Response of soil organisms to dimethyl disulfide fumigation

Sadikshya R. Dangi[1,2,*], J. Alfonso Cabrera[1,3] James Gerik[1], and Husein Ajwa[2]

[1]Water Management Research Unit, USDA-ARS, Parlier, CA 93648, USA.
[2]Department of Plant Sciences, University of California, Davis, CA 95616, USA.
[3]Department of Environmental Sciences, University of California, Riverside, CA 92521, USA.

After the commonly used soil fumigant methyl bromide (MeBr) was phased out in the United States, alternatives to MeBr such as dimethyl disulfide (DMDS) which is known to have broad pest control spectrum, is increasingly used. However effectiveness of DMDS has been mainly investigated to study target soil borne pathogens and nematodes but their effect on microbial community structure are largely unknown. Soil microorganisms are essential in sustaining health of agricultural soil and hence, it is very important for them to recover after treatment with fumigants for the development of healthy soils. The primary objective of this study is to examine and compare the impact of different rates of DMDS on target (Citrus nematodes, *Pythium* spp., *Fusarium oxysporum* etc.) and non-target soil organisms (fungi, gram positive bacteria, gram negative bacteria, actinomycetes, Arbuscular Mycorrhizal Fungi (AMF), protozoa).

Materials and Methods

DMDS was applied at 32, 64, 128, or 256 mg a.i./L air space per vine. One treatment remained without DMDS fumigation and served as control. Immediately after fumigation, 3.7 L water was applied to each vine in a 2 h period to seal the soil surface. One soil sample per vine at 1-60 cm soil depth was taken 15, 45 and 60 and 90 days after fumigation with a 2.5 cm diameter auger. From the top soil samples phospholipid fatty acids were extracted from 10-g soil samples using a modified Bligh–Dyer methodology. Fatty acids were directly extracted from soil samples using a 1:2:0.8 chloroform/methanol/phosphate buffer mixture. Phospholipid fatty acids were separated from neutral and glycolipid fatty acids in a solid-phase extraction column. After mild alkaline methanolysis, PLFA samples were qualitatively and quantitatively analyzed using an Agilent 6890 gas chromatograph with autosampler, split-splitless injector, and flame ionization detector. The system was controlled with Agilent Chemstation and MIDI Sherlock software. Individual PLFA signatures were used to quantify the abundances of specific microbial groups in soil samples. Treatments were arranged in a complete randomized block design. Each treatment had six replicates. The experiment was conducted twice. Efficacy of DMDS on target and non-target soil organisms will be discussed.