

Andy Taylor abstract

The cryptic nature of fungi growing within opaque substrates and the general uniformity of their vegetative forms has greatly hindered our ability to detect, characterise and monitor fungal communities. With few exceptions, all of our current knowledge of species distributions, and consequently any conservation strategy, is based upon observations made on macroscopic fruiting structures produced by fungi. This situation is rapidly changing with the application of metagenomic approaches to determining the phylogenetic and functional diversity of fungi in a wide range of ecosystems. In this talk I will highlight two examples where whole community approaches have been applied to the evaluation of fungal diversity. The first study focussed on the tooth fungi, which are covered by a group Biodiversity Action Plan. Many of these fungi are considered threatened or near threatened and often regarded as indicative of old growth Scots pine forests, to which many are thought to be restricted. Our recent work has demonstrated that they may in fact much more frequent than previously thought and their conservation status is likely to require a re-evaluation. The other study examined the mutualistic fungi associated with four declining montane plant hosts in the Scottish arctic-alpine zone. The fungi form obligate mycorrhizal associations with the roots of the host plants and are essential for the growth and survival of the plants. High species richness was encountered in these extreme environments with 257 species detected, of which 34 were new to the UK. Remarkably, an additional 23 species are considered to be new to science. This figure is even more surprising since it refers only to species found as fruiting structures - including the below ground sequence data increases this number to ca. 101. In addition, the data are derived from only 23 arctic-alpine sites - i.e. a small fraction of potential sites. The continuing decline of the host plants in montane habitats means that these fungi are in danger of being lost even before they are known. The application of community level approaches to assessing fungal communities is still very much work in progress but there is clearly huge potential. The main current constraints are with handling the extreme small-scale spatial heterogeneity in taxon distribution and in the severe lack of reference sequence data in most fungal groups.