Biomarker Analysis of Carbon Rich Shales in the Bambuí Group

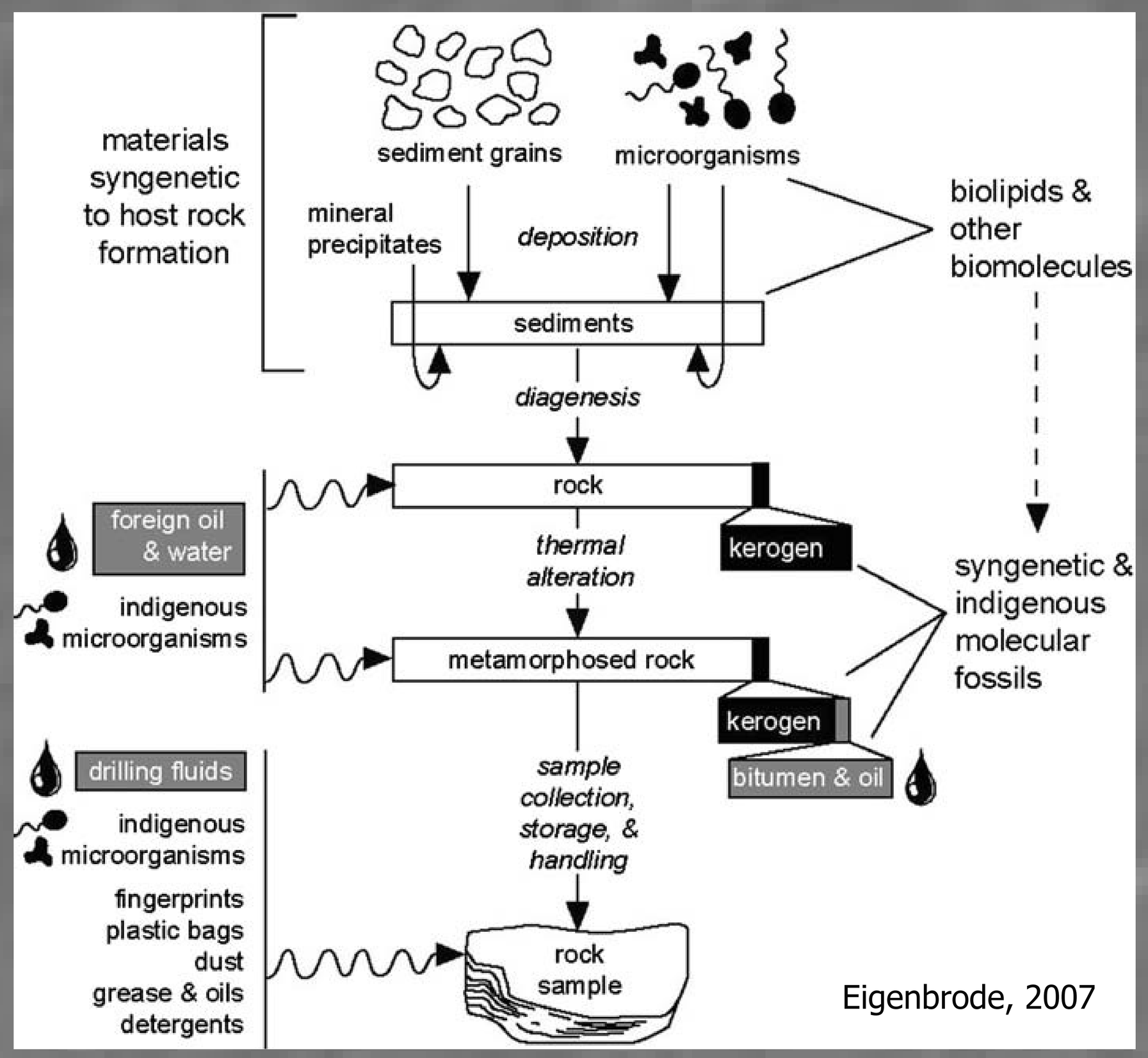
Jess Little, Geology Department, University of Maryland-College Park

