‘Marine fungi’ and ‘marine-derived fungi’ in natural product chemistry research: Toward a new consensual definition

Article *in* Fungal Biology Reviews · September 2016

DOI: 10.1016/j.fbr.2016.08.001

FUNGAL BIOLOGY REVIEWS XXX (2016) 1–13

British Mycological Society promoting fungal science

journal homepage: www.elsevier.com/locate/fbr

Review

'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition

Ka-Lai PANG[a,*], *David P. OVERY*[b,c], *E. B. Gareth JONES*[d], *Maria da Luz CALADO*[e], *Gaëtan BURGAUD*[f], *Allison K. WALKER*[g], *John A. JOHNSON*[h], *Russell G. KERR*[b,i], *Hyo-Jung CHA*[a], *Gerald F. BILLS*[j]

[a]*Institute of Marine Biology and Centre of Excellence for the Oceans, National Taiwan Ocean University, 2 Pei-Ning Road, Keelung, 20224, Taiwan, ROC*

[b]*Department of Chemistry, University of Prince Edward Island, 550 University Ave., Charlottetown, Prince Edward Island, C1A 4P3, Canada*

[c]*Department of Pathology and Microbiology, Atlantic Veterinary College, University of Prince Edward Island, 550 University Ave., Charlottetown, Prince Edward Island, C1A 4P3, Canada*

[d]*Botany and Microbiology Department, College of Science, King Saud University, Riyadh, 1145, Saudi Arabia*

[e]*Departamento de Biologia Vegetal, Faculdade de Ciências da Universidade de Lisboa, Campo Grande, Edifício C2, 4° Piso, 1749–016, Lisbon, Portugal*

[f]*Université de Brest, EA 3882, Laboratoire Universitaire de Biodiversité et Ecologie Microbienne, ESIAB, Technopôle Brest-Iroise, 29280, Plouzané, France*

[g]*Department of Biology, Acadia University, 33 Westwood Avenue, Wolfville, Nova Scotia, B4P 2R6, Canada*

[h]*Department of Biological Sciences, University of New Brunswick, Saint John, New Brunswick, PO Box 5050, E2L 4L5, Canada*

[i]*Department of Biomedical Sciences, Atlantic Veterinary College, University of Prince Edward Island, 550 University Ave., Charlottetown, Prince Edward Island, C1A 4P3, Canada*

[j]*Texas Therapeutics Institute, The Brown Foundation Institute of Molecular Medicine, University of Texas Health Science Center, 1881 East Road, Houston, TX, 77054, USA*

ARTICLE INFO

Article history:
Received 18 June 2016
Accepted 4 August 2016

Keywords:
Deep-sea
Genomics
Mangrove endophytes

ABSTRACT

The discovery of new natural products from fungi isolated from substrata in marine environment has increased dramatically over the last few decades, cumulating in over 1000 new metabolites. The term 'marine-derived fungi' is used extensively in these reports, and it refers to the environment from which the fungi are isolated, in contrast to the classical ecological definition of 'marine fungi' as obligate and facultative inhabitants of the marine environment. In a significant number of reports, the origins of substrata or habitat relationships of strains referred to as 'marine-derived fungi' are unknown or whether a seawater medium was used for their isolation. In August 2014, a workshop held at the University of Prince Edward Island, Canada was convened to discuss a series of topics related

* *Corresponding author*. Fax: +886 2 24633152.
E-mail addresses: klpang@ntou.edu.tw (K.-L. Pang), dovery@upei.ca (D. P. Overy), torperadgj@gmail.com (E.B. G. Jones), mdcalado@fc.ul.pt (G. Calado), gaetan.burgaud@univ-brest.fr (G. Burgaud), a.k.walker@eagles.usm.edu (A. K. Walker), jaj@unb.ca (J. A. Johnson), rkerr@upei.ca (R. G. Kerr), hyojung.a@gmail.com (H.-J. Cha), Gerald.F.Bills@uth.tmc.edu (G. F. Bills).
http://dx.doi.org/10.1016/j.fbr.2016.08.001

Secondary metabolites
Transcriptomics

to marine fungal natural product research. A central discussion topic was "What constitutes a marine fungus?" There was a general agreement that a review of the definition of a marine fungus would be beneficial to the marine fungal natural product community, together with an evaluation of the suitability and relevance of the use of the term 'marine-derived fungi'. We here propose a revised, broad definition of a marine fungus as 'any fungus that is recovered repeatedly from marine habitats because: 1) it is able to grow and/or sporulate (on substrata) in marine environments; 2) it forms symbiotic relationships with other marine organisms; or 3) it is shown to adapt and evolve at the genetic level or be metabolically active in marine environments'.

1. Introduction – history of marine mycology and associated natural products discovery

The field of marine mycology has evolved tremendously since its inception. The first marine fungi were described in the 1850s, and early studies of marine fungi focused mainly on seaweeds (Sutherland, 1915, 1916). The subdiscipline of marine mycology was conceived based on Barghoorn and Linder's exhaustive investigation of wood-inhabiting marine fungi (Barghoorn and Linder, 1944). Pioneering efforts in the field were dedicated to deciphering the diversity of marine fungi from different marine substrata, *i.e.* submerged wood, seaweeds and salt marsh grasses in temperate areas, mainly in Europe and North America (Sutherland, 1915, 1916; Barghoorn and Linder, 1944; Kohlmeyer and Kohlmeyer, 1979). As the field advanced into the late 1970's, morphological studies of marine fungi, especially those affiliated with the Halosphaeriaceae, using light and electron microscopy, were subsequently used to classify taxa (Jones and Moss, 1978; Jones, 1995). All of these marine fungi were collected on substrata in intertidal zones, and classified based on characteristics of sporulating (sexual or asexual) structures. Since the 1990s, molecular-based studies of marine fungi, using rDNA phylogenetic analyses, have dominated the field (Spatafora *et al.*, 1998; Jones *et al.*, 2009; Suetrong *et al.*, 2009; Sakayaroj *et al.*, 2011; Hyde *et al.*, 2013). In 1996, diversity estimates of marine fungi were placed at around 1500 species and by 2011, diversity estimates were projected to include over 10,000 species (Jones, 2011). To date, a total of 1112 marine fungi have been documented (including yeasts) from marine sources (Jones *et al.*, 2015). According to Jones *et al.* (2009), classification of many marine fungi remains a confused and unresolved issue; particularly because of a narrow, prior definition of what constitutes a marine fungus.

Concurrent to the development of the field of marine mycology, there has been a voluminous output in natural product research from fungi isolated from substrata in different marine habitats, including marine animals, seaweeds and sediments, with many new bioactive compounds being described each year (Rateb and Ebel, 2012; Blunt *et al.*, 2013; Ebada and Proksch, 2015). An exponential increase in the rate of discovery of new natural products from "marine-derived" fungi has occurred over a period spanning 1970–2010, cumulating in over 1000 new metabolites described by the middle of 2010 (Overy *et al.*, 2014). These so-called 'marine-derived' fungi had an impact early on in the history of drug discovery from fungi. The cephalosporin β-lactam antibiotics (Fig. 1A–C) were discovered about 15 y after the penicillins from *Acremonium chrysogenum* (previously known as "*Cephalosporium acremonium*"). Giussepe Brotzu, a professor of Hygiene at the University of Cagliari, Sardinia, Italy formulated a hypothesis about why young people that were swimming at "Su Siccu" Bay, at the site where the city sewer system drained into the sea never contracted typhoid fever (Hamilton-Miller, 2000). Although the disease was endemic to the area, there were no cases of typhoid fever related to bathing in these sewage-contaminated waters. He decided to take a water sample from the bay and tested its effect on *Salmonella enterica* subsp. *enterica* (serovar Typhi), *Yersinia pestis*, *Brucella melitensis*, *Vibrio cholerae*, and *Staphylococcus aureus*, leading to observations of potent antibacterial activities which he followed with improvised experiments with humans using concentrated culture broths. Investigations on Brotzu's fungus in England eventually led to the isolation of cephalosporins P, N and C (Burton and Abraham, 1951; Newton and Abraham, 1954; Abraham and Newton, 1961).

In recent decades, renewed interest in fungi obtained from marine substrata has significantly expanded the catalog of fungal natural products, including many novel chemical scaffolds. One metabolite, halimide (Fig. 1D), a potently cytotoxic diketopiperazine phenylahistine from a marine-derived *Aspergillus ustus* isolate, led to the synthesis of plinabulin (NPI-2358) – a molecule that reached phase II trials as an angiogenesis inhibitor for preventing tumors and scar tissue development (Mita *et al.*, 2010). A current issue in the field of marine fungal natural product research is that an increasing majority of fungal isolates obtained from marine habitats and examined for new and novel natural products belong to well-known terrestrial genera, such as *Aspergillus* (Fig. 2C) and *Penicillium*. This raises questions as to whether these genera are capable of growth in saline habitats, do they constitute stable and active populations in the marine environment and what is their associated ecological role(s) (Höller *et al.*, 2000; Jensen and Fenical, 2002; Kohlmeyer and Volkmann-Kohlmeyer, 2003; Overy *et al.*, 2014). Inversely correlated with the increased attention given to chemistry of marine-derived fungi has been an apparent rejection of the exploration of terrestrial soil fungi because they are perceived as exhausted sources of new natural products, even though genomics clearly indicates this is not the case (Bérdy, 2012). A

Please cite this article in press as: Pang, K.-L., et al., 'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition, Fungal Biology Reviews (2016), http://dx.doi.org/10.1016/j.fbr.2016.08.001

