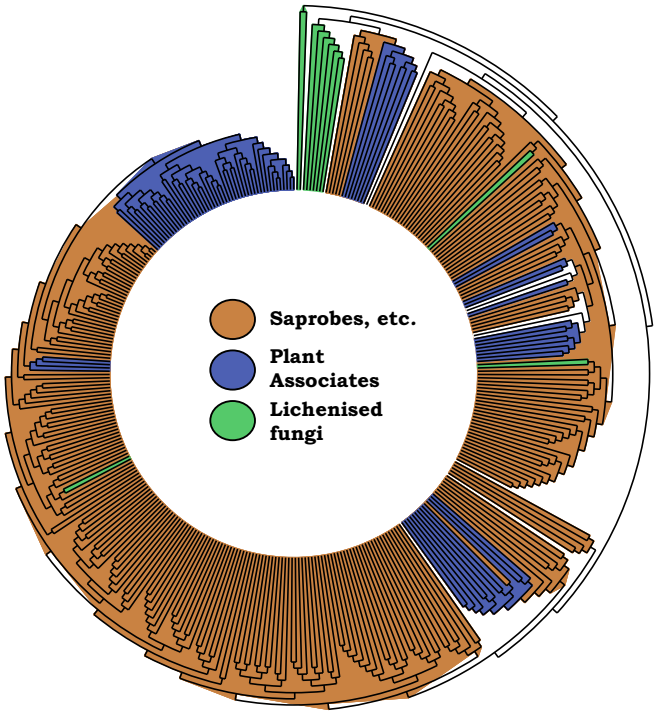
Were the first ascomycetes lichenized?

In the "Protolichenes Hypothesis", which was stimulated by the discovery of the early Devonian *Palaeopyrenomycites devonicus*, Eriksson (2005) postulated that *Pezizomycotina* – the class that includes all ascomycetes that form fruit bodies apart from *Neolecta* – most probably evolved from a group of ascomycetes lichenized with cyanobacteria and/or green algae, *Protolichenes*. This hypothesis was reached after carefully analyzing other possible scenarios, and paying attention to fossil fungal remains as well as molecular phylogenetic trees.

Hypotheses are there to be tested, and as new data accrue, that can be used to challenge them in the best traditions of science. Lutzoni *et al*. (2001) argued that the major fungal lineages were derived from lichenized ancestors, but since that date substantial amounts of new molecular data have become available. First, Schoch *et al*. (2009) presented a six-gene tree including sequences from 420 species of ascomycetes and endeavoured to reconstruct the ancestral character states. They concluded that ascomata had originated twice, once in common ancestor of *Pezizomycotina*, and once in that of *Neolectomycetes*. The first ascomata were considered to have had an exposed hymenium (apothecia) with multiple derivations of partially or completely closed hymenia (perithecia or cleistothecia). The ancestral fungi were interpreted as most probably saprobes with lichenization occurring multiple times, but also being lost infrequently and then mainly in groups of closely related species. There was, however, a problem posed by the possibility that *Palaeopyrenomycites devonicus* belonged to the advanced *Sordariomycetes*, as had previously been thought to be the case.



Molecular clock data had previously yielded divergent views – Did the ascomycetes originate 600 Myr or 1.5 Byr ago? The issue was revisited by Lücking *et al*. (2009) who re-assessed the systematic placement of *P. devonicus* and prepared newly calibrated molecular clock trees. Their results placed the origins of fungi at between 760 Myr and 1.06 Byr years ago, and that of the ascomycetes at 500-650 Myr ago. They did not consider that their results supported the "Protolichenes Hypothesis".

A critical factor is the calibration of the molecular clock, is the interpretation of the asci of *Palaeopyrenomycites*; were they really operculate as stated by Lücking *et al*. or not? The issue was revisited by Eriksson (2009) who discussed the asci in detail, and concluded that they were fissurate as in *Neolectales* and *Rhytismatales*, and not idemtical to the operculate type characteristic of *Pezizales*. He also points to the existence of other early fossils, including the Devonian *Winfrentia reticulata* which is considered to have been lichenized, and points to an origin at a time when there were few or no vascular plants.

Interestingly, and independently of the 2009 papers mentioned, Blair (2009) concluded from molecular time-trees that the major fungal lineages arose in the Pre-Cambrian, much earlier than their first appearance as unequivocal fossils in the Ordovician He places the origins of ascomycetes at about 900 Myr, with the *Pezizomycotina*/*Saccharomycotina* divergence at about 850 Myr ago, but does not cite or comment on the "Protolichenes Hypothesis".

