

# Chapter 13

## Biology and Ecology of Freshwater Fungi

Clement K.M. Tsui, Christiane Baschien, and Teik-Khiang Goh

### Introduction

Freshwater fungi complete at least one part of their life cycle in water and distribute propagules (spores, conidia, sporangia) in or above water. It has been estimated that there are more than 3000 species of fungi occurring in the aquatic habitats (Abdel-Aziz 2008). Taxonomically, aquatic fungi comprise taxa from all fungal phyla (*Cryptomycota*, *Chytridiomycota*, *Blastocladiomycota*, *Mucoromycotina*, *Glomeromycota*, *Dikaryomycota*).

Fungal morphology in freshwater ranges from zoospores and nonmotile single cells of *Cryptomycota*, *Chytridiomycota*, *Blastocladiomycota*, yeasts, and aseptate and septate hyphae up to interwoven hyphae in more or less complex plectenychma in higher fungi. Sporangiohores and sporangia (*Chytridiomycota*, *Blastocladiomycota*, and *Mucoromycotina*), ascomycetous and basidiomycetous

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Our work is dedicated to John Webster (1925–2014) for his pioneer and influential work on freshwater fungi.

C.K.M. Tsui, Ph.D. (✉)

Department of Pathology and Laboratory Medicine, University of British Columbia,  
Vancouver, BC, Canada, V6T 1Z4  
e-mail: [clementsui@gmail.com](mailto:clementsui@gmail.com)

C. Baschien, Ph.D.

Department of Microbial Ecology and Diversity, Leibniz Institute  
DSMZ-German Collection of Microorganisms and Cell Cultures,  
Inhoffenstr. 7 B, 38124 Braunschweig, Germany

T.-K. Goh, Ph.D.

School of Biological Sciences, Faculty of Integrative Sciences and Technology,  
Quest International University Perak, No. 227, Plaza Teh Teng Seng (Level 2),  
Jalan Raja Permaisuri Bainun, 30250 Ipoh, Perak Darul Ridzuan, Malaysia  
e-mail: [teikkhiang.goh@qiup.edu.my](mailto:teikkhiang.goh@qiup.edu.my)

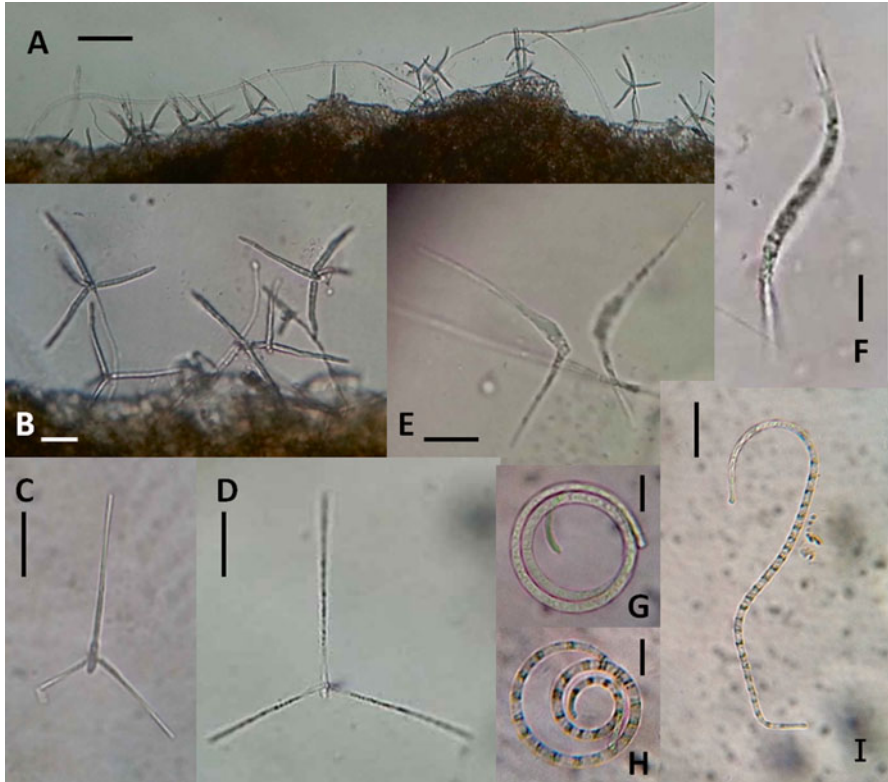
yeasts, conidiophores, and a high diversity of more or less conspicuous conidia (*Ascomycota* and *Basidiomycota* derived) are also visible under the microscope. In addition, complex structures such as acervuli, pycnidia, and ascocarps and basidiocarps as well as lichens can be found on substrates in freshwaters. Over the past few decades, various morphological and ecological groups of water-associated fungi have been identified (Fuller and Jaworski 1987; Goh and Hyde 1996; Hyde et al. 1997; Ingold 1975; Jones 1981). These include the zoosporic fungi, the aquatic ascomycetes, the “Ingoldian fungi,” the aero-aquatics, and a great diversity of mitosporic fungi (asexual *Ascomyceta*) occurring on submerged plant materials.

Worldwide, freshwater comprises diverse habitats such as groundwater, streams, rivers, canals, and lakes but also includes amphibious habitats, such as ditches, peats, and swamps (Shearer et al. 2007). Generally, most freshwater fungi are associated with organic matter derived from decaying plants and animals. However, there are many microhabitats in and adjacent to freshwater, which provide space and possibilities for different fungal life strategies. These microhabitats include roots and other parts of submerged and riparian plants, the canopy, the ambient soil, and sediments. Indeed, freshwater fungi are recorded from the tree canopy (Ando 1992; Ando and Tubaki 1984a, b; Sridhar et al. 2009), rainwater (Gönczöl and Révay 2004), and soil (Park 1974). Also leaf litter in treeholes (Gönczöl and Révay 2003), dew drops (Tubaki et al. 1985), and honey (Magyar et al. 2005) have been identified as locality for spores of freshwater fungi. Fungi have been observed within cooling towers (Eaton and Jones 1971a, b), groundwater (Krauss et al. 2005), and potable water distribution systems (Doggett 2000; Nagy and Olson 1982) including tap water (Heinrichs et al. 2013).

## Who Are the Members of Freshwater Fungi?

Traditional taxonomy and identification of fungi is mostly based on fruiting bodies and spores. Freshwater fungi are divided into various morphological and ecological groups (Shearer et al. 2007; Goh and Hyde 1996). The different groups require specialized methods to examine their biodiversity, taxonomy, distribution, population dynamics, and ecological functions. Traditionally, it has been a challenge to characterize all the different groups of freshwater fungi within a freshwater habitat.

The first group is (*I*) the aquatic hyphomycetes (more than 300 described mitosporic fungi) (Figs. 13.1 and 13.2), also known as “the Ingoldian fungi” in honor of the pioneer mycologist Prof. C. T. Ingold, which comprises conidial states of mainly *Ascomycota* and a few *Basidiomycota* (Shearer et al. 2007; Jones et al. 2014). Ingold (1942) discovered the conidia in the foam of streams and showed the connection to their associated mycelia on submerged leaves. Most aquatic hyphomycetes produce conspicuous stauroconidia (e.g., tetra- or polyradiate [*Alatospora*, *Articulospora*] or other branched forms [*Varicosporium*]) or scolecoconidia (sigmoid, curved, or straight [*Anguillospora*, *Flagellospora*]). The conidial shape is an adaptation to survival and



**Fig. 13.1** Ingoldian fungi. (a, b) *Triscelophorus acuminatus*. Conidia production seen at the edge of submerged leaf. Each conidium has four arms. (c, d) *Triscelophorus monosporus*. Conidia with three arms. (e) *Lunulospora cymbiformis*. Conidia which are sickle-shaped and distinctly bent more or less at right angle. (f) *Anguillospora crassa*. Typical sigmoid-shaped conidium. (g, h) *Helicomyces roseus*. Typical coiled conidia. (i) *Helicomyces roseus*. Conidium which has uncoiled and become more or less sigmoid shaped in water. Scale bars: a=50  $\mu\text{m}$ ; b–i=20  $\mu\text{m}$

dispersal in aquatic habitats discussed below (Dix and Webster 1995; Webster 1959). Aquatic hyphomycetes are known as important decomposers in the turnover of leaf litter in woodland streams [overview in (Gessner et al. 2007)]

