# ABSTRACT

Molecular Microbial Ecology and Nitrifying Communities of Tropical Composts and Soils

Vidya de Gannes

Some key questions remain regarding the dynamics of prokaryotic and fungal communities in the composting process. One of these is that it remains unknown whether unifying patterns in one or both groups of microbes can be identified as composting progress that might be informative of processes important in composting and compost safety. Another important question is, how microbial community composition varies throughout the composting process. While nitrification is a key process in composting and in soils, there is limited information about the environmental factors that shape the community structure of ammonia-oxidizing archaea (AOA) and ammonia-oxidizing bacteria (AOB) mediating nitrification in those systems.

Hence, the overall goals of this research were: 1) to determine the prokaryotic and fungal successions in three composting systems and to develop a census of their diversities, 2) to investigate how AOA and AOB communities vary

between compost types and phases and 3) to gain an understanding of nitrification and ammonia-oxidizing prokaryotes in soils of Trinidad.

Next-generation (next-gen) sequencing was applied to analyze prokaryotic and fungal patterns in three composting systems across the three main phases. For the prokaryotes, in all composts, diversity expanded as composting progressed. Analysis of similarity revealed compost phase was a significant source of dissimilarity ($p$ = 0.011), compost type was not ($p$ = 0.401). Based on sequence abundance, mature-phase compost was a preferred niche for the *Archaea*, *Planctomycetes*, *Chloroflexi* and *Deltaproteobacteria*, while *Gammaproteobacteria* were predominant in earlier phases. Thus, the mature phase pattern could have implications in the development of biomarker assays for compost maturity.

In all composts, fungal diversity in the mature phase exceeded that of the mesophilic phase. A total of 102 fungal genera, 120 species and 222 operational taxonomic units (> 97% similarity) were identified. *Ascomycota* represented most (93%) of the 27,987 fungal sequences and thirty genera predominated (*ca*. 94% of the sequences). Fifteen species of potential human pathogens were identified, eight of which have not been previously identified in composts. This study demonstrated that this information can have important implications for compost use and safety.

The AOA were more abundant than AOB in composts of tropical agricultural wastes. These communities in the composts were diverse and the structure of these diverged between compost types and phases. Nitrification patterns and levels differed in the composts which, for the mature material, could have signifcant effects on its performance as a plant growth medium.

In soils from Trinidad, nitrification potential was positively correlated with clay content and pH ($p < 0.001$). AOA were detected by qPCR (*ca.* $10^5$ to $10^6$ copies archaeal *amoA* $g^{-1}$ soil), but AOB levels were low and infrequently detected. AOA abundance showed a significant negative correlation ($p < 0.001$) with levels of organic carbon, clay and ammonium, but no correlation to pH. Variation in AOA terminal restriction fragment analysis (TRF) profiles was best explained by ammonium-N and either Kjeldahl N or total N ($p < 0.001$) while variation in AOB TRF profiles was best explained by phosphorus, bulk density and iron ($p < 0.01$). Hence AOA and AOB communities were affected by differing sets of edaphic factors, and pH was not a major driver for either community.

**Keyword**s: compost, soils, prokaryotes, fungi, ammonia-oxidizing archaea, ammonia-oxidizing bacteria, diversity, nitrification.