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The Fungus Fossil Record: A Major Problem for Darwinism

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Abstract

Fungi are complex life-forms that play a major role in modern ecology. A wide variety of fungal types exists from microscopic yeasts to large mushrooms. The estimated 100,000 species of fungi comprise approximately one-quarter of the earth's entire biomass. The fungus fossil record, which is examined in this paper, does not provide evidence of neo-Darwinism for the members of the Kingdom Fungi. As a result of this lack of evidence, speculation by Darwinists has resulted in many conflicting theories of fungus evolution, all unconstrained by fossil evidence.

Introduction

Fungi are highly successful life-forms. The atmosphere normally contains enormous numbers of their tiny spores, which are light and easily germinate on a wide variety of substances (Thomas, 1981, p. 30). Fungi are so common and widespread that they comprise an estimated 1.5 million species, fewer than 5% of which have been described, and 25 % of the biomass on the entire planet (Bruns, 2006; Moore, 1998). As a result, human exposure to fungi is ubiquitous. They are found in all ecosystems and show a great diversity of lifestyles (Redecker, 2002a).

Although approximately a hundred thousand species of fungi and molds have been identified by mycologists, less than 150 have been demonstrated to produce infectious disease and/or allergies in humans (Hiipakka and Buffington, 2000; Karunasena et al., 2000). The vast majority are ecologically and economically important (Ingold, and Hudson, 2000). They play many significant roles in nature everywhere some types exist (Brodo et al., 2001). Because some types cause health problems, the disease-causing fungi are often the best-known types. About 90% of all fungi found indoors are associated with the biodeterioration of plants, and a few of these fungus types can produce certain organic products that cause allergies. Some of the more common allergy-causing organisms include *Penicillium*, *Aspergillus*, *cladeosporium*, *Alternaria*, and *Aureobasidium*. A few fungi also produce mycotoxins that can result in a variety of adverse health effects.

Fungi include a wide variety of complex, usually nonmotile, filamentous, multicellular plantlike, spore-producing organisms characterized by the absence of chlorophyll. In terms of evolution, they are considered one of the most successful forms of life (Christensen, 1965). Lacking plastids and photosynthetic pigments such as chlorophyll, they cannot photosynthesize, and, for this reason, must utilize other organic matter (Brodo et al., 2001). Common examples of fungi include molds, mildews, yeasts, lichens, mushrooms, and toadstools. Fungi have several critical functions in ecology, including colonizing bare rock as the first step in converting unusable land to fertile areas that can support a wide variety of plant life. Their major role is to decompose and recycle organic waste materials produced by other organisms, notably lignin and cellulose (Taylor and Taylor, 1997, p. 83). This role is necessary for life to exist on earth.

Fungi also are critical as mutualistic symbionts of plants and animals. Yeasts are important in making a variety of foods, including bread, wine, and many other food products. Fungi are a major source of antibiotics, including those in the penicillin and griseofulvin families,

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and also of many other kinds of medicine (Kavaler, 1965).

Fungus Feeding Systems

Four basic feeding systems of fungi exist: *parasites* (those that grow in, and feed on, living tissues or cells), *epiphytes* (those that grow on the surface of other living organisms and use them for structural support only), *saprophytes* (those that live in and feed on dead plants or animals, their tissues, or products, such as seeds), and *mycorrhiza*. Saprophytic fungi play a critical role in breaking down or decomposing a wide variety of dead plants and animals, including wood logs, nuts, grass, and even animal dung (Sterflinger, 2000). A few fungi types (the parasitic fungi) live on living organisms, especially trees. The fourth type, the mycorrhiza, lives in a unique symbiotic association with the roots of plants. Redecker et al. (2000, p. 1920) conclude that some fungi, such as arbuscular mycorrhiza, played an important role in the success of early terrestrial plants.

Fungus Taxonomy

Fungal taxonomy has undergone numerous major changes during the last decade or so, partly due to the use of DNA sequence comparisons. The Kingdom Fungi now contains four main nonflagellated phylums, also called divisions, Glomeromycota, Zygomycota, Ascomycota, Basidiomycota, and the flagellated Chytridiomycota (James et al., 2006; Guarro et al., 1999, pp. 454–500). The current scheme of fungus is described in Table I. Most of the groups once called lower fungi—like the cellular and plasmodial slime molds, the oomycetes, and the hyphochytrids—are no longer classified as fungi, or even considered closely related to fungi (see Table II). For an older scheme of fungal phyla, see Table III. For an explanation of terms, see the glossary at the end of this paper.