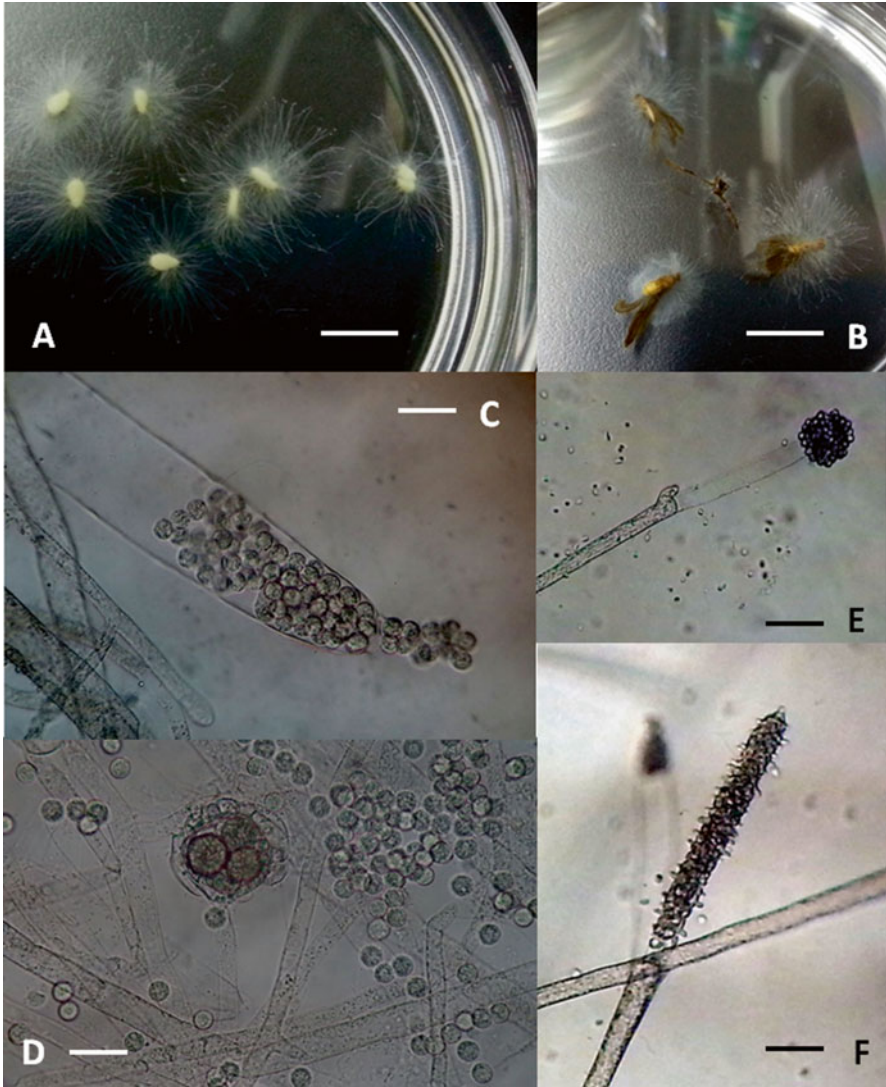
The second group is called the (II) aero-aquatic fungi (mitosporic ascomycetes) (~90 species described) (Fig. 13.1g, h), which are found on submerged plant litter and wood in flat lentic waters, such as woodland ponds and ditches, which may have periodical levels of water. In contrast to aquatic hyphomycetes, the aero-aquatic fungi release their propagules aerially. Therefore, they produce conspicuous air-trapping dispersal units, which can flow on the water surface; for example, some spores are helicoid in more than one plane (Fig. 13.1g, h) (e.g., *Helicoma*, *Helicoon*) or spiral into a sphere or a net [e.g., *Candelabrum*, *Spirosphaera* (Voglmayr 2004, 2011; Voglmayr and Delgado-Rodriguez 2003; Voglmayr et al. 2011)]. The aero-aquatic life strategy was first described by Agathe van Beverwijk (1951).



**Fig. 13.2** *Lumulospora curvula*. Conidiogenesis of crescent-shaped unbranched conidia. Bar = 25  $\mu$ m

The third group is named (*III*) freshwater ascomycetes (~600 species described meiosporic fungi), which comprise the sexual states of phylogenetically heterogeneous ascomycete fungi occurring worldwide in freshwater habitats on herbaceous and woody substrates (Shearer et al. 2007, 2009; Goh and Hyde 1996; Shearer 1993a; Vijaykrishna et al. 2006). In addition, they are also collected from submerged dead macrophytes (Shearer 1993a; Fallah and Shearer 2001). The morphologies in asci and ascospores are very diverse and noticeable. Asci of freshwater ascomycetes are either deliquescent, with apical apparatus (e.g., *Massarina*, *Jahnula*), or fissitunicate (ectoascus and coiling endoascus, e.g., *Kirschsteiniothelia* (transferred to *Helicascus*)) (Shearer 1993b). Many freshwater ascomycetes produce ascospores with appendages, which facilitate attachment to substrates (Shearer et al. 2007; Shearer 1993a; Wong et al. 1998). Gelatinous gel-like sheaths and/or thick-walled hyphae (Shearer et al. 2009; Ingold 1955) are thought to enhance attachment and adhesion to plant materials (Digby and Goos 1987; Ingold and Chapman 1952). However, spores borne with gelatinous sheath and the active discharge of ascospores are also present in strictly terrestrial ascomycetes. In comparison to aquatic and aero-aquatic hyphomycetes, freshwater ascomycetes seem to be less exclusively adapted to life in aquatic habitats (Vijaykrishna et al. 2006).

The fourth group of freshwater fungi is the (*IV*) zoosporic fungi (Fig. 13.3), which produce flagellate zoospores as part of their life cycle. They are known for



**Fig. 13.3** Oomycetes. (a) Baiting of oomycetes, using sesame seeds. (b) Baiting of oomycetes, using insect carcasses. (c) *Saprolegnia* sp., zoosporangium releasing zoospores. (d) *Saprolegnia* sp., oogonium, with attached antheridia, and many encysted primary zoospores. (e) *Achlya* sp., zoosporangium showing discharged and encysted zoospores at the apical pore. (f) *Dictyuchus* sp., a dictyoid zoosporangium in the process of zoospore discharge. Scale bars: a, b = 5 mm; c = 10  $\mu$ m; d–f = 20  $\mu$ m

