

Rapid determination of soil quality and earthworm impacts on soil microbial communities using fluorescence-based respirometry

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We applied a fluorescence-based respirometry method currently devised for aquatic ecotoxicology studies to rapidly measure soil microbial oxygen consumption as a function of soil quality. In this study, soil was collected from an arable wheat field and the field margin. These two soil habitats are known to differ in their soil quality due to differences in their use and management as well as plant, microbial and earthworm community. The earthworm *Lumbricus terrestris* was incubated in arable or margin soil for three weeks. After this initial phase, a transfer experiment was then conducted to test the hypothesis that earthworm 'migration' alters soil microbial community function and diversity. In this transfer experiment, earthworms incubated in margin soil were transferred to arable soil. The converse transfer (i.e. earthworms incubated in arable soil) was also conducted. Soils of each type with no earthworms were also incubated as controls. After a further four week incubation, the impact of earthworm migration on the soil microbial community was tested by measuring oxygen consumption.

Replicated soil slurry subsamples were aliquoted into individual respirometer wells (600 μl volume) on a glass 24-well microplate (Loligo Systems, Denmark) fitted with non-invasive, reusable oxygen sensor spots. The sealed microplate was then attached to an oxygen fluorescence sensor (SDR SensorDish Reader, PreSens, Germany). Oxygen consumption was measured in real-time over a 2 hr period following standard operating procedures. Soil microbial activity was measured with and without an added carbon source (glucose or cellulose, 50 mg C L⁻¹). Using this system, we were able to differentiate between soil type, earthworm treatment and C source. Earthworm-driven impacts on soil microbial oxygen consumption were also supported by changes in soil microbial community structure and diversity revealed using DNA-based sequencing techniques.

This method provides a simple and rapid system for measuring soil quality and has the potential for use in a variety of scenarios investigating impacts on soil microbial function.