

WEED SEED MORTALITY IN SOILS WITH CONTRASTING AGRICULTURAL MANAGEMENT HISTORIES. Adam S. Davis*, Kathleen I. Anderson, Steven G. Hallett, Karen A. Renner, Ecologist, USDA-ARS Invasive Weed Management Unit, Urbana, IL 61801; Research Technician and Assistant Professor, Purdue University, West Lafayette, IN 47907; Professor, Michigan State University, East Lansing, MI 48824.

It has been proposed that cropping systems can be managed to promote the development of soil microbial communities that accelerate weed seed mortality. We examined soil fungal and bacterial communities, soil C:N ratio, soil particle size fractions, and weed seed mortality in soil from five fields with over 10 years of contrasting agricultural management histories. Seed mortality of giant foxtail and velvetleaf were greatest in soil from the conventionally managed systems and lowest in soil from a compost-amended corn-corn-soybean-wheat rotation. Principal components analysis of soil microbial communities showed distinct differences in the fungal and bacterial profiles among the study soils, with the first two principal components explaining over 50% of the variation in the study soils. The first principal component of the 18S rDNA PCR-DGGE analysis of fungal community composition showed a strong negative correlation with both giant foxtail (-0.52 , $P < 0.05$) and velvetleaf (-0.57 , $P < 0.01$) seed mortality, as did ordination with non-metric multidimensional scaling (NMS) [giant foxtail (-0.54 , $P < 0.01$) and velvetleaf (-0.60 , $P < 0.01$)], suggesting that seeds of the two species were affected similarly by changes in the soil fungal community. For giant foxtail, weed seed mortality was also positively correlated ($r = 0.48$, $P < 0.05$) with the first NMS axis of the bacterial 16S rDNA analysis. None of the other measured soil properties were significantly correlated with weed seed mortality. These results demonstrate that soil management history, microbial community composition and weed seed mortality are linked. More work is needed to identify components of the fungal and bacterial communities that are active in seed degradation, and to develop conservation biocontrol recommendations for these species.