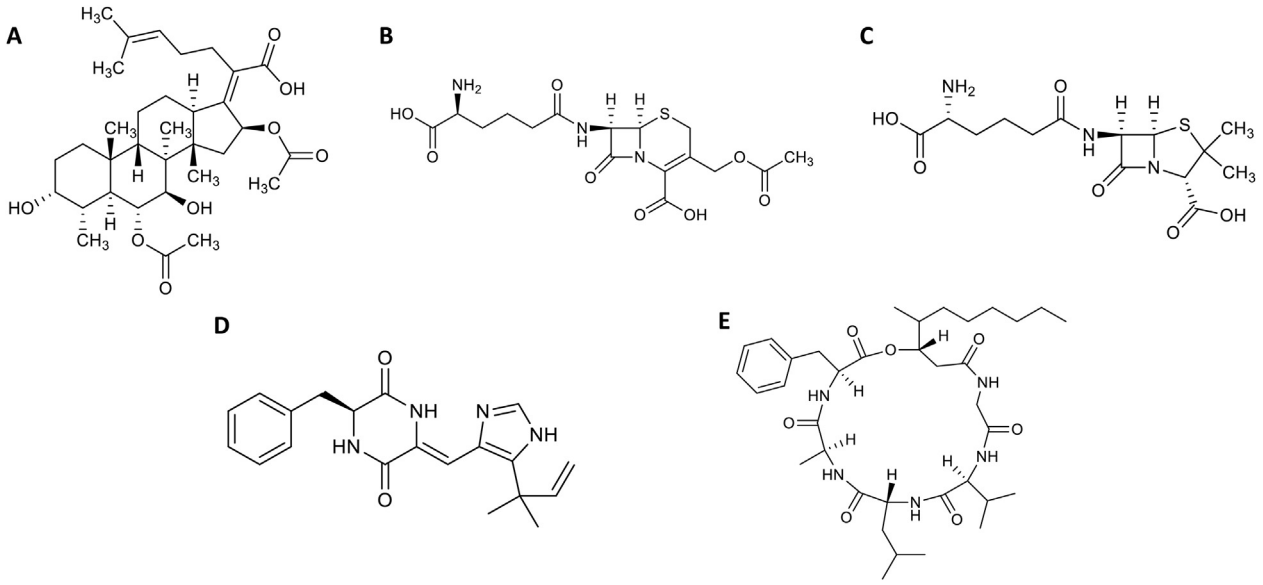

Fig. 1 – (A) Cephalosporin P1, (B) Cephalosporin C, (C) Cephalosporin N, (D) Halimide ((−)-phenylahistin), (E) Scopularide A.

related issue is the apparent lack of effort and resources devoted by the natural product community to explore fungi that are unequivocally marine in nature (those forming fruiting bodies on substrata in marine habitats), and therefore, likely to provide chemistry exclusive to the marine environment. The latter group of marine fungi often grows very slowly in culture which possibly hinders detection and scale up of their metabolites when employing ordinary fermentation methods (Miller, 2000).

In August 2014, a workshop held at the University of Prince Edward Island, Charlottetown, Canada brought together marine mycologists and marine fungal natural product chemists to discuss topics relevant to marine fungal natural product research. The MaFNaP (Marine Fungal Natural Product) consortium was consequently established. In response to one discussion topic "What constitutes a marine fungus?", in this short article, we: (1) review the history of the definition of a marine fungus, (2) evaluate suitability and relevance of the term 'marine-derived fungi' which is commonly used in marine fungal natural product research, (3) summarise the current research in identifying which fungi are of marine origin, and (4) propose a revised definition of what a marine fungus is.

2. Prior definitions of marine fungi

Historical definitions of what constitutes a marine fungus were based on whether the fungus could grow and reproduce in seawater or freshwater conditions. Indeed, Johnson and Sparrow (1961) defined marine fungi as 'capable of developing to reproductive maturity even though exposed at some point in their growth to salinities of 30 ‰ or more, either while continually submerged or intermittently inundated by tidal waters'. Tubaki (1969) proposed a similar definition wherein marine fungi exhibit 'better growth and reproductive occurrence on substrata with a wide range of salinity than those with freshwater, or growth of nearly the same degree on substratum with salinity of seawater and with freshwater'. Defining a marine fungus based on these physiological parameters is problematic as fungi are highly adaptable microorganisms, and thus, many can grow equally well under a range of saline and freshwater conditions (Tubaki, 1969; Alderman and Jones, 1971; Jones, 1976; Pang *et al.*, 2011). This led to extensive studies on the salinity tolerance of marine fungi, and examination of the movement of ions in and out of fungal cells (Jones and Jennings, 1964, 1965; Jennings, 1983; Booth and Kenkel, 1986; Jennings and Garrill, 2000). Likewise, many terrestrial filamentous fungi and yeasts, especially those in the Ascomycota, are adapted to low water activity (a_w), or are even halophilic, and thus, can grow in salinities higher than seawater (Tresner and Hayes, 1971; Kis-Papo *et al.*, 2003; Kutty and Philip, 2008).

During the 1970s, Jan Kohlmeyer and his colleagues began examining fungi associated with salt marsh grasses and documented over 100 species occurring on submerged as well as on aerial parts of *Juncus roemerianus* in North Carolina, USA (summarized in Calado and Barata, 2012). Following this work, previous definitions of marine fungi were reevaluated by Kohlmeyer and Kohlmeyer (1979), who proposed a broad ecological definition dividing marine fungi into obligate and facultative groups; obligate marine fungi were defined as 'those that grow and sporulate exclusively in a marine or estuarine habitat' and facultative marine fungi as 'those from freshwater or terrestrial milieus able to grow (and possibly also to sporulate) in the marine environment'. This definition has been adopted and cited by most studies for the last 35 y, in particular, it was applied to classify fungi occurring vertically on salt marsh plants including *Juncus roemerianus*, *Spartina alterniflora* (Kohlmeyer and Volkmann-Kohlmeyer, 2000; Al-Nasrawi and Hughes, 2012) and *Spartina maritima* (Barata, 2002) and the mangrove plant *Acanthus illicifolius* (Sadaba *et al.*, 1995). A similar definition was also suggested by Kohlmeyer and Kohlmeyer (1979) to define marine yeasts:

Please cite this article in press as: Pang, K.-L., et al., 'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition, Fungal Biology Reviews (2016), http://dx.doi.org/10.1016/j.fbr.2016.08.001

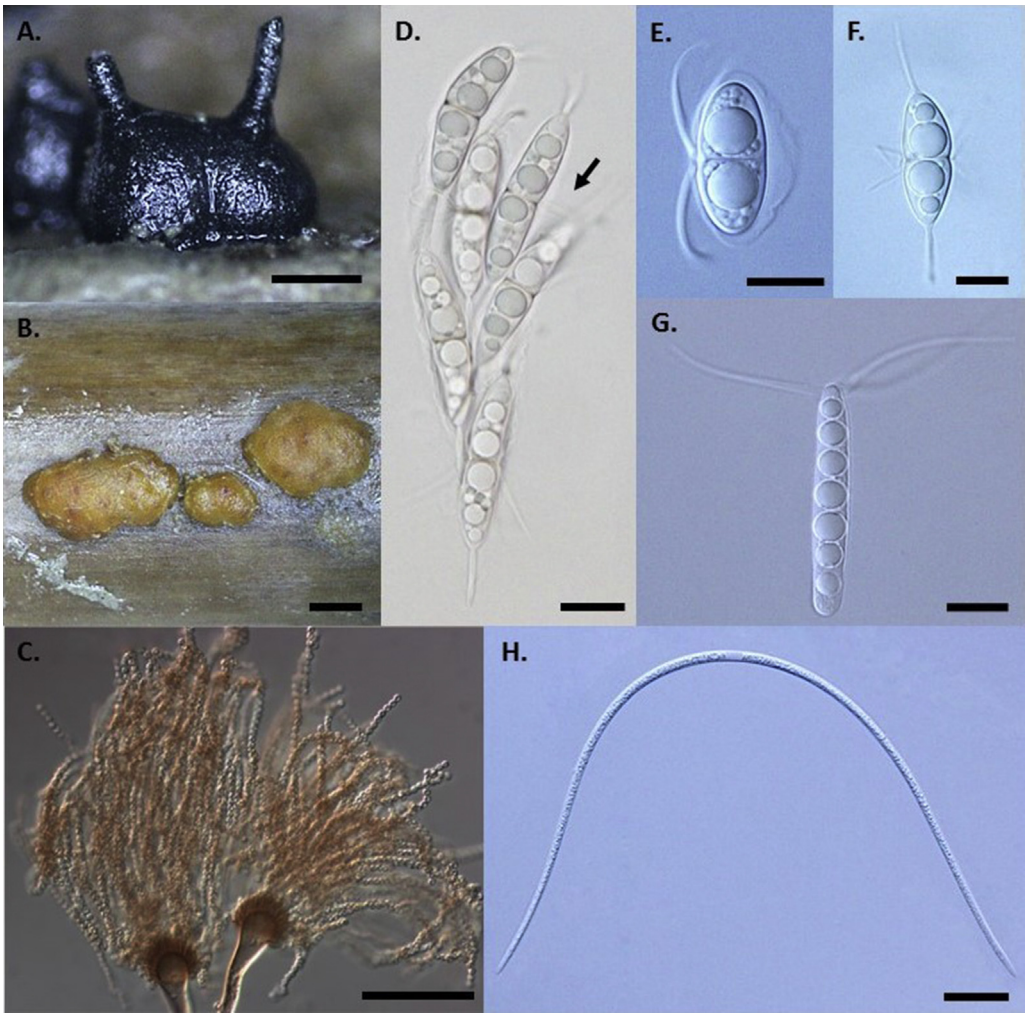

Fig. 2 – (A) Black ascomata of the deep-sea fungus *Alisea longicolla*, (B) Fleshy ascomata of the deep-sea fungus *Oceanitis scuticella*, (C) A marine *Aspergillus* sp., (D) Deliquescing ascus, (E) *Nimbospora effusa* with a sheath and equatorial appendages, (F) Ascospore of *Corollospora maritima*, (G) Ascospore of *Torpedospora radiata*, (H) Ascospore of *Lulworthia* sp. Scale bar: A = 500 μm, B = 1 mm, C = 50 μm, D-G = 10 μm, H = 30 μm.

'obligate marine yeasts are those yeasts that, thus far, have never been collected anywhere but in the marine environment, whereas facultative marine yeasts are also known from terrestrial habitats'.

