

# MICROBIAL QUALITY OF RECLAIMED MINE SOILS FOLLOWING TIME AND TREATMENT BASED INFLUENCES<sup>1</sup>

J.P Brooks<sup>2</sup>, A. Adeli, J.J. Read, D. J. Lang, M.R. McLaughlin, and J. Willers

**Abstract:** Loss of soil organic C following mining operations can lead to soil degradation and loss in vital microbial diversity, enrichment, and ultimately function. Returning soils to a productive state requires a return of soil organic C, nutrients, and microbial constituents. Traditionally, mining operations are required to return the land to a state near to its original quality. In its most simple form, this involves reclaiming the land by applying nutrient fertilizer and introducing grass followed by eventual introduction of trees. The process is a time-consuming affair and can take >4 years to accomplish. A process which may enhance soil reclamation is the use of manure and municipal sewage sludge residuals. The purpose of this study was to follow soil microbial quality over time and fertilizer (manure/conventional) based treatments. The time-based study focuses on the time necessary for the traditional reclamation approach to bring the land to suitable microbial pre-mining quality. 0, 2, 5 and 10-year-old reclaimed sites corresponding to reclamation beginning in 2011 to 2000 respectively, were chosen for the study. The treatment based study follows soil reclamation using poultry litter and other residuals. Soil samples were collected from each of three replicate treatment-based and time-based plots. Soil samples for 0-15 and 15-30 cm depths were collected from each of three spatially diverse locations within each reclaimed site. Soil samples were culturally processed for the presence of heterotrophic plate count bacteria. Molecular analyses consisted of clone-library sequence analysis from each site and quantitative PCR (qPCR) to discern differences in microbial diversity and enrichment and functional genes, respectively. Overall, increasing microbial diversity and gene enrichment occurred as a function of time and manure-based treatments. MOTHR and the Ribosome Database Project II will be used to determine the effect of time and treatment had on microbial diversity.

**Additional Key Words:** Need Listing of those not in the title.

<sup>1</sup> Paper was presented at the 2012 National Meeting of the American Society of Mining and Reclamation, Tupelo, MS *Sustainable Reclamation* June 8 - 15, 2012. R.I. Barnhisel (Ed.) Published by ASMR, 3134 Montavesta Rd., Lexington, KY 40502.

<sup>2</sup> Brooks, J.P., A. Adeli, J.J. Read, M.R. McLaughlin, and J. Willers. Research Scientists, Precision Agricultural Research Unit, ARS-USDA ,P.O. Box 5367, Mississippi State, MS 39762 and D.J. Lang, Associate Professor, Plant and Soil Sciences, Mississippi State University, Mississippi State, MS 39762