Table I. The New Fungus Phylum Classification

1.	**Phylum Chytridiomycota**, the chytrid, represent a group of primitive aquatic fungi characterized by having gametes called zoospores that are motile by means of flagella. They are the only members of the kingdom Fungi that produce motile cells sometime during their life cycle.
2.	**Phylum Zygomycota** have unenclosed, or naked, sexual spores called zygospores that are not contained within a specialized fruiting body or sac. Zygospores form when the haploid nuclei at the ends of two hyphae fuse together to form a diploid zygote. The zygote then undergoes meiosis to form haploid cells that develop into zygospores. An example of a zygomycete is the common black bread mold, *Rhizopus nigricans*.
3.	**Phylum Ascomycota** are also called sac fungi because their sexual spores (ascospores) are enclosed in tubelike sacs called asci. Ascospore formation is similar to that of zygospores, except ascospores are formed by meiosis enclosed in the asci. *Neurospora crassa* is an ascomycete mold important in genetic linkage studies.
4.	**Phylum Basidiomycetes** are also known as club fungi, because their sexual spores (basidiospores) are produced from tiny clubs called basidia. Basidiomycetes include many of the more complex fungi, including mushrooms and puffballs.
5.	**Phylum Deuteromycetes**, also called imperfect fungi, contain species for which no sexual stage has been discovered. Many parasitic fungi were once classified into this group but were reclassified when the sexual stage was discovered. An example of a deuteromycete is *Candida albicans*, a dimorphic fungus responsible for many human yeast infections.
6.	**Phylum Glomeromycota** is a new fungal phylum known to be ecologically and economically important (Schüsler, et al., 2001). The Glomeromycota were part of the Zygomycota phylum but were removed on the basis of molecular, morphological and ecological characteristics (Schüsler, et al., 2001). They are mutualistic symbionts that form intracellular associations with the vast majority of tropical trees and herbaceous plants. They receive carbohydrates from their host and function as an extended root system, called an arbuscule, dramatically improving the plant hosts' mineral uptake (Redecker, 2005). The Glomeromycota phylum contains ten genera and approximately 150 described species.

The exception is the chytrids, which are still thought to be ancestral to all other fungi and retain what evolutionists assume are primitive fungal ancestor characteristics. It is also now believed that, except for the chytrids, fungi are more closely related to animals than to plants, algae, or any of the lower fungi as noted above (see Werner, 2003, pp. 1–5). Werner also reported that recent research findings have forced some surprising revisions in fungus taxonomy.

> Most notably, it has been demonstrated that the Zygomycota are not a real monophyletic group, but instead represent a polyphyletic assemblage of parts of at least four different lineages, including a lineage that does not belong to the Kingdom Fungi at all (Werner, 2003, p. 3).

Gene analysis also has resulted in other reclassifications. *Amoebidium*, for example, is a trichomycete that lives in the intestines of arthropods. Amoebidi-

Table II. The Lower Fungi (Lower fungi are fungus-like organisms that are not included in Kingdom Fungi by most modern taxonomists).

1.	**Plasmodiophoromycota,** also called **Phytomyxea**, are a group of protists that are parasites of plants. They typically develop within plant cells, causing the infected tissue to grow into a gall or scab (thus are endoparasitic slime molds). Important diseases that they cause include club root in cabbage and its relatives and powdery scab in potatoes.
2.	**Dictyosteliomycota** are eukaryote cellular slime molds. When water or food resources are limiting, they release pheromones as acrasin to aggregate amoebal cells in preparation for movement as a large (thousands of cells) bloblike mass called a grex, or "slug," that glides along on its own secretions, engulfing bacteria, fungi, and decaying organic matter for food as it travels.
3.	**Acrasiomycota** are eukaryote acrasid cellular slime molds related to protists. The name *acrasio-* comes from the Greek *akrasia*, meaning "acting against one's better judgment." Some mycologists consider Acrasiomycota a kingdom, because of conflicting molecular and developmental data, a debate not yet settled.
4.	**Myxomycota** are eukaryote true slime molds is a group related to protists. The name *myxomycota* comes from the Greek *myxo*, meaning "slime," and *mycota*, meaning fungus. They are also known as plasmodial or acellular slime molds. Some mycologists consider Myxomycota a kingdom because of conflicting molecular and developmental data.
5.	**Oomycota** are eukaryotes that include the so-called water molds and downy mildews. The 500 known Oomycota species are filamentous protists that must either absorb their food from the surrounding soil or they may invade another organism to parasitically live off of it. Oomycetes play a critical role in the decomposition and recycling of decaying matter. Oomycota means "egg fungi."
6.	**Hyphochytriomycota** are a small but important group of zoospore-producing organisms that look much like the Chytridiomycota except that they have flagella.
7.	**Labyrinthulomycota** are eukaryote net slime molds
8.	**Eufungi** are eukaryote nonciliated fungi, which, unlike other fungi, have unstacked Golgi cisternae
9.	**Chytridiomycota** (chytrids) are considered the most primitive fungi. They are mostly saprobic, and many are aquatic, living mostly in fresh water. The approximately 1,000 chytrid species use flagella to travel in their watery world.

Table III. An Older Fungus Classification.

Kingdom: Plants.

