ABSTRACT

There is a limited amount of scientific literature regarding the diversity of soil microorganisms. Diversity and recognition of soil organisms is important because of the ever-growing agricultural need; soil microorganisms contribute to the overall quality of the soil and could be the key to improving farming soil. This investigation analyzed the living community within a soil sample collected on the Baylor University campus under a Southern Live Oak tree (*Quercus virginiana)* with the objective of determining experimental metadata and soil microorganism diversity. The soil was collected with a plastic spoon and transferred to a small plastic bag, then taken to the lab for metadata to be collected. The soil texture was sandy loam with a 2.27% water content and 7.2 pH. After metadata was collected, DNA was extracted through the silica bead method. The extracted DNA was then purified with 80% isopropanol alcohol and run through a vacuum manifold multiple times. The purified DNA was then run through gel electrophoresis to identify the general presence of DNA. PCR was then run and tested positive. The 18s, v4 region of DNA was amplified and will be sent out for sequencing.