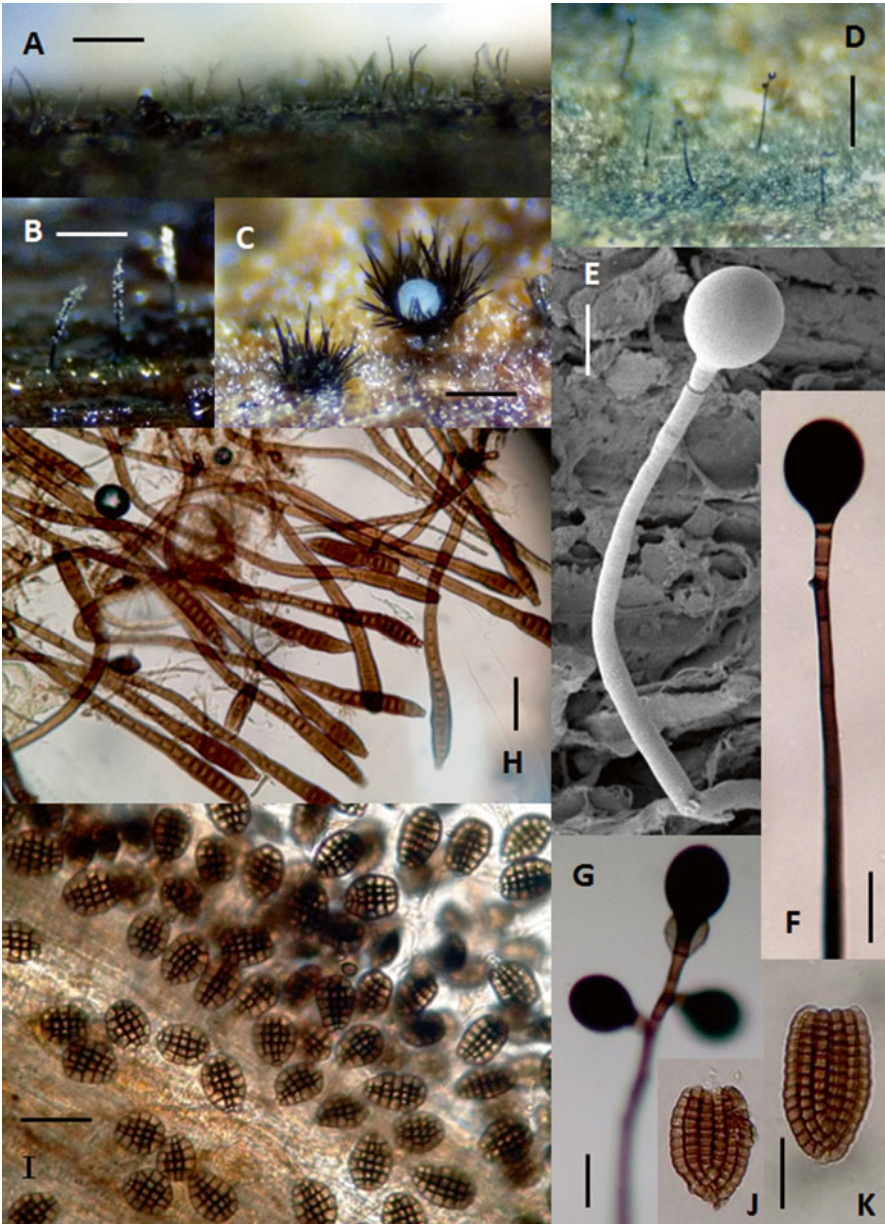
their parasitic life strategies but they are also involved in the decomposition of organic matter (Sparrow 1960). Historically, they have been known as the members of “phycomycetes,” a functionally defined group. They have also been traditionally termed the “lower fungi” which basically comprises species without a septate hyphal system. With the advent of molecular studies and recent taxonomic treatments based on phylogenetics, the “phycomycetes” is in fact heterogeneous, comprising of members from the *Eumycota* (“true fungi”) and the *Chromista* (*Oomycetes* and *Labyrinthulomycetes*). The biology, taxonomy, and phylogenetic relationship of these aquatic organisms have been well documented (Fuller and Jaworski 1987; Beakes 2003; Bowman et al. 1992; Buczacki 1983; Powell 1993).

The freshwater zoosporic fungi belong mostly to the *Chytridiomycetes* and the fungal-like *Oomycetes*, which are microscopic organisms not producing any fruiting bodies visible to the naked eye. Members of the *Chytridiomycetes* are generally called chytrids, whereas those belonging to the *Oomycetes* are usually called water molds. They usually reproduce asexually by means of zoospores, but in *Oomycetes*, sexual reproduction may occur by means of oogamy, resulting in the formation of oospores, which are survival structures generally resistant to adverse environmental conditions. The chytrids produce unflagellate haploid zoospores, whereas those of the water molds are biflagellate and diploid. These taxa are associated with dead and living plant materials but also with algae, cyanobacteria (Sonstebo and Rohrlack 2011), invertebrates, fish, and amphibians (Powell 1993; Longcore et al. 1999; Powell et al. 2013).

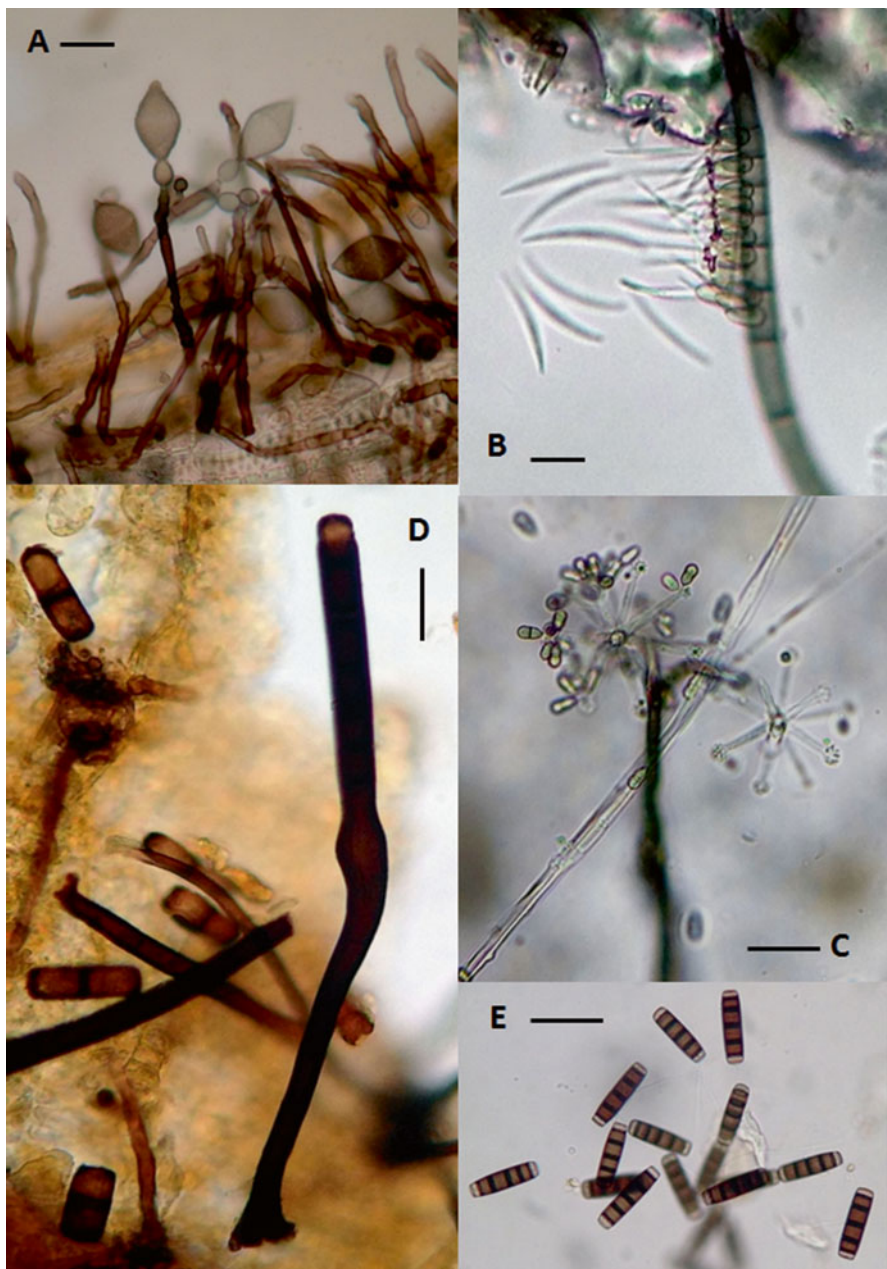
The main orders of *Chytridiomycetes* are *Chytridiales*, *Spizellomycetales*, and *Monoblepharidales*. Furthermore members of *Neocallimastigomycota* and *Blastocladiomycota* occur in aquatic habitats (Powell and Letcher 2014). Members of *Chytridiales* and *Blastocladales* are more frequently encountered in freshwater systems. The main orders of *Oomycetes* found in aquatic environments are the *Saprolegniales*, *Leptomitales*, and *Peronosporales*. Common genera of *Saprolegniales* frequently isolated from the aquatic systems are *Saprolegnia*, *Achlya*, and *Dictyuchus*.

Apart from chytrids, *Cryptomycota* is a recently discovered (Jones et al. 2011) phylum with endoparasitic lifestyle (James et al. 2013; Lazarus and James 2015). They differ from other filamentous fungi in that they lack chitinous cell walls in the trophic stage. Based on molecular markers, they have been detected in lakes and wetlands (Ishii et al. 2015; Wurzbacher et al. 2014).