Subdivison D: True Fungi defined as thallophytes without chlorophyll

Class 1: Phycomycetes (Algal Fungi), vegetative hyphae usually without cross walls. Reproduces sexually by zygospores or oospores.

Class 2: Ascomycetes (sac fungi) has hyphae with cross walls and Ascospores formed after sexual fusions.

Class 3: Basidiomycetes (club fungi) has hyphae with cross walls and Basidospores formed after sexual fusions.

Class 4: Imperfecti (Imperfect Fungi), sexual reproduction unknown (from Wilson, 1945, pp. 278–279).

um was originally classified as a fungus but has been reclassified in the Mesomycetozoea, which are a small group of parasitic protists. Amoebidium are also closely allied to choanoflagellates. The mesomycetozoans and choanoflagellates form a clade that Werner believes to have diverged from the animal line at a point in animal evolution when the ancestors of animals had not yet strongly differentiated from the ancestors of fungi. Werner (2003) added that it is very likely that further analysis will reveal many other trichomycetes to be mesomycetozoans rather than fungi. In addition, according to Werner (2003), the majority of taxa once classified with the classic *Rhizopus* bread mold in the phylum Zygomycota are now in a lineage consisting of the core zygomycetes plus the Blastocladiales (which were once classified as chytrids).

The next most basal clade consists of the chytrids (excluding the Blastocladiales), plus several genera formerly classified as zygomycetes, including the genus *Endogone*. *Endogone* is the only known fungal taxon outside of the Ascomycota and Basidiomycota whose members can form ectomycorrhizae with plants.

The remaining zygomycete clade consists of certain mycorrhizal fungi that recently have been designated phylum Glomeromycota (see Table 1). This group is now considered to be a basal member of the same clade as both Ascomycota and Basidiomycota.

This revolution in taxonomy is largely caused by the use of gene comparisons for classification as opposed to morphology, which was the system used in the past (Guarro et al. 1999, p. 455). Werner (2003) concluded,

> This new understanding of the basal phylogeny of fungi throws much of our prior understanding of fungal evolution into disarray. When the chytrids were thought to be the most basal clade in the fungi, the evolution of a predominantly hyphal fungal morphology from a zoosporic one was thought to have taken place only once. It now seems that this evolutionary event took place at least three times, or perhaps there may have been several shifts back and forth between predominantly zoosporic life histories and predominantly hyphal ones. (p. 4)

DNA comparisons not only have forced a polyphylogeny theory on the older monophylogenetic zoospore theory but also have forced a major revolution on the phylogeny of all life-forms. One reason for favoring the polyphylogeny theory is the fact that molecular studies have found the so-called lower fungi are much more complicated than previously thought (Redecker, 2002a, p. 126).

Fungal taxonomy is still in a state of flux (see Tables 1 and 3), and the relationships of different groups within the main groups will likely continue to change, and some mycologists disagree with the classification described here from Werner (2003). Another problem is that what different mycologists consider to be a species can vary widely, and there are different approaches for delineating species (Guarro et al. 1999, p. 455).

The Phylogeny (Evolution) of Fungi

It was once believed that algae, lichens, mosses, and other primitive plants spontaneously generated from decomposing water (see Howe and Armitage, 2003, p. 247). Although the details have changed considerably, for the last century Darwinists have likewise taught that fungi evolved from some other simpler life-forms that originated by spontaneous generation (Padovan et al., 2005; Gaumann, 1952). It also was once believed that fungi are degenerate plants that lost their chlorophyll during evolution. Since genetic research on rRNA has indicated that fungi were never photosynthetic (Raven, 2002), it is now argued that they split off by evolution before plants had evolved chloroplasts.

Others argue that genetic symbiosis (the exchange of genes) better explains the evolution of fungi (Margulis, 1996). In other words, this theory argues that it is the lateral transfer of genes from one unrelated life-form to other unrelated evolutionary clads, causing unexpected similarities, that produced the variety and similarity we see today in the fungal kingdom. No direct evidence exists for the theory of symbiosis, although it is well established that viruses and other vectors can transfer genes and cause disease such as cervical cancer. Creationists attribute these differences to a designer, a view that is supported by the fact that these different genes are well integrated to the different organisms in which they are found.

The classical view proposed by mycologists and still accepted by many is that fungi evolved from chytridomycotes (chytrids) or similar organisms. Their ancestors are assumed to have been aquatic, either marine or freshwater, mostly single-celled life traditionally classified as protists. Other mycologists hold different views of fungi evolution. For example, Pearson (1995, p. 162) suggested that they evolved from extinct seaweeds in the order of solenoporales. Specifically, fungi are now commonly assumed to have originally evolved about a billion years ago from flagellated protists similar to present-day choanociliates (Moore, 1998). Confusion over their evolution is indicated by the fact that

> mycologists have long maintained that the fungi represent different phylogenetic lineages, probably evolving from different protist ancestors. A widely held and longstanding view of fungal phylogeny assumes that the chytrids, or organisms similar to the chytrids, were ancestral to the true fungi (Moore-Landecker, 1996, p. 245).

