Ploughing up the wood-wide web?

Key species groups that affect major ecological processes are vital components of community diversity. Many such key groups are found in the soil, including the mycorrhizal fungi that may connect plants into a functional "wood-wide web"[1]. Arbuscular mycorrhizal associations are formed by fungi of the order Glomales with 90% of land plant families, and many arbuscular mycorrhizal fungi are thought to have a broad host range[2]. Here we show that, despite this broad host range, the diversity of arbuscular mycorrhizal fungi is strikingly low in arable sites compared with a woodland.

The arbuscular mycorrhizal fungi that colonize roots cannot be reliably identified below the genus level except by molecular methods. We examined roots from five abundant woodland plant species at four sites within a broadleaved wood dominated by oak (*Quercus petraea*, colonized by ectomycorrhizal fungi), and sycamore (*Acer pseudoplatanus*, colonized by arbuscular mycorrhizal fungi), at Castle Howard, North Yorkshire, UK. Partial fungal small-subunit ribosomal RNA sequences were amplified, cloned and screened for differences in restriction pattern by restriction-fragment length polymorphism (RFLP). We sequenced selected clones to determine their phylogenetic position (Fig. 1). For comparison, we sampled pea, maize and wheat crops on three farms within a 55-km radius of the woodland site.

There are three families in the Glomales, represented in our samples by the genera *Glomus*, *Acaulospora* and *Scutellospora*, and these are readily distinguished as distinct sequence clusters (Fig. 1). Morphological studies confirmed that these three genera were present in these roots[3]. In arable sites, 92% of sequences represented *Glomus mosseae* or closely related taxa, whereas those from woodland were much more diverse (Fig. 1). This was true even though the arable sites were separated by up to 66 km and three host species were sampled. The combined woodland samples had a much higher diversity of RFLP types (Shannon–Weiner $H = 0.144$) than the combined arable samples ($H = 0.398$). In both wood and field, we often obtained identical sequences from different plant species, suggesting that the broad host range exhibited by many cultured arbuscular mycorrhizal fungi[2] may also be realized in nature.

Given the broad host range of some arbuscular mycorrhizal fungal taxa, the change in sequence composition and low diversity of the fungi in arable fields is probably not a result of plant monoculture *per se*, but reflects other aspects of the agronomic regime such as ploughing, fertilization or fungicide application. In all the arable fields, regardless of host plant or location, the dominant arbuscular mycorrhizal fungal type was a putative *G. mosseae* not found in the woodland. This species sporulates abundantly and colonizes readily from spores, which may be more important in a field that is ploughed annually than in woodland[4].

Arbuscular mycorrhizal fungi differ widely in their biological properties, and presumably have several different roles in ecosystems[5]. The low taxonomic diversity of arbuscular mycorrhizal fungi in arable fields indicates that their functional contribution may be less there than in woodland. It has been suggested that low ecosystem diversity may be associated with impaired function[6,7] and reliability[8,9]. Our results show that microbes need to be considered in any assessment of the effects of agriculture on biological diversity and that intensive arable agriculture may be operating at minimum levels of diversity for at least one key functional group.

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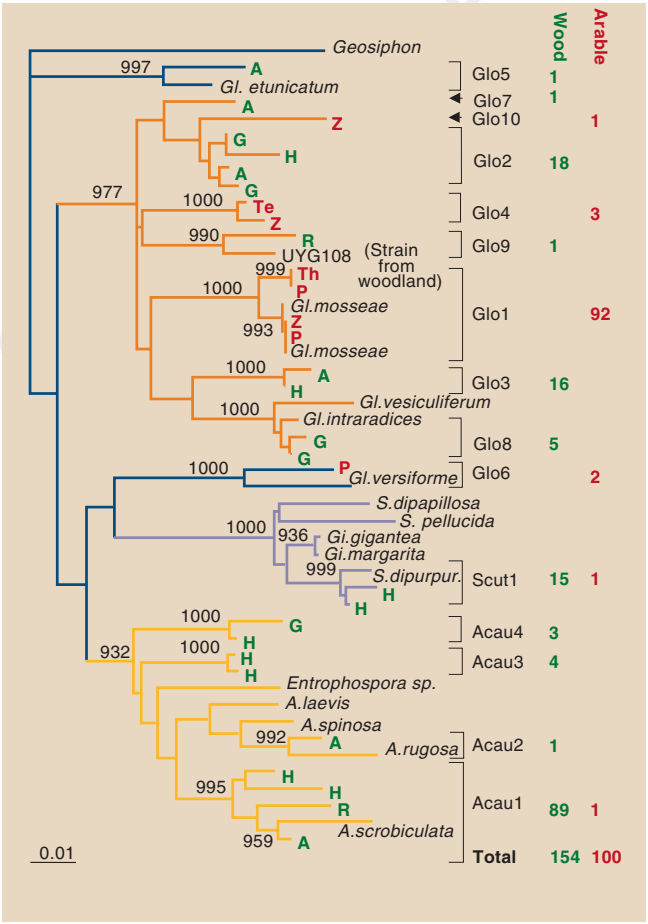

Figure 1 Neighbour-joining phylogeny of arbuscular mycorrhizal fungal DNA sequences amplified from plant roots sampled at woodland (green letters) and arable (red letters) sites. Fungal sequences are identified by the host plant from which they were isolated. A, *Ajuga*; H, *Hyacinthoides*; E, *Epilobium*; G, *Glechoma*; R, *Rubus* (from the woodland site, sampled in July 1996). P, *Pisum* and Te, *Triticum* from Escrick; Th, *Triticum* from High Mowthorpe; Z, *Zea* from Bedale (arable sites, sampled at three time points during 1997). Orange branches correspond to the arbuscular mycorrhizal fungus family Glomaceae, purple branches to Gigasporaceae, yellow branches to Acaulosporaceae, and dark blue branches to the two taxa that do not cluster with any of these families. Partial small-subunit ribosomal DNA fragments of about 550 base pairs were amplified using *Pfu* DNA polymerase and primers NS31 (ref. 10) and AM1 (5′-GTT TCC CGT AAG GCG CCG AA-3′, designed to amplify fungal and exclude plant DNA sequences). Cloned products were digested with *Hin*fI and *Alu*I and selected samples sequenced. Named sequences are from GenBank or from library cultures sequenced in our laboratory. Bootstrap values of >90% are shown at the nodes. RFLP types defined for analysis are shown on the right (Glo, *Glomus*; Acau, *Acaulospora*; Scut, *Scutellospora*), along with the number of clones of each type found in woodland (green numbers) and arable land (red numbers). Previously unpublished sequences have been deposited in GenBank under accession numbers AF074340–AF074373.

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