Advisors: Kristen Miller and Dr. Alan J. Kaufman

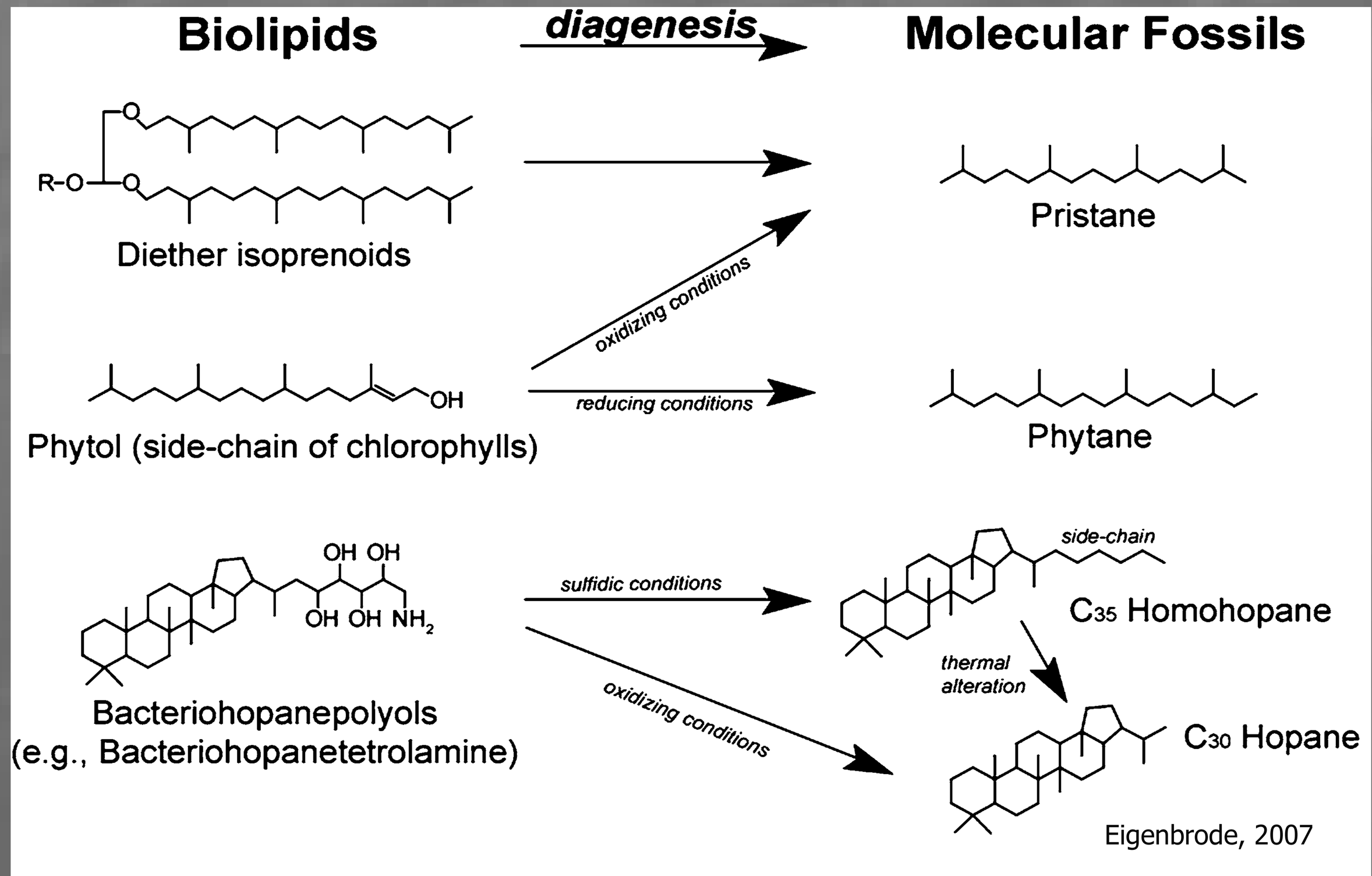
Abstract

My project will focus on the structural biomarker analysis of carbonate shales from the Neoproterozoic Bambuí Group of Brazil. The study of biomarkers is an important tool for understanding biological evolution during the Neoproterozoic. My samples are from the Lagoa do Jacaré Formation within the Bambuí Group. This is the first study to analyze biomarkers from the Lagoa do Jacaré Formation. Biomarkers will be extracted from 30 samples from one continuous exploratory core (PSB-14-MG). The samples collected from the core range in depth from 12.6 m to 145.55 m with an average spacing of approximately 4.7 m. The biomarkers will be extracted from these samples and fractionated into saturated compounds, aromatic compounds, and polar compounds. The saturated and aromatic compounds will then be analyzed using a Gas Chromatograph-Mass Spectrometer (GC-MS) at the Carnegie Institute for Science. The resulting mass chromatograms and mass spectrometer will be used to identify the biomarkers and calculate key ratios that are indicative of thermal maturity. The extracted biomarkers will also be structurally identified to determine if they are syngenic to the host rock and biologic in origin. Ultimately my project will provide insight about the organisms that were present during an interglacial interval of the Neoproterozoic and the environment in which they lived.