Although no accepted phylogenetic hypothesis exists for the evolution of fungi, one view is they evolved from flagellated cells (James et al., 2006). They also are commonly assumed to have evolved in an aquatic habitat and to have left this environment by becoming parasitic and living off of the first land plants (Heckman et al., 2001). To support this view, evolutionists point to evidence that some of the earliest known fungi coexisted with various organisms in nonmarine ecosystems (Gray and Boucot, 1993; Urbani, 1980). The moist tissues of their hosts would have shielded them from desiccation, allowing them to live on land (Neushul, 1974). Other researchers disagree, holding that fungi evolved on land and that some forms left the land and went into the water, where they evolved further.

Still others argue that different groups of fungi evolved separately in water and on land. Many researchers think that fungi evolved separately several times, producing the wide array of types existing today (Redecker, 2002a). Kendrick even assumed that fungi seem to have arisen independently in no fewer than fourteen families of agarics (2000). Another view fostered by James et al. (2006) claims that the ancestors of fungi are simple, aquatic forms with flagellated spores, similar to the extant Phylum Chytridiomycota (chytrids). This view indicates that fungi lost their flagella at least four separate times in evolution and the loss of swimming spores coincided with evolution of entirely new methods of spore dispersal (James et al., 2006).

The matter of determining the evolution of fungus as a group is a major problem because even the basic classification of Fungi

> has been a matter for considerable discussion and debate. Fungi, for example, were previously placed in the Plant Kingdom along with the photosynthetic plants. Now, the organisms studied as fungi by mycologists fall into three [different] kingdoms (the Protoctista, Chromista, and Fungi), but none are considered to be plants. Similarly, the phylogeny of the fungi themselves has been debated and various hypotheses proposed (Moore-Landecker, 1996, p. 245).

An excellent summary of the problems determining fungus phylogeny concluded that

> diagrams, evolutionary trees, and statements regarding the *course* of evolution and relationship among the higher categories are of necessity largely speculative.... Such phylogenic syntheses often vary with the individual biologist who proposes them, and they are subject to continuing modification as new evidences become available (Bold et al., 1987, p. 5).

Bold et al. (1987) concluded that the most trustworthy evidence on which evolutionary relationships can be postulated is the fossil record and the comparative morphology of both extinct and extant organisms. We will now turn to that evidence.

Fossil Evidence

To demonstrate an evolutionary origin of fungi requires fossil evidence. Guarro et al. (1999) in a review of the literature concluded that currently little is known about evolutionary relationships among fungi and even the phylogenic relationships among higher fungal taxa remains uncertain, mainly because of a lack of sound fossil evidence. As a result, their phylogeny remains a source of much controversy.

The problem is not due to a lack of a fossil record. Fossil fungi are especially well preserved as permineralized remains or epiphyllous types (Taylor, 1993). Fossil fungi dated by evolutionists back to 600 million years by using their dating system have been found throughout the world, and many studies have been completed on these discoveries (Yuan et al., 2005; Sterflinger, 2000; Waggoner, 1994). Fossil finds include glomaleans (see Glossary) with an assigned date as far back as 720 million years ago. A diverse collection of fungi has also recently been unearthed in Scotland (Yuan et al., 2005). Many of those found were higher fungi, including Ascomycota and Basidiomycota groups (Rokas and Carroll, 2006; Redecker, 2006).

Aquatic fungi were some of the first fossil fungi reported from carboniferous plant materials, and chlamydospores are one of the most common fungal elements in carboniferous coal (Taylor and Taylor, 1997). So far, approximately 500 species and 250 genera have been discovered in the fossil record, and many are exactly like modern fungi, even with respect to their life cycle (Stewart and Rothwell, 1993).

The close similarity between fossil fungi and modern forms was noted by Arnold as far back as 1947. He documented the fact that the early fossil record includes well-preserved examples of both modern-appearing mycelium and spores (Arnold, 1947). Many fungi have been preserved in amber, and fine details have been preserved by the silicification of chert in which many fossils are embedded. Many different species of fungi, including yeast, have been preserved in amber, and the most common type found is saprophytic fungi (Poinar, 1992). Even well preserved fossil fungi living within host tissue (endogenaceous fungi) have been found (Stewart and Rothwell, 1993). Although most fossil fungi are small, even large fossil fungi (such as mushrooms) have been found in amber. All of the evidence discovered to date shows that nearly all of these fossil fungi are very similar to modern fungi and the rest are extinct.

In addition, fungi are found in the fossil record where they were living off the plants on which they live today. This indicates that the plant-fungi symbiotic or parasitic relationship has not changed much over time. For examples see Rodriguez et al. (1998).

