.00	0.00	0.00	0.05	0.54	0.03
Galveston	Control	T18	19.50	0.37	1.55	1.36	1.06	0.09	0.21	0.00	0.00	0.00	0.04	0.62	0.02
C. therm.	Control	T19	N/D	N/D	1.23	1.08	0.84	0.06	0.17	0.00	0.00	0.00	0.04	0.46	0.02
No Inoculum	Control	T20	N/D	N/D	1.37	1.19	0.91	0.05	0.23	0.00	0.00	0.00	0.04	0.45	0.02
CBHS 1	Buckeye Hot Spring	U01	11.10	0.57	0.03	0.03	0.02	0.00	0.01	0.00	0.00	0.00	0.12	0.00	0.00
CBHS 2	Buckeye Hot Spring	U02	24.59	1.84	0.92	0.80	0.62	0.05	0.13	0.00	0.00	0.00	0.10	0.14	0.01
CBHS 3	Buckeye Hot Spring	U03	15.30	0.47	2.83	2.40	1.74	0.15	0.50	0.00	0.01	0.00	0.11	0.37	0.04
CBHS 4	Buckeye Hot Spring	U04	78.53	18.83	1.36	1.18	0.89	0.09	0.21	0.00	0.00	0.00	0.06	0.34	0.02
MLNB 1	Mono Lake Navy Beach	U05	39.35	7.88	1.33	1.15	0.87	0.06	0.22	0.00	0.00	0.00	0.08	0.23	0.02

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
MLNB 2	Mono Lake Navy Beach	U06	49.41	3.64	1.44	1.27	1.00	0.07	0.20	0.00	0.00	0.00	0.10	0.21	0.02
MLNB 3	Mono Lake Navy Beach	U07	52.15	4.98	1.46	1.26	0.95	0.10	0.21	0.00	0.00	0.00	0.16	0.13	0.02
MLNB 4	Mono Lake Navy Beach	U08	27.77	2.16	0.42	0.36	0.27	0.02	0.07	0.00	0.00	0.00	0.10	0.06	0.01
MLNB 5	Mono Lake Navy Beach	U09	28.10	1.49	0.34	0.29	0.21	0.02	0.05	0.00	0.00	0.00	0.06	0.08	0.00
MLIS 1	Mono Lake Island Hot Springs (Paoha Island)	U10	42.40	3.46	1.06	0.93	0.72	0.06	0.15	0.00	0.00	0.00	0.13	0.11	0.01
MLIS 2	Mono Lake Island Hot Springs (Paoha Island)	U11	47.75	3.06	1.79	1.55	1.17	0.09	0.29	0.00	0.00	0.00	0.14	0.17	0.02
MLIS 3	Mono Lake Island Hot Springs (Paoha Island)	U12	35.63	4.29	0.51	0.44	0.34	0.02	0.08	0.00	0.00	0.00	0.07	0.11	0.01
MLIS 4	Mono Lake Island Hot Springs (Paoha Island)	U13	83.14	7.30	1.52	1.35	1.07	0.08	0.19	0.00	0.00	0.00	0.11	0.20	0.02
MLIS 5	Mono Lake Island Hot Springs (Paoha Island)	U14	62.53	4.28	1.13	0.97	0.72	0.07	0.18	0.00	0.00	0.00	0.11	0.14	0.01
MLIS 6	Mono Lake Island Hot Springs (Paoha Island)	U15	47.33	3.77	2.53	2.21	1.68	0.18	0.35	0.00	0.00	0.00	0.05	0.70	0.04
MLIS 7	Mono Lake Island Hot Springs (Paoha Island)	U16	43.02	5.28	2.36	2.08	1.63	0.12	0.33	0.00	0.00	0.00	0.06	0.56	0.03
HCMA 1	Hot Creek at Mammoth	U17	38.51	4.25	1.55	1.35	1.02	0.09	0.24	0.00	0.00	0.00	0.07	0.33	0.02
HCMA 2	Hot Creek at Mammoth	U18	39.10	3.62	1.65	1.41	1.04	0.08	0.29	0.00	0.00	0.00	0.08	0.30	0.02
HCMA 3	Hot Creek at Mammoth	U19	34.70	2.87	1.98	1.72	1.31	0.10	0.31	0.00	0.00	0.00	0.05	0.56	0.03
HCMA 4	Hot Creek at Mammoth	U20	38.34	6.11	5.25	4.58	3.50	0.32	0.74	0.02	0.00	0.00	0.17	0.44	0.07
HCMA 5	Hot Creek at Mammoth	U21	43.88	4.19	4.21	3.71	2.92	0.19	0.60	0.00	0.00	0.00	0.25	0.25	0.06
OLCA 1	Owens Lake (dry lake)	U22	48.54	14.17	6.41	5.56	4.21	0.35	1.00	0.00	0.00	0.00	0.36	0.25	0.09
OLCA 2	Owens Lake (dry lake)	U23	10.96	30.85	2.23	1.97	1.55	0.10	0.31	0.01	0.00	0.00	0.25	0.12	0.03
OLCA 3	Owens Lake (dry lake)	U24	10.62	27.14	5.30	4.65	3.64	0.25	0.76	0.00	0.00	0.00	0.31	0.22	0.07
Galveston	Control	U25	17.70	3.95	2.71	2.37	1.82	0.15	0.40	0.00	0.00	0.00	0.18	0.21	0.04
C. therm.	Control	U26	N/D	N/D	2.53	2.21	1.69	0.13	0.38	0.01	0.00	0.00	0.31	0.12	0.04
No Inoculum	Control	U27	N/D	N/D	4.16	3.69	2.95	0.19	0.55	0.00	0.00	0.00	0.18	0.31	0.06
HBSP1	Hapuna Beach SP	V01	20.10	3.60	0.62	0.55	0.44	0.03	0.08	0.00	0.00	0.00	0.10	0.09	0.01
HBSP2	Hapuna Beach SP	V02	22.09	3.50	0.84	0.70	0.48	0.03	0.19	0.00	0.00	0.00	0.06	0.17	0.01
HBSP3	Hapuna Beach SP	V03	22.64	5.10	1.15	0.98	0.74	0.03	0.21	0.00	0.00	0.00	0.11	0.15	0.02
APHW1	Alchiline ponds	V04	37.19	4.50	1.11	0.96	0.73	0.06	0.17	0.00	0.00	0.00	0.17	0.09	0.02