Background

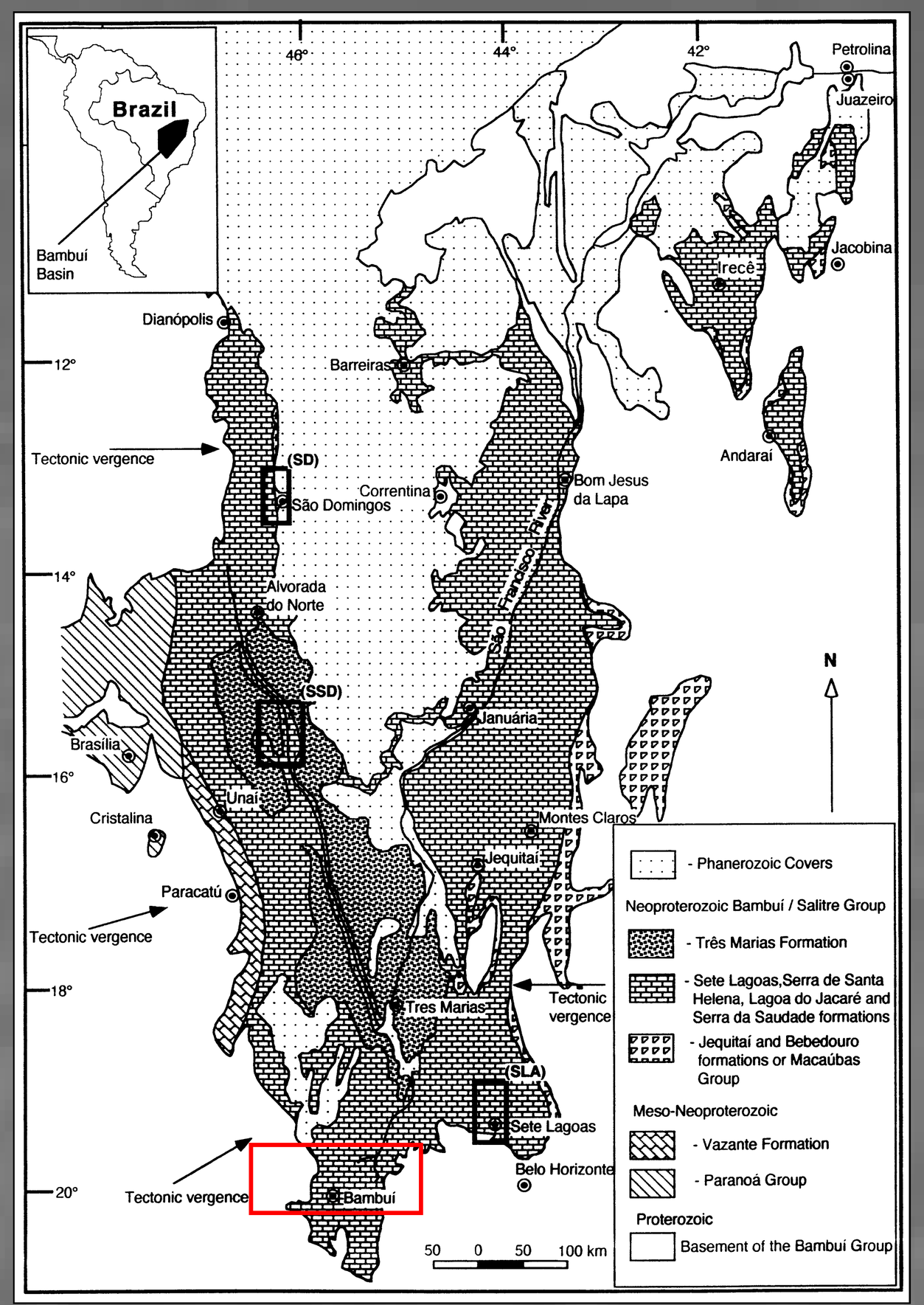


Biomarkers are fossilized lipids which have survived degradation (Eigenbrode, 2007). Biomarkers occur in sedimentary rocks and are incorporated into the sediment as kerogen or bitumen (Waldbauer et al., 2008). Biomarkers may be syngenic or non-syngenic. Syngenic biomarkers were deposited as the rock was forming. Non-syngenic biomarkers are biomarkers which were deposited by a secondary media as it flowed through the host rock. Biomarkers are sensitive to contamination (Waldbauer et al., 2008). In the field the core may be contaminated by the drill fluid which is used with the drill which takes the core. Contamination in the lab can come from lab equipment which has not been properly cleaned.



As lipids undergo diagenesis, they break down into more thermodynamically stable forms by clearing their functional side chains and sometimes their multiple bonds hence becoming more saturated. The structure of the diagenetic product depends on the structure of the original lipid and the type of degradation, or