

MICROBIAL INTERACTIONS WITH WEED SEEDS. Joanne C. Chee-Sanford¹, Adam S. Davis², Martin M. Williams II², Lynn M. Connors³, Teresa J. Holman³, and Gerald K. Sims¹, ¹Research Microbiologist, ²Research Ecologist, and ³Biological Science Technician, USDA-ARS, Invasive Weed Management Unit, Urbana, IL 61801.

Buried seed reserves in soil (seed banks) are a major source of future plant emergence. Seed production from many annual weed species is high and the longevity of seed banks suggests existing mechanisms of seed protection against natural decay processes. This environment also offers opportunities for numerous seed-microbe interactions, with potential importance to plant and microbial community development. Studies conducted earlier demonstrated seeds of velvetleaf (*Abutilon theophrasti*) were subject to extensive decay mediated by soil microorganisms, in contrast to other species like giant ragweed (*Ambrosia trifida*), Pennsylvania smartweed (*Polygonum pennsylvanicum*), jimsonweed (*Datura stramonium*), and woolly cupgrass (*Eriochloa villosa*). We investigated the hypothesis that if accessed, seeds provide significant nutritional resources for soil microbial populations with focus on velvetleaf seed as a model. Microbial community analysis using terminal restriction fragment length polymorphisms (TRFLP) and rDNA clone libraries, along with cultivation and microscopic examination, were used to characterize microbial species and community assemblages associated with seeds following exposure to soil microorganisms. Multidimensional scaling analysis of TRFLP profiles indicate bacterial assemblages generally differed between weed seeds of different species, and particularly with velvetleaf seed, the associated populations differed in accordance with the origin of the soil inoculum. While TRFLP analysis did not indicate a specific community composition associated with seed type, the dominant presence of several bacterial sequences in clone libraries derived from individual seeds did indicate closely related species were present on replicate seeds exposed to the same soil inoculum. This suggests certain species within complex soil microbial communities may likely be found in seed associations, but weed seeds may support overall associations with a wide range of soil bacteria. Most of the dominant bacteria identified in association with decaying velvetleaf seed were native soil species, such as members found within the phyla *Bacteroidetes* and *Proteobacteria*. In contrast to bacteria, species belonging to the major fungal phylum *Ascomycota* were present, regardless of soil origin indicating specific relationships between certain species of seeds and soil-borne fungi may occur. Microscopic examination indicated densely populated surfaces of seeds following incubation where seeds provided the major source of carbon nutrition for microbial growth. The results suggest seeds can provide a selective environment for microbial associations, and leads to further investigation on whether these relationships are common in natural soil environments. The results further suggest that native soil microbial populations are active in association with seeds, and identifying the species and factors that influence these associations in natural soil, will determine whether these relationships can be manipulated or exploited for use in seed bank depletion.