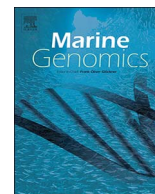




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Method paper

How to boost marine fungal research: A first step towards a multidisciplinary approach by combining molecular fungal ecology and natural products chemistry

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ABSTRACT

Marine fungi have attracted attention in recent years due to increased appreciation of their functional role in ecosystems and as important sources of new natural products. The concomitant development of various “omic” technologies has boosted fungal research in the fields of biodiversity, physiological ecology and natural product biosynthesis. Each of these research areas has its own research agenda, scientific language and quality standards, which have so far hindered an interdisciplinary exchange. Inter- and transdisciplinary interactions are, however, vital for: (i) a detailed understanding of the ecological role of marine fungi, (ii) unlocking their hidden potential for natural product discovery, and (iii) designing access routes for biotechnological production. In this review and opinion paper, we describe the two different “worlds” of marine fungal natural product chemists and marine fungal molecular ecologists. The individual scientific approaches and tools employed are summarised and explained, and enriched with a first common glossary. We propose a strategy to find a multidisciplinary approach towards a comprehensive view on marine fungi and their chemical potential.

1. Introduction

Marine fungi have a broad diversity in terms of species richness, phylogenetic distribution, and their natural products (NPs). Compared to other marine organisms, the diversity of marine fungi and their NPs had been largely neglected and only recent research has started to provide in-depth data on this understudied organism group (Bhadury et al., 2006; Richards et al., 2015; Imhoff, 2016; Rämä et al., 2016; Taylor and Cunliffe, 2016).

Cultivation-dependent and molecular studies demonstrate that marine macroorganisms, such as sponges and algae, are a rich source for fungi (Debbab et al., 2010). In consequence of this recognition, an increasing number of new NPs from marine fungi have recently been characterised and reported. There is no doubt that these organisms produce a large number of interesting secondary metabolites, which often show pharmaceutically relevant bioactivities and may be candidates for the development of new drugs. The last few years have seen an explosion of research interest in marine fungi and their NPs, as reflected in the formation of the MaFNap consortium (<http://mfnpc.vre3.upei.ca/>), a network of research groups with interests in the diversity of marine fungi and investigation of their NPs in the context of drug

discovery). When reviewing these recent developments (Bhadury et al., 2006; Saleem et al., 2007; Imhoff, 2016; Silber et al., 2016), it became obvious that current research has some limitations: The diversity of marine fungi is not adequately represented in investigations on their secondary metabolites; most of the published work on secondary metabolites of marine fungi has focused on just a few genera, mainly *Penicillium*, *Aspergillus*, *Fusarium* and *Cladosporium* (Imhoff, 2016). Although next-generation DNA sequencing (NGS) methods are now standard approaches for the detection of multiple genes of interest (Culligan et al., 2014) and provision of genomewide information is largely employed for several fungi (Grigoriev et al., 2014), genome and genetic data on marine fungi and especially secondary metabolite biosynthesis genes are poorly represented in the current databases.

Another drawback for marine fungal research is that data collected for the single taxa are far from being comprehensive and often not publicly available. However, the data would be of utmost importance for ecological, taxonomic and biotechnological research. Furthermore, many studies use either culture-dependent or culture-independent approaches and available datasets are not interlinked. The availability of data and tools is additionally imbalanced between the two “worlds” of NP research and marine fungal molecular ecology: several tools and

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Box IHow to name a fungal taxon according to the *Code*?

For many situations in the daily work of a fungal researcher, knowledge of nomenclature is essential for producing comparable research results. Examples are the literature research, BLASTn output with several best hits or phylogenetic analysis, where a clade can be comprised by several different named fungal taxa. In all these cases, different taxon names could be the consequence of dual naming rather than standing for different taxa or bad marker gene resolution. Further, the taxon names of the lab's own culture collections should follow the rules of the *International Code of Nomenclature for algae, fungi, and plants* (McNeill et al., 2012) to ensure good communication among scientists. Basic knowledge on the rules of the *Code* is thus critical.