Characteristics of the Fungus Fossil Record

The plant, fungus, and animal kingdoms are thought by many evolutionists to "have diverged from each other roughly a billion years ago" (Bruns, 2006, p. 758). They believe the fossil record of fungi dates back to over 650 million years ago (Moore, 1998). Fossil spores also are commonly found—the oldest have been dated back to about 601 million years ago—many of which are highly distinctive and extremely similar to present-day species (Moore, 1998). The major groups of fungi, including the Zygomycota (fungi producing a multinucleate zygospore; see Table 1), Ascomycota, and Basiomycota are thought to have diverged about one billion years ago because modern members of these divisions are found very early in the fossil record (Simon et al., 1993). Taylor and Taylor (1997) noted that research on fungus-host interactions indicates that most modern fungus groups extend well back into the Precambrian.

The oldest confirmed fungus discovered so far (a chytrid-like form) was found in northern Russia and has been given a date in the late Precambrian. Several other fungus groups can be traced back to strata that are classified as Paleozoic (Taylor and Taylor, 1997). All major groups of modern fungi have been found as far back as strata assigned to the Devonian. The primary method used to determine evolutionary phylogeny involves morphological traits such as spore characteristics, cuticle structure, and an evaluation of a variety of macroscopic features (Moore-Landecker, 1996). In one study alone about 500 fossil fungi were evaluated (Alexopoulos et. al., 1996).

Although an abundant fossil record exists for many fungi, there is no evidence to show their evolution from their putative evolutionary ancestors, a topic that has been much debated in the journals. For this reason, many mycology text authors include only a few paragraphs on the evolution of fungi, and some totally ignore the topic (see Ingold and Hudson, 2000). Other writers admit that fungi, bacteria, algae, and bryophytes all lack fossil evidence of any of their putative evolutionary stages (Scagel et al., 1984; Scagel et al., 1969). Scagel et al. (1984) noted that because of this lack of fossil evidence for neo-Darwinism, theories of the origins of fungal groups are always speculative, and are based upon inadequate factual information.

The same is true in publications from the 1990s. Stewart and Rothwell (1993) stressed that conclusions about the evolutionary original(s) and relationships of the major groups of fungi are speculative and often based on equivocal interpretations of the fossil evidence. Moore (1998) reported that most aspects relating to the origins and subsequent evolution of fungi are impossible to establish from any fossil record, so ideas and concepts must be gleaned from other sources. Their chitin skeleton seems to have showed up so suddenly in the fossil record that its appearance was called "dramatic" by Lowenstam and Margulis (1980).

A study of the fossil record reveals either essentially modern types or extinct forms of fungi (Stewart and Rothwell, 1993). Because their pattern of life and structure is in marked contrast to plants, a large number of transitional forms would be required to bridge fungi to other similar life-forms (Thomas, 1981). In the fossil record, for example, Redecker et al (2000) found that

> fossilized fungal hyphae and spores from the Ordovician of Wisconsin (with an age of about 460 million years) strongly resemble modern arbuscular mycorrhizal fungi (*Glomales*, *Zygomycetes*). These fossils indicate that Glomales-like fungi were present at a time when the land flora most likely only consisted of plants on the bryophytical level. (p. 1920)

Rikkinen and Poinar (2000) described a recent find of a remarkably well preserved fungus called *Chaenothecopsis bitterfeldensis* in Bitterfeld amber dating back to at least 20 million years ago (near the Miocene-Oligocene boundary) and possibly closer to 40 million years ago. They concluded that the fungi were strikingly similar to some modern species living in East Asia. Protein sequence estimates also date major modern lineages of fungi back to one billion years ago (Heckman et al., 2001). Even ultrastructural comparisons indicate ancient fungi are remarkably similar to modern forms (Stubblefield et al., 1985).

Poinar and Poinar (1994) add that their findings push back the time of the fossil record of glomalean fungi by 55 to 60 million years and also suggest that *these* fungi were present before the first vascular plants arose (p. 179). Typical of the fossil studies that have found either extinct or modern types in the fossil record is a review by Redecker (2002a):

> The Rhynie Chert [see Glossary] also contained a wealth of specimens from other fungal groups. Among them are a blastocladealean chytrid, strikingly well preserved and very similar to today's genus *Allomyces*. Another fungus has fruiting structures resembling today's Ascomycete groups of *Pyrenomycetes* or *Loculoascomycetes*. The quality of the specimens even led to distinguishing individual asci, the microscopic sac-like structures containing meiospores. (p. 128)

The Rhynie Chert beds in Aberdeenshire (northeastern Scotland) are important fossil sites that reveal a great deal about life in the Early Devonian (dated by evolutionists at approximately 408–360 million years ago).

