

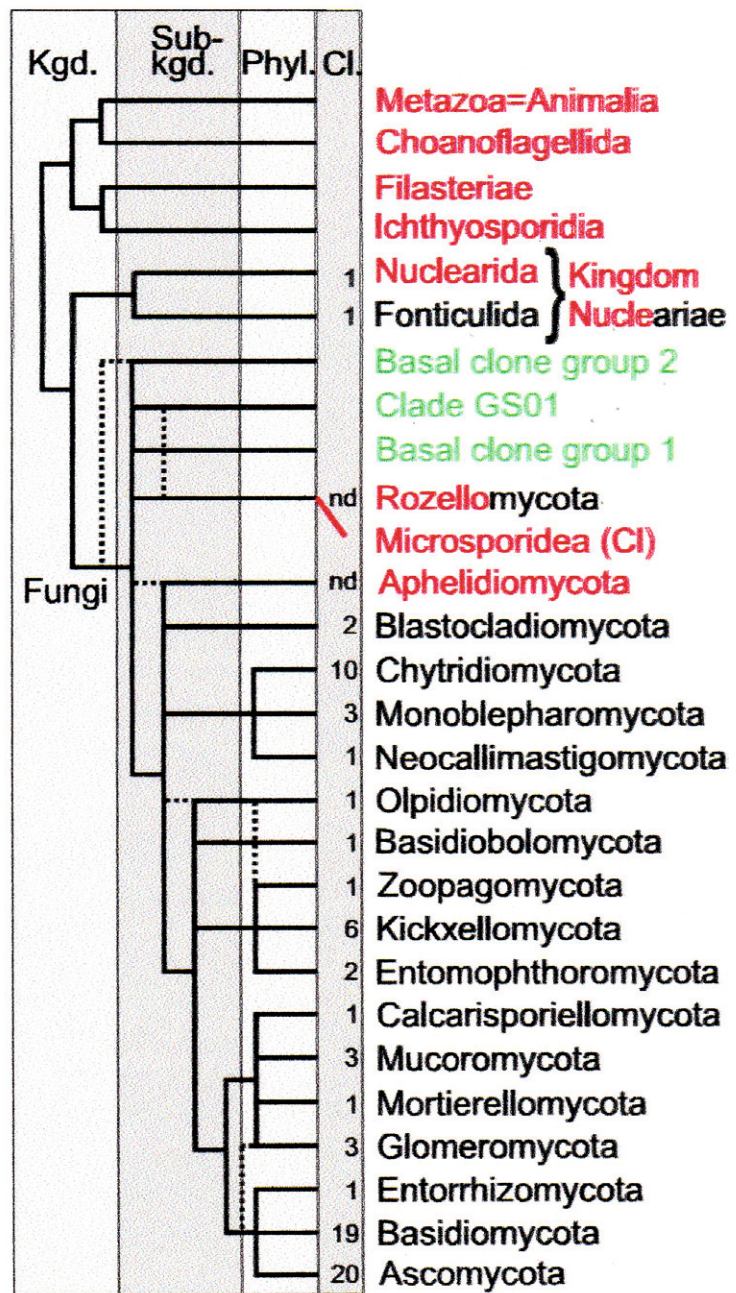
How many phyla of *Fungi* – eight, eighteen, or even more?

In the major overview of the classification of the kingdom *Fungi* by Spatafora *et al.* (2018), just eight phyla were recognized: *Cryptomycota*, *Microsporidia*, *Blastocladiomycota*, *Chytridiomycota*, *Zoopagomycota*, *Mucoromycota*, *Ascomycota*, and *Basidiomycota*. Now an updated system has been proposed (Tedersoo *et al.* 2018) which aims to take account of monophyly and divergence times so that the main ranks are more informative, and “a user-friendly tool for both taxonomists and ecologists” (p. 2).

