

The New Forest is one of the best surveyed areas in the country and probably the world, with well over 2000 species recorded over the centuries.

However, recording fungal diversity has historically been limited to finding and identifying their (mainly) ephemeral spore-producing structures, in the most part from the more obvious and distinctive species.

With the arrival of molecular techniques, not only are many existing taxonomies having to be revised completely but the number of named species is “mushrooming” (pun intended!).

Even so, it has been appreciated for some time that only a small proportion of fungal species have been described, which limits eDNA techniques to largely recording the diversity of “Operational Taxonomic Units” (OTUs) and “sporophore counting” still remains the principle approach employed by most fungus surveys including those carried out by the Hampshire Fungus Recording Group (HFRG).

However, HFRG also now employs molecular techniques to help identify more unusual collections and more complex species groups, which increases both the coverage and quality of the records and most of the resulting sequences are published on a public database.

Interestingly, a reasonable fraction of specimens produce sequences which match nothing in the public databases. Some of these are morphologically identifiable and the publication of their sequence increases the coverage. Others fall into the “none of the above” category and may be undescribed species needing more work.

The talk will cover the limitations of traditional fungus surveying, an overview of the DNA sequencing protocol and some examples from the New Forest.