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
APHW2	Alchiline ponds	V05	24.77	2.30	1.08	0.93	0.70	0.03	0.19	0.00	0.00	0.00	0.08	0.18	0.02
APHW3	Alchiline ponds	V06	48.68	8.10	0.63	0.55	0.42	0.02	0.11	0.00	0.00	0.00	0.08	0.12	0.01
APHW4	Alchiline ponds	V07	28.92	2.80	3.61	3.17	2.44	0.23	0.49	0.00	0.00	0.00	0.11	0.46	0.05
NELH1	Natural Energy Lab Hawaii	V08	59.46	10.90	2.05	1.77	1.35	0.07	0.35	0.00	0.00	0.00	0.10	0.29	0.03
NELH2	Natural Energy Lab Hawaii	V09	20.25	2.80	2.63	2.24	1.64	0.14	0.46	0.00	0.00	0.00	0.09	0.38	0.04
NELH3	Natural Energy Lab Hawaii	V10	35.15	6.80	2.51	2.18	1.67	0.10	0.41	0.00	0.00	0.00	0.12	0.28	0.03
NELH4	Natural Energy Lab Hawaii	V11	20.47	2.60	0.29	0.25	0.17	0.02	0.05	0.00	0.00	0.00	0.11	0.04	0.00
KKHW1	Kekahi Kai State Park	V12	15.82	2.80	3.22	2.76	2.02	0.23	0.51	0.00	0.00	0.00	0.15	0.30	0.04
KKHW2	Kekahi Kai State Park	V13	87.49	44.80	1.50	1.31	1.01	0.05	0.25	0.00	0.00	0.00	0.03	0.81	0.02
KKHW3	Kekahi Kai State Park	V14	84.20	38.30	4.38	3.83	3.00	0.15	0.68	0.00	0.00	0.00	0.10	0.63	0.06
KKHW4	Kekahi Kai State Park	V15	85.96	50.40	3.97	3.47	2.70	0.17	0.60	0.00	0.00	0.00	0.16	0.36	0.06
KKHW5	Kekahi Kai State Park	V16	65.23	19.00	4.24	3.71	2.90	0.14	0.67	0.00	0.00	0.00	0.08	0.80	0.06
Galveston	Control	V17	24.30	0.40	2.79	2.38	1.76	0.13	0.49	0.00	0.00	0.00	0.06	0.59	0.04
No Inoculum	Control	V18	0.00	0.00	3.25	2.81	2.12	0.18	0.51	0.00	0.00	0.00	0.07	0.61	0.04
ONHW1	Onekahakaha Beach park	V19	72.46	28.70	3.38	2.90	2.13	0.20	0.56	0.00	0.00	0.01	0.09	0.48	0.04
ONHW2	Onekahakaha Beach park	V20	46.38	10.60	7.11	6.31	5.02	0.38	0.91	0.01	0.00	0.00	0.12	0.80	0.10
ONHW3	Onekahakaha Beach park	V21	41.12	7.10	2.38	2.08	1.60	0.14	0.34	0.00	0.00	0.00	0.08	0.40	0.03
ONHW4	Onekahakaha Beach park	V22	19.80	3.30	3.26	2.69	1.81	0.17	0.71	0.00	0.00	0.00	0.15	0.28	0.04
WRHW1	Wailoa River State Park	V23	62.57	15.50	2.56	2.29	1.85	0.10	0.34	0.00	0.00	0.00	0.17	0.22	0.04
AFHW1	Akaka Falls State Park	V24	44.31	10.20	2.54	2.24	1.75	0.16	0.33	0.00	0.00	0.00	0.09	0.39	0.04
AFHW2	Akaka Falls State Park	V25	78.66	49.90	2.84	2.41	1.73	0.19	0.50	0.00	0.00	0.00	0.12	0.31	0.04
AFHW3	Akaka Falls State Park	V26	73.57	51.50	2.46	1.94	1.18	0.09	0.68	0.00	0.00	0.00	0.11	0.27	0.03
CPHW1	Carlsmith County Park	V27	81.14	22.50	2.18	1.77	1.15	0.10	0.52	0.00	0.00	0.00	0.05	0.52	0.03
CPHW2	Carlsmith County Park	V28	22.97	0.70	2.84	2.43	1.75	0.23	0.45	0.00	0.00	0.00	0.06	0.64	0.04
CPHW3	Carlsmith County Park	V29	83.16	28.80	2.96	2.59	2.08	0.01	0.47	0.03	0.00	0.00	0.10	0.39	0.04
CPHW4	Carlsmith County Park	V30	51.00	12.40	1.64	1.40	1.07	0.01	0.31	0.02	0.00	0.00	0.11	0.20	0.02