In general, a name must have been validly published and the denomination has to follow the rules of the *Code* to become the correct name. In the case that several names for the same taxon fulfil the demand of being validly published and legitimate, the correct name is the one, which was published earliest (“priority”). However, several exceptions exist. To understand the *Code*, the most important vocabularies should be known:

Basionym:	The original (legitimate and previously published) name on which a new name at new rank is based. This can be a helpful starting point for solving nomenclatural problems.
Conserved name:	(<i>nomen conservandum</i>) A name that has become the correct and legitimate name although it might have been illegitimate or lack priority. Only names on species, genus and family level can become conserved.
Correct name:	The name that has to be used for a taxon in accordance with the rules.
Legitimate name:	A validly published name that is in accordance to the rules (opposite: illegitimate).
Replacement name:	(<i>nomen novum</i>) A name created to replace another scientific name, but only when this other name cannot be used for technical, nomenclatural reasons.
Rejected name:	(<i>nomen rejiciendum</i>) A name ruled out for use. This can be the consequence of a formal action (over a proposal), where the rejection is in favor of a conserved name or it does simply not follow the <i>Code</i> .
Suppressed name:	(<i>nomen utique rejiciendum</i>) A name that has been ruled out for use. Such an outright rejection can be done for names of any rank.
Synonyms:	Validly published names other than the correct name.
Validly published:	The name has correctly been published and the minimal required information on the taxon is provided with the publication.

The *Code* offers different options how to name a fungal taxon. Here, we provide examples of the two most frequently occurring cases:

1. Example: Priority rule

In general, if several validly published names exist for the same taxon and all the names are legitimate, the rule of priority is applied, thus the oldest published name will supersede the other names.

Example: The family *Ophiocordycipitaceae* comprises several genera; among them are *Tolypocladium*, *Chaunopycnis* and *Elaphocordyceps*. *Elaphocordyceps* taxa are mainly described as teleomorphic forms and the few described asexual morphs showed similarity to *Tolypocladium* taxa (Sung et al., 2007). For most of the *Tolypocladium* taxa, no sexual morphs have been identified. However, a high similarity of the conidiogenesis between *Tolypocladium* and the asexually typified genus *Chaunopycnis* was recognised (Gams, 1980). The results of a multiple-locus phylogenetic tree indicated that these three genera form one monophyletic clade (Quandt et al., 2014). As all names were validly published and followed the *Code*, they are synonyms and the rule of priority has to be applied.

The entries of *Mycobank* (Crous et al., 2004) can help to find the correct name (discussion of pros and cons of nomenclatural repositories see section 2.1). Under “summary”, the name and the publication, which introduced the name, is listed. “Remarks” indicate possible changes to the name. The row “synonyms” lists all possible synonyms to the taxon name indicated under “summary”.

Chaunopycnis W. Gams, Persoonia 11 (1): 75 (1979); Remarks: Listed as synonym of *Tolypocladium* in Quandt et al. (2014).

Elaphocordyceps G.H. Sung & Spatafora, Studies in Mycology 57: 36 (2007); Remarks: Listed as synonym of *Tolypocladium* in Quandt et al. (2014).

Tolypocladium W. Gams, Persoonia 6 (2): 185 (1975); Synonyms: *Chaunopycnis* and *Elaphocordyceps*.

Conclusion: *Tolypocladium* is the oldest name among the three validly published and legitimated names. Thus, it has priority over the two other names and taxa have to be named accordingly. The other names have been proposed to become a *nomen utique rejiciendum* (Quandt et al., 2014), a name not to be used any longer. Such an outright rejection is possible for a name at any rank.

2. Example: Conservation over rejection rule

The purpose of conserving a name is “to avoid disadvantageous nomenclatural changes entailed by the strict application of the rules, and especially of the principle of priority [...]” (Art. 14.1) (McNeill et al., 2012). Conservation is possible only for names at the rank of *family*, *genus* or *species*.

Penicillium chrysogenum belongs to the most important penicillin producing filamentous taxa. Phylogenetic analysis showed that its taxonomy can be subdivided by four clades including isolates of other related taxa (Scott et al., 2004) and some of them were identified to be conspecific.

The entries in *Mycobank* indicate the following: *P. chrysogenum* is the conserved name (*nomen conservandum*) and thus, naming has not

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