



## **Evaluation of Microbial Transitions in Human Impacted Soil Systems Using DNA Analytical Procedures**

R. L. Tate III\*, C. San Miguel, J. Kist and R. Mikita

Department of Environmental Science, Rutgers University, New Brunswick, NJ USA

It is reasonable to hypothesize that slight changes in the dynamics and composition of the soil microbial community can have meaningful impacts on the soil ecosystem function and the nature of the interaction between the soil microbial community and aboveground plants and animals—including associated and more distant human populations. Until recently, only major changes in those portions of the soil microbial community that could be easily cultivated could be quantified. With the advent of DNA molecular methods and the continued development of and relative availability of reasonably inexpensive DNA sequencing procedures, more detailed questions regarding somewhat minute changes in the soil microbial community composition, structure, and dynamics can be asked. These procedures are proven to be particularly useful in evaluating human-induced environmental changes. Three diverse current environmental concerns—role of soil microbes in remediation of zinc contaminated soils, impact of wild-fires and controlled burns on soil microbial community diversity, and dynamics of antibiotic resistant genes in animal waste impacted soils—serve as examples of how techniques such as polymerase chain reaction and denaturing gradient gel electrophoresis can be used to examine small, but meaningful, changes in the soil microbial community structure and the role of the specific microbes in ecosystem function and sustainability.