H19 The Assessment of GeoChip™ Functional Gene Microarray as an Aid for Soil Provenance

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The goal of this presentation is to demonstrate the use of the functional gene microarray GeoChip™ 5.0. This array can be used for discrimination and provenance of soil samples. This technique is a useful platform to study microbial communities and how their functional guild associations can strengthen the forensic investigations of soil.

This presentation will impact the forensic science community by demonstrating the utility of functional gene analyses to refine the use of microbial community profiles for soil provenance. The GeoChip™ microarrays are rapid, robust, and can analyze approximately 180,000 functional genes with known taxonomic affiliations.

Soils have served as an important evidence in forensic investigations owing to their mineral and organic properties.[1] Nevertheless, the physical examination of soils does not always result in successful categorization of the samples. Therefore, complementary approaches such as DNA profiling of soil bacterial communities using Terminal Restriction Fragment Length Polymorphism (T-RFLP) for forensic comparison and discrimination of soils have been done in the past.[2] Although soil microbial profiles characterized using 16S ribosomal RNA (rRNA) hypervariable domains have been successful in discrimination of soil samples, the 16S rRNA domain is not adequate to establish microbial functional diversity.[3] As soil microbial community plays an important role in maintaining the fertility and stability of soils by cycling the biochemical nutrients, it is imperative to understand the function of these microbial communities and add those data to existing methods to refine the ability to discriminate between soil samples.[4]

GeoChip™ is a functional microarray that contains oligonucleotides probes for genes involved in all of the biogeochemical cycles, stress-related genes, *gyrB*-based phylogenetic markers, antibiotic resistance genes, and many others. Hence, it can detect thousands of microbial functional genes and phylogenetic markers at the same time.[5,6] The objective of the study was to compare the functional gene profiles of bacterial, archaeal, fungal, protists, and viral communities between two different soil types: Lauderhill Dania-Pahokee (Soil type 2; represented as Krome North Tower (KNT) transect) and Perrine-Biscayne-Pennsuco (Soil type 4; represented as Card Sound (CS) transect) of Miami-Dade County, FL.

DNA was extracted from soil samples (n=15) collected from one transect belonging to each soil type. DNA was precipitated with 100% ethanol and 0.3M NaOAc and DNA purity was assessed using Ultraviolet (UV) absorbance, dried and shipped to the Institute of Environmental Genomics (IEG), University of Oklahoma, Norman, OK, for processing the GeoChip™ 5.0 microarray. The raw data was pre-processed using the IEG data analysis pipeline and Principal Component Analysis (PCA) on carbon and sulfur cycle genes was performed.

PCA analysis of carbon and sulfur cycle genes resulted in clustering of the two soil samples onto different principle components. In addition, unpaired Student's t-test revealed the genes (*AceB*, *CsoS1_CcmK*, *CsoS2*, *FBP_aldolase*, *FBPase*, *GAPDH_Calvin*, *PRI*, and *TIM*) representing the carbon cycle and sulfur cycle genes (*APS_APrB*, *APS_kinase_protist*, *Sir*, *dsrB*, *dsra*, *soxA*, and *soxB*) that were significantly different ($p < 0.05$) for KNT and CS. In conclusion, this study was able to discriminate these different soil types from each other. The assessment of both the phylogenetic and functional genes of soil communities together will assist in higher discrimination of soil samples for provenance and forensic applications.

Reference(s):

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GeoChip™ Microarray, Functional Genes, Microbial Community