

A Fast and Inexpensive Molecular Biological Assay to Assess Soil Health

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Soil health and biology is capturing public imagination due to its significance in organic and regenerative agriculture and its role in mitigating climate change (a location for potential carbon sequestration). Programs centred on soil health are supported by farmers and funding bodies such as the Soil Biology Initiative (Grains Research and Development Corporation), the National Landcare Program, and the Cooperative Research Centre for High Performance Soils. Additionally, global businesses are diverting resources into understanding soil and crop microbiomes to develop novel technologies that increase soil health and crop productivity to commercialise a variety of products including soil amendments (e.g. sea weeds, humic acids, other prebiotics) or microbial inocula (often termed “biologicals”, “probiotics”, “biopesticides”, or “biofungicides”). Farmers thus have a plethora of products and management options at their disposal to improve their soil health. However, there is a lack of fast, reliable, low-cost test for farmers to assess whether their efforts in restoring soil health have been fruitful. Therefore, our aim was to develop a molecular biological assay that can inform farmers of changes in their soil or plant microbiome that is not based on intact phospholipid fatty acids, activity measurements (e.g. substrate-induced respiration) or soil enzyme activities but rather on microbial DNA. The assay we developed involves the PCR amplification of the 16S-23S intergenic spacer region of the ribosomal RNA operon. This is used to elucidate the diversity of Archaea, Dikarya, and Bacteria. For the latter, several subgroups are targeted that are prevalent in soils including Acidobacteria, Actinobacteria, Bacteroidetes, Firmicutes, and Gammaproteobacteria. Amplicons are subjected to automated ribosomal intergenic spacer analysis (ARISA) using an ABI 310 genetic analyzer (Perkin-Elmer). Bioinformatic analysis reveals the number of operation taxonomic units (OTUs) and both alpha and beta diversity estimates are generated. Here we showcase different examples from our database that contains microbial profiles of more than 2000 samples from Western Australian agricultural soils. The ARISA assay can easily distinguish between samples taken from different locations ($P < 0.001$) and crops ($P < 0.001$) across the state. Furthermore, we can detect differences in alpha diversity between areas in the same paddock where plant growth is poor or good, or where different soil amendments (e.g. compost pellets) or different fertiliser treatments have altered the soil microbiome. Our ARISA assay represents a reliable, fast, and inexpensive tool for anyone interested in assessing their soil regeneration efforts. Comparing submitted samples to our database informs clients of their soil health to soils from similar crop and farming systems.