The study was based on 111 taxa, with at least two taken from each phylum. Maximum Likelihood phylogenies were constructed, and for dating fossil-based calibration points were used. The kingdom *Fungi* itself is placed within a superkingdom, *Holomycota*, along with some groups generally the domain of zoologists and some unnamed major clades. The name *Holomycota*, however, is inappropriate at such a high level as the suffix “-mycota” is used only as an indication of the rank of phylum in the *International Code of Nomenclature for algae, fungi, and plants* (Turland *et al.* 2018). The *Holomycota* also includes the kingdom *Nucleariaria*, and is sister to the superkingdom *Holozoa*.

A formal nomenclatural treatment of names in all the ranks used down to class is provided, which includes the validating descriptions of numerous newly recognized higher taxa. Amongst these are the new phylum names *Aphelidiomycota*, *Calcarisporiellomycota*, and *Mortierellomycota* in *Fungi*, and *Fonticuilida* and *Nuclearida* in *Nucleariaria*.

It remains to be seen how readily such a drastic change will be taken up by other mycologists, and how robust it will be to challenges from the vast amounts of data coming from environmental sequences.



Updated phylum-level classification, names in red are taxa generally treated in zoology, in green are unnamed clades, and the numbers are those of the classes included. Adapted from Tedersoo *et al.* (2018).

Spatafora JW, Aime MC, Grigoriev IV, Martin F, Stajich JE, Blackwell M (2018) The fungal tree of life: from molecular systematics to genome-scale phylogenies. In: *The Fungal Kingdom* (Heitman J, Howlett BJ, Crous PW, Stukenbrock EV, Gow NAR, eds): 3–34. Washington DC: American Society for Microbiology.

Tedersoo L, Sánchez-Ramírez S, Kõljalg U, Bahram M, Döring M, *et al.* (2018) High-level classification of the *Fungi* and a tool for evolutionary ecological analyses. *Fungal Diversity*: DOI 10.1007/s13225-018-0401-0.

Turland NJ, Wiersema JH, Barrie FR, Greuter W, Hawksworth DL, *et al.* (2018) *International Code of Nomenclature for algae, fungi, and plants*

(Shenzhen Code) adopted by the Nineteenth International Botanical Congress Shenzhen, China, July 2017. [Regnum Vegetabile no. 159.] Oberreifenberg: Koeltz Botanical Books.



Artist's impression of *Prototaxites* sporophores, that can be almost 9 m tall. Artist: Geoffrey Kibby.

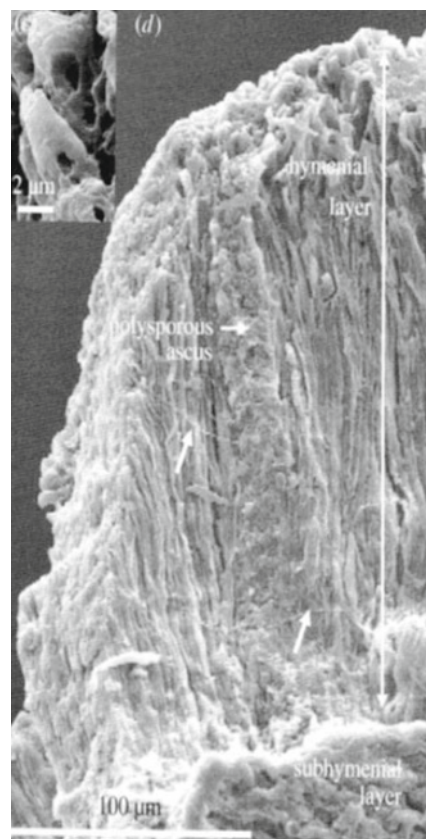
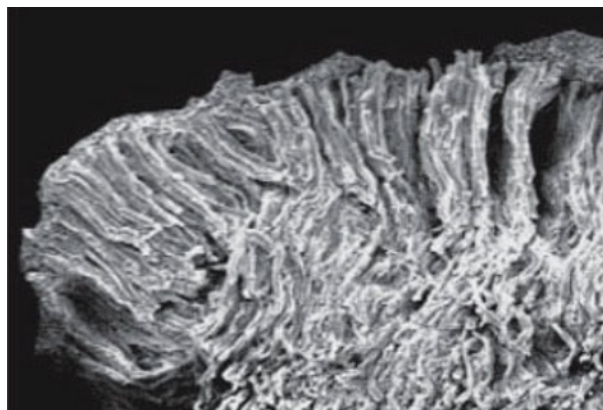
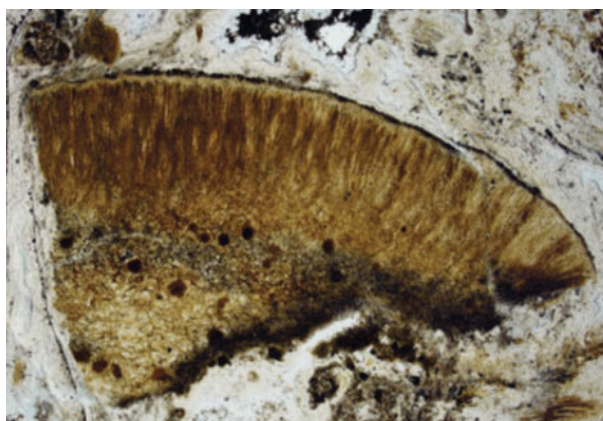
Prototaxites revealed as a basal ascomycete that may have been lichenized

