TOP 50 MOST WANTED FUNGI

A continuing problem in mycology is the issue of fungal sequences being obtained from environmental samples not matching any named species, or in some times even higher ranks such as class, that are represented in public databases. This is not entirely surprising in view of the still relatively low proportion of known species represented in sequence repositories such as GenBank, and the huge number of undescribed fungi considered to be in existence.

While single sequences with no matches may in some cases be attributable to artefacts of various kinds, when identical ones are recovered by different researchers from different sites that seems unlikely. In some cases, these have even led to the discovery of previously unknown major groups such as *Cryptomycota* and *Archaeorhizomycetes*. Nilsson *et al.* (2016) have now highlighted the extent of the problem of "orphan" sequence in the UNITE database in such higher ranks down to order. They identified clusters of sequences which, as deduced from the extent of molecular divergence, did not fall into any order, or higher categories. Information is given on the 50 most recovered clusters of unknown sequences. The largest unknown group comprised 60 sequences, many by independent researchers in different studies; one had been found in 23 separate investigations.

An analysis of the information on these unknown higher taxa by geographical distribution revealed that about two-thirds came from Europe and North America. Perhaps somewhat surprisingly as these are by far the mycologically best studied regions of the world. A substrate analysis, not unexpectedly, showed that most of these unknown clusters were obtained from soils, especially ones at phylum and class levels. The pattern at the ordinal level was rather different, with clusters coming from soil (34 %), living plants (27 %), mycorrhizas (10 %), dust (9 %), lichens (8 %), and dead wood (6 %).

The authors point out that "it is frustrating, in the year 2016, not to be able to assign a name to a fungal sequence even at the phylum level". This is a long-standing issue, but a formal proposal to enable this to be done has now been submitted (*see below*). In the interim, until scientific names are available, UNITE is assigning DOI numbers to them to facilitate exchange across databases.

Nilsson RH, Wurzbacher C, Bahram M, Coimbra VRM, Larsson E, *et al.* (2016) Top 50 most wanted fungi. *MycoKeys* **12**: 29–40.

FTA CARDS SIMPLIFY DNA EXTRACTION IN THE FIELD AND FROM DRIED MATERIAL

GE Healthcare (UK) produce a range of cards designed for the collection of specimens for DNA analysis for use in criminal investigations. One of these is the Whatman FTA Classic card in which a small sample of the material to be analysed is placed in the centre of a disc on a card flapped open at the point where the sample is to be taken. The disc includes chemicals that lyse cells, denature proteins, and protect nucleic acids from nucleases.

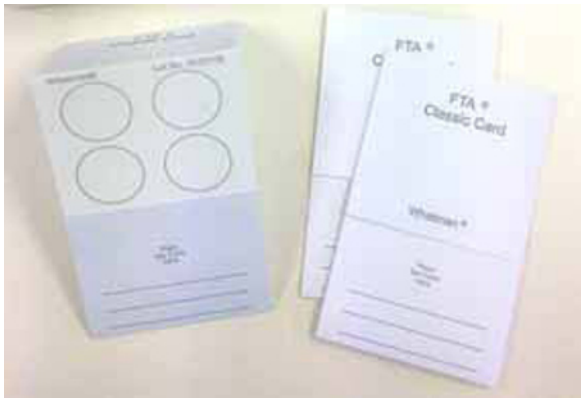

Fig. 1. An open but unused Whatman FTA Classic Card. Photo: GE Healthcare.

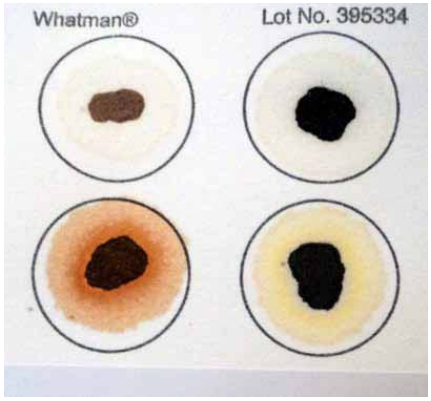

Fig 2. Detail of lichen extracts applied to FTA Classic Card discs. Photo: Cecile Gueidan.