In recent years, the long-standing Kohlmeyers' definition of what constitutes a marine fungus has been found by some researchers to be overly restrictive. Jones *et al.* (2009) have expressed their opinion that distinguishing whether or not a fungus is obligatorily or facultatively marine depends largely on personal opinion, especially with respect to saprobic species routinely isolated from marine sediments and from intertidal substrata, such as, maritime grasses and mangrove plants. Fungi isolated from marine sediments have been largely ignored by marine mycologists (Kohlmeyer and Volkmann-Kohlmeyer, 2003) as they are typically labeled as terrestrial, however, the repeated isolation of these species from different sites and by different laboratories has prompted marine mycologists to consider these fungi as being marine (Jones *et al.*, 2015). These conflicting interpretations require more rigorous experimentation to understand how the propagules of terrestrial fungi that are constantly transported from the atmosphere and terrestrial and freshwater habitats survive in marine habitats. A parallel set of issues have plagued the studies of Actinobacteria in marine environments, and after extensive phylogenetic and ecological dissections of marine populations, specific lineages of Actinobacteria were eventually recognized as being indigenous to the marine environment, while the majority recovered were of terrestrial origin (Mincer *et al.*, 2002; Prieto-Davó *et al.*, 2008; Ziemert *et al.*, 2014). Many wood-inhabiting marine ascomycetes have evolved morphological adaptations for a marine (or aquatic) occurrence: 1. deliquescing asci (ascospores are pushed up through the ostiole, accumulate outside and are washed away during high tide, Fig. 2D) and 2. ascospores or conidia with appendages, gelatinous sheaths, or both (Fig. 2E), to facilitate for prolonged suspension in seawater and foam, and their attachment to solid surfaces (Pang, 2002). However, these features are also present in

Please cite this article in press as: Pang, K.-L., et al., 'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition, Fungal Biology Reviews (2016), http://dx.doi.org/10.1016/j.fbr.2016.08.001

some freshwater and terrestrial fungi adapted to dispersal in rainwater and aqueous films. Therefore, gross anatomical features alone cannot distinguish the marine mycota from their terrestrial counterparts.

Many factors influence the occurrence and distribution of marine fungi including hydrogen ion activity, hydrostatic pressure, ionic composition and concentration, osmotic response, oxygen availability, salinity, tidal exposure, temperature, availability of substrata for growth and the fungal taxonomic group under discussion. In trying to determine what constitutes a marine fungus, little thought is given to why so few terrestrial fungi occur in marine habitats. Chytrids and fungal-like organisms with a zoosporic stage are more susceptible to variations in salinity (Jones and Harrison, 1976; Leaño *et al.*, 1998, 2000; Fan *et al.*, 2002). Harrison and Jones (1974) demonstrated that the sporulation of freshwater oomycetes was the principle factor governing their restriction to freshwater or low salinity levels. In the chytrid *Rhizophylctis rosea*, normal cleavage of sporangia and release of zoospores occurred in 10 % seawater, but at 30 % seawater only malformed sporangia were formed with no zoospore release. Although the vegetative phase of saprolegniaceous organisms investigated is more or less tolerant of low salinity conditions, the inhibition imposed by salinity on their reproduction confines them to freshwaters or waters of extremely low salinity (Harrison and Jones, 1975). Likewise the terrestrial ascomycete *Neurospora crassa* formed perithecia at salinities of 30 % seawater but none at 50 % seawater (Jones and Byrne, 1976). However, salinity is only one parameter to be taken into consideration; other co-factors have an effect upon spore germination. For example, the conidia of a new species of marine *Acremomium*, *Acremonium fuci*, germinated in the presence of *Fucus serratus* tissue or its aqueous tissue homogenates, but not in seawater alone (Zuccaro *et al.*, 2004).

In attempting to define what a marine fungus is, too much attention has been focused on salinity. Most studies on the salinity requirements of fungi have dealt only with vegetative growth which may be more adaptable to different concentrations of sea water (Gray *et al.*, 1963). The marine environment covers a broad spectrum of habitats ranging from deep water environments, oceanic waters, intertidal habitats such as mangroves with a range of salinities. For examples, salinity of the water at Deep Bay mangrove, Hong Kong, ranges from 1 to 30 ‰ (average 10–15 ‰) depending on whether it is the dry or wet season; while waters of Red Sea mangroves in Egypt vary between 39.9 and 46.0 ‰ (Abdel-Wahab and El-Sharouney, 2002). All are regarded as marine habitats.

Jennings (1986) opined "there is still debate about those major properties of such fungi which allow them to grow in the sea or for that matter make them less able to grow in freshwater". So what are the problems faced by a fungus in the marine environment? Seawater has a relatively low water potential and contains relatively high concentrations of ions which potentially exert toxic effects on cell processes, and finally, seawater has an alkaline pH (Jennings, 1986). It has been demonstrated that solute transport in all fungi growing in the sea may be based on a proton economy, with primary active transport being the expulsion of protons, with an alkaline external medium reducing the pH gradient of the proton motive force (Commerford *et al.*, 1985; Davies *et al.*, 1990). It is also important for the fungus to maintain a high protoplasmic osmotic potential bearing in mind the external medium. In the marine hyphomycete *Paradendryphiella salina*, osmolytes such as the polyols sorbitol and mannitol have been shown to play a role in osmotic regulation (Clipson and Jennings, 1990b). The maintenance and efflux of the ions potassium and sodium, and the role of divalent ions, are also critical for the growth of marine fungi (Jones and Jennings, 1964; Clipson and Jennings, 1990a). However, more detailed discussion of these issues remains outside the scope of this article.

Mahé *et al.* (2014) categorized marine fungi into three groups based on the criteria of an 'active/passive role' in the sea: (1) strict endemic active marine fungi, (2) ubiquist metabolically active marine fungi, and (3) ubiquist passive fungi. Strict endemic active marine fungi refer to those which produce fruiting bodies on marine substrata. Ubiquist metabolically active marine fungi and ubiquist passive fungi are mostly asexual fungi and can be differentiated based on an active role in the marine environment using the following methods: (1) taxon-specific fluorescent staining of fungal structures, (2) taxa present in both isolation and culture-independent techniques, (3) production of 'marine-derived' secondary metabolites, (4) repeated isolation from independent studies from different geographical locations, (5) having a functional role in the marine environment, and (6) prediction using a fungal metagenomic approach through identification of metabolic function of genes.

3. What are marine-derived fungi?

The adjective 'marine' in the term 'marine fungi', in most cases, refers to the environment from which the fungi are isolated; whereas, the terms 'obligate marine' or 'facultative marine' are ecologically-based terms imparting an understanding of active vegetative colonization of the habitat, physiological activity, and effective ecological role(s) of the fungi in the marine environment. The term 'marine-derived fungi' has been used extensively to describe fungi isolated from marine or marine-related habitats/substrata in the field of natural product chemistry (Jensen and Fenical, 2002). A search using the keywords 'marine-derived fungi' in the Web of ScienceTM (Thomson Reuters) resulted in >600 publications, and the majority of papers were related to secondary metabolites/natural products/bioactive compounds. These fungi were predominantly isolated from sediment, seawater, marine animals (corals, sponges, bryozoans, etc.), algae/seaweeds and leaves of marine-adapted mangrove plants. Examination of the numerous publications using 'marine-derived fungi' as keywords revealed the majority of taxa most frequently cited were taxa associated with ruderal substratum relationships, that are often characteristic of terrestrial soils and plant surfaces (Overy *et al.*, 2014). Similar to the adjective 'marine', the term 'marine-derived' can be defined as 'obtained from a marine source'. Unfortunately, the term 'marine-derived fungi' has often been misconstrued as referring to an ecological niche of fungi. 'Isolation' is the operational word responsible for this ambiguous definition because, in nearly all cases, the

Please cite this article in press as: Pang, K.-L., et al., 'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition, Fungal Biology Reviews (2016), http://dx.doi.org/10.1016/j.fbr.2016.08.001

kind of propagule that initiated the cultured strain and its origin are unknown. In other words, they were not observed sporulating or growing vegetatively on the substratum where the fungus was isolated. The isolation of a fungus from a propagule embedded in a substratum does not necessarily mean the fungus depends on the substratum as its habitat and therefore does not confirm an ecological/physiological affiliation of the fungus to the marine environment. The overuse and misuse of the word "endophyte" has similar parallel issues when referring to fungi and bacteria isolated from living plants without regard to true origins or role of the cells that initiate the cultured strain.

The origin of many of the 'marine-derived' isolates is unknown, neither is it known whether they play any ecological role(s) in the sea, or if they form stable relationships with other living organisms, such as algae, sponges, and corals. As the use of the term 'marine-derived fungi' has become well-established (as has the word endophyte), suggestion of a new alternative term seems of little value; however, it should be recognized that the use of the term 'marine-derived fungi' does little to convey ecological meaning, as the isolates may be of terrestrial, freshwater, or marine origin. Halotolerance and osmotolerance are widespread traits of terrestrial fungi, especially among the Eurotiomycetes. Therefore, unless behavior of a "marine-derived" fungus is tested in appropriate media, we cannot even assume that they are halophilic or halotolerant.

4. Unfounded assumptions and misuse of terminology

Fungi occurring on salt marsh grasses and other plants have been referred to be obligately marine, facultatively marine, or salt-tolerant based on the absolute vertical distribution of fruiting bodies at the bottom, middle and top portions of the plants with respect to the rhizome and exposure to tidal influences (Kohlmeyer *et al.*, 1995). Fructification of the Dothideomycetes occurs on the more exposed portion of the plant, while fruiting bodies of the Sordariomycetes mostly form on the basal parts (Barata, 2002). The Dothideomycetes produce bitunicate/fissitunicate asci for which dispersal on the exposed part of the plant may be more efficient, while many marine Sordariomycetes have deliquescing asci, a character possibly evolved for aquatic dispersal (Pang, 2002). However, some fungi on salt marsh plants overlap in their distributions, blurring these distinctions (Kohlmeyer and Volkmann-Kohlmeyer, 2000). The continuous nature of environmental factors and gradients in plant height, tidal amplitude, and levels of salinity in salt marshes in different geographical locations also confound the delineation between obligate and facultative ecological groups. Calado *et al.* (2015) investigated the vertical distribution of fungi on *S. maritima* at two sites in Portugal and discovered that the absolute vertical position of the shared fungi on the plant between the two sites differed but their relative vertical positions were maintained. Many marine fungi occur as mycelia on/in substrata for which fructification may occur only under ideal environmental conditions, *e.g.*, temperature, salinity, etc. (Jones, 2000; Pang and Mitchell, 2005).