The massive enigmatic structures referred to *Prototaxites* occur from the Silurian to the Upper Devonian (ca.360–430 Myr) can be more than 1 m diam and to 8.8 m tall. They are thought to have projected vertically as narrow cones and must have been a spectacular sight, which several artists have endeavoured to provide impressions of. About 14 species have been recognized, and these come from as far apart as Australia, Europe, the Middle East, North Africa and North Africa. Their interpretation has been a long-standing matter of debate amongst palaeontologists, and elucidation has been frustrated by the outer surfaces not being preserved intact.

Prototaxites has been thought to be fungal, and possibly a basidiomycete, for some years (Selosse 2002), but evidence of the nature of the reproductive structures has been lacking, and its' biology has remained particularly obscure. Now some material of *P. taiti* with the surface intact from the Rhynie chert in Scotland has been studied in thin section using a laser-scanning confocal microscope and autofluorescence techniques (Honegger *et al.* 2018). The

surface layer was established as being the hymenium of an ascomycete, with narrowly cylindrical polyspored asci packed amongst vertically orientated paraphyses. Although no similar ascomycetes are extant, there are families which have the hymenium formed over the outer surface of erect structures (e.g. *Geoglossaceae*, *Morchellaceae*,

Neolectaceae) and which are long-lived as these organisms are presumed to have been (e.g. *Cladoniaceae*). The asci were found to be inoperculate, opening with a split, and to arise from what were interpreted as croziers. The authors consequently conclude that the genus is a basal ascomycete, but not an ancestor of *Pezizomycotina* as other members



Prototaxites taiti, thin section of hymenium (above); *Prototaxites* sp., SEM of charcoaled hymenial layer (below); and detail showing polyspored asci and narrow unbranched paraphyses (side). Reproduced from Honegger *et al.* (2018).

of the subphylum were contemporaneous. Similarities to the diminutive genus *Neolecta* are, however, rather striking.

Two major uncertainties remain: how the massive *Prototaxites* structures retained their integrity, and how they obtained the nutrients they needed. The stromata do, however, appear to have been robust and some are reported to show growth-rings; there have also been speculations that there may have been some kind of anchoring root-like structures. The question of nutrition is especially intriguing. It seems unlikely that such large structures would be of a saprotroph as there would be no advantage in investing energy to form such huge aerial structures. While no microscopic evidence for the occurrence of algae or cyanobacteria in the

structures has been obtained, it is well-known that these do not readily fossilize and may just not have been preserved, so the possibility that *Prototaxites* was lichenized cannot be excluded – indeed, depending on included photosynthetic partners is an optimal means of obtaining required sugars. Perhaps the next step is for there to be a more concerted search for algal or cyanobacterial remains within the structures.

