



Application of Phenotype Microarray technology to soil microbiology

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It is well established that soil microorganisms are extremely diverse and only a small fraction has been successfully cultured in the laboratory. Furthermore, addressing the functionality of genomes is one of the most important and challenging tasks of today's biology. In particular the ability to link genotypes to corresponding phenotypes is of interest in the reconstruction and biotechnological manipulation of metabolic pathways.

High-throughput culture in micro wells provides a method for rapid screening of a wide variety of growth conditions and commercially available plates contain a large number of substrates, nutrient sources, and inhibitors, which can provide an assessment of the phenotype of an organism. Thus, over the last years, Phenotype Microarray (PM) technology has been used to address many specific issues related to the metabolic functionality of microorganisms. However, computational tools that could directly link PM data with the gene(s) of interest followed by the extraction of information on gene-phenotype correlation are still missing.

Here potential applications of phenotype arrays to soil microorganisms, use of the plates in stress response studies and for assessment of phenotype of environmental communities are described.

Considerations and challenges in data interpretation and visualization, including data normalization, statistics, and curve fitting are also discussed. In particular, here we present DuctApe, a suite that allows the analysis of both genomic sequences and PM data, to find metabolic differences among PM experiments and to correlate them with KEGG pathways and gene presence/absence patterns.