The fifth group (V) belongs to aquatic–terrestrial hyphomycetes (mitosporic ascomycetes) (Figs. 13.4, 13.5 and 13.6) that comprise a huge morphological diversity of conidial (mitosporic) fungi growing on decaying plant material (Shearer et al. 2007; Hu et al. 2014) and capable of sporulating underwater (Bärlocher et al. 2008; Baschien et al. 2009). They are distinguished based on the features of conidia, conidiophores, and the conidiogenesis. For example, common fungi include *Dactylaria*, *Dictyoachaeta*, *Canalisporium*, and *Sporoschisma*; some of these fungi are linked with their corresponding sexual relatives using cultural or molecular studies. Some studies also demonstrate the presence of fungi of terrestrial origin, including saprobes from plants and soil, such as *Cladosporium*, *Alternaria*, and *Penicillium* species. Fungi on leaves from the canopy (Gönczöl and Révay 2006) may fall into the water.

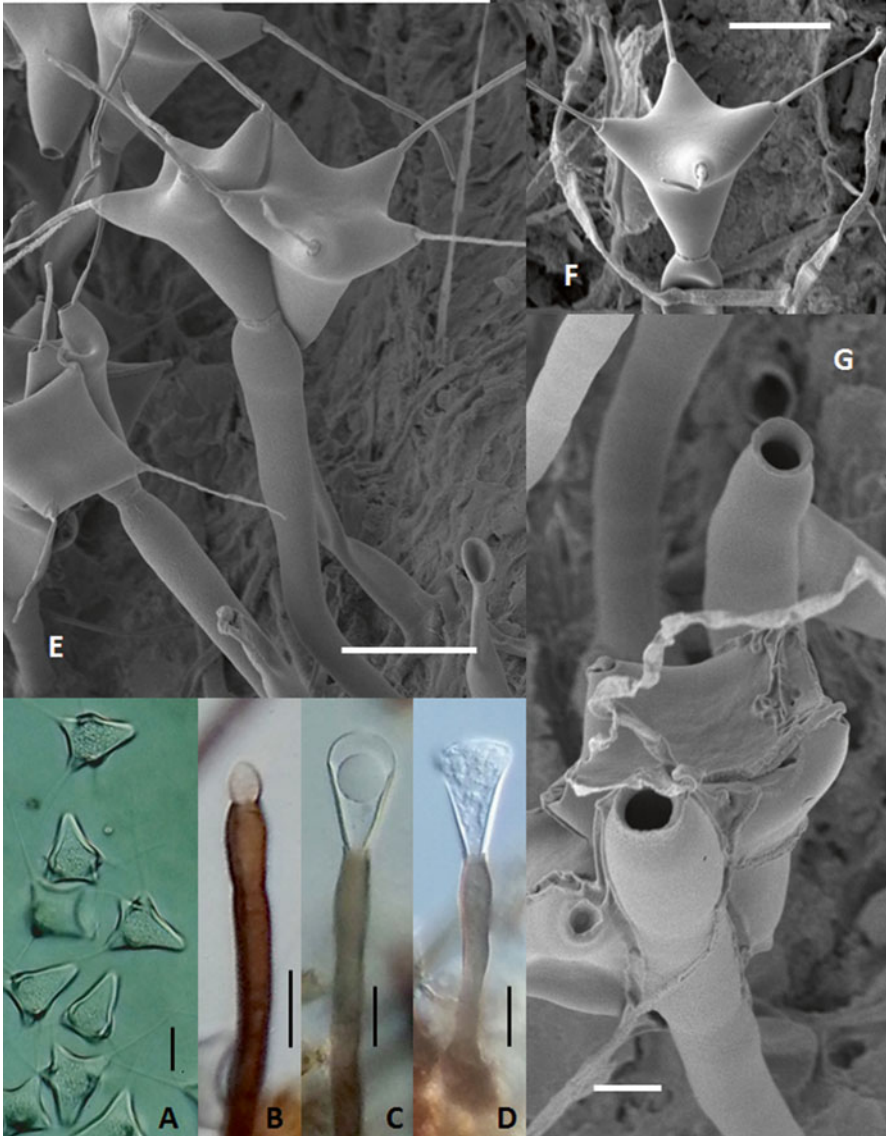


**Fig. 13.4** Lignicolous hyphomycetes. (a) *Ellisembia adscendens*. Colony on submerged wood. Conidia are long and projecting upward on the wood surface. (b) *Phaeoisaria clementidis*. Colony on submerged wood. Conidiophores are in the form of long synnemata projecting upward on the wood surface. (c) *Vermiculariopsiella* sp. Colony on submerged wood. Conidiophores are in the form of dense sporodochia on the wood surface, surrounded by long setae and producing conidia in the form of white slimy mass. (d) *Monotosporella setosa*. Colony on submerged wood. Conidiophores are long, erect, and projecting from the wood surface. (e-g) *Monotosporella setosa*. Conidiophores producing conidia at their apex. (h) *Ellisembia adscendens*. Conidia. (i) *Canalisporium elegans*. Conidia, which were produced in the form of sporodochia on the surface of submerged wood. (j, k) *Dictyosporium elegans*. Conidia. Scale bars: a-d=200 µm; e-h, j, k=20 µm; i=50 µm



**Fig. 13.5** Lignicolous hyphomycetes. (a) *Beltrania africana*. Conidiophores and conidia from submerged wood. (b) *Cryptophialoidea secunda*. Part of setiform conidiophore showing the fertile region, bearing unilateral phialidic conidiogenous cells, producing falcate conidia. (c) *Pseudobotrytis terrestris*. Conidiophore bearing umbellately arranged polydentate conidiogenous cells, producing two-celled conidia. (d) *Sporoschisma uniseptatum*. Conidiophore which has a swollen venter, producing endogenous conidia, usually in basipetal chains. (e) *Sporoschisma mirabile*. Conidia, initially borne on chains, have become disarticulated in water mount. Scale bars: a=20  $\mu$ m; b=10  $\mu$ m; c, d=20  $\mu$ m; e=50  $\mu$ m





**Fig. 13.6** *Nawawia quadrisetulata*. (a) Conidia, bearing 4–5 setulae at the corners of the distal end. (b–d) Conidiophores showing sequential development of conidia. (e, f) Scanning electron micrographs of setulate conidia produced at the apex of conidiophores. (g) Conidiophores showing the terminal phialides. Scale bars: a–d = 20 µm; g = 5 µm

## How Are They Adapted to an Aquatic Lifestyle?

Spores are the dispersal propagules of fungi. Aquatic fungi need to produce spores that can be dispersed in water, and then become entrapped to, and subsequently colonize new substrates. The completion of the life cycle and hence the survival of the species is reliant on the spores.

The zoosporic fungi release motile spores that can actively disperse/swim in the lentic aquatic environments (e.g., ponds, lakes, ditches, pools, and swamps). They are usually chemotactic, being sensitively attracted to their host or substrates that release specific sugars and amino acids (Fuller and Jaworski 1987). Usually the zoospores swim for a few minutes to hours before they stop and encyst. At the initial stage of zoospore encystment, depending on the species, the flagella are either retracted or shed before the zoospore assumes a spherical shape. An important property of the zoospores in general is their ability to stick firmly to the surfaces of the substrates upon which they settle down to encyst. Adhesion ensures that the zoospore, upon reaching a favorable substrate, accidentally, or through specific tactic responses, would remain firmly attached. Evidently, this behavior has great ecological value for both saprobes and parasites as it establishes a permanent contact between the fungus and its potential food source. Swimming zoospores are for dispersal and thus are not adhesive but become so in the initial stage of encystment before a cyst wall is made. The adhesive phase lasts only about 30–60 s (Sing and Bartnicki-Garcia 1972). Apparently, the timing of the adhesive phase, coinciding with the change from motile to sessile form, provides obvious ecological advantage to the fungus. Once the cysts mature, i.e., after a well-defined wall is made, the cells lose their ability to attach themselves to solid surfaces. After successful adhesion and encystment of the spore, germination of the cyst leads to penetration and colonization of the substrate.

