T-RFLP analysis of nematode assemblages

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Soil faunal communities may be used as indicators of soil health. However, identification based on morphology is time consuming and problematical. Molecular methods offer an alternative.

Terminal Restriction Fragment Length Polymorphism (T-RFLP) is proposed as a means of nematode community analysis and will be used to profile nematode communities from different habitats.

DNA extraction

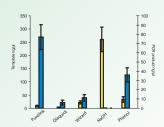


Fig 1. Mean concentration of template DNA ☐ and PCR product ☐ for 3 replicates of each of 5 habitat types. Bars show standard error, n=15

Nematodes were extracted from 5 habitats and DNA extractions performed using various techniques. Quality of the extract was assessed by quantification of PCR product. Tissue disruption, by bead beating, followed by purification through the Purelink PCR purification kit (Invitrogen, Paisley, UK) was

Morphological vs molecular

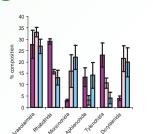


Fig 2. % community composition as calculated from ■ individual counts, ■ biomass and ■ clone number.

PCR products amplified from 3 arable samples were cloned, sequenced and assigned to taxonomic order by phylogenetic anlysis.

100 nematodes from each sample were identified under the microscope to order level and their biomass calculated. Clone number corresponds more closely to biomass than to counts.

Effects of organic ammendment revealed by T-RFLP

method.

selected as the optimal



Fig.3 Compost, slurry and no ammendment treatments were applied to spring barley, *Hordeum vulgare*, along with an irrigation treatment.

Directed T-RFLP

Nematodes extracted from 200g soil

Community DNA extracted

500bp of SSU rDNA amplified using fluorescently labelled primers

Digestion of PCR product with Hinfl

Analysis of terminal fragments on capillary sequencer

Multivariate analysis of relative abundance of fragments

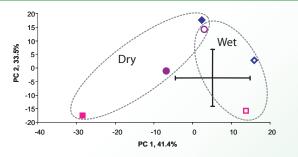


Fig.4 Communities extracted from compost treatment∎ were significantly different to the slurry● and no ammendment ◆ treatments, PC2 ANOVA p=0.034. Open symbols represent irrigated treatments, PC1 ANOVA. p=0.029. Bar = L.S.D.



Fig. 5 With careful design of the enzyme digest, from known nematode sequences, signature T-RFLP peaks may be assigned to taxonomic groups. This will allow us to integrate T-RFLP data with established nematode ecological indices.

References

Donn et al. (2007) DNA extraction from soil nematodes for multi-sample community studies. Appl. Soil Ecol., 38, 20-26 Griffiths et al. (2006) Molecular sequencing and morphological analysis of a nematode community. Appl. Soil Ecol., 32, 325-337.