diagenetic conditions Common diagenetic fluids vary in their reduction potential and the amount of H2S which is available, so that the conditions may be oxic, anoxic, or sulfidic.

Geologic Setting



Santos, 2000

The Bambuí Group is a thick carbonate succession which overlies a glacial unit (Cruz-Vieira et al., 2007). Approximately 250 m above the glacial deposits is the Lagoa do Jacaré Formation, which primarily consists of siltstones, marls, and black organic rich oolitic limestones (Cruz-Vieira et al., 2007, Kaufman, Pers. Com.). The Lagoa do Jacaré Formation is approximately 740 Ma although radiometric constraints are lacking (Alkmim et al., 2006). This formation is of lower greenschist metamorphic grade (Iyer et al., 1995). The low metamorphic grade makes this an ideal location for a biomarker study (Guido et al., 2007).

Hypotheses

I hypothesize the thermal maturity of the samples will be low.

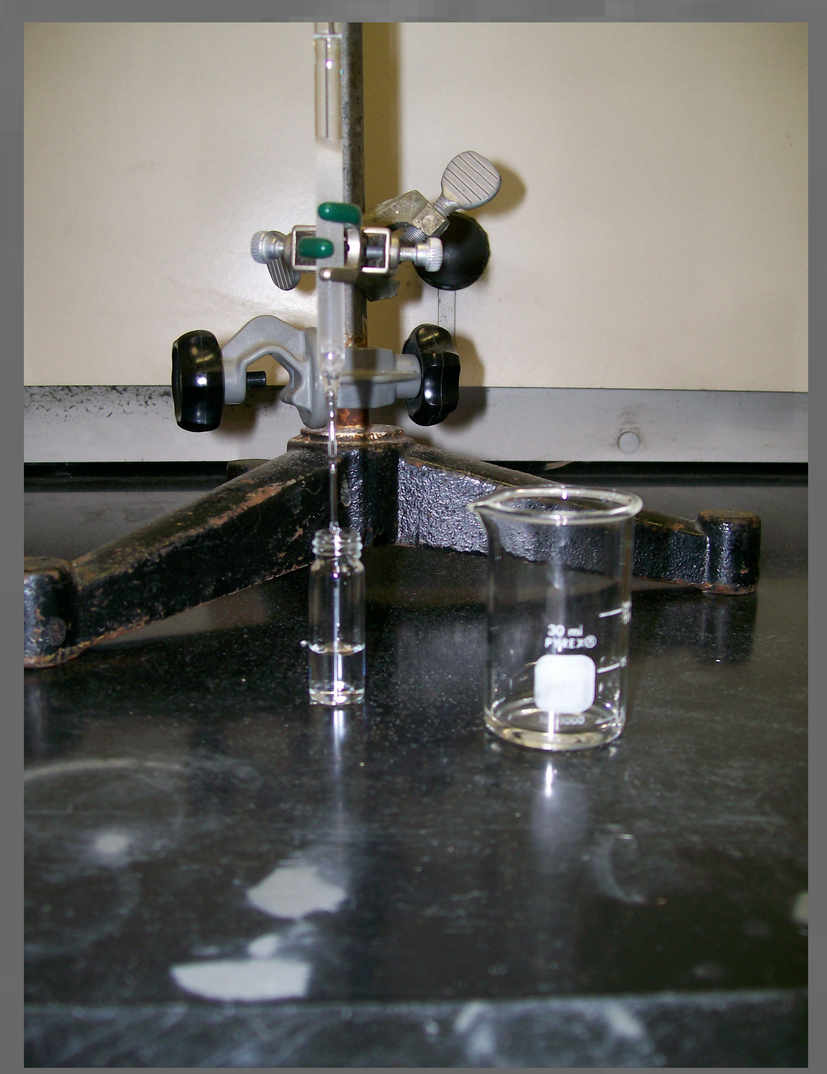
I also hypothesize the biomarkers in these samples are syngenic and were not deposited by the flow through of another media