Parallel difficulties in characterizing the marine-terrestrial fungus transition occur in mangrove communities. In the last decade, secondary metabolites of mangrove fungi, especially endophytes of leaves/fruits of mangrove plants, have been extensively studied (Wang *et al.*, 2013). We believe referring to these fungi as 'marine-derived' is incorrect because healthy leaves of mangrove plants grow on the aerial part of the trees and are rarely in contact with tidal seawater (Chaeprasert *et al.*, 2010). In some studies that refer to strains as 'marine-derived fungi', their origin in terms of substrata or specific habitats is unknown (Niu *et al.*, 2012; Zhou *et al.*, 2013) or whether the isolation medium was amended with seawater (Zeng *et al.*, 2012; An *et al.*, 2013). In some cases, it is difficult to understand the investigators' experimental rationale; in one case (Kong *et al.*, 2014), a freshwater medium was used for the isolation of a 'marine-derived' *Phoma* sp., a fungal genus typical of terrestrial plants and soil, from a fruit of the mangrove plant *Kandelia candel*. Subsequently, three new thiodiketopiperazines were isolated from a seawater fermentation liquid of the fungus.

Before labeling a fungus as marine, the substratum from where it was collected or isolated should be classified based on type of substratum of its origin: animals (sponges, corals, molluscs, ascidians, fish), seawater, sediment, cyanobacteria, plants including mangroves, and algae. The tissue where the fungus was isolated from should also be specified, especially for mangrove plants, as only the lower part of the trunk and roots are immersed in seawater during high tide. Mangroves are marine-adapted plants, and they can lose salt through cuticular transpiration or salt glands, maintaining higher water potential in the tissues than the surrounding seawater (Tomlinson 1986). As a result, endophytic fungi of healthy leaves experience a rather freshwater environment, and freshwater media have always been used for their isolation (Pang *et al.*, 2008); therefore, these fungi are not truly marine. An exception is the endophytic fungi isolated from roots and pneumatophores of mangrove plants, where typical marine fungi, such as *Lulworthia* spp. (Fig. 2H), *Hydea pygmea*, *Trichocladium alopallonellum* and *Zalerion maritimum* have been isolated (Ananda and Sridhar, 2002). Salt is only partially excluded at the roots (Tomlinson, 1986), thus maintaining an elevated saline environment.

5. Current research in identifying fungi of a marine origin

Pathogens of marine organisms are more reliably categorized as marine because they cause visible symptoms on their marine hosts, and can include skin ulcers and gill lesions of fish. They can be inferred to actively colonize the hosts. Species in the genera *Fusarium*, *Ochroconis*, *Exophiala* and *Scytalidium* can cause diseases of marine fish, prawns (Hatai, 2012), or even deep-sea mussels (van Dover *et al.*, 2007). *Mycaureola dilseae*, a parasitic basidiomycete of the red alga *Dilsea carnosa*, causes necrosis of the host tissues leaving a lesion where fruiting bodies form around it (Porter and Farnham, 1986; Binder *et al.*, 2006). Furthermore, appearance of the fungus appears to be seasonal, only sporulating in the late autumn (Stanley, 1992). Mutalistic/commensalistic relationships between a

Please cite this article in press as: Pang, K.-L., et al., 'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition, Fungal Biology Reviews (2016), http://dx.doi.org/10.1016/j.fbr.2016.08.001

marine fungus and other marine organisms require timely observations in the field to generate hypothesis regarding the trophic dependence of the fungus on its host. Mutualistic relationships between intertidal fungi and the marine snail *Littoraria irorata* on the cord grass *S. maritima* have been documented (Silliman and Newell, 2003). The snail grazes on the cordgrass to promote fungal colonization. Faecal pellets from the snail inoculate the wounded surface. The resulting mycelial biomass in the lesion is then consumed by the snail.

Fungi recovered from marine sediment and seawater are difficult to define as marine because mycelia and spores of these fungi may be washed off from terrestrial and freshwater habitats and are constantly rained in from the spores and particulate matter in the atmosphere. Fröhlich-Nowoisky *et al.* (2012) surveyed the fungal composition of continental, coastal and marine air samples and found that an astonishing diversity of ascomycetes, including dominant *Penicillium* spp., *Cladosporium* spp., was prevalent in marine and coastal air. The propagules of these fungi may remain viable for a long time, but they may have no ecological role in the marine environment. However, repeated isolation of *Penicillium* spp. and *Cladosporium* spp. from the marine substrata may suggest their marine affiliation (Jones *et al.*, 2015). Isolation of cultures or detection of sequences from metagenomes with significant abundance and discernable physical pattern in sediments or other substrata may provide clues to the marine nature of a fungus (Nagahama *et al.*, 2001, 2011). DSF-group 1 related to the genera *Metschnikowia* and *Candida* in the Ascomycota was originally identified by sequences of the ITS and 28S rDNA from a few deep-sea sediment samples off the Japanese coast (Nagano *et al.*, 2010), and it was also later identified by ITS clone libraries in sediment samples from other locations of the Pacific Ocean (Xu *et al.*, 2014). Another example is the Cryptomycota which was originally described as a group of 18S rDNA sequences named LKM11 (van Hannen *et al.*, 1999). Members of the Cryptomycota are present in a wide range of marine environments: marine anoxic sediments (Dawson and Pace, 2002), deep-sea sediments (Nagano *et al.*, 2010), deep-sea methane cold-seep sediments (Nagahama *et al.*, 2011) and the marine upper water column (Livermore and Mattes, 2013; Richards *et al.*, 2015), although it is also present in freshwater and terrestrial environments (Jones *et al.*, 2011). Recently, Stern *et al.* (2015) found the Cryptomycota to be abundant in open water samples in the English Channel using 18S rDNA 454-sequencing. If molecular studies tend to indicate the occurrence of many phylotypes representing mainly basal fungal lineages (Cryptomycota and Chytridiomycota), deep-sea fungal communities appear dominated by higher fungal lineages. Some of them are endemic, such as the recently described *Candida oceani* (Burgaud *et al.*, 2011) or *Rhodotorula pacifica* (Nagahama *et al.*, 2006) isolated from deep-sea hydrothermal vents or the deep sunken wood-associated *Alisea longicolla* (Fig. 2A) and *Oceanitis scuticella* (Fig. 2B) (Dupont *et al.*, 2009). However, a large fraction of the fungal sequences were from ubiquitous ascomycetes and basidiomycetes. What proportions of these sequences were amplified from active mycelium versus from a dormant spore bank will require further study.

Recently, one record-depth sediment core, representing a distance of a few meters to almost 2000 m below the seafloor was extensively examined for culturable fungal communities and led to the isolation of many well-known terrestrial fungi (Rédou *et al.*, 2015). However, ecophysiological analyses indicated a shift from terrestrially-adapted to marine-adapted lifestyles along the core for some fungal species. Such results indicate the occurrence of non-marine species in the uppermost layers of sediment and endemic or adapted strains at deeper layers. Some terrestrial fungi could conceivably adapt to deep-sea sediment conditions, responding to different physical and chemical stressors (salinity, temperature, pressure), while some might simply be microbial zombies (Rédou *et al.*, 2015).

Filamentous fungi isolated from the deep-sea were shown to be able to grow at high pressure, *i.e.* 100 bar (10 MPa)/10 or 30 °C (Raghukumar and Raghukumar, 1998). Deep-sea yeasts, especially basidiomycetous yeasts, displayed growth at even higher pressure, up to 60 MPa (Lorenz and Molitoris, 1997; Burgaud *et al.*, 2015). Similarly, terrestrial fungi were shown to grow at 100–200 bar (20 MPa)/5 or 30 °C; some showed comparative growth with deep-sea-derived isolates (Damare *et al.*, 2006). Manohar *et al.* (2015) studied the denitrification activity of fungi (isolated from sea water and sediment samples 500–1100 m deep at the oxygen minimal zones of the Arabian Sea) under simulated deep-sea conditions (anoxic, 100 bar, 10 °C) and found that selected fungi were capable of nitrate reduction, as was the control terrestrial isolate. Spore germination, on the other hand, did not occur for a terrestrial isolate of *Aspergillus terreus* while 66 % of spores germinated for the deep-sea isolate of *A. terreus* under 200 bar/30 °C (Damare *et al.*, 2006). A further increase in pressure from 200 to 500 bar/30 °C was shown to cause a decrease in spore germination for some unidentified deep-sea filamentous fungi (Singh *et al.*, 2010). These studies suggest that fungi isolated from deep marine habitats (autochthonous and allochthonous) can grow under simulated deep-sea conditions (high pressure) and they may participate in nutrient turnover.

Many asexual fungi have been rejected as marine species (Kohlmeyer and Volkmann-Kohlmeyer, 2003) as they are common in terrestrial habitats; however, they are often isolated from seawater, diseased marine animals or marine sediments. For example: *Aspergillus sydowii*, a well-known terrestrial fungus, has frequently been isolated from diseased sea fans (Geiser *et al.*, 1998; Nieves-Rivera, 2002). In a study examining the fungal bloom in eastern Australian coastal waters after a dust storm, *A. sydowii* was also found to be the dominant fungus, forming masses of spores and mycelia on the sea surface (Hayashi *et al.*, 2016). A marine-derived dust storm isolate of *A. sydowii* shared a profile of major metabolites (including sydonic acid, a signature metabolite of *A. sydowii*) with a few terrestrial isolates and a pathogenic isolate from Florida, USA, although they showed differences in their co-metabolite profile. However, extracts of the marine-derived dust storm isolate at a concentration of 0.3 mg exerted a stronger adverse effect on the photophysiological performance of the coral reef dinoflagellate endosymbiont *Symbiodinium* than one of the terrestrial isolates. *Fusarium oxysporum*, another well-known terrestrial fungus, was revealed as a pathogen of crustaceans (Khoa and Hatai, 2005). Thus, it seems that these fungi have some capacity to colonize and persist in marine animals. Similarly, sequence analysis of

Please cite this article in press as: Pang, K.-L., et al., 'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition, Fungal Biology Reviews (2016), http://dx.doi.org/10.1016/j.fbr.2016.08.001

the ITS (including the 5.8S rRNA) and intron 3 of the β-tubulin genes showed the monophyly of a 4-clade group, encompassing *Emericellopsis*, *Stanjemonium* and some marine-derived *Acremonium* species (Zuccaro *et al.*, 2004). One clade, distinct from terrestrial isolates, contained isolates originating from marine sources and saline lakes. Such examples indicate that some lineages of terrestrial fungi have the capacity to colonize the marine environment, highlighting the limitation of using the term 'facultative marine fungi' (Kohlmeyer and Kohlmeyer, 1979). This is supported by the study of Kumar *et al.* (2015) which postulated that the sponge-associated fungus *Scopulariopsis brevicaulis* originated from the terrestrial soil environment based on a comparative genome analysis; a plethora of genes related to cellulose breakdown and an over representation of genes related to uptake/transport of small charged solutes and metabolites were indeed characterized in the genome.

