

High-throughput sequencing of soil nematode communities for ecological research

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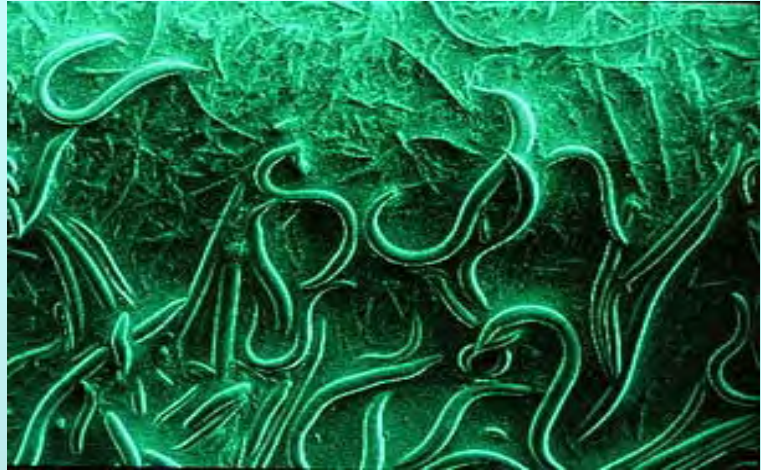


Introduction

Although nematode community analysis is widely quoted as a useful environmental indicator, a major impediment to its wider adoption is the morphological identification of individual nematodes. Molecular techniques offer an alternative to time-consuming traditional methods of faunal identification based on morphology.

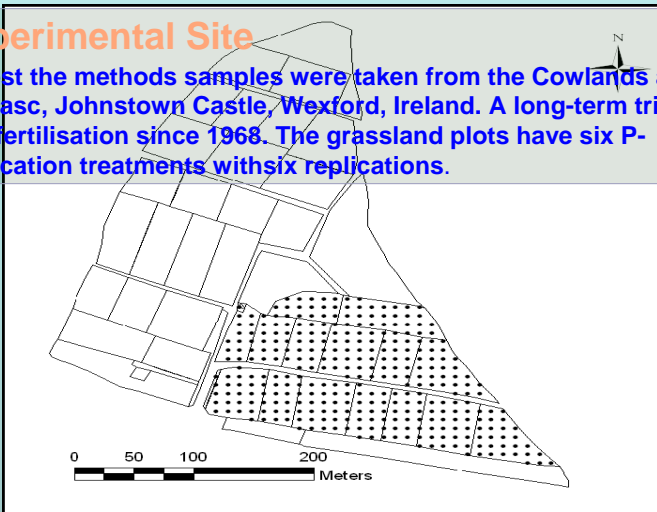
Objective

This study will combine morphological and molecular sequencing to establish the potential for analysing nematode communities by molecular biological characterization.



Experimental Site

To test the methods samples were taken from the Cowlands at Teagasc, Johnstown Castle, Wexford, Ireland. A long-term trial of P fertilisation since 1968. The grassland plots have six P-application treatments with six replications.



Fertilizer P Treatment (kg ha⁻¹ yr⁻¹)

year	Treatment No.					
	1	2	3	4	5	6
	P0-0	P0-30	P30-30	P30-0	P15-15	P15-5
1968-1998	0	0	30	30	15	15
1999-2008	0	30	30	0	15	5

Methods

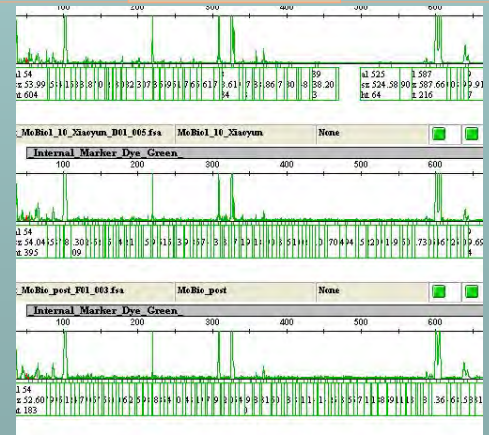
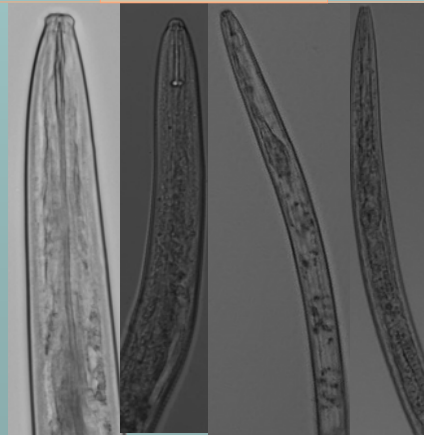
Nematode extraction

morphological identification

18 days to finish

molecular identification (T-RFLP)

2 days to finish



Conclusion

This Walsh Fellowship project is going to determine if molecular methods can augment morphological identification for soil nematode community analysis.

Acknowledgments

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