Because of the lack of evidence for transitions, possible phylogenies of fungi require numerous assumptions and much speculation:

> Although no clear link exists between procaryotes and fungi, possible relationships occur between fungi, flagellates, and perhaps even red algae. It is widely thought that diverse ancestral flagellates have given rise to the lower fungi. These [as yet undiscovered organisms] are thought to have resembled the flagellated reproductive stages of existing Chytridiomycetes and Oomycetes.... These ancestral types are also assumed to have been able to use inorganic sulfur and nitrogen and to synthesize a wide variety of compounds. (Neushul, 1974, p. 178)

After noting that the phylogenetic history of fungi is based on little evidence and much speculation, Moore-Landecker (1996) admitted that the phylogenetic framework outlined by mycologists for over a century is a hypothesis that has become

> part of mycological history, whether or not it is factual in its entirety. Until molecular biology techniques were developed, there was little resolution about the validity of the proposed hypotheses. Arguments were particularly vehement about whether or not the red algae were ancestral to the Ascomycota. (p. 247)

One example of this hypothetical mycological history was summarized by a leading mycologist, Moore-Landecker (1996). After admitting that ancestral chytrids were much like their modern counterparts, he theorized that ancient chytrids lost their flagella and evolved zoospores. Then they gave rise to the Zygomycota, speculating that the most primitive Zygomycota

> might have been similar to *Mucor*, which forms large multispored sporangia. ...It is possible that the link between the phylum Zygomycota and phylum Ascomycota was made in the evolutionary transition of a fungus resembling our present-day *Endogone* into one resembling *Dipodascopsis*.... *Dipodascopsis* is a key organism, perhaps yielding the unicellular yeasts by reduction, and also giving rise to more advanced organisms as an extended dikaryophase was acquired. Once a dikaryophase had been acquired, the ancestral organism was much like our present-day *Taphrina*. *Taphrina*-like ancestors gave rise to the remaining members of the phylum Ascomycota as multicellular ascomata evolved. Evolution of the bitunicate ascus [also] occurred, probably producing a divergent line. (Moore-Landecker, 1996, p. 247)

Moore-Landecker (1996) concludes that it is currently speculated that Basidiomycota evolved from a *Taprhina*-like ancestor and that the Basidiomycota in turn

> gave rise to two lines. One was the primitive rusts, which may have been similar to the present-day *Uredinopsis*, a short-cycled rust that produces only teliospores and basidiospores, that in turn produced the modern-day rusts. The second line from the *Taphrina*-like ancestor led to a primitive member of the Auriculariales, which had a transversely-septate basdium, superficially resembling a mycelium, and sporadic clamp formation. The nonseptate basidium evolved, giving rise to the remaining members of the Basidiomycota, which also have diverse forms of basidiomata (p. 247).

Note that Moore-Landecker admits that his phylogeny is largely speculation. The current status of the evolution of fungi is identical to that noted by Thomas (1981) over 25 years ago—that the evolution of the fungi themselves is very difficult to unravel. For this reason evolutionary relationships are still very controversial (Padovan et al., 2005). In spite of the fact that very few fungi have hard parts, primitive fungi have been found in the earliest fossil-bearing rocks, the Precambrian cherts (Thomas, 1981). This fossil evidence does not support evolution; therefore scientists have used molecular data to try to infer phylogeny (Basgall, 2007; Moore, 1998). I am preparing a future paper that will review these fungal molecular data.

Recent molecular clock studies have produced results that are difficult to accommodate with the traditional interpretations of the fossil record of plants and fungi (Redecker, 2002a). Molecular studies also have found other conflicts with morphology-based taxonomy, such as molecular evidence supporting the conclusion that one fungus, which is currently put in two different families, actually belongs in another family (Redecker, 2002b).

Carlile et al. (2001) noted that biochemical studies sometimes confirm conclusions that had been reached on other grounds, for example that some of the organisms studied by mycologists are only distantly related to the mushrooms and toadstools. A problem is the majority of fungal species have never been the subject of physiological, biochemical, or molecular study, and with these morphological features remain the only basis for identification (see Carlile et al., 2001, p. 286). As more data come in, I predict that it not only will contradict our current assumptions about the fossil record, but also will contradict our assumptions derived from morphology. The difficulty in using genetic comparisons has motivated innovative ways of trying to understand the evidence, such as the hypothesized lateral gene transfer (the movement of genes from one type of fungus to other types).

Fossil Lichen and Mushrooms

A lichen is a symbiotic association between a fungus and an alga or a cyanobacterium. Although some evidence exists of Precambrian lichens and other fungi, the oldest unequivocal fossil lichen dates back to the Early Devonian (Heckman et al., 2001; Doerfelt and Striebich, 2000; and Taylor et al., 1995). Preserved in high detail, cyanobacterium shares numerous morphological features with several extant cyanobacteria (Raven, 2002). Study of this earliest fossil lichen found nothing to indicate that it was any less evolved than modern lichens (see also Howe and Armitage, 2002; 2003). Another fossil lichen assigned to early to middle Miocene (12–24 million years ago) bears a remarkable resemblance to *Lobaria pulmonaria*, a species that occurs in the area today (Peterson, 1999). Kendrick (2000) concluded that lichens have no common ancestor; only a widely shared symbiotic process that has arisen time and time again as a result of natural affinity, opportunity, or need.

