# **Dominant Bacterial Populations in EPTC-Enhanced and Unenhanced Soils. (S03-wang095946-Poster)**

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### Abstract:

The herbicide, S-ethyldipropylthiocarbamate (EPTC), has been extensively used for weed control in agricultural crops. Little information exists concerning the effect of EPTC application on the soil microbial community. Terminal Restriction Fragment Length Polymorphism (T-RFLP) analysis revealed a pronounced shift in the microbial community between EPTC-Enhanced (Soil E) and Unenhanced (Soil-U) soil. Specific EPTC-degrading genes were present in Soil-E but not in Soil-U. This strongly suggests bacterial populations containing EPTC-degrading genes significantly increased in Soil-E. The dominant bacterial populations, determined by RFLP analysis of 16S rDNA clone libraries, were almost all in the Cytophaga-Flexibacter-Bacteroides (CFB) group of bacteria for Soil-U. Dipareforma spartinacae accounted for the majority of this group. For Soil-E, the majority of the clones were closely affiliated with the Sphingomonas spp. Thus, Sphingomonas spp. are potential novel EPTC-degraders in soils in addition to the known Rhodococcus spp. EPTC treatment changes the microbial community population and we identify EPTC-degraders that have, as yet, not been isolated from soil and characterized.

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