It is evident that the debate will continue and require future reassessments as more early fossils are found, and also as greater numbers of gene sequences become available in a wider range of genera and families of ascomycetes. I suspect the fossils will prove to hold the day . . . . and wish more energy could be directed into palaeomycology to elucidate these fundamental questions of fungal evolution.

Blair JE (2009) Fungi. In: *The Timetree of Life* (Hedges SB, Kumar S, eds): 215–219. Oxford: Oxford University Press.

Eriksson OE (2005) Ascomyceternas ursprung och evolution – Protolichenes-hypotesen. [Origin and evolution of *Ascomycota* – the Protolichenes hypothesis.] *Svensk Mykologisk Tidskrift* **26**: 22–33.

Eriksson OE (2009) Ascomyceternas ursprung – argument granskade. [The origin of the ascomycetes - argument scrutinized.] *Svensk Mykologisk Tidskrift* **30**: 61–64.

Lücking RL, Huhndorf S, Pfister DH, Rivas-Plata E, Lumbsch HT (2009) Fungi evolved right on track. *Mycologia* **101**: 810–822.

Lutzoni F, Pagel M, Reeb V (2001) Major fungal lineages are derived from lichen ancestors. *Nature* **411**: 937–940.

Schoch CL, Sung G-H, López-Giráldez F, [and 61 others] (2009) The Ascomycota tree of life: a phylum-wide phylogeny clarifies the origin and evolution of fundamental reproductive and ecological traits. *Systematic Biology* **58**: 224–239.

A new devastating fungal pathogen of bats

Bats in the northeastern USA are being affected by a fungal pathogen, the recently described *Geomyces destructans* (Gargas *et al*. 2009). The disease was first noted in the winter of 2006, and the fungus is expressed as a powdery mass of conidia and hyphae on the bat's muzzles, leading to the coloquial name of "Bat white-nose syndrome" (WNS). ITS and SSU data show that he fungus is an anamorphic *Pseudogymnoascus* species. It invades the living tissues and is associated with a high rate of mortality. The species is so far known from four species of bats: *Eptesicus fuscus*, *Myotis lucifugus*, *M. septentrionalis*, and *Perimyotis subflavus*. The effects have been devastating, and it is estimated that over one million bats have died from WNS in the last three years, with some hibernation sites losing 90–100 % of their populations, with 10,000 to 20,000 dead bats being found on the cave floor of a single site last year (Buchen 2010). The mode of action is still unknown, and, fascinatingly, the species may have been infecting European bats for at least 23 years – it is reported from France, Germany, Hungary, and Switzerland. However, the European bats are not killed and it is speculated that they may have developed immune resistance to the fungus, which does not kill them.

Buchen L (2010) Disease epidemic killing only US bats. *Nature* **463**: 144–145.
Gargas A, Trest MT, Christensen M, Volk TJ, Blehert DS (2009) *Geomyces destructans* sp.nov. associated with bat white-nose syndrome. *Mycotaxon* **108**: 147–154.

Secretive sex

While the sexual states of fungi are characterized by the ability to form asci, basidia, or teliospores, an increasing number of fungi in which no sexual structures are known are being found to have mating locus genes (MAT-loci). Kück & Pöggeler (2009) list 23 species of "asexual" fungi in which MAT genes have been discovered; in only six of these has either sexual reproduction or mating ever been confirmed. These include species of *Acremonium*, *Alternaria*, *Aspergillus*, *Bipolaris*, *Candida*, *Cercospora* (as "*Cerospora*"!), *Cladosporium*, *Coccidioides*, *Fusarium*, *Penicillium*, *Rhynchosporium* (as "*Rhynchsporium*"), *Septoria*, and *Trichoderma*. In such cases it is uncertain whether sexual stages ever occur in nature, but in a few instances laboratory matings have given rise to sexual sporing bodies, as in *Aspergillus fumigatus* and *A. parasiticus*. In other cases, meiotic division and genetic recombination may both occur within the hyphae themselves as part of the so-called "parasexual cycle" with no production of sexual spores or sporing bodies. Interestingly, some of the species in which the parasexual cycle has been documented are ones which have also been found to be capable of forming sexual structures under particular conditions, such as *Aspergillus fumigatus* and *A. nidulans* (Swart & Debets (2004). The continued findings of MAT genes in fungi traditionally regarded as asexual, adds to the view that the division of pleomorphic fungi into discrete and separately named categories, i.e. a sexual teleomorph and one or more asexual anamorphs, is artificial. This adds to the case for an end to the dual naming system, which is appearing increasingly superfluous in the molecular age.