The released nucleic acids are entrapped and preserved in the fibres of the matrix, immobilize and protecting any DNA present until required for analysis. The flap on the card is then closed, and pressed hard (I have seen a hammer used). The manufacturers claim that samples collected in this way can be preserved for at least 17 years.

A superb and pioneering example of the use of these cards in the field and from collections is provided by the study of Gueidan *et al.* (2016) of the tropical corticolous lichenized family *Pyrenulaceae*. New DNA sequences were generated using both DNA extractions from material of 100 taxa, 52 when freshly collected in several countries in south-east Asia and Brazil (yielding 116 sequences) and 48 from material after it had been shipped back to the Natural History Museum in London (115 sequences). They did not, however, place material directly on the cards, but first ground up small samples carefully selected under a stereomicroscope with a PBS buffer and applied them with a pipette to the discs.

rDNA nuLSU, mtSSU, and ITS genes were sequenced, and the phylogenetic trees produced show promise for the eventual production of a much improved taxonomy for the family when many more taxa and collections from different regions are included in the data set.

If you are contemplating acquiring DNA samples from tropical material, especially if there are problems over the export of specimens, the method is clearly one that merits consideration.

Gueidan C, Aptroot A, da Silva Cáceres MA, Binh NQ (2016) Molecular phylogeny of the tropical lichen family *Pyrenulaceae*: contribution from dried herbarium specimens and FTA card samples. *Mycological Progress* **15** (7): 1–21.

INTRODUCED MUSHROOM USED BY NATIVE BIRDS

Bowerbirds are endemic to Australia and New Guinea, and the males of most species construct and adorn a bower to attract females. All sorts of coloured objects can be selected, which can include modern artefacts as well as natural objects. Some bowerbird species favour objects of a particular colour. Elliott & Marshall (2016) note that there are several reports from the 1800s of birds using fungi, although the identification of those is often uncertain. However, in 2010 they came across a case in New South Wales where bluish objects, including a blue livestock ear tag, had been collected, along with pecked specimens of the bluish-gilled mushroom *Lepista nuda*. The bowerbird engaged in this activity was observed over the next five years, and found to be *Ptilonorhynchus violaceus,* which is known for its preference for collecting objects with various shades of blues.

The choice of this mushroom is of particular interest as the species is not native to Australia and seems to have been introduced into the area in the 1860s along with the cork oak, *Quercus suber*, from Europe. The mushroom has now become established in the area of activity of this bowerbird, where it now forms basidiomes regularly.

Perhaps there are other cases as well in which particular bowerbirds have been responsible for the establishment of mushrooms, native or introduced, into the vicinity of their bowers? This is clearly something for ornithologists to be aware of, and for mycologists to consider when coming across colonies of mushrooms not to be expected in an area.

Bird in bower. Photo: Mark Nairn.

Elliott TF, Marshall PA (2016) Animal-fungal interactions 1: Notes on bowerbird's use of fungi. *Australian Zoologist* **38**: 59–61.

STOP PRESS!

Proposal to enable sequence data to be used as types of new scientific names

A formal proposal to permit the type of a voucherless environmental taxon of fungi of any rank to consist of DNA sequence data alone, deposited a publically accessible database, has now been submitted for consideration by the Nomenclature Section of the International Botanical Congress, which next meets in Shenzhen, China, in July 2017 (Hawksworth et al. 2016). It is anticipated that the full text will be included in the August 2016 issue of *Taxon*.

This proposal, if eventually accepted, should meet the concerns expressed by, amongst others, Hibbett *et al.* (2010), Nilsson *et al.* (2016; see above), and Taylor (2011).

Hawksworth DL, Hibbett DS, Kirk PM, Lücking R (2016) Proposal to permit DNA sequence data to serve as types of names of "fungi". *Taxon* **65**: in press.

Hibbett DS, Ohman A, Glotzer D, Nurhi M, Kirk PM, Nilsson RH (2011) Progress in molecular and morphological taxon discovery in fungi and options for formal classification of environmental sequences. *Fungal Biology Reviews* **25**: 38–47.

Nilsson RH, Wurzbacher C, Bahram M, Coimbra VRM, Larsson E, *et al.* (2016) Top 50 most wanted fungi. *MycoKeys* **12**: 29–40.

Taylor JW (2011) One fungus = one name: DNA and fungal nomenclature twenty years after PCR. *IMA Fungus* **2**: 113–126.