Molecular biology has greatly advanced our knowledge of the ecology and diversity of marine fungi. Sequencing of the fungal barcoding gene, *i.e.* the internal transcribed spacer region (ITS) of the rDNA cluster, for the identification of non-sporulating fungi has helped to assess marine fungal diversity. Rämä *et al.* (2014) isolated fungi from washed-up marine logs which were identified using ITS sequencing. Ascomycota was dominant on the wood while fungi affiliated with the Basidiomycota, Mucoromycotina and Chytridiomycota were also isolated. *Tolypocladium cylindrosporum* was one of most common species in the study and probably represents a marine species, although it is not recognized as marine in the most recent treatise (Jones *et al.*, 2015). Using pyrosequencing of 28S rDNA amplicons obtained from direct nucleic acid extraction of *Acropora hyacinthus* coral colonies, 11 kinds of fungi, spanning two phyla and four classes, were found in 90 % of the coral colonies, and four of these were found in all samples. These fungi included an unknown species in the Malasseziales (where the type species is yeast-like fungus, generally associated with sebaceous glands of mammalian hosts), a group of black yeast-like fungi related to *Hortaea werneckii*, characteristic of high salt environments and occasionally form rashes in human hosts (Petrovic *et al.*, 2002), and a sordariomycete species closely related to *Lindra* (species undetermined), a genus associated with marine algae and wood. These fungi were thought to be the likeliest candidates for an ecologically significant association and/or coevolution with the *A. hyacinthus* colonies. Arfi *et al.* (2012) investigated the diversity of fungi on aerial and intertidal portions of two mangrove trees *Avicennia marina* and *Rhizophora stylosa* using ITS and partial 18S rDNA pyrosequencing and found distinct patterns of taxonomic diversity; for instance, the Sordariomycetes showed preferential distribution in submerged samples. Comparative metagenomics analyses of samples spanning terrestrial to fully submerged gradients should help to resolve what components belong to truly marine fungi.

Detection of fungal gene expression in the substratum using RT-PCR and metatranscriptomics is another way to evaluate the activity of marine fungi. Edgcomb *et al.* (2011) and Rédou *et al.* (2014) studied deep subseafloor sediment core samples of the Peru Margin, the Peru Trench and the Canterbury Basin using sequencing of cDNA clone library analysis; basidiomycetes in the genera *Cryptococcus*, *Trichosporon* and *Malassezia* were dominant, suggesting their active role in such environments. Direct sequencing of V4 18S rRNA reverse-transcripts using the 454 platform also revealed the active role of *Cryptococcus* and *Trichosporon* in Peru Margin, together with the genera *Mycena* and *Rhodotorula* (Orsi *et al.*, 2013). Burgaud *et al.* (2013), also using cDNA clone library analysis, mapped the diversity of fungi in sediment at three stations along the Delaware River estuary and bay and found active fungal community structure transitioned from the freshwater station (*Preussia*, *Phoma*, *Westerdykella*, *Eremodothis*) to the more saline stations (*Penicillium*, *Thysanophora*, *Aspergillus*). Studies like these can demonstrate the growth of fungi in marine substrata, and will be required before many ubiquitous species are generally accepted as being facultative marine by the mycological community.

Comparative genomics can directly address the question of differences in physiological adaptations and secondary metabolism between terrestrial and marine fungi. The genomes and transcriptomes of three halophilic fungi, *Eurotium rubrum*, *Hortaea werneckii*, and *Wallemia ichthyophaga*, indicate that differentially expressed genes encoding ion and metabolite transporters are involved in halotolerance (Lenassi *et al.*, 2013; Zajc *et al.*, 2013; Kis-Papo *et al.*, 2014). Similar to halotolerant bacteria, these fungi are rich in genes that encode for proteins with a significantly higher proportion of acidic amino acid residues. However, the three fungi also use different strategies for osmoregulation. In *E. rubrum* isolated from the Dead Sea, genes related to stress response (A-/B-barrel proteins, catalases) are enriched in the genome and transcripts related to compatible solute synthesis (*e.g.*, glycerol-3-phosphate dehydrogenase) and cell wall integrity (beta-glucan biosynthesis, chitin binding) were up-regulated in response to increase in salinity (Kis-Papo *et al.*, 2014). The saltern fungus *W. ichthyophaga* has genes coding for hydrophobins and polyol synthesis in the genome, both of which have key functions in osmoregulation while high salinity triggered higher expression of enzyme in lipid degradation and a stress protein (Zajc *et al.*, 2013). Compared with the terrestrial *Wallemia sebi*, *W. ichthyophaga* has an expansion of proteins related to DNA processing and damage (Zajc *et al.*, 2013). Genome duplication in *H. werneckii* may be an adaptation to salt stress (Lenassi *et al.*, 2013).

Comparative genome/transcriptomic analysis of marine and terrestrial/freshwater isolates of the same species of a fungus should be able to determine if their genomic structure varies with origin and how their transcriptomic composition responds when grown in their respective salinities. With the available data of halophilic fungi, their genome characteristics include: (1) proteins with a higher proportion of acidic amino acids, (2) enrichment of genes related to stress response proteins, ion/metabolite transporters, hydrophobins (as in *W. ichthyophaga*), polyols biosynthesis (including HOG pathway), and (3) genome duplication (as in *H. werneckii*) (Lenassi *et al.*, 2013; Zajc *et al.*, 2013; Kis-Papo *et al.*, 2014). Some of these genes were highly expressed when grown in high salinity conditions. In a study investigating the transcriptomes of the marine fungus *Corollospora maritima* (Fig. 2F) grown in both freshwater and seawater media, genes related to cell wall modification and biosynthesis, sugar or amino acid transmembrane transporters, ion channels,

Please cite this article in press as: Pang, K.-L., et al., 'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition, Fungal Biology Reviews (2016), http://dx.doi.org/10.1016/j.fbr.2016.08.001

transcription factors, endoplasmic reticulum transmembrane protein MPS, a protein with ligase activity and a choline sulfatase family protein were up-regulated in the seawater medium (Velez *et al.*, 2015). More detailed identification of gene composition and responses are needed to test the hypothesis that "marine-derived" strains differ from terrestrial strains in their genetic makeup and gene expression. Such experiments are also an important step and may hold vital clues as to the genes that are specifically expressed in a marine fungus. Such analyses, coupled with comparative metagenomic and metatranscriptomic data sets representing the uncultured component of fungal communities, may highlight specific markers of fungal adaptation to marine habitats in order to verify the marine nature of a fungus detected in the marine environment.

At the time of writing this report, the genome sequences and putatively classified proteomes of four marine-exclusive fungi, *Verruculina enalia*, *Torpedospora radiata* (Fig. 2G), *Lindra thalassiae*, and *Corollospora maritima*, are available at the Joint Genome Institute (http://genome.jgi.doe.gov/programs/fungi/index.jsf). Although, restrictions on publishing the primary investigators' results prevent us from presenting a complete analysis of their secondary metabolite encoding capacity, a basic analysis of their assembled scaffolds with AntiSmash indicates that these fungi have an abundance of recognizable secondary metabolite gene clusters (Weber *et al.*, 2015). Identification of non-ribosomal peptide synthetase (NRPS) genes, polyketide synthase (PKS) genes and other genes (such as terpene-encoding genes) in the genome, together with RNA-seq data confirming their expression, evidence the molecular basis for the production of bioactive secondary metabolites. Whole genomic sequencing and transcriptome analysis of *S. brevicaulis* isolated from a sponge have revealed the likely genes/gene clusters responsible for the production of the anticancerous scopularides and other metabolites, including melanin and stilbenes (Kumar *et al.*, 2015). The biosynthetic pathway for the production of scopularide A (Fig. 1E) was proposed to involve a nonribosomal peptide synthetase (NRPS1), a polyketide synthase (PKS2), a CoA ligase, an acyltransferase, and a transcription factor based on the genome annotation of *S. brevicaulis* (Lukassen *et al.*, 2015).

Trichoderma spp. produce long-sequence peptaibols such as longibrachins and trichokonins (20-residue peptaibols). Poirier *et al.* (2007) detected these peptaibols in sediment samples (5.2±2.1 ng/g of sediment) collected at Fier d'Ars along the French Altantic coast by reverse phase liquid chromatography (LC)/electrospray ionization-ion trap-mass spectrometry (ESI-IT-MS) analysis. This *in situ* detection of secondary metabolites suggests active fungal growth in the sediment and strongly supports the idea that metabolomics can be useful to reveal the marine nature of fungi isolated from the marine environment.

6. Conclusions and recommendations – new definition?

With thousands of names of marine and marine-derived fungi in the literature, Jones *et al.* (2015) recognised a total of 1112 species of marine fungi which were mainly collected or isolated from plant materials and algae; many so-called 'marine-derived' or 'facultative marine' fungi were also included in the treatise. Their consideration may represent a step forward towards recognizing whether these fungi play an active ecological role in marine environments (Jones *et al.*, 2015); as for example, do they contribute to biogeochemical processes? Jones *et al.* (2015) identified 129 families and 65 orders of fungi with marine taxa, and many of these lineages were predominantly marine, such as taxa in the Halosphaeriaceae, Lulworthiales, Torpedosporales, and others. Recognition of new isolates or sequences from omic-based approaches with phylogenetic affinity with these groups may suggest these fungi have a marine origin. Arriving at a definition that will be acceptable to all mycologists will always be difficult as so many parameters have to be taken into consideration, as outlined above. A broad definition of a marine fungus is proposed as follows 'any fungus that is recovered repeatedly from marine habitats because: 1) it is able to grow and/or sporulate (on substrata) in marine environments; 2) it forms symbiotic relationships with other marine organisms; or 3) it is shown to adapt and evolve at the genetic level or be metabolically active in marine environments'.