Besides the zoosporic fungi, most aquatic fungi are saprobes that grow/colonize on submerged wood or waterlogged leaves in freshwater. The spores of freshwater ascomycetes and Ingoldian fungi are not motile in the aquatic environment. These fungi usually occur in lotic habitats (e.g., streams, creeks, rivers, brooks), and thus they possess strategies to survive in turbulent water. Their propagules are released from conidiophores growing out of substrates and thus are able to detach from the surface of the substrates, disperse (float) in water, and eventually become entrapped (settled) or attached (adhere) to new substrates, which they can colonize by penetration of a germ tube. The mechanisms of fungal adhesion and the role of mucilage in fungal attachment in the aquatic environment have been well documented (Wong et al. 1998; Au et al. 1996; Ingold 1966; Jones 2006). An excellent review of the adaptations for dispersal in filamentous freshwater fungi is given by Goh and Hyde (1996).

Many freshwater ascomycetes have ascospores with various sheaths, appendages, or wall ornamentations, which probably function in dispersal and/or attachment of the spores. Shearer (1993a) provided a list of ascomycete species possessing ascospores surrounded by mucilaginous sheaths. There are ascospores that possess

unfurling mucilaginous appendages, which uncoil in water to form long viscous threads. Several unique appendage types have now been shown to exist in freshwater ascomycetes, which account for their success in the aquatic environments (Jones 2006; Wong and Hyde 1999).

The Ingoldian fungi have been known for decades to have sigmoid or tetra- radiate spores (Ingold 1975; Goh 1997). Sigmoid conidia often become attached at their sticky poles and straighten in the direction of the water current so that they are less likely to be washed away in a lotic habitat (Webster and Davey 1984). Tetra- radiate and variously branched spores act as an anchor and allow their entrapment to the substrates or in surface foam (Ingold 1966). Tetra- radiate spores can also effectively attach to the substrate with three “legs” forming a strongly adhesive tripod (Webster and Descals 1981). Adhesive mucilaginous material is also produced at each arm of the tetra- radiate spore in contact with a surface and attaches them firmly to the substrate.

The aero-aquatic hyphomycetes, such as *Beverwykella*, *Cancellidium*, and *Clathrophaerina*, are normally found on decaying plant materials in slow-flowing streams and stagnant ponds (Gessner et al. 2007; Voglmayr and Delgado-Rodriguez 2001, 2003; Voglmayr and Krisai-Greilhuber 1997). Their propagules are beautiful, extraordinary, and interesting as they possess a special floatation device, usually composed of intricate branching hyphal network and thus air trapping, enabling these fungi to be dispersed from one static water habitat to another. Conidia of *Helicoon* species are composed of tightly coiled filaments, which assume a barrel shape, and can trap air in water for floating (Goh and Hyde 1996). For further discussion of the adaptation strategies in the aero-aquatic fungi, see Fisher (Fisher et al. 1977) and Webster and Descals (1981).

A great diversity of dematiaceous hyphomycetes have been discovered from wood submerged in freshwater (Goh and Tsui 2003). Among these lignicolous hyphomycetes, many possess long mononematous stiptate conidiophores, which stand erect from the submerged substrates and bear masses of conidia at the apices. Examples of such hyphomycetes are *Acrogenospora*, *Cryptophiale*, and *Spadicoides*. Others produce erect synnemata (e.g., *Bactrodesmium longisporum*, *Nawawia dendroidea*, and *Phaeoisaria clematidis*) or occur as sporodochia (e.g., *Dictyosporium*, *Canalisporium*, and *Yinmingella*). Producing easily detachable conidia at the apex of long, erect conidiophores, or having conidia produced in dense masses from sporodochia, may be adaptation strategies conducive to effective spore dispersal in the aquatic habitats. Moreover, certain features observed in some of the commonly found hyphomycetes from submerged wood are worth mentioning, because they may represent special adaptation features for dispersal in the aquatic habitats. For example, *Chalara*, *Sporoschisma*, and *Sporoschismopsis* (Goh et al. 1997) produce long chains of conidia from erect conidiophores, which eventually disarticulated in water for ease of dispersal. The muriform conidia of *Canalisporium* have distinct pores or canals in the septa (Goh et al. 1998) which enable air to trap inside the conidia for floating. The various spore types of these lignicolous hyphomycetes in freshwater also are provided with modified appendages, mucilaginous sheaths, setulae, or arms (Goh 1997), and these are functionally comparable to those of aquatic ascomycetes and Ingoldian fungi.

## How Did They Evolve?

The absolute age of fungal phyla is an area of active research, and only broad estimates exist for the oldest clades (Taylor and Berbee 2006). Currently, the divergence of younger phyla from the *Cryptomycota*, *Chytridiomycota*, and *Blastocladiomycota* clades—and the loss of the zoospore stage—is thought to have occurred during the Neoproterozoic, approximately 600–800 Myr (Stajich et al. 2009). The first divergence of terrestrial fungi (*Endogonales* and *Glomales*) has been estimated to have occurred about 600 Myr or even earlier, while *Ascomycota* and *Basidiomycota* separated 500 Myr (Berbee and Taylor 2001). The origin and radiation of *Euascmycetes* (whose groups commonly produce conidia adapted in aquatic habitats) may have taken place in the Mesozoic, about 240 Myr. This puts a lower limit to the earliest appearance of aquatic ascomycetes and relatives. Did the majority of the taxa appear in a brief burst of rapid radiation, or was this spread out over an extended period of time? Are new species still invading running waters today (Schlütz and Shumilovskikh 2013)?

Fungi in freshwater are grouped ecologically and morphologically, and it is not surprising that they have evolved independently from multiple lineages. Shearer (Shearer 1993a) first proposed the multiple origins of freshwater ascomycetes, which are present as endophytes, pathogens, or saprobes on plants, and have become adapted to aquatic environment when these plants invaded water. 18S rRNA data (Vijaykrishna et al. 2006; Baschien et al. 2006; Belliveau and Bärlocher 2005) showed that freshwater fungi (sexual and asexual ascomycetes) evolved from terrestrial fungi in (more than) four different classes, *Sordariomycetes*, *Dothideomycetes*, *Leotiomyces*, and *Orbiliomycetes*. Many freshwater fungi have terrestrial relatives, supporting the fact of secondary adaptation to the freshwater environment. A comprehensive study of 84 fungi of described and undescribed freshwater *Dothideomycetes* and 85 additional ascomycetes representative of the major orders and families of *Dothideomycetes* based on ribosomal genes also confirmed the polyphyletic origins of freshwater ascomycetes (Shearer et al. 2009). Apart from these, molecular studies of fungi on submerged leaves using denaturing gradient gel electrophoresis [DGGE; (Kelly et al. 2010; Nikolcheva et al. 2003)] and the analysis of terminal restriction fragment length polymorphism [TRFLP; (Nikolcheva et al. 2003; Nikolcheva and Bärlocher 2005)] and of clone libraries (Clivot et al. 2014; Harrop et al. 2009) provided evidence for the presence of fungi of terrestrial origin.

Many genera of freshwater fungi (ascomycetes and their asexual relatives) are also not monophyletic. The polyphyletic origin of aquatic hyphomycetes has been reinforced by additional studies (Baschien et al. 2006, 2013; Campbell et al. 2006, 2009). For example, Ingoldian fungi are assigned to four classes: *Sordariomycetes* (~11 spp.), *Dothideomycetes* (~10 spp.), *Pezizomycetes* (1 sp.), *Orbiliomycetes* (3–5 spp.), and *Leotiomyces* (>75 spp.). The morphology of tetra- and sigmoid conidial shape has been recognized as convergent development in unrelated aquatic hyphomycete taxa (Ingold 1966; Webster 1980). Molecular studies of ribosomal

genes also reassured the convergence of the conidial shape (Baschien et al. 2006, 2013; Campbell et al. 2006; Belliveau and Bärlocher 2005). Also, the helicosporous aero-aquatic fungi have evolved from multiple lineages within the ascomycetes (Tsui and Berbee 2006).

