
H26 Biodiversity of Functional Genes: An Aid in Soil Provenance

Priyanka Kushwaha, MS*, Florida International University, 11200 SW 8th Street, Miami, FL 33174; Jacqueline Zayas, BS, Florida International University, 11200 SW 8th Street, Miami, FL 33199; Yanie Oliva, BS, Florida International University, 11200 SW 8th Street, Miami, FL 33199; Maria A. Mendoza, PhD, 11200 SW 8th Street, Biological Sciences, OE 167, Miami, FL 33199; Beatrice Kallifatidis, MS, 11200 SW 8th Street, Bldg. OE/Room 167, Miami, FL 33199; and DeEtta Mills, PhD, Florida International University, OE 167, Biological Sciences, 11200 SW 8th Street, Miami, FL 33199

The goal of this presentation is to acquaint attendees with the use of DNA microbial profiling for discrimination/comparisons of soil samples. Also, attendees will gain insight on the use of functional markers to define microbial communities and how their use will strengthen the crime scene investigations involving soil as evidence.

This presentation will impact the forensic science community by laying the foundation to adopt the use of functional markers over universal markers as they represent the true microbial community profile and would be better for studying soil structure.

Soils are treated as important pieces of evidence in forensic investigations owing to their mineral and organic properties. Most often, soils are examined utilizing physical properties such as color, particle size, and mineral content; however, these techniques do not always result in successful categorization of the samples. Hence, laying the path to complementary approaches such as that proposed by Horswell et al. DNA profiling of soil bacterial communities using terminal restriction fragment length polymorphism can be employed for forensic comparison and discrimination of soils. This method is advantageous as it does not require a large sample size and the equipment is already owned by the forensic laboratories for human DNA analysis, making it more cost-effective.

Studies have demonstrated that microbial soil community structure can be determined from small soil samples across different locations and can be used for comparisons. Based on the existing ecological literature, it is suggested that variations exist in microbial community profiles across land management and vegetation types. Thus, microbial community profiling can potentially be employed as an intelligence tool for the providence of unknown soil samples collected from crime scenes.

Soil bacterial community profiles have been categorized using 16S rRNA hypervariable domains. These domains are effective in constructing a DNA profile that would enable discrimination between various soil samples; however, 16S rRNA profile alone is not adequate to establish the functional diversity of these microbes. Microbes play an important role in maintaining the stability of soils by cycling the biochemical nutrients such as carbon, phosphorus, nitrogen, sulfur, and iron. These processes are carried out by the enzymes produced by soil microorganisms. Thus, investigation of these functional enzymes can provide a better understanding of the function of the soils.

The objective of this study was to compare the functional diversity of microbial communities among different soil types: Lauderhill Dania-Pahokee (soil type 2) and Perrine-Biscayne-Pennsuco (soil type 4) of Miami-Dade County, FL.

DNA was extracted from samples (n=36) collected from one transect belonging to each soil type. Degenerate primers for *mcrA*, *cel48*, and *dsrA* were used to amplify the gene using polymerase chain reaction followed by cloning and sequencing. Sequences were analyzed by Basic Local Alignment Search Tool (BLAST) and subsequently aligned to construct a phylogenetic tree.

Comparison of sequences of the *mcrA* gene obtained from KNT and CS transect with sequences from other Florida studies resulted in close alignment with *Methanothermobacter thermautotrophicus*; however, many were not associated with any known reference samples. The KNT- and CS-labeled sequences associated almost exclusively with either uncultured archaea or with the uncultured euryarchaeote from oligotrophic soils in the northern Everglades. While some of the clones from the two soil types examined in Miami-Dade County grouped together with a particular soil type, there was overlap in the clones from the different soil types. These overlaps for the gene *mcrA* are indicative of saturated anoxic soils which are also useful for discrimination of environmental ecosystems. Thus, the study of these overlaps is important as it can also provide useful information.

The assessment of phylogenetic and functional abilities of microbial communities will clarify the importance of microbes for soil function and hence define its structure. A well-characterized structure can thus be of extreme importance in soil provenance.

Functional Genes, Microbial Community Profiling, Soils