Different mushrooms manifest a very wide variety of morphological forms. The common names for the basic types of mushrooms are boletes, agaric chanterelles, tooth polypores, puffballs, jelly fungi, bracket fungi, stinkhorns, and cup fungi. One mushroom (*Corprinites dominicana*) found in Dominican amber is considered to be the best-preserved mushroom fossil (Poinar and Poinar, 1994). Its delicate scales, and even its spores, are very well preserved (Poinar and Poinar, 1994, 1999).

Even some rotifers (small invertebrates) living in the mushroom gills located beneath the cap, and mites on the cap, were both still well preserved (Poinar and Poinar, 1994). The oldest mushroom trapped in amber has been dated at 90 to 94 million years old (Redecker, 2002a). Its morphology is so similar to modern forms that Redecker concluded it shows all the characteristics of today's Basidiomycete genera *Marasmius* or *Marasmiellus*. Such excellent preservation argues for very rapid fossilization.

Various Types of Fungi Are Radically Different from Each Other

Fungi were once classified as plants but now are recognized as so widely different from plants that they have been put into their own separate kingdom called Kingdom Fungi. The different types of fungi are so diverse, even within one classification, that they are often also grouped into *threadlike fungi* (bread mold), *club fungi* (mushrooms, puffballs, and bracket fungi that grow on rotting logs), and *sac fungi*, including yeasts, mildews, and morels. Even these groups are so different from each other that difficulties exist in finding or imagining credible intermediates. Some fungus types even can live in very hostile environments, such as under snow in cold parts of the earth. The number of species is enormous. One authoritative guide lists almost 5,000 species of mushrooms in North America alone, including many types that are very different from other mushrooms (Bessette et. al., 2000; see also, Phillips, 2005). The stark contrasts between these basic types of fungi should be accompanied by many unambiguous transitional forms in the fossil record, but after over a century of intensive looking, none has yet been found.

In spite of the many fossils found so far, Gamlin and Vines (1987) noted that almost nothing is known about how fungi evolved since no fossil evidence exists for their evolution. They also expressed the belief that the origin of fungi is polyphyletic, that is, fungi include several separate lineages, each of which evolved independently. The reason for this assumption is that modern fungus types differ so widely from each other that no one common ancestor is a feasible ancestor for all of them. Molds are as different from mushrooms as insects are from mammals. As a result of these contrasts evolutionary relationships of

> fungi to each other and to other living plants and animals are unclear, although ultimately they may have descended from some simple single-celled flagellated ancestor. The evolutionary relationships of the several classes of fungi have not been established. They may have evolved from one or another of the algae by taking up heterotrophic nutrition and losing chlorophyll. Alternatively they may have descended directly from primitive heterotrophs without ever passing through an autotrophic stage.... Finally, the evolutionary origin of the basidiomycetes [mushrooms and toadstools] is truly shrouded in mystery, for they show no relationships with any of the algae (Villee and Dethier, 1976, pp. 360).

This 1976 conclusion of Villee and Dethier is still valid today. Because current evolution theories are unconstrained by fossil evidence, many widely differing opinions of fungus origins are now held by experts. Most long-held theories of fungal evolution have not been supported by modern research findings. For example, it was once widely believed that algae were the ancestors of the true fungi, but this is now a discredited idea (Gamlin and Vines, 1987). Although some scientists still believe that oomycetes evolved from algae, other experts disagree with that conclusion (Gamlin and Vines, 1987).

Summary and Conclusions

We might expect that if fungi evolved from some primitive ancestor, the abundant fossil record of fungi should contain clear evidence of fungus transitional forms documenting this theory. The fossil record is very clear: all fossil fungi are either of extinct types or of essentially modern forms. No convincing transitional fungus forms are found in the enormous fossil record known to exist. Arnold's (1947) conclusion that the fossil record has thrown no light on the problem of the evolution or origin of the fungi, although made more than a half century ago, is still true today.

A diagram of the fungus fossil record shows a creationist orchard instead of demonstrating a tree spreading from one common ancestor. Fossils appear and sometimes disappear, but they do not evolve into other very different types of fungi (see Taylor, 1993, pp. 10–11). Furthermore, fossil research has verified Arnold's conclusion that throughout the long geological past, fungi have played the same role in nature as at present, that of acting as scavengers and thereby preventing an endless accumulation of dead vegetable matter (Arnold, 1947). This supports the intelligent design argument that fungi had an important role from the beginning of creation.

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Glossary

Agarics fungi, also known as gilled mushrooms for their distinctive gills, are usually referred to as toadstools and mushrooms. They are a large Class of Basidiomycetes.

Agrobacterium is a genus of bacteria that causes tumors in plants. The most commonly studied species in this genus is *Agrobacterium tumefaciens*. Agrobacterium is comparatively effective in transferring DNA between itself and plants, and for this reason is an important tool for plant genetic engineering.