Acknowledgments

Ka-Lai Pang thanks the president of National Taiwan Ocean University, Prof. Ching-Fong Chang, for a special fund to attend the workshop held in Charlottetown, Canada in 2014 where the idea of this article was discussed. Gareth Jones acknowledges support by the International Research Group Program (IRG-14-27), Deanship of Scientific Research, King Saud University, Saudi Arabia. Gerald Bills received support from the University of Texas Health Science Center at Houston new faculty start-up funds and the Kay and Ben Fortson Endowment. Gaëtan Burgaud acknowledges support from the European Union's Seventh Framework Programme (FP7/2007-2013) under grant agreement no 311975.

REFERENCES

Abdel-Wahab, M.A., El-Sharouney, H.M., 2002. Ecology of subtropical mangrove fungi with emphasis on *Kandelia candel* mycota. In: Hyde, K.D. (Ed.), Fungi in Marine Environments. Fungal Diversity Press, Hong Kong, pp. 247–265.

Abraham, E.P., Newton, G.G.F., 1961. The structure of cephalosporin C. Biochem. J. 79, 377–393.

Alderman, D.J., Jones, E.B.G., 1971. Shell Disease of Oysters, Fishery Investigation, London Ser. II, 8, pp. 1–19.

Al-Nasrawi, H.G., Hughes, A.R., 2012. Fungal diversity associated with salt marsh plants *Spartina alterniflora* and *Juncus roemerianus* in Florida. Jordan J. Biol. Sci. 5, 247–254.

An, C.Y., Li, X.M., Li, C.S., Gao, S.S., Shang, Z., Wang, B.G., 2013. Triazoles and other n-containing metabolites from the marine-derived endophytic fungus *Penicillium chrysogenum* EN-118. Helv. Chim. Acta 96, 682–687.

Ananda, K., Sridhar, K.R., 2002. Diversity of endophytic fungi in the roots of mangrove species on the west coast of India. Can. J. Microbiol. 48, 871–878.

Arfi, Y., Buée, M., Marchand, C., Levasseur, A., Record, E., 2012. Multiple markers pyrosequencing reveals highly diverse and host-specific fungal communities on the mangrove trees *Avicennia marina* and *Rhizophora stylosa*. FEMS Microbiol. Ecol. 79, 433–444.
Barata, M., 2002. Fungi on the halophyte *Spartina maritima* in salt marshes. In: Hyde, K.D. (Ed.), Fungi in Marine Environments. Fungal Diversity Press, Hong Kong, pp. 179–193.
Barghoorn, E.S., Linder, D.H., 1944. Marine fungi: their taxonomy and biology. Farlowia 1, 395–467.
Bérdy, J., 2012. Thoughts and facts about antibiotics: where we are now and where we are heading. J. Antibiot. 65, 385–395.
Binder, M., Hibbett, D.S., Wang, Z., Farnham, W.F., 2006. Evolutionary relationships of *Mycaureola dilseae* (Agaricales), a basidiomycetes pathogen of a subtidal Rhodophyte. Am. J. Bot. 93, 547–556.
Blunt, J.W., Copp, B.R., Keyzers, R.A., Munroa, M.H.G., Prinsep, M.R., 2013. Marine natural products. Nat. Prod. Rep. 30, 237–323.
Booth, T., Kenkel, N., 1986. Ecological studies of lignicolous marine fungi: a distribution model based on ordination and classification. In: Moss, S.T. (Ed.), The Biology of Marine Fungi. Cambridge University Press, Cambridge, pp. 297–310.
Burgaud, G., Arzur, D., Sampaio, J.P., Barbier, G., 2011. *Candida oceani* sp. nov., a novel yeast isolated from a Mid-Atlantic Ridge hydrothermal vent (−2300 meters). Antonie Van Leeuwenhoek 100, 75–82.
Burgaud, G., Hué, N.T.M., Arzur, D., Coton, M., Perrier-Cornet, J.M., Jebbar, M., Barbier, G., 2015. Effects of hydrostatic pressure on yeasts isolated from deep-sea hydrothermal vents. Res. Microbiol. 166, 700–709.
Burgaud, G., Woehlke, S., Rédou, V., Orsi, W., Beaudoin, D., Barbier, G., Biddle, J.F., Edgcomb, V.P., 2013. Deciphering the presence and activity of fungal communities in marine sediments using a model estuarine system. Aquat. Microb. Ecol. 70, 45–62.
Burton, H.S., Abraham, E.P., 1951. Isolation of antibiotics from a species of *Cephalosporium*. Cephalosporins P1, P2, P3, P4 and P5. Biochem. J. 50, 168–174.
Calado, M.D.L., Barata, M., 2012. Salt marsh fungi. In: Jones, E.B.G., Pang, K.L. (Eds.), Marine Fungi and Fungal-Like Organisms. De Gruyter, Berlin, pp. 345–381.
Calado, M.D.L., Carvalho, L., Pang, K.L., Barata, M., 2015. Diversity and ecological characterization of sporulating higher filamentous marine fungi associated with *Spartina maritima* (Curtis) Fernald in two Portuguese salt marshes. Microb. Ecol. 70, 612–633.
Chaeprasert, S., Piapukiew, J., Whalley, A.J.S., Sihanonth, P., 2010. Endophytic fungi from mangrove plant species of Thailand: their antimicrobial and anticancer potentials. Bot. Mar. 53, 555–564.
Clipson, N.J.W., Jennings, D.H., 1990a. *Dendryphiella salina* and *Debaryomyces hansenii*: models for ecophysiological adaptation to salinity by fungi that grow in the sea. Can. J. Bot. 113, 2097–2105.
Clipson, N.J.W., Jennings, D.H., 1990b. The role of potassium and sodium in the generation of the osmotic potential of the marine fungus *Dendryphiella salina*. Mycol. Res. 94, 1017–1033.
Commerford, J.G., Spencer-Philips, P.T.H., Jennings, D.H., 1985. Membrane-bound ATPase activity, properties of which are altered by growth in saline conditions, isolated from the marine yeast *Debaryomyces hansenii*. Trans. Br. Mycol. Soc. 85, 431–438.
Damare, S., Raghukumar, C., Raghukumar, S., 2006. Fungi in deep-sea sediments of the Central Indian Basin. Deep-Sea Res. I 53, 14–27.
Davies, J.M., Brownlee, C., Jennings, D.H., 1990. Measurement of intracellular pH in fungal hyphae using BCECF and digital imaging microscopy: evidence for a primary proton pump in the plasma-lemma of a marine fungus. J. Cell Sci. 96, 731–736.
Dawson, S.C., Pace, N.R., 2002. Novel kingdom level eukaryotic diversity in anoxic environments. PNAS 99, 8324–8329.
Dupont, J., Magnin, S., Rousseau, F., Zbinden, M., Frebourg, G., Samadi, S., Richer de Forges, B., Jones, E.B.G., 2009. Molecular and ultrastructural characterization of two ascomycetes found on sunken wood off Vanuatu Islands in the deep Pacific Ocean. Mycol. Res. 112, 1351–1364.
Ebada, S.S., Proksch, P., 2015. Marine-derived fungal metabolites. In: Kim, S.K. (Ed.), Handbook of Marine Biotechnology. Springer-Verlag, Berlin Heidelberg, pp. 759–788.
Edgcomb, V.P., Beaudoin, D., Gast, R., Biddle, J.F., Teske, A., 2011. Marine subsurface eukaryotes: the fungal majority. Environ. Microbiol. 13, 172–183.
Fan, K.W., Vrijmoed, L.L.P., Jones, E.B.G., 2002. Physiological studies of subtropical mangrove thraustochytrids. Bot. Mar. 45, 50–57.
Fröhlich-Nowoisky, J., Burrows, S.M., Xie, Z., Engling, G., Solomon, P.A., Fraser, M.P., Mayol-Bracero, O.L., Artaxo, P., Begerow, D., Conrad, R., Andreae, M.O., Despŕes, V.R., Pöschl, U., 2012. Biogeography in the air: fungal diversity over land and oceans. Biogeosciences 9, 1125–1136.
Geiser, D.M., Taylor, J.W., Ritchie, K.B., Smith, G.W., 1998. Cause of sea fan death in the West Indies. Nature 394, 137–138.
Gray, W.D., Pinto, P.V.C., Pathak, S.G., 1963. Growth of fungi in sea water medium. Appl. Microbiol. 11, 510–505.
Hamilton-Miller, J.M.T., 2000. Sir Edward Abraham's contribution to the development of the cephalosporins: a reassessment. Int. J. Antimicrob. Agents 15, 179–184.
Harrison, J.L., Jones, E.B.G., 1975. The effects of salinity on sexual and asexual sporulation of members of the Saprolegniaceae. Trans. Br. Mycol. Soc. 65, 389–394.
Harrison, J.L., Jones, E.B.G., 1974. Patterns of salinity tolerance displayed by the lower fungi. Veroff Inst Meeresforschung Bremerhaven (Suppl. 5), 197–220.
Hatai, K., 2012. Disease of fish and shellfish caused by marine fungi. In: Raghukumar, S. (Ed.), Biology of Marine Fungi. Springer-Verlag, Berlin, pp. 15–52.
Hayashi, A., Crombie, A., Lacey, E., Richardson, A.J., Vuong, D., Piggott, A.M., Hallegraeff, G., 2016. *Aspergillus sydowii* marine fungal bloom in Australian coastal waters, its metabolites and potential impact on *Symbiodinium* dinoflagellates. Mar. Drugs 14, 59. http://dx.doi.org/10.3390/md14030059.
Höller, U., Wright, A.D., Matthee, G.F., Konig, G.M., Draeger, S., Aust, H.J., Schulz, B., 2000. Fungi from marine sponges: diversity, biological activity and secondary metabolites. Mycol. Res. 104, 1354–1365.
Hyde, K.D., Jones, E.B.G., Liu, J.K., Ariyawansha, H., Boehm, E., Boonmee, S., et al., 2013. Families of Dothideomycetes. Fungal Divers. 63, 1–313.
Jennings, D.H., Garrill, A., 2000. Physiological studies. In: Hyde, K.D., Pointing, S.P. (Eds.), Marine Mycology – A Practical Approach. Fungal Diversity Press, Hong Kong, pp. 92–113.
Jennings, D.H., 1986. Fungal growth in the sea. In: Moss, S.T. (Ed.), The Biology of Marine Fungi. Cambridge University Press, Cambridge, pp. 1–10.
Jennings, D.H., 1983. Some aspects of the physiology and biochemistry of marine fungi. Biol. Rev. 58, 423–459.
Jensen, P.R., Fenical, W., 2002. Secondary metabolites from marine fungi. In: Hyde, K.D. (Ed.), Fungi in Marine Environments. Fungal Diversity Press, Hong Kong, pp. 293–315.
Johnson, T.W., Sparrow, F.K., 1961. Fungi in Oceans and Estuaries. J. Cramer, Germany.
Jones, E.B.G., Jennings, D.H., 1965. The effect of cations on the growth of fungi. New Phytol. 64, 86–100.