Table 23 continued

Sample Name	*Site Name*	*Fermen-tation ID*	*M %*	*V %*	*Aeq*	*Change in Acid Conc g L^{-1}*	*Acetic g L^{-1}*	*Propionic g L^{-1}*	*Butyric g L^{-1}*	*Valeric g L^{-1}*	*Caproic g L^{-1}*	*Heptanoic g L^{-1}*	*Conv.*	*Select.*	*Yield*
Galveston	Control	V31	17.57	0.90	0.42	0.36	0.27	0.01	0.08	0.00	0.00	0.00	0.05	0.12	0.01

Abbreviations: C. therm, *Clostridium thermocellum*; M, moisture ; V and VS, volatile solids; Aeq, acetic acid equivalents; Conc, concentration; Conv., conversion; Select., selectivity;
VS: All combustible materials (i.e., biomass)
Aeq: Equivalents of acetic acid in all higher molecular weight acids
Conversion: (Proportion of VS converted to products)= VS digested/VS loaded
Selectivity: (Proportion of digested VS becoming acids)= Total carboxylic acids produced/VS digested
Yield: Total carboxylic acids produced/VS loaded

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Hollister EB, **Hammett AM**, Holtzapple MT, Gentry TJ, Wilkinson HH. (2011) Microbial community composition and dynamics in a semi-industrial-scale facility operating under the MixAlco™ bioconversion platform. *Journal of Applied Microbiology* **110**:587-596.

Hollister EB, Engledow AS, **Hammett AJM**, Provin TL, Wilkinson HH, Gentry TJ. (2010). Shifts in microbial community structure along an ecological gradient of hypersaline soils and sediments. *The ISME Journal* **4**:829-838.

Honors and Awards:

Texas A&M University Regents Fellowship, 2007-2008
First place in the Genomics Education Poster Scholarship program, a nationwide competition sponsored by LI-COR Biosciences Corporation, 2006
Texas Woman's University Biology Department Scholarship, 2006
Chancellor's Student Research Scholars Award at Texas Woman's University, 2006