Methods

Thirty organic rich black shale samples were collected from one core (PSB-14-MG). The samples were collected by Nick Geboy in 2005. The core was separated into individual samples based on depth (Table 1). The depths were chosen for my samples were based on which parts of the core were most organic rich, had not shown any secondary mineralization, or veining.

Approximately 100g of each sample were taken from the core. The outer 0.5 cm was removed first, and then the sample was broken in 0.5 cm3 pieces. These pieces were cleaned with Milli-Q water and dipped in dichloromethane. The cleaned pieces were then crushed into powder using a mill and puck shatter box. All of my samples have been crushed by Kristen Miller. Next the samples will be extracted.

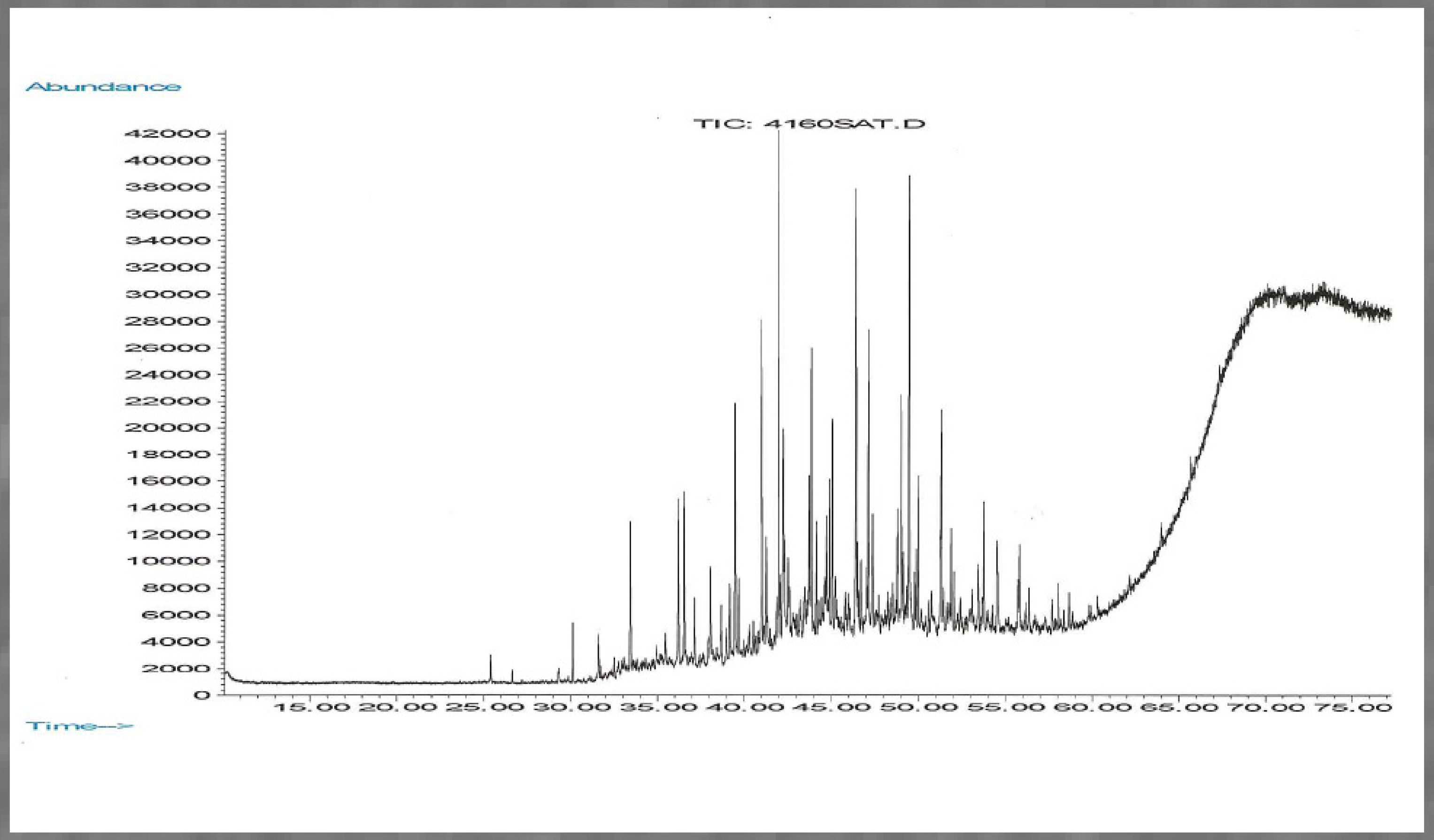
Initially 40-90 g of the powdered sample is weighed and placed into an ashed jar. Each jar will contain 15 g of powdered sample. Approximately 25 mL will be added to each sample. The samples will then sonicate twice for 30 minutes and will be left allowing the rock powder to settle (Waldbauer et al. 2008). The extract and solvent are then pooled and filtered through a wide bore column packed with silica gel and then run over acid activated copper pellets to remove elemental sulfur (Waldbauer et al. 2008).