Arbuscular mycorrhizae are mycorrhizal fungi that penetrate the cortical cells of vascular plant roots. They are the most common type of mycorrhizae on earth. Ninety percent of all plant families contain *Arbuscular mycorrhizae* species.

Blastocladiales are fungi that reproduce asexually by thick-walled spores that produce zoospores upon germination. Sometimes placed in class Oomycetes, they are saprobes and parasites that live off of a broad range of substrates, especially decaying fruits (e.g., rose hips) and partially decorticated twigs.

Chert is a type of fine crystalline quartz that occurs in veins throughout the rocks in Rhynie Scotland. Rhynie fossils were preserved when mineral sediments settled on top of them, effectively preserving them. As a result, this area of Scotland is a major source of small fossils.

Chlamydospores are the thick-walled spores of several kinds of fungi. Spores are a multicellular life stage that can survive in unfavorable conditions, such as in dry or very hot environments. They are the basic reproductive unit of a fungus. Chlamydospores are usually spherical with a dark-colored, smooth (non-ornamented) surface.

Choanoflagellates are a group of small single-celled flagellate protozoa found in both fresh waters and the oceans. They are considered by evolutionists to be the closest living relatives of animals and the last unicellular ancestors of animals. They have a single flagellum, surrounded by a ring of closely packed slender fingerlike projections (microvilli) that form a cylindrical collar, which is the source of their name ("collar-flagellates"). The actin-filled protrusions are microvilli that surround the single flagellum by which choanoflagellates both move and take in food. Evolutionists believe choanoflagellates must have existed on the earth since the Late Precambrian, because they are believed to be the closest living protist relatives of the most primitive metazoans, sponges. No fossil record exists of choanoflagellates, although some marine choanoflagellates secrete an outer covering made of fine, interwoven silica bars called loricae that would be expected to be preserved in the fossil record.

Choanociliate is another term for a choanoflagellate.

Chytrids is an older classification term referring to a group of fungi that were placed in the Class Phycomycetes under the Subdivision Myxomycophyta of the Kingdom Fungi. Also, in an older and more restricted sense the term "chytrids" referred only to those fungi in the order Chytridiales. The term Chytrid is now a common name for any small, simple life-forms in the phylum Chytridiomycota in the fungus kingdom.

Cyanobacteria are photosynthetic microorganisms that contain chlorophyll. Formerly called blue-green algae, the classification was changed because it has been shown they are more similar to bacteria than algae.

Epiphyllous refers to some life-form that is growing on, or inside of, a leaf.

Glomaleans is a term referring to a member of the phylum Glomeromycotan. See Table 1.

Hyphochytrids are uniflagellate fungus-like organisms that live in freshwater either as symbiotrophs of fungi or algae, or as saprobes that live on the carcasses of plant debris or on insects.

Mastigonemes are lateral "hairs" that cover the flagella of heterokont and cryptophyte algae. The approximately 15 nm diameter structures usually consist of a tubular shaft that terminates in even smaller "hairs." Their roles include assisting in locomotion by increasing the flagellum surface area.

Mesomycetozoea is a small group of heterogeneous microorganisms, most of which are parasites of fish, birds, and even mammals, including humans. The protozoon-like Mesomycetozoea are at the boundary between the animal and fungus "kingdoms." Because of conundrums such as this, dropping the "kingdom" rank for fungi has been seriously proposed by some taxonomists.

Mycelium is the vegetative part of a fungus, consisting of a mass of branching, threadlike hyphae. Hyphae are long, branching, and filamentous structures.

Oomycetes are the largest group of heterotrophic Stramenopiles (see below). They are facultative or obligate parasites found worldwide in fresh and saltwater habitats. Some terrestrial Oomycetes are important plant pathogenic organisms including Phytophthora of Irish potato famine fame, and Pythium, which causes seed rot and damping off.

Rotifers are microscopic, aquatic, animal life-forms in the phylum Rotifera. They are found in many freshwater environments and in moist soil where they inhabit still-water environments, such as lake bottoms and the thin films of water formed around soil particles, as well as flowing-water environments, such as rivers or streams. Rotifers also are commonly found on mosses and lichens.

Saprobic refers to an organism that is able to degrade chitin and keratin and utilize the nutrients. Saprobic organisms often feed on dead and decaying material as opposed to parasitic creatures that feed on living hosts.

Stramenopiles (also called heterokonts) are a major line of eukaryotes presently containing about 10,500 known species. As a group they have flagella with hollow or "strawlike" mastigonemes. Unlike the fungi, all members of this group have mitochondria with tubular cristae and synthesize lysine by a diaminopimelic acid pathway. Most are algae, ranging from the giant multicellular kelp to the unicellular diatoms, which are a primary component of plankton, and Oomycetes.

Trichomycete are a class of obligate fungi that grow in the alimentary canal, especially the intestine and stomach, of insects, crustaceans, and millipedes that live in terrestrial freshwater or marine habitats.