

# Predominant Microbial Assemblages and Enzyme Activities during Record Drought and Heat in Agricultural Soils

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## Abstract

Identification of microbial assemblages predominant under natural extreme climatic events will aid in our understanding of the resilience and resistance of microbial communities to climate change. From November 2010 to August 2011, the Southern High Plains (SHP) of Texas, U.S., received only 39.6 mm of precipitation (vs. the historical average of 373 mm) and experienced the three hottest months (June-August 2011) since record keeping began in 1911. The objective of this study was to characterize soil bacterial (16S rRNA gene) and fungal (Internal Transcribed Spacer 1-4, ITS1-ITS4) species distribution and diversity via pyrosequencing during the peak of the drought/heat wave in July 2011 and when the drought index and temperatures were lower in March 2012. Samples were collected from two different soil types (loam and sandy loam) under two different dryland cropping histories (monoculture vs. rotation). Fungal diversity indexes were significantly higher after the drought/heat wave while bacterial indexes were similar. Bacterial phyla distribution in July 2011 was characterized by lower relative abundance of *Acidobacteria* and *Verrucomicrobia*, and greater relative abundance of *Proteobacteria*, *Chloroflexi*, *Actinobacteria* and *Nitrospirae* than March 2012 samples. Further grouping of pyrosequencing data revealed approximately equal relative proportions of Gram positive (G+) and Gram negative (G-) bacteria in July 2011, while G- bacteria predominated in March 2012. Fungal class *Dothideomycetes* was approximately two times greater in July 2011 than in March 2012, while the class *Sordariomycetes* and a group of unidentified OTUs from *Ascomycota* increased from July 2011 to March 2012. Microbial community composition was less influenced by management history than by the difference in climatic conditions between the sampling times. Correspondence analysis identified assemblages of fungal and bacterial taxa associated with greater enzyme activities (EAs) of C, N, or P cycling found during the drought/heat wave. Microbial assemblages associated with arylsulfatase activity (key to S cycling), which increased after the drought/heat wave, were identified (*Streptomyces parvisporogenes*, *Terrimonas ferruginea* and *Syntrophobacter* sp.) regardless of the soil and management history. The distinct microbial composition found in July 2011 may represent assemblages essential to maintaining ecosystem function during extreme drought and intense heat waves in semiarid agroecosystems.