Diversity of AM Fungi Over a Physical and Temporal Gradient

Jennifer Kennedy[1], John Raven[2] and Tim Daniell[1]
1. Scottish Crop Research Institute, Invergowrie, Dundee DD2 5DA Scotland.
2. Biological Sciences Institute, University of Dundee, Dundee DD1 4HN Scotland.

Introduction

Arbuscular mycorrhizal (AM) fungi are obligate symbionts, forming an intimate association with over 90% of plant species.
The importance of this symbiosis and the role that AM fungi play in plant health and productivity is becoming increasingly apparent, as is the preference between fungi and host plant species[1,2,3].
It has been shown that AM fungal diversity is much lower in disturbed, intensive arable sites when compared with semi - natural woodland sites[4].
AM fungi have been sampled from commercially grown raspberry plants (838 root samples in total) over a temporal and physical gradient in order to test two hypotheses:

1. Species diversity of AM fungi increases with time from physical disturbance in arable field sites.

2. Community structure of AM fungi will change over a gradient of physical disturbance and time showing succession in AM species composition.

Presented are preliminary results of molecular analysis of AM fungal populations found within samples of varying ages and at the beginning and end of a growing season.

Methods

DNA extraction

↓

Selected samples
PCR amplification
SSU fragment 550bp
NS31 - AM1

↓

Clone pGEM-T easy

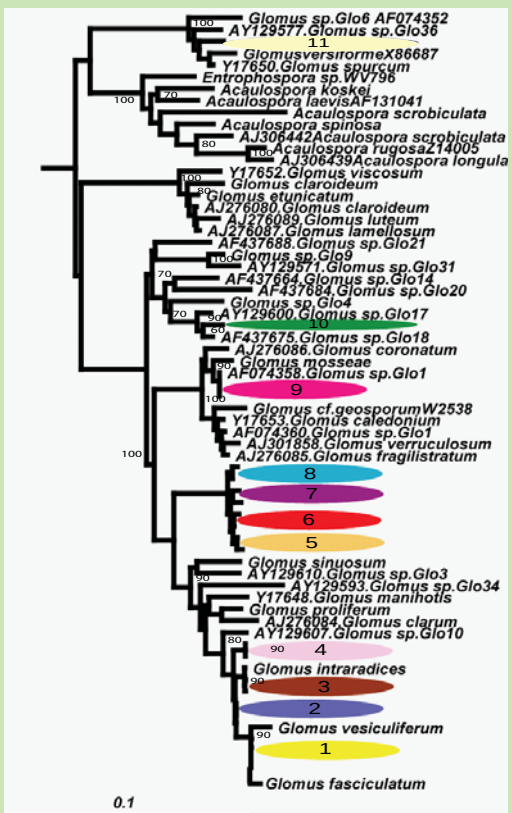
↓

Sequence clones from each sample

↓

Phylogenetic analysis

Results



Neighbor-joining phlyogenetic tree. Clones sequenced from root samples from various ages of raspberry plant. All sequences fall within Glomus spp. However, clear differences can be seen between groups.

The distribution of sequence types suggest changes in AM diversity and also indicate a seasonal shift. However, these results are preliminary, high throughput analysis will be performed on all samples in order to reveal other differences and confirm patterns observed.

		Sequence Group											Total	H
		1	2	3	4	5	6	7	8	9	10	11		
Spring	25yrs	11	8		6								25	1.069
	8yrs													
	0yrs	19	1										20	0.199
Autumn	25yrs		5	1	3	8	4	9	1	2	1	1	35	1.99
	8yrs	9	22	2	2				1				36	1.063
	0yrs			20									20	0

Distribution of sequence groups, with total number of clones, from each sampling point. Shannon - Weiner diversity index (H) is shown. 25 year old plants in Autumn contain the greatest diversity of sequence types and 0 year old plants in Autumn contain the least.

Future Work

Sequence types will be exhausted by high throughput sequencing as measured by rarefaction analysis. Sequences will then be used to design a high throughput T-RFLP strategy to be applied on all samples.

References

1. van der Heijden M. et al. Mycorrhizal fungal diversity determines plant biodiversity, ecosystem variability and productivity. Nature 396, 69-72, 1998.
2. van der Heijden M; Scheublin TR; Brader A. Taxonomic and functional diversity in arbuscular mycorrhizal fungi - is there any relationship? New Phytologist 164(2), 201-204, 2002.
3. Vandenkoornhuyse P, Husband R, Daniell TJ, Watson IJ, Duck JM, Fitter AH, Young JPW. 2002. Arbuscular mycorrhizal community composition associated with two plant species in a grassland ecosystem. Molecular Ecology 11: 1555-1564.
4. Helgason,T.; Daniell,T.J.; Husband,R.; Fitter,A.H.; Young,J.P.W. Ploughing up the wood-wide web? Nature 394, 431, 1998.

Acknowledgements

This project is funded by the Perry Foundation.
We thank Peter Thomson for access to commercial raspberry fields.