

Characterization of Bacterial Communities in Soil during the Transition to Organic Agriculture.

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The “Strategies for Transition to Organic Systems” project, being conducted at the Center for Environmental Farming Systems in Goldsboro, NC, is a large-scale, long-term study, initiated in 1999 to determine the best strategy, economically and ecologically, to complete the transition from conventional to organic farming. A major challenge for farmers and researchers in the field of organic agriculture is the occurrence of a period of suppressed yields that often follows the removal of conventional inputs and institution of certified organic methods. As a part of this study, soil microbiological properties are being examined along with soil chemical and physical properties, crop yield and quality, pest and beneficial organism dynamics, and the economics of the transition strategy. Bacterial communities in agricultural soils represent a key factor in healthy ecosystem functioning. Several bacterial groups play significant roles in sustainable soil systems and in plant health, making them important members of the soil community. In particular, *Burkholderia* and fluorescent *Pseudomonas* species have been studied because of their association with plant disease-suppressive and plant growth-promoting effects. Members of both of these genera have been shown to fix nitrogen, induce resistance in plants to pathogens, promote plant growth and act as biocontrol agents by producing antibiotics or competing with pathogens for nutrients.

Soil samples for microbial assays were taken in April, June (and/or) July, and September. Each sample was composed of 30 cores and a thoroughly mixed subsample placed on ice immediately for microbial analysis. Samples were diluted 10-fold by adding 1 gram of soil to 9ml of sterile distilled water and a dilution series was prepared using 96-well microtiter plates inoculated in triplicate and containing King’s B, to quantify fluorescent *Pseudomonas*, PCAT, to quantify *Burkholderia* and R2A to quantify ‘total’ culturable bacteria. After incubation, the most probable number (MPN) of bacterial cells per gram of dry soil was calculated based on the number of wells with growth.

Year and Date of sampling and Start (see Creamer et al. for details) dramatically impacted the number of culturable bacteria (Figure 1). Distinct and consistent trends in each population were observed. Bacterial populations were typically relatively high in the early spring, declined during the summer and increased again by September. Total culturable bacteria (R2A) oscillated from 6.18 to 7.55 log MPN; *Burkholderia* populations had a narrow range of growth with a high value of 5.99 and a low value of 4.94 log MPN over the 4 yr time frame; fluorescent *Pseudomonad* populations were much more dynamic ranging from 2.68 to 6.05 log MPN (Figure 1). Populations appeared to be most impacted by time of sampling, presumably due to environmental conditions, despite very different cropping histories (effect of Start) and treatment effects. In Start 1, conventional plots had significantly lower *Burkholderia* populations over the 4 yr time frame as compared to population sizes in the organic and transitional plots (Figure 2). A similar trend was not observed in Start 2 plots and in most cases,

transitional treatment (1-6) did not impact these microbial populations. Genomic fingerprint analysis revealed a high level of diversity amongst the *Burkholderia* populations (Figure 2) and sequence analysis confirmed all strains to be *Burkholderia* species representing a range of genomovars. All soil samples, bacterial cultures and DNA (when extracted) have been archived for future analysis. This and future work enhances our understanding of the dynamics and diversity of microbial populations at the CEFS research site.

Figure 1: Dynamics of selected bacterial communities as affected by time and START.

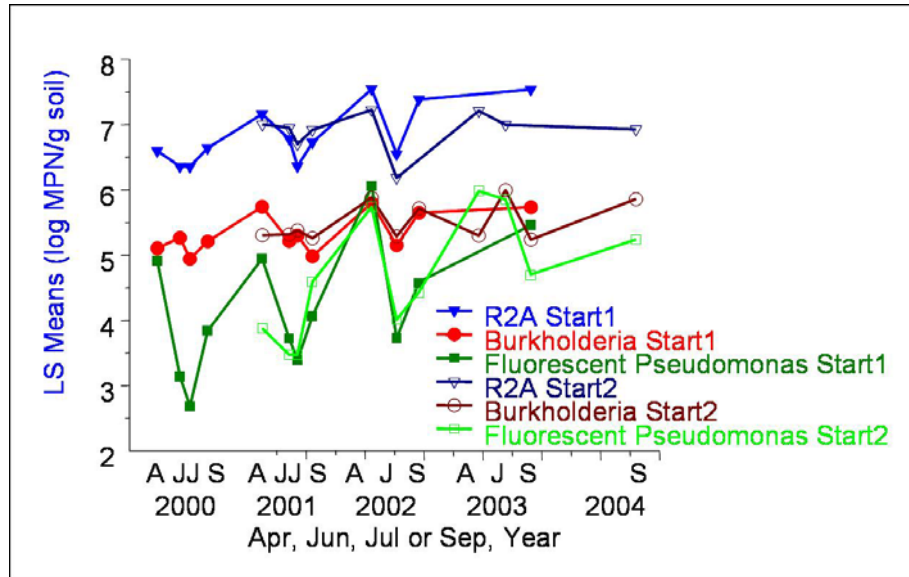


Figure 2: Effect of treatment on *Burkholderia* populations (left) and genetic diversity of selected strains representative of each sampling point (right).