[This study forms one of a collection of 16 papers on the Rhynie Chert arising from a discussion meeting held in the rooms of the Royal Society of London in March 2017 (Edwards *et al.* 2018). It includes three papers concerning fungi associated with the Rhynie chert plants in addition to that on

Prototaxites, so should be consulted by all interested in palaeomycology.]

Geoffrey Kibby kindly allowed a copy of his painting to be used in this report.

Edwards D, Dolan L, Kenrick P (eds) (2018) The Rhynie cherts: our earliest terrestrial ecosystem revisited. *Philosophical Transactions of the Royal Society of London, B 373*: issue 1739.

Honegger R, Edwards D, Axe L, Strullu-Derrien CS (2018) Fertile *Prototaxites taiti*: a basal ascomycete with inoperculate, polysporous asci lacking croziers. *Philosophical Transactions of the Royal Society of London, B 373*: 20170146.

Selosse MA (2002) *Prototaxites*, a 400 Myr old giant fossil, a saprophytic basidiomycete, or a lichen. *Mycological Research* 106: 641–644.

Immunity to *Aspergillus fumigatus* infections

Aspergillosis in humans, caused by *Aspergillus fumigatus*, is a major and sometimes fatal disease, particularly in those with suppressed immune systems, and including those who have had transplant surgery. The conidia are so small (*ca.* 2 µm diam) that when inhaled they can penetrate into the smallest and deepest recesses of the lungs, where they can establish mycelia and become invasive and even form substantial growths. The number of people infected around the world is unknown, but could run into many 100 000s, especially as internal fungal infections can be overlooked or misdiagnosed by generalist practitioners.

There have been enormous advances in our understanding of the disease processes and the nature of immune responses involved in recent years (Bignell 2014), but the precise mechanism which results in some people being more resistant than others has remained obscure. Elegant work by a team of 33 researchers scattered through six countries has now shed new light on this question. Stappers *et al.* (2018) investigated what triggered mammalian C-type lectin receptors to respond to an invading organism and initiate an immune response. They discovered a melanin-recognizing receptor (MelLec) that reacted to the melanin in the conidia of *A. fumigatus* and some other fungi, triggering the production of cytokine that can attract and stimulate neutrophil cells that can target the invading conidia; the process is well-illustrated in a news item in the same issue of the journal that describes this work (Casadevall 2018). Tests with mutated strains of the *Aspergillus*

revealed that responses were not initiated when these genes were knocked-out in experiments with mice. However, when mice were immunosuppressed by corticosteroids, those that lacked this gene substantially increased in susceptibility to *Aspergillus* conidia compared with wild-type controls.

The group then proceeded to ascertain if a parallel situation occurred in humans, where the MelLec has been detected, but differs in a single nucleotide polymorphism (SNP) from that in mice. There was a significant association between this SNP and the risk of aspergillosis in stem-cell transplant recipients. Further, macrophages isolated from healthy patients with the SNP produced a significantly less immune response when challenged by *A. fumigatus* conidia compared with controls. Consequently, identifying organ donors carrying this SNP could help reduce the incidence of this disease.

The authors speculate that the MelLec gene may also have an important role in human immunity to other fungi with melanized walls, such as those involved in chromatoblastomycosis, mycetomas, and phaeophycomycoses. This result may therefore be the start of a new era in understanding and addressing human reactions to a wide range of melanized fungi.



Aspergillus fumigatus (photo: Rob Samson).

Bignell E (2014) *Aspergillus fumigatus*: saprotroph to pathogen. In: *The Mycota*. Vol. XII. *Human Fungal Pathogens* (Kurzei O, ed.): 19–43. 2nd edn. Berlin: Springer.

Casadevall A (2018) Melanin triggers antifungal defences. *Nature* 555: 319–320.

Stappers MHT, Clark AE, Aimaniananda V, Bidula S, Reid DM, *et al.* (2018) Recognition of DHN-melanin by a C-type lectin receptor is required for immunity to *Aspergillus*. *Nature* 555: 382–386.