Please cite this article in press as: Pang, K.-L., et al., 'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition, Fungal Biology Reviews (2016), http://dx.doi.org/10.1016/j.fbr.2016.08.001

Jones, E.B.G., Harrison, J.L., 1976. Physiology of marine phycomycetes. In: Jones, E.B.G. (Ed.), Recent Advances in Aquatic Mycology. Elek, London, pp. 260–278.
Jones, E.B.G., Byrne, P.J., 1976. Physiology of the higher marine fungi. In: Jones, E.B.G. (Ed.), Recent Advances in Aquatic Mycology. Elek, London, pp. 135–176.
Jones, E.B.G., Moss, S.T., 1978. Ascospore appendages of marine ascomycetes: an evaluation of appendages as taxonomic criteria. Mar. Biol. 49, 11–26.
Jones, E.B.G., 2000. Marine fungi: some factors influencing biodiversity. Fungal Divers. 4, 53–73.
Jones, E.B.G., 2011. Are there more marine fungi to be described? Bot. Mar. 54, 343–354.
Jones, E.B.G., Sakayaroj, J., Suetrong, S., Somrithipol, S., Pang, K.L., 2009. Classification of marine Ascomycota, anamorphic taxa and Basidiomycota. Fungal Divers. 35, 1–187.
Jones, E.B.G., 1976. Recent Advances in Aquatic Mycology. Elek, London.
Jones, E.B.G., Suetrong, S., Bahkali, A.H., Abdel-Wahab, M.A., Boekhout, T., Pang, K.L., 2015. Classification of marine Ascomycota, Basidiomycota, Blastocladiomycota and Chytridiomycota. Fungal Divers. 73, 1–72.
Jones, E.B.G., 1995. Ultrastructure and taxonomy of the aquatic ascomycetous order Halosphaeriales. Can. J. Bot. 73, S790–S801.
Jones, E.B.G., Jennings, D.H., 1964. The effect of salinity on the growth of marine fungi in comparison with non-marine species. Trans. Br. Mycol. Soc. 47, 619–625.
Jones, M.D.M., Forn, I., Gadelha, C., Egan, M.J., Bass, D., Massana, R., Richards, T.A., 2011. Discovery of novel intermediate forms redefines the fungal tree of life. Nature 474, 200–205.
Khoa, L.V., Hatai, K., 2005. First case of *Fusarium oxysporum* infection in cultured kuruma prawn *Penaeus japonicas* in Japan. Fish. Pathol. 40, 195–196.
Kis-Papo, T., Oren, A., Wasser, S.P., Nevo, E., 2003. Survival of filamentous fungi in hypersaline Dead Sea water. Microb. Ecol. 45, 183–190.
Kis-Papo, T., Weig, A.R., Riley, R., Peršoh, D., Salamov, A., Sun, H., Lipzen, A., Wasser, S.P., Rambold, G., Grigoriev, I.V., Nevo, E., 2014. Genomic adaptations of the halophilic Dead Sea filamentous fungus *Eurotium rubrum*. Nat. Commun. 5, 3745.
Kohlmeyer, J., Volkmann-Kohlmeyer, B., 2000. Fungi on *Juncus roemerianus* 14. Three new coelomycetes, including *Floricola*, anam.-gen. nov. Bot. Mar. 43, 385–392.
Kohlmeyer, J., Volkmannn-Kohlmeyer, B., 2003. Marine Ascomycetes from algae and animal hosts. Bot. Mar. 46, 285–306.
Kohlmeyer, J., Kohlmeyer, E., 1979. Marine Mycology – The Higher Fungi. Academic Press, New York.
Kohlmeyer, J., Volkmann-Kohlmeyer, B., Eriksson, O.E., 1995. Fungi on *Juncus roemarianus* 3. New ascomycetes. Bot. Mar. 38, 175–186.
Kong, F.D., Wang, Y., Liu, P.P., Dong, T.H., Zhu, W.M., 2014. Thiodiketopiperazines from the marine-derived fungus *Phoma* sp. OUCMDZ-1847. J. Nat. Prod. 77, 132–137.
Kumar, A., Henrissat, B., Arvas, M., Syed, M.F., Thieme, N., Benz, J.P., Sørensen, J.L., Record, E., Pöggeler, S., Kempken, F., 2015. De novo assembly and genome analyses of the marine-derived *Scopulariopsis brevicaulis* strain LF580 unravels lifestyle traits and anticancerous scopularide biosynthetic gene cluster. PLoS One 10, e0140398.
Kutty, S.N., Philip, R., 2008. Marine yeasts – a review. Yeast 25, 465–483.
Leaño, E.M., Vrijmoed, L.L.P., Jones, E.B.G., 1998. Physiological studies on *Halophytophthora vesicula* (Staminipilous fungi) isolated from fallen mangrove leaves from Mai Po, Hong Kong. Bot. Mar. 41, 411–419.
Leaño, E.M., Jones, E.B.G., Vrijmoed, L.L.P., 2000. Why are *Halophytophthora* species well adapted to mangrove habitats? Fungal Divers. 5, 131–151.
Lenassi, M., Gostinčar, C., Jackman, S., Turk, M., Sadowski, I., Nislow, C., Jones, S., Birol, I., Cimerman, N.G., Plemenitaš, A., 2013. Whole genome duplication and enrichment of metal cation transporters revealed by de novo genome sequencing of extremely halotolerant black yeast *Hortaea werneckii*. PLoS One 8, e71328.
Livermore, J.A., Mattes, T.E., 2013. Phylogenetic detection of novel Cryptomycota in an Iowa (United States) aquifer and from previously collected marine and freshwater targeted high-throughput sequencing sets. Environ. Microbiol. 15, 2333–2341.
Lorenz, R., Molitoris, H.P., 1997. Cultivation of fungi under simulated deep sea conditions. Mycol. Res. 101, 1355–1365.
Lukassen, M.B., Saei, W., Sondergaard, T.E., Tamminen, A., Kumar, A., Kempken, F., Wiebe, M.G., Sørensen, J.L., 2015. Identification of the scopularide biosynthetic gene cluster in *Scopulariopsis brevicaulis*. Mar. Drugs 13, 4331–4343.
Mahé, S., Rédou, V., Le Calvez, T., Vandenkoornhuyse, P., Burgaud, G., 2014. Fungi in deep-sea environments and metagenomics. In: Martin, F. (Ed.), The Ecological Genomics of Fungi. John Wiley-Blackwell, Ames, Iowa, pp. 325–354.
Manohar, C.S., Menezes, L.D., Ramasamya, K.P., Meena, R.M., 2015. Phylogenetic analyses and nitrate reducing activity of fungal cultures isolated from the permanent, oceanic oxygen minimum zone of the Arabian Sea. Can. J. Microbiol. 61, 217–226.
Miller, J.D., 2000. Screening for secondary metabolites. In: Hyde, K.D. (Ed.), Marine Mycology – A Practical Approach. Fungal Diversity Press, Hong Kong, pp. 158–171.
Mincer, T.J., Jensen, P.R., Kauffman, C.A., Fenical, W., 2002. Widespread and persistent populations of a major new marine actinomycete taxon in ocean sediments. Appl. Environ. Microbiol. 68, 5005–5011.
Mita, M.M., Spear, M.A., Yee, L.K., Mita, A.C., Heath, E.I., Papadopoulos, K.P., Federico, K.C., Reich, S.D., Romero, O., Malburg, L., Pilat, M., Lloyd, G.K., Neuteboom, S.T., Cropp, G., Ashton, E., LoRusso, P.M., 2010. Phase 1 first-in-human trial of the vascular disrupting agent plinabulin (NPI-2358) in patients with solid tumors or lymphomas. Clin. Cancer. Res. 16, 5892–5899.
Nagahama, T., Takahashi, E., Nagano, Y., Abdel-Wahab, M.A., Miyazaki, M., 2011. Molecular evidence that deep-branching fungi are major fungal components in deep-sea methane cold-seep sediments. Environ. Microbiol. 13, 2359–2370.
Nagahama, T., Hamamoto, M., Horikoshi, K., 2006. *Rhodotorula pacifica* sp. nov., a novel yeast species from 702 sediment collected on the deep-sea floor of the north-west Pacific Ocean. Int. J. Syst. Evol. Microbiol. 56, 295–299.
Nagahama, T., Hamamoto, M., Nakase, T., Takami, H., Horikoshi, K., 2001. Distribution and identification of red yeasts in deep-sea environments around the northwest Pacific Ocean. Antonie Van Leeuwenhoek 80, 101–110.
Nagano, Y., Nagahama, T., Hatada, Y., Nunoura, T., Takami, H., Miyazaki, J., Takai, K., Horikoshi, K., 2010. Fungal diversity in deep-sea sediments—the presence of novel fungal groups. Fungal Ecol. 3, 316–325.
Newton, G.G.F., Abraham, E.P., 1954. The degradation, structure and some derivatives of cephalosporin N. Biochem. J. 58, 103–111.
Nieves-Rivera, A.M., 2002. Sea fan aspergillosis. What is it? Inoculum 53, 10–13.
Niu, C.P., Cai, M.H., Zhang, Y.X., Zhou, X.S., 2012. Biosynthetic origin of the carbon skeleton of a novel anti-tumor compound, haloroquinone, from a marine-derived fungus, *Halorosellinia* sp. Biotechnol. Lett. 34, 2119–2124.

