

Can AM Fungi Recolonise Arable Fields From Refugia?

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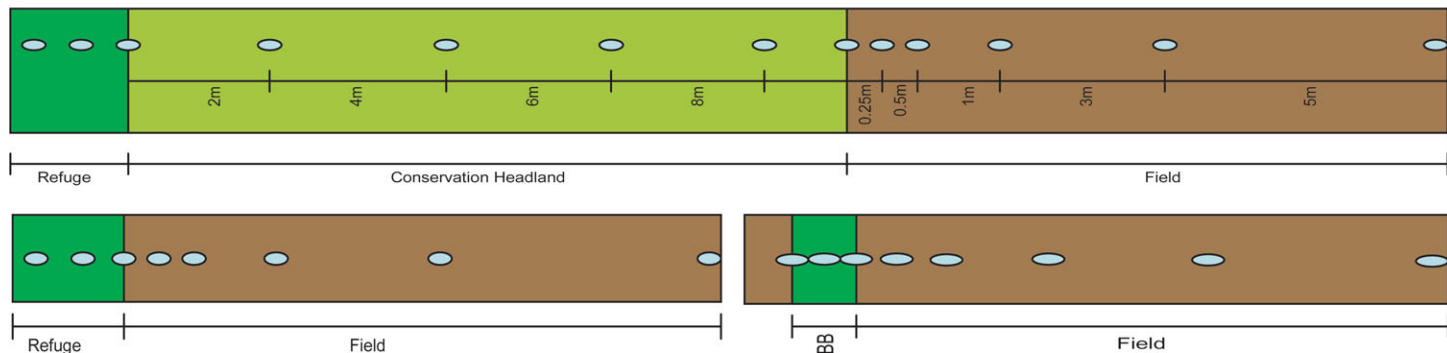
Introduction

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^{1,2}, as is the preference between fungi and host plant species³. It has been shown that fungal species diversity is much lower in disturbed, arable sites compared with semi-natural woodland sites. Little is known about the re-colonisation dynamics of AM.

This experiment aims to test the following hypothesis:

Re-colonisation of low fungal diversity, arable land will occur from adjacent high diversity refugia rather than from low abundance sequence types intrafield.

Experimental Design



Roots were collected at measured distances from undisturbed refuge or beetle banks, either directly or through a conservation headland. Roots were also collected from highly disturbed field sites (as shown above). Three replicate transects were sampled at each of a number of sites

Methods - Undirected TRFLP

DNA extraction → PCR amplification (SSU fragment 550bp, NS31 - AM1) → Restriction Digest (Hinfi and Hsp 92II)

Discussion

Preliminary analysis suggests that community structure of AM fungi do not differ between refuge and field and therefore is no clear pattern of recolonisation of AM types from an area of no disturbance to one that is highly disturbed. However, conservation headlands have a distinct community structure (Fig1c). These differences may be due to plant preference of the AM and the differences seen in the field may be due to monoculture rather than physical disturbance.

References

1. van der Heijden M. et al. Nature 396, 69-72, 1998.
2. van der Heijden M et al New Phytologist 164(2), 201-204, 2002.
3. Vandenkoornhuyse P et al 2002. Molecular Ecology 11: 1555-1564.

Acknowledgements

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Results

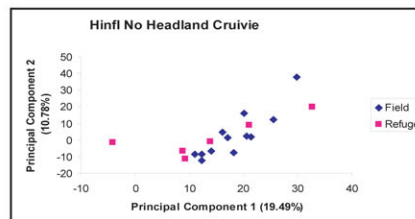


Fig1a

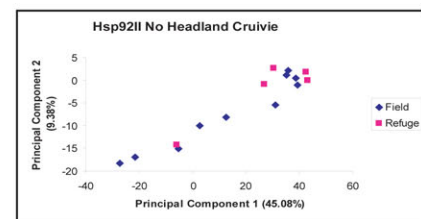


Fig1d

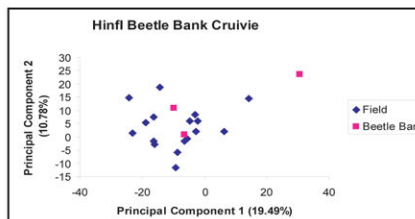


Fig1b

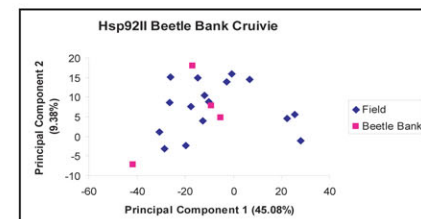


Fig1e

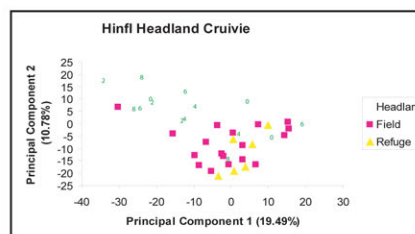


Fig1c

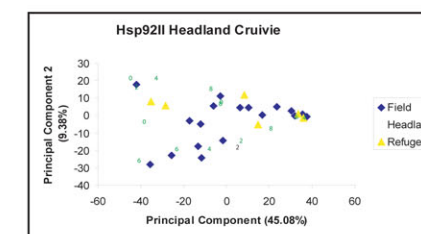


Fig1f

Fig 1: Principal component analysis of samples digested with Hinfi and Hsp 92II restriction enzymes. Position of the samples from each site indicates that there is little difference between AM types found in undisturbed refuges and highly disturbed field sites (a,b,d,e,f). However, there appears to be some variation in the types found in conservation headlands compared to field and refuge sites (c).