The molecular studies mentioned above showed that many ascomycetous and basidiomycetous freshwater fungi are closely related to terrestrial fungi. A few species of the genera *Varicosporium*, *Tetracladium*, *Filospora*, and *Anguillospora* have been isolated as endophytes from aquatic or terrestrial roots (Fisher et al. 1991; Kohout et al. 2012; Nemeč 1969; Sati and Belwal 2005; Watanabe 1975). The step back from terrestrial to aquatic life cycles could have been aided by an endophytic lifestyle (Selosse et al. 2008). Furthermore, the localization of freshwater fungi inside roots or other amphibious plant parts may function as temporary reservoir during different stages within a life cycle. The production of different conidial shapes and synanamorphs may also be an adaptation to shifts between aquatic, semiaquatic, and terrestrial habitats (Baschien et al. 2013). Kohout and co-workers (Kohout et al. 2013) proposed the scenario that terrestrial ancestors of recent aquatic plants interacted with different root-associated fungi (RAF). The aquatic hyphomycetes could have evolved from non-mycorrhizal RAF that once entered aquatic habitats together with their host plants.

## What Are They Doing in Freshwater Habitats?

The primary ecological role of fungi in aquatic habitats is to decompose dead plant material—both woody and herbaceous debris. When Kaushik and Hynes (1971) demonstrated the crucial role of fungi in the decomposition of plant materials to detritus in streams, limnologists recognized the important ecological function of aquatic hyphomycetes. Bärlocher and Kendrick (1974) showed that aquatic hyphomycetes condition leaf material for aquatic invertebrates (Plecoptera, Trichoptera, Coleoptera, Crustacea, Gastropoda) by increasing the palatability using exoenzymes [cellulases, pectinases, laccases; (Abdel-Raheem and Shearer 2002; Chamier 1985)]. Most aquatic fungi have the ability to decompose a wide range of organic substrates, although a few species may be limited to one or a few types of substrates. For example, Gulis (2001) showed that wood/twig substrates bear fungal communities distinct from those on leaves. In general, aquatic ascomycetes and basidiomycetes are thought to be responsible for the decomposition of woody debris while Ingoldian fungi decompose either leaves or herbaceous debris. Through decomposition, freshwater fungi can facilitate the transfer of nutrients and energy between trophic levels in the food web (Gessner et al. 2007).

Wood is a complex substance and its major chemical constituents contain cellulose, hemicellulose, and lignin. The degradation mechanisms of wood are well known in terrestrial fungi, and it is assumed that similar mechanisms are present in freshwater fungi. Cellulose hydrolysis is achieved by endoglucanases and cellobiohydrolases, collectively termed cellulases (Eaton and Hale 1993). Hydrolysis of

hemicellulose, a mixed polymer, occurs via the action of hydrolytic xylanases, mannanases, and possibly other hydrolases with broad substrate specificity (Eaton and Hale 1993). The degradation of lignin involves two peroxidases, lignin peroxidase and Mn-dependent peroxidase, and a polyphenol oxidase, laccase, known as lignin-modifying enzymes (LMEs) (Pointing 2001). The vast majority of freshwater ascomycetes, regardless of eco-climate, habitat, and substrate distributions, are capable of breaking down cellobiose, hemicellulose, and xylan and starch, which are important carbon compounds in plant-based debris (Bucher et al. 2004; Simonis et al. 2008; Yuen et al. 1998).

Three fungal wood decay types are recognized on the basis of whether or not they can degrade cellulose and lignin or just cellulose alone, namely, soft rot, white rot, and brown rot (Eaton and Hale 1993). Soft rots occur in wood that has an unusually high level of moisture, which is often the case for woody substrates in aquatic environments. Most of the freshwater fungi are capable to form soft rot decay and to produce cellulases (Bucher et al. 2004; Abdel-Raheem and Shearer 2002). White-rot fungi normally have the enzymes to degrade both cellulose and lignin simultaneously. The residual material that is left behind has a somewhat fibrous appearance and is very pale in color, looking as if it had been bleached. In contrast, members of brown-rot fungi can degrade cellulose. After decomposition, wood is brown in color and tends to be broken up into cubical fragments that quickly disintegrate into a powdery brown residue. It has been questionable whether or not freshwater ascomycetes can form white rot or brown rot because the breakdown of lignin in woody debris is primarily accomplished by basidiomycetes that do not seem common in the aquatic habitat. However, Junghanns et al. (2005) showed that the aquatic hyphomycete *Clavariopsis aquatica* produced laccases. Five putative laccase genes (*lcc1* to *lcc5*) identified in *C. aquatica* were differentially expressed in response to the fungal growth stage and potential laccase inducers (Sole et al. 2012). Recently, Kerr and co-workers (2013) showed the oxidation of lignin in leaf litter by undetermined aquatic fungi using high spatial resolution infrared microspectroscopy. The modification of lignin by freshwater fungi degrades lignin into carbohydrate-depleted recalcitrant carbon, which may influence the carbon pool in aquatic environments.

Leaves and other nonwoody plant parts (e.g., fruits and seeds) represent a different type of substrate than wood and bark. In general, angiosperm leaves are readily decomposed. When a leaf falls from a tree from the riparian zone, it would be colonized by soil-inhabiting fungi—those already present in the layer of litter at the soil surface or various aquatic fungi when the leaf becomes submerged. Most aquatic hyphomycetes can degrade cellulose, various hemicelluloses, and pectin (Chamier 1985; Abdel-Raheem and Ali 2004; Chandrashekar and Kaveriappa 1991; Zemek et al. 1985). Many studies have examined the enzymatic activities of freshwater fungi and reported amylase,  $\beta$ -glucosidase,  $\beta$ -xylosidase, endoglucanase, endoxylanase, lipase, pectinase, and protease activity (Chamier 1985).

To which extent aquatic—terrestrial—hyphomycetes play an important role in aquatic systems is still unclear, although they are common on leaves and wood. It is generally assumed that the so-called aquatic—terrestrial fungi are not able to compete

against aquatic hyphomycetes and hence are removed after the first 2–3 days of the decomposition process (Harrop et al. 2009; Bärlocher and Kendrick 1974; Nikolcheva et al. 2005; Perez et al. 2012). However, aquatic–terrestrial fungi are present on longer-exposed leaves in streams [e.g., (Hameed et al. 2008; Smither-Kopperl et al. 1998)]. Kelly et al. (2010) studied fungal communities on decomposing maple and aspen leaves, and his group reported that the majority of operational taxonomic units (OTUs) represented terrestrial *Cladosporium* species, whereas aquatic hyphomycete sequences were not observed. Indeed, several aquatic–terrestrial hyphomycetes are able of decomposing leaf litter (Bucher et al. 2004; Singh et al. 2014). For example, the terrestrial leaf litter ascomycete *Torula herbarum*, isolated from a tropical stream, has been found to be able to break down lignin (Bucher et al. 2004).

Few aquatic fungi form a symbiotic mycorrhizal relationship with the roots of trees and other plants and macrophytes. This association is mutually beneficial to both the plant and the fungus. The fungus enables the plant to take up nutrients that are unavailable, and the plant provides nutrition for the fungus. There are two fundamentally different types of mycorrhizal associations—ectomycorrhizal (usually involving a basidiomycete) and endomycorrhizal (most often involving a member of the *Glomeromycota*). In the former, the fungus produces a covering of hyphae (called a sheath, Hartig net, or mantle) around the outside of smaller rootlets of the host plant. Other hyphae invade the cortex of the rootlet but do not disrupt the individual cells. In endomycorrhizal associations, no sheath is formed and hyphae of the fungus actually invade cells of the cortex of the rootlet. Perhaps 80 % of all vascular plants form mycorrhizal associations with fungi. First aquatic vesicular–arbuscular mycorrhiza was discovered in *Littorella uniflora*, *Lobelia dortmanna*, and *Isoetes lacustris* by Sondergaard and Laegaard (1977). Vesicular–arbuscular mycorrhizas (VAM) in *Isoetes* plants were later also observed by Sudova et al. (2011).