Please cite this article in press as: Pang, K.-L., et al., 'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition, Fungal Biology Reviews (2016), http://dx.doi.org/10.1016/j.fbr.2016.08.001

Orsi, W., Biddle, J.F., Edgcomb, V., 2013. Deep sequencing of subseafloor eukaryotic rRNA reveals active fungi across marine subsurface provinces. PLoS One 8, e56335.
Overy, D.P., Bayman, P., Kerr, R.G., Bills, G.F., 2014. An assessment of natural product discovery from marine (*sensu strictu*) and marine-derived fungi. Mycology 5, 145–167.
Pang, K.L., Mitchell, J.I., 2005. Molecular approaches for assessing fungal diversity in marine substrata. Bot. Mar. 48, 332–347.
Pang, K.L., 2002. Systematics of the Halosphaeriales: which morphological characters are important? In: Hyde, K.D. (Ed.), Fungi in Marine Environments. Fungal Diversity Press, Hong Kong, pp. 35–57.
Pang, K.L., Vrijmoed, L.L.P., Goh, T.K., Plaingam, N., Jones, E.B.G., 2008. Fungal endophytes associated with *Kandelia candel* (Rhizophoraceae) in Mai Po Nature Reserve, Hong Kong. Bot. Mar. 51, 171–178.
Pang, K.L., Chow, R.K.K., Chan, C.W., Vrijmoed, L.L.P., 2011. Diversity and physiology of marine lignicolous fungi in Arctic waters: a preliminary account. Polar Res. 30, 1–5.
Petrovic, U., Gunde-Cimerman, N., Plemenitas, A., 2002. Cellular responses to environmental salinity in the halophilic black yeast *Hortaea werneckii*. Mol. Microbiol. 45, 665–672.
Poirier, L., Amiard, J.C., Mondeguer, F., Quiniou, F., Ruiz, N., Pouchus, Y.F., Montagua, M., 2007. Determination of peptaibol trace amounts in marine sediments by liquid chromatography/electrospray ionization-ion trap-mass spectrometry. J. Chromatogr. A 1160, 106–113.
Porter, D., Farnham, W.F., 1986. *Mycaureola edulis*, a marine basidiomycete parasite of the red alga, *Dilsea carnosa*. Trans. Br. Mycol. Soc. 87, 575–582.
Prieto-Davó, A., Fenical, W., Jensen, P.R., 2008. Comparative actinomycete diversity in marine sediments. Aquat. Microb. Ecol. 52, 1–11.
Raghukumar, C., Raghukumar, S., 1998. Barotolerance of fungi isolated from deep-sea sediments of the Indian Ocean. Aquat. Microb. Ecol. 15, 153–163.
Rämä, T., Nordén, J., Davey, M.L., Mathiassen, G.H., Spatafora, J.W., Kauserud, H., 2014. Fungi ahoy! Diversity on marine wooden substrata in the high North. Fungal Ecol. 8, 46–58.
Rateb, M.E., Ebel, R., 2012. Secondary metabolites of fungi from marine habitats. Nat. Prod. Rep. 28, 290–344.
Rédou, V., Ciobanu, M.C., Pachiadaki, M.G., Edgcomb, V., Alain, K., Barbier, G., Burgaud, G., 2014. In-depth analyses of deep subsurface sediments using 454-pyrosequencing reveals a reservoir of buried fungal communities at record-breaking depths. FEMS Microbiol. Ecol. 90, 908–921.
Rédou, V., Navarri, M., Meslet-Cladière, L., Barbier, G., Burgaud, G., 2015. Species richness and adaptation of marine fungi from deep-subseafloor sediments. Appl. Environ. Microbiol. 81, 3571–3583.
Richards, T.A., Leonard, G., Mahé, F., del Campo, J., Romac, S., Jones, M.D.M., Maguire, F., Dunthorn, M., De Vargas, C., Massana, R., Chambouvet, A., 2015. Molecular diversity and distribution of marine fungi across 130 European environmental samples. Proc. R. Soc. B 282, 20152243.
Sadaba, R.B., Vrijmoed, L.L.P., Jones, E.B.G., Hodgkiss, I.J., 1995. Observations on vertical distribution of fungi associated with standing senescent *Acanthus ilicifolius* stems at Mai Po mangrove, Hong Kong. Hydrobiologia 295, 119–126.
Sakayaroj, J., Pang, K.L., Jones, E.B.G., 2011. Multi-gene phylogeny of the Halosphaeriaceae: its ordinal status, relationships between genera and morphological character evolution. Fungal Divers. 46, 87–109.
Silliman, B.R., Newell, S.Y., 2003. Fungal farming in a snail. PNAS 100, 15643–15648.
Singh, P., Raghukumar, C., Verma, P., Shouche, Y., 2010. Phylogenetic diversity of culturable fungi from the deep-sea sediments of the Central Indian Basin and their growth characteristics. Fungal Divers. 40, 89–102.
Spatafora, J.W., Volkmann-Kohlmeyer, B., Kohlmeyer, J., 1998. Independent terrestrial origins of the Halosphaeriales (marine Ascomycota). Am. J. Bot. 85, 1569–1580.
Stanley, S.J., 1992. Observations on the seasonal occurrence of marine endophytic and parasitic fungi. Can. J. Bot. 70, 2089–2096.
Stern, R.F., Picard, K.T., Hamilton, K.M., Walne, A., Tarran, G.A., Mills, D., McQuatters-Gollop, A., Edwards, M., 2015. Novel lineage patterns from an automated water sampler to probe marine microbial biodiversity with ships of opportunity. Progr. Oceanogr. 137, 409–420.
Suetrong, S., Schoch, C.L., Spatafora, J.W., Kohlmeyer, J., Volkmann-Kohlmeyer, B., Sakayaroj, J., Phongpaichit, S., Tanaka, K., Hirayama, K., Jones, E.B.G., 2009. Molecular systematics of the marine Dothideomycetes. Stud. Mycol. 64, 155–173.
Sutherland, G.K., 1916. Marine Fungi Imperfecti. New Phytol. 15, 35–48.
Sutherland, G.K., 1915. New marine fungi on *Pelvetia*. New Phytol. 14, 33–42.
Tomlinson, P.B., 1986. The Botany of Mangroves. Cambridge University Press, Cambridge, UK.
Tresner, H.D., Hayes, J.A., 1971. Sodium chloride tolerance of terrestrial fungi. Appl. Microbiol. 22, 210–213.
Tubaki, K., 1969. Studies on the Japanese marine fungi lignincolous group (III), algicolous group and a general consideration. Ann. Rep. Inst. Fermentation, Osaka 4, 12–41.
van Dover, C.L., Ward, M.E., Scott, J.L., Underdown, J., Anderson, B., Gustafson, C., Whalen, M., Carnegie, R., 2007. A fungal epizootic in mussels at a deep-sea hydrothermal vent. Mar. Ecol. 28, 54–62.
van Hannen, E.J., Mooij, W.M., van Agterveld, M.P., Gons, H.J., Laanbroek, H.J., 1999. Detritus-dependent development of the microbial community in an experimental system: qualitative analysis by denaturing gradient gel electrophoresis. Appl. Environ. Microbiol. 65, 2478–2484.
Velez, P., Alejandri-Ramírez, N.D., González, M.C., Estrada, K.J., Sanchez-Flores, A., Dinkova, T.D., 2015. Comparative transcriptome analysis of the cosmopolitan marine fungus *Corollospora maritima* under two physiological conditions. G3:Genes Genomes Genetics 5, 1806–1814.
Wang, X., Mao, Z.G., Song, B.B., Chen, C.H., Xiao, W.W., Hu, B., Wang, J.W., Jiang, X.B., Zhu, Y.H., Wang, H.J., 2013. Advances in the study of the structures and bioactivities of metabolites isolated from mangrove-derived fungi in the South China Sea. Mar. Drugs 11, 3601–3616.
Weber, T., Blin, K., Duddela, S., Krug, D., Kim, H.U., Bruccoleri, R., Lee, S.Y., Fischbach, M.A., Müller, R., Wohlleben, W., Breitling, R., Takano, E., Medema, M.H., 2015. AntiSMASH 3.0-A comprehensive resource for the genome mining of biosynthetic gene clusters. Nucl. Acid Res. 43, W237–W243.
Xu, W., Pang, K.L., Luo, Z.H., 2014. High fungal diversity and abundance recovered in the deep-sea sediments of the Pacific Ocean. Microb. Ecol. 68, 688–698.
Zajc, J., Liu, Y., Dai, W., Yang, Z., Hu, J., Gostincar, C., Gunde-Cimerman, N., 2013. Genome and transcriptome sequencing of the halophilic fungus *Wallemia ichthyophaga*: haloadaptations present and absent. BMC Genomics 14, 617.
Zeng, Y.B., Wang, H., Zuo, W.J., Zheng, B., Yang, T., Dai, H.F., Mei, W.L., 2012. A fatty acid glycoside from a marine-derived fungus isolated from mangrove plant *Scyphiphora hydrophyllacea*. Mar. Drugs 10, 598–603.

Please cite this article in press as: Pang, K.-L., et al., 'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition, Fungal Biology Reviews (2016), http://dx.doi.org/10.1016/j.fbr.2016.08.001

Zhou, W.Q., Cai, M.H., Zhou, J.S., Jiang, T., Zhou, J., Wang, M.X., Zhou, X.S., Zhang, Y.X., 2013. Nutrition and bioprocess development for efficient biosynthesis of an antitumor compound from marine-derived fungus. J. Ind. Microbiol. Biotechnol. 40, 1131–1142.

Ziemert, N., Lechner, A., Wietz, M., Millañ-Aguiñaga, N., Chavarria, K.L., Jensen, P.R., 2014. Diversity and evolution of secondary metabolism in the marine actinomycete genus *Salinispora*. PNAS 111, E1130–E1139.

Zuccaro, A., Summerbell, R.C., Gams, W., Schroers, H.J., Mitchell, J.I., 2004. A new *Acremonium* species associated with *Fucus* spp., and its affinity with a phylogenetically distinct marine *Emericellopsis* clade. Stud. Mycol. 50, 283–297.

Please cite this article in press as: Pang, K.-L., et al., 'Marine fungi' and 'marine-derived fungi' in natural product chemistry research: Toward a new consensual definition, Fungal Biology Reviews (2016), http://dx.doi.org/10.1016/j.fbr.2016.08.001