J Fundam Renewable Energy App 2016, 6:6(Suppl)
http://dx.doi.org/10.4172/2090-4541.C1.021

Biofumigation compounds from biofuel oilseed meals differentially impact soil bacterial and fungal populations

Terry J Gentry[1], **Frank M Hons**[1], **Emily B Hollister**[2] and **Ping Hu**[1]
[1]Texas A&M University, USA
[2]Baylor College of Medicine, USA

The seed meals (SMs) from some dedicated biofuel oilseed crops have potential application as soil biofumigants due to their release of biocidal compounds such as isothiocyanates (ITCs). Various ITCs are known to inhibit numerous plant pathogens; however, much less is known about how the soil microbial community responds to different oilseed meals and the specific ITCs they release. A series of experiments were conducted to determine the impact of various SMs and ITCs on soil fungal and bacterial communities. In one set of experiments, soil was amended with a glucosinolate-containing brassicaceous SM (*Brassica juncea*; mustard), a non-glucosinolate-containing, non-brassicaceous SM (*Linum usitatissimum*; flax), and a non-oilseed biomass (*Sorghum bicolor*). In a subsequent experiment, soil was directly amended with four types of ITCs (allyl, butyl, phenyl, and benzyl ITC) along with 1% flax SM. Microbial communities were analyzed based on the ITS region for fungi and *16S rRNA* gene for bacteria using qPCR and tag-pyrosequencing. Distinct separation of the bacterial and fungal communities occurred along amendment-type lines, with mustard inducing large, short-lived increases in the abundance of bacterial groups known to include many fungal disease-suppressing bacteria. Likewise dramatic shifts were seen among the fungi, with fungal phylotype richness decreasing by >60% following mustard SM addition. Similarly, a dramatic decrease in fungal populations (~85% reduction) was observed after allyl ITC addition. Fungal community compositions also shifted following specific ITC amendments. Bacterial populations were less impacted by ITCs, although there was a transient increase in the proportion of *Firmicutes*, related to bacteria known to be antagonistic to plant pathogens, following amendment with allyl ITC. Our results indicate that SMs releasing different ITCs can result in differential impacts on soil microorganisms. This information will aid selection and breeding of oilseed crops for biofumigation-based control of soil-borne pathogens while minimizing the impacts on non-target microorganisms.

tjgentry@tamu.edu