Furthermore, dark septate endophytes (DSE) and fungal root associates (RAF) from aquatic habitats were reported (Kohout et al. 2012; Seena et al. 2008). Mycorrhiza and some DSE are known to be mutualistic. On the other hand, endophytism can be the balance between rather antagonistic relationships between fungus and host which may even develop into a pathogenic outcome (Schulz and Boyle 2005). Several species of aquatic hyphomycetes were isolated as endophytes from aquatic or terrestrial plants (Sati and Belwal 2005). Some aquatic hyphomycetes were also found in roots of terrestrial habitats [e.g., (Tedersoo et al. 2007)]. However, there are few reports about the transmission of freshwater fungi either vertical to the next generation of the same host or horizontal between hosts. It is not known if endophytic aquatic hyphomycetes have a harmful or beneficial effect on the hosts. Further thorough studies are needed to elucidate the aspects of endophytic life of aquatic hyphomycetes.

For instance, all the described *Minutisphaera* spp. (*M. fimbriatispora*, *M. japonica*, *M. aspera*, and *M. parafimbriatispora*) have been isolated from submerged wood in freshwater habitats so far (Ferrer et al. 2011; Raja et al. 2013), suggesting that they play an ecological role in nutrient cycling and organic matter decomposition

in freshwater habitats (Pointing 2001). A recent BLAST search (Altschul et al. 1990) of newly sequenced ITS strains of *M. aspera* and *M. parafimbriatispora* in GenBank identified two ITS sequences from endophytes (“*Pleosporales* sp. 39 g,” JX244063, and “*Didymosphaeria* sp. TS\_04\_050,” HQ713763) as the top BLAST matches with high percent identity values and coverage. Based on the uncorrected p-distances calculated in PAUP\*, the two ITS sequences from endophytes were identical to each other and shared 99 % sequence similarity with ITS sequences of *M. aspera*. The high ITS sequence similarity between these fungal endophytes and *M. aspera* could imply that *Minutisphaera* may have a dual mode of lifestyle as saprobes on submerged wood as well as fungal endophytes inside the roots of trees. However, additional studies are warranted to test this ecological hypothesis (Selosse et al. 2008).

In contrast to the aquatic ascomycetes (meiosporic and mitosporic fungi), which generally colonize organic matter, which are comparatively larger in size, such as fallen leaves, submerged wood, or aquatic plants, the zoosporic fungi are colonizers of smaller substrates. They are particularly fond of substrates which contain chitin, keratin, or cellulose (Wong et al. 1998). In case of small particles such as algae, pollen grains, seeds, and zooplankton carcasses, and other temporarily available substrates decomposition is achieved by the much smaller chytrids (*Chytridiomycetes*) and water molds (*Oomycetes*), rather than the aquatic hyphomycetes. This is because the zoosporic fungi are relatively simpler in structures. They do not depend on macroscale hyphal networks and thus are capable of very fast responses to changes in their environment. Being actively motile, the zoospores of these aquatic fungi actively search for adequate substrates using chemotaxis. Once a suitable substrate has been reached, the zoospore encysts. An appressorium or a penetration tube is formed and the food particle (substrate) is invaded by tiny rhizoids tapping the internal nutrient reservoirs. Zoosporogenesis can occur in a short time, producing a prolific number of zoospores from zoosporangia. Their life cycle can be completed in days, either endobiotic, epibiotic, endophytic, or ectophytic, depending on the relationship of the thallus with the host or organic substrate.

Like other aquatic fungi, the chytrids and water molds are heterotrophs. Most of the species are benign saprobes, but they often exist as parasites, sometimes as symbionts, and of course as decomposers. The aquatic systems harbor a wealth of organisms that can serve as suitable hosts for the parasitic zoosporic fungi: algae from different phyla, cyanobacteria, protists, zooplankton, fish, birds, mussels, eggs of liver flukes, nematodes, crayfish, mites, insect larvae, amphibians, mammals, plants, and other aquatic fungi. For the decomposers, resources of organic matters derived from animals include fish scales, fish eggs, carcasses, feathers, and hair, while plant-derived resources include pollen, spores, seeds, small fruits, and plant debris (Cole et al. 1990).

Chytrids are surprisingly abundant on filamentous algae, phytoplanktons, and diatoms, and some species are known to severely deplete local populations of their algal hosts. The abundance of chytrids in aquatic systems are considered much higher than traditionally thought (Kagami et al. 2014). The phytoplanktons infected with chytrid zoospores could become an excellent food source for zooplanktons in terms of size, shape, and nutritional quality, and the nutrients from



within the planktons can be transferred to the zooplanktons through the “mycoloop” pathway in the aquatic ecosystems (Kagami et al. 2014). Also pollen deposited in lakes could be consumed by saprotrophic chytrids, rather than parasitic relatives (Masclaux et al. 2013).

Ibelings and co-workers studied the host–parasite interactions between freshwater phytoplankton and chytrid fungi and found that algal population was naturally regulated by the parasitism of these fungi (Ibelings et al. 2004). Encounters with these parasitic chytrids can be fatal to algae, particularly if their defense mechanism is breached by the fungal parasites. When the alga is attacked by the fungus, it undergoes a “suicide” response, which is a controlled hypersensitive reaction. This hypersensitivity is regarded as a common defense mechanism in algae. If this controlled “suicide” progress is initiated at the right moment during fungal infection, it results in the successful interruption of the fungal infection cycle, because the parasite’s ability to reproduce via spore production is inhibited. This mechanism is conducive to maintaining a healthy algal population because it reduces the abundance of the deadly fungal parasite in the environment. If such control is unsuccessful, however, the parasitic chytrid prevails and thus resulting in mass mortality of the algal species. The ecological relevance of this negative interaction between the two parties is obvious. The failure of the algal “suicide” mechanism in response to fungal infection can lead to shifts in the algal community composition in a given aquatic system.

In rare, but important cases, some zoosporic fungi cause severe damage to larger aquatic organisms. They infect frogs, shrimps, fishes, or fish eggs (Chukanhom and Hatai 2004; Noga 1993) and thereby exert strong population pressure. Such damage is of great importance for aquaculture and often demands antifungal treatments. Some oomycetes, especially species of *Aphanomyces* and *Saprolegnia*, are aggressive pathogens of fish and crustacea. For example, *Aphanomyces astaci* causing the crayfish plague has driven the European crayfish population to the edge of extinction (Reynolds 1988). The most notorious parasitic chytrid is *Batrachochytrium dendrobatidis*, which cause worldwide extinction of several known and unknown species of frogs (Berger et al. 1998; Skerratt et al. 2007). Aquatic plants are also greatly affected by some oomycetes. For example, *Pythium phragmites* has been found to cause reed decline (Nechwatal et al. 2005). For more discussion on diseases of freshwater fishes caused by zoosporic fungi, see Willoughby (2003).

## Distribution and Biodiversity

### *Distribution Pattern*

Regarding the distribution pattern of freshwater fungi, some may be restricted to tropical, temperate, or cold water habitats, while others are cosmopolitan. The geographical distribution of Ingoldian mitosporic ascomycetes (=anamorph or asexual fungi) are relatively well studied compared to those of the freshwater ascomycetes. The Ingoldian fungi most commonly occur on shed leaves in streams and rivers, and

they are documented by stream biologists. Some are cosmopolitan and some are restricted in distribution. Also the phylogeographic pattern varies among and within a species. Molecular barcoding (ITS) of 130 isolates of six Ingoldian fungi revealed significant genetic differentiation between continents within a single fungal species (Duarte et al. 2012). The knowledge on the distribution pattern of freshwater ascomycetes is accumulating even though most investigations are concentrating in tropical and subtropical Asia, North America, as well as the neotropics.

Some studies have reported shifts in fungal community composition by latitude and temperature (Arnold and Lutzoni 2007). Such spatial shifts/turnover in community is also expected in freshwater fungi. Wood-Eggenschwiler and Bärlocher (1985) used distribution data obtained from the literature (Webster and Descals 1981) for over 150 species of Ingoldian mitosporic fungi and they concluded, “on a worldwide scale, temperature together with its influence on vegetation in different climatic regions is the major factor in determining distribution patterns of Ingoldian mitosporic fungi.” Wood-Eggenschwiler and Bärlocher (1985) discovered that there was a higher similarity in species composition of Ingoldian fungi between geographically distinct tropical locations (South America, West Africa) than between tropical and temperate regions that were located on the same continent, either African or North and South American. Raja et al. (2009) also reported a change in species composition of freshwater ascomycetes along the temperate–subtropical latitudinal ecotone in Florida, USA.