Kück U, Pöggeler S (2009) Cryptic sex in fungi. *Fungal Biology Reviews* **23**: 86–90.
Swart K, Debets AJM (2004) Genetics of *Aspergillus*. In: *The Mycota*. Vol. 2. *Genetics and Biotechnology* (Kück U, ed.): 21–36. 2nd edn. Berlin: Springer-Verlag.

Measuring the relationship between dead timber and wood-decay fungi

A recurring theme in developing woodland management plans is the issue of the extent to which dead standing and fallen timber should be in order to maximize the conservation of organisms of all kinds that occupy that habitat. This is of especial concern to mycologists as many of the rarest macromycetes are ones associated with dead wood. Now, Hottola *et al*. (2009) have endeavoured to generate a unified measure that takes into account the number, volume, and diversity of dead timber – and relates this to the diversity of the fungal communities. In order to characterize the amount of dead wood in a plot, a formula was devised:

$S(x) = \sum_i {}^{Vx}{}_i$ where Vi is the volume of log i, and x is a parameter that tunes the weighting between the number of logs and their volume or size; S(0) counts the number of logs irrespective of size, and S(1) the total volume of logs irrespective of their number. At the limit of $x \to \infty$, the value of S (x) is determined by the volume

of the largest individual log. Additional calculations were made to allow for the diversity of logs. The method was applied to 47 study plots dispersed through a 150 x 150 km area of boreal forest in Finland. Data were obtained on the occurrences of 116 wood-decaying polypores, counting all sporing bodies of a single species on an individual tree as one occurrence. The field surveys were carried out 2000, 2001, and 2003.

Possible explanatory variables were compared, and it was concluded that the abundance of common species is related to the number of downed logs, while occurrences of rarer Red-listed species was best explained by the total volume of logs – and especially the abundance of large logs. The Red-listed species were additionally affected by spatial connectivity to adjacent old-growth forest.

It will be no surprise to experienced field mycologists to find that the best method of ensuring the continuance of Red-listed polypores is to allow the amount of large downed logs to increase through the adopted management practices. However, what is valuable is for conservationists to have a critical study such as this to cite when making management proposals.

Hottola J, Ovaskainen O, Hanski I (2009) A unified measure of the number, volume and diversity of dead trees and the response of fungal communities. *Journal of Ecology* **97**: 1320–1328.

Funga and fungarium

Mycologists need to assert their independence from botanists, (other) microbiologists, and zoologists as a part of the long road to increased recognition amongst the life sciences. This is topic on which I have drawn attention to previously (e.g. Hawksworth 2000, 2003, 2006). One issue is to adopt a word for the fungi (including lichens) that occur in a particular area, or a major publication on those of a particular geographical region. In many cases it is possible to just use "fungi" by careful wording. I have not personally favoured the often-used "mycota" as that is the termination that indicates the rank of phylum, and the fungi are now universally accepted as a kingdom in their own right. I have consequently encouraged the use of "mycobiota" where some word was required. However, the alternative of "funga" was proposed by Gravesen (2000), and hardly taken up until recently relaunched in the title of *Funga Nordica* (Knudsen & Vesterholt 2008) – a key work which all field mycologists will now be coming familiar with. As the term "mycology" may not be as familiar to naturalists in general as "fungi", I now consider that "funga" has much to commend it.

In transferring the collections of the former International Mycological Institute (IMI) to the Royal Botanic Gardens at Kew at the end of 2009, to make the largest fungal collection in the world with some 1.25 million specimens, Spooner & Cannon (2010) introduced the term "fungarium" (pl. "fungaria") as a counterpart to "herbarium" (a collection of dried plants). This also seems logical and surely merits wider adoption – at least where the more encompassing "biosystematic reference collections" is not appropriate.

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Gravesen S (2000) Microbiology on Indoor Air '99 – what's new and exciting? An overview of selected papers presented in Edinburgh, August, 1999. *Indoor Air* **10**: 74–80.
Hawksworth DL (2000) Mycobiota, mycota or funga? *Mycological Research* **104**: 1283.
Hawksworth DL (2003) Monitoring and safeguarding fungal resources worldwide: the need for an international collaborative MycoAction Plan. *Fungal Diversity* **13**: 29–45.
Hawksworth DL (2006) Mycology and mycologists. In: *8th International Mycological Congress, Cairns (Australia), August 20-25, 2006* (W Meyer & C Pearce, eds): 65–72. Bologna: Medimond.
Knudsen H, Vesterholt J (eds) (2008) *Funga Nordica: agaricoid, boletoid and cyphelloid genera*. Copenhagen: Nordsvamp.
Spooner B[M], Cannon P[F] (2010) World's largest collection of fungi held at Kew Gardens. *Mycologist News* **2010** (1): 8–9.