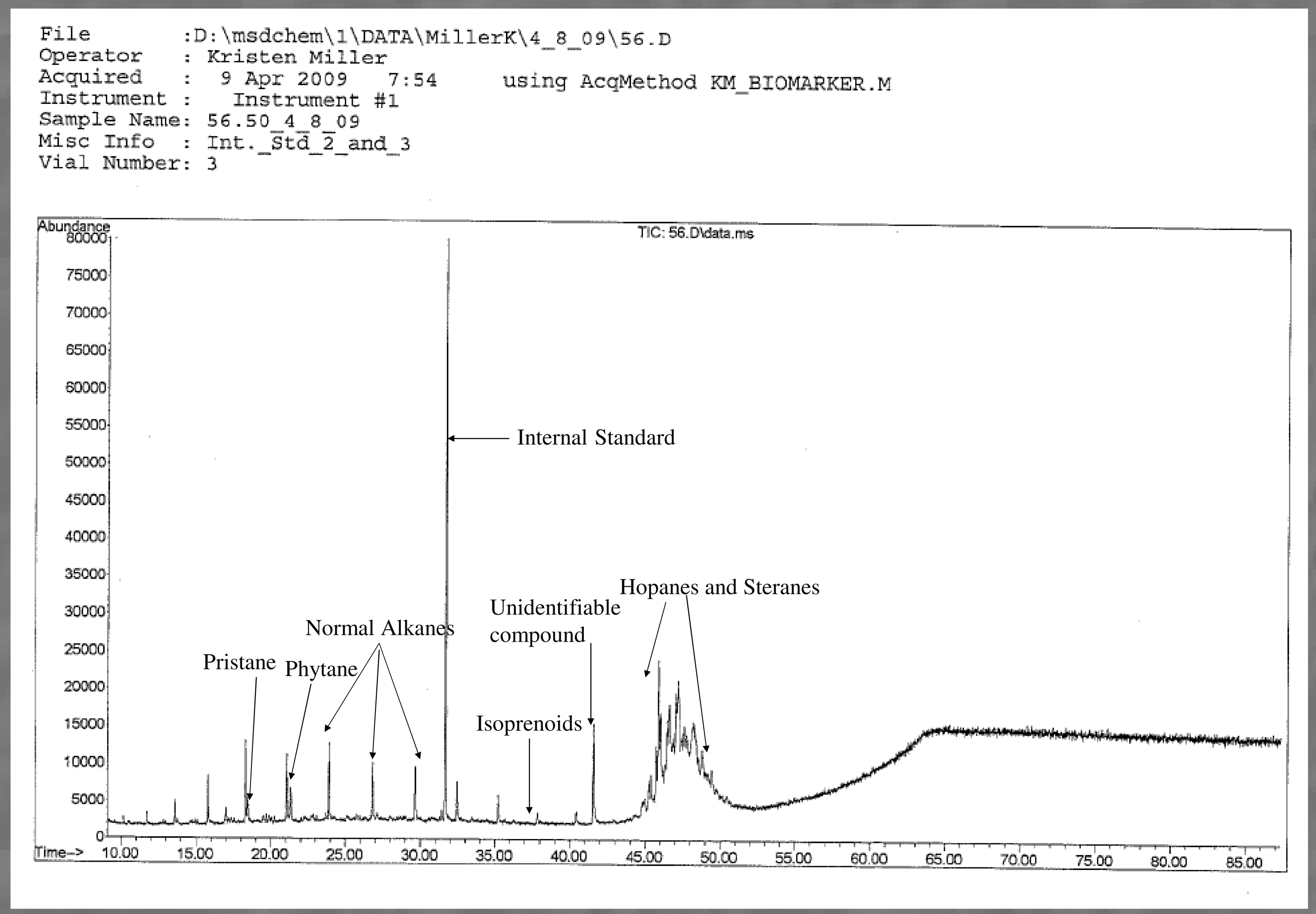
The samples concentrated by evaporation with a vacuum to a volume of approximately 40 μL. 20 μL of each sample is then set on activated silica gel in an ashed aluminum cup and left to dry over night. The sample is then poured into a pipette with 0.6 g of activated silica gel. Using liquid column chromatography the samples are fractionated into saturated compounds using 1.5 mL of hexane, aromatic compounds with 3 mL hexane:dichloromethane (4:1 ratio), and polar compounds with dichloromethane:methanol (7:3 ratio). The saturated and aromatic compounds are then analyzed for each sample in a GC-MS.