Apart from the macroclimatic factors, microenvironmental factors also affect the distribution and abundance of freshwater fungi. Chauvet (1991) studied the distribution of Ingoldian mitosporic fungi at 27 stations in France, and he concluded that the most important environmental factors are altitude, pH, temperature, and season, although the relationship between species composition and each environmental factor is hard to establish. Longitudinal distribution patterns in freshwater fungi along a river and stream are reported for both leaf litter and woody substrates (Gönczöl 1989; Shearer and Webster 1985a, 1991; Tsui et al. 2001a). Tsui et al. (2001a) reported changes in fungal communities and taxonomic compositions from upstream to downstream in responses to salinity and riparian vegetation. Shearer and Webster (1985a) reported that Ingoldian mitosporic fungi communities in headwater streams were distinctly different from the downstream communities in the River Teign. Using water filtration, leaf pack baiting, and collection of naturally occurring substrates, lower species diversity with a lower frequency occurrence of species was observed in the headwaters (Shearer and Webster 1985a). Using molecular data of DGGE, Miura and Urabe (2014) also demonstrated that taxonomic composition and richness of epilithic fungal assemblages change along the longitudinal gradient of the river, according to the water temperature, and the spatial variation in abundance and composition of dissolved organic matter and nutrients. While species diversity could change spatially, the genetic variability within a species does not vary locally. Using eight microsatellite markers, Anderson and Shearer (2011) revealed small genetic differentiations among populations of *Tetracladium marchalianum* from Wisconsin and Illinois, USA. They concluded that the fungal populations may be highly connected in local habitats.

## ***Substrate Preference***

Freshwater fungi demonstrate substrate specialization, even though they are saprobes. For instance, of the 548 species of freshwater ascomycetes reported up to 2009 (<http://fungi.life.uiuc.edu/>), 60 % are reported only from submerged woody debris and about 30 % are reported only from herbaceous substrates, while only about 10 % species are reported from both submerged wood and herbaceous substrates [reviewed in (Raja et al. 2009)]. During the substrate distribution pattern investigation of freshwater ascomycetes in the Florida Peninsula (Raja et al. 2009), the results implied substrate preference among freshwater fungi. Of the 132 fungal taxa collected in freshwater habitats, 100 were reported only on woody debris, 14 species occurred exclusively on herbaceous debris, and 18 species were found on both woody and herbaceous debris (Raja et al. 2009). Cai et al. (2003) also reported substrate preferences in freshwater fungi during an investigation on the biodiversity of freshwater fungi on submerged bamboo and submerged wood in Liput River in the Philippines. Fifty-eight and 38 fungal taxa were collected on bamboo and wood, respectively, but only 16 among them were in common on both substrates (Cai et al. 2003).

Thomas et al. (1992) observed *Alatospora acuminata* more frequently on *Acacia* leaves, while *Tetrachaetum elegans* was more common on *Eucalyptus* leaves. The authors suggested five possible reasons: First, different substrates have different nutrients, favoring the growth of some fungi over others. Second, different substrates contain different inhibitory chemicals, for example, tannin, impacting sporulation and spore germination. Third, variations in the gross physical structure of substrates affect differentially the impaction efficiency of various fungal spores. Fourth, variations in fine physical structure of substrates affect penetration and colonization by fungi. Fifth, different substrates vary in their decay rate—durable substrate has a much longer exposure time to the spores and to fungal colonization. Gulis (2001) investigated five different substrate types from 92 watercourses of Belarus for aquatic hyphomycete colonization (52 species). He found specific fungal assemblages correlating with leaf litter types which suggests possible substrate preferences of aquatic hyphomycetes triggered in particular by lignin content.

## ***Seasonal Variation***

Seasonal occurrence with fluctuations in conidial numbers has been reported in many parts of the world (Thomas et al. 1989). Although most species can be collected throughout the year, their relative abundance (measured in terms of conidial production) is influenced by the seasonal availability of substrates, which is in agreement with seasonal input of deciduous tree litter in temperate regions (Bärlocher 1992). For instance, the conidial peak in summer in Australia was also highly correlated with the leaf fall of eucalypt forests in summer (Thomas et al. 1989), and the timing of conidial maxima in New Zealand streams was well

correlated with the prevailing litter fall patterns (Aimer and Segedin 1985). Recent studies employing DGGE illustrated seasonal changes in fungal communities in a lake in Japan (Ishii et al. 2015).

### ***Human Disturbance***

Most freshwater habitats are vulnerable to human disturbance such as agriculture, urbanization, and industrialization. Any perturbation around the riparian environment affects significantly the in-stream fungal communities and the biogeochemical cycles through runoff processes. Organic pollution caused by the mass discharged of domestic or agricultural wastes reduces the amount of oxygen in the water. Most freshwater fungi cannot survive in such anoxic and polluted environments. For example, organic pollution reduced substantially the diversity of aquatic hyphomycetes (Raviraja et al. 1998) and ascomycetes (Tsui et al. 2001b). Toxic metal entering the rivers as a result of mining and industrialization also impact negatively the fungal communities. Spore production, biomass, and fungal diversity are severely depleted under high concentrations of coal, copper, zinc, and cadmium (Krauss et al. 2001; Niyogi et al. 2009; Sridhar et al. 2005). Similarly, the application of chemical pesticides can also change the fungal communities. For example, the antigen and biomass production of *Neonectria (Heliscus) lugdunensis* was influenced by the herbicide mecoprop (Birmingham et al. 1998). Recent pyrosequencing (metagenomics) data also showed declining fungal diversity in most eutrophic streams (Duarte et al. 2014). However, previous studies demonstrated the opposite—anthropogenic nutrients stimulated fungal spore production and mycelial biomass on leaves (Gulis and Suberkropp 2003).

### **Functional Biodiversity/Outlook: Who Is Doing What?**

The most prominent ecological function of freshwater fungi is the decomposition of allochthonous organic matter in aquatic systems. The research of freshwater fungal ecology has been focused on stream-inhabiting aquatic hyphomycetes mostly in temperate low-order streams (Bärlocher 2010). Properties of ecosystem functions, such as fungal biomass, fungal productivity, and fungal impact on the decomposition process (Lecerf and Richardson 2010a), have been investigated in hundreds of field and laboratory (microcosm) studies [meta-analyzed in (Ferreira et al. 2014)]. These studies were accompanied by inventory biodiversity (morphological and molecular) approaches of aquatic hyphomycetes [e.g., (Nikolcheva et al. 2003; Seena et al. 2008; Duarte et al. 2014; Casas et al. 2011; Pascoal et al. 2005; Shearer and Webster 1985b)]. However, the results of studies investigating the functional consequences of biodiversity changes often remained unpredictable or inconsistent [summarized in (Graça et al. 2015)]. Within the last decade, it has

become apparent that species traits and functional diversity may be better correlated with ecosystem function than taxonomic identity (Gessner et al. 2010; Lecerf and Richardson 2010b).

Nowadays we have the methods at hand to even more thoroughly elucidate species assemblages and, furthermore, investigate the possible and active traits of freshwater fungi. The progress in sequencing and annotating fungal genomes will soon shed light on the genetic diversity and metabolic potential of freshwater fungi from all fungal phyla. Transcriptomes [e.g., using RNA-seq; (Wang et al. 2009)] from single cultures or microcosm studies of freshwater fungi will enable us to study the metabolism during decomposition and/or degradation processes. For the identification of metabolic pathways, the quality of genome annotation is crucial (Kuske et al. 2015). The optimal study design is to have very well-annotated reference genomes, the transcriptome (the expressed genes), and the corresponding proteome (the produced enzymes) as shown by Hori and co-workers (2014). Freshwater fungal communities are complex assemblages of mostly filamentous fungi, single-celled chytrids, and yeasts. They are members of food webs and mediators of biogeochemical pathways for the energy transfer between different trophic levels. Future methodical improvements will hopefully ease the challenges of meta-analyses to understand the “why-is-who-doing-what” in the ecology of freshwater fungi.

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