Preliminary Observations and Results

To this date three saturate fractions have been analyzed by GC-MS. Based on the metamorphic grade for the host rock of my samples, which is lower greenschist. There is also little evidence that liquid hydrocarbon has flowed through my samples because of the absence of veins. During the Neoproterozoic life was largely microbial (Eigenbrode, 2008) and mainly consisted of cyanobacteria, green sulfur bacteria, aerobic eukaryotes, as well as other microbial life, but another molecular fossil which will be interesting if found is 24-Isopropylcholestane (24-IPC) which is likely indicative of demosponges. This is important because carbon evidence of sponges has been found in this time period, but only in the form of carbon evidence and so far is rare. If carbon evidence is found in these samples for demosponges, it will be very important for the geologic community.



This is the original chromatogram for sample 41.60. 41.60 is the depth of the sample in meters. SAT is written at the end of the sample to denote the sample being run through the GC-MS is the saturated fraction. During this run, there was an issue with the GC-MS and pieces of the column falling into the sample and being counted as data.



This is the chromatogram for sample 56.50, the saturate fraction. This chromatogram is good example of what a chromatogram should look like. In this chromatogram the different saturated compounds are clearly shown. Each peak represents a compound. The larger peaks are normal alkanes. There is an outstanding large peak which is the internal standard. This internal standard is a saturate and has a chain of 22 carbons. The peak directly next to the C17 normal alkane is pristane. The peak directly next to the C18 normal alkane is phytane. The even smaller peaks on the chromatograms are acyclic isoprenoids. This chromatogram shows there are biomarker compounds in our samples.

Time Line

I will be working in the Kaufman Laboratory this summer and plan to have finished extracting and fractionating my samples by the first week of August and I plan to have chromatograms for all of my samples by September 1st, 2009. The results will be obtained by running each sample through the GC-MS at the Carnegie Institute for Science with the help of George Cody at a predetermined access interval. I will then analyze the compounds present in each sample and their ratios before the last week of November.