



## Mycosphere Essay 6: Why is it important to correctly name *Colletotrichum* species?

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### Abstract

*Colletotrichum* is one of the most important plant pathogenic genera worldwide. There have been many studies on this genus, as species are important in many disciplines, especially in plant disease diagnostics. In this paper we discuss the importance of accurately naming *Colletotrichum* species. In most cases we conclude that it is important to know the correct identity of species, as the name is the key to all data for that taxon. The entire knowledge and data on a species relies on it being correctly named. The naming of *Colletotrichum* species have become “mostly fit-for-purpose”, with the use of molecular data. The aim of this contribution is to illustrate the importance of naming *Colletotrichum* species using several essential examples.

**Key words** – agriculture – evolutionary history – nomenclature – plant pathology – species complex – taxonomy

### Introduction

Species of *Colletotrichum* have traditionally been identified based on morphology, host association and more recently, phylogenetic analyses (Shenoy et al. 2007, Than et al. 2008a,b, Cai et al. 2009, Hyde et al. 2009a, b, 2014). Molecular data has allowed us to identify species more precisely with analysis of only a few genes (Hyde et al. 2014). Therefore, we can now relatively easily identify collections of *Colletotrichum* to species level. However, this paper asks the question, how important is it to know a collection of *Colletotrichum* by its species name, or is the genus level adequate? The aim of the present paper is to explore whether we need to name *Colletotrichum* to species level with regard to species identification and diversity, plant pathology and quarantine, human infections, agriculture, bio-control, plant breeding, whole genome sequencing, developing and maintaining knowledge bases, commercial applications and understanding evolutionary history. The importance of names, correct identification and problems due to misidentification, with examples, are discussed here.

### *What are names?*

Names are the foundation by which, information is communicated about an organism (Jayasiri et al. 2015). There are two types of names: common names and scientific names. Common names can vary from place to place and among different languages (Rossman & Palm-Hernández 2008). Therefore they are less precise and of less use. In contrast, scientific names define an organism accurately and are the key to accumulated knowledge, properties and uses of a species (Hawksworth 2015, Jayasiri et al. 2015). Accurately naming a fungus allows us to communicate precisely about this organism. The names allow us to organize and categorize and predict the behaviour or biology of the species, based on the knowledge associated with the name (Hawksworth 2001, Rossman & Palm-Hernández 2008, Jayasiri et al. 2015). Accurate scientific names given to fungi, eradicate any species confusion which may occur if the species is designated different names. Therefore, naming a taxon provides a platform for the organism and eliminates any uncertainty that might occur, if the same species is studied in different countries. When naming a fungus, it is important to deposit a type or a voucher specimen in known herbaria for future study and an ex-type living strain should be deposited in more than one culture collection. Due to various changes in the nomenclatural history, the name of the fungus can change, but the fungus itself remains the same (Minnins 2015). *Colletotrichum* is an asexual morph genus with a *Glomerella* sexual morph. *Colletotrichum* is the most common morph found in the natural environment. The use of *Colletotrichum* is recommended over *Glomerella* as it is the older, as well as the most widely used generic name (Hyde et al. 2014, Maharachchikumbura et al. 2015).

### *Colletotrichum*

The genus *Colletotrichum* was introduced by Corda (1831), with *C. lineola* as the type species. This genus belongs to the family *Glomerellaceae* (Glomerellales, Sordariomycetes) and is the sole member of this family (Réblová et al. 2011, Maharachchikumbura et al. 2015). Species in this genus occupy various lifestyles, ranging from necrotrophy to hemibiotrophy and endophytism (Crouch et al. 2014). Species of this genus are important plant pathogens on economically important crops such as avocado, banana, chilli, grapes, maize, mango, orchids, strawberry, tea and yam in both tropical and temperate regions (Mills et al. 1992, Johnston & Jones 1997, Freeman et al. 2001, Promputtha et al. 2005, 2007, Chung et al. 2006, Than et al. 2008b, Hyde et al. 2009a, b, 2014, Yang et al. 2009, Rojas et al. 2010, Cannon et al. 2012, Sharma et al. 2013, Udayanga et al. 2013, Yan et al. 2015). Several *Colletotrichum* species have been identified as endophytes from asymptomatic healthy angiosperms, conifers, ferns, lichens and grasses (Bussaban et al. 2001, Liu et al. 2007, Manamgoda et al. 2013, Tao et al. 2013, Hyde et al. 2014). Lu et al. (2007) pointed out that some endophytes may be latent become pathogens. The study of Liu et al. (2015) support this hypothesis, as *C. camelliae*, *C. fructicola*, *C. gloeosporioides*, *C. jiangxiense*, *C. karstii* and *C. siamense* were isolated from both symptomatic and asymptomatic leaf tissues of *Camellia sinensis* in China. *Colletotrichum* species have been also identified as saprobes on dead plant material (Photita et al. 2005). A few species of *Colletotrichum* are known to be pathogenic to humans (Shivaprakash et al. 2011, Natarajan et al. 2013). *Colletotrichum fioriniae* is entomopathogenic on *Fiorinia externa*, a scale insect (Damm et al. 2012b).

In the 20<sup>th</sup> century, inadequate laboratory facilities and scarcity of well trained mycologists/plant pathologists in many institutes have resulted in *Colletotrichum* being identified and named based on host association (Hyde et al. 2009a,b, Cannon et al. 2012). Once a species was found on a previously unknown host, that species was described as a new species, even in the absence of unique morphological diagnostic characters, which resulted in an erroneous taxonomy of this genus (Cannon et al. 2012). For an example, Index Fungorum (2016) lists 813 epithets under the genus *Colletotrichum*, but around only 200 names are currently accepted (Hyde et al. 2014).

The taxonomy of *Colletotrichum* has undergone numerous revisions and recent polyphasic approaches undertaken towards *Colletotrichum* systematics (e.g Cai et al. 2009) have made significant changes in its nomenclature. Species concepts are now less confused and the genus

comprises several major monophyletic clades (Cannon et al. 2012, Crouch et al. 2014, Hyde et al. 2014). There has been significant research on this genus regarding its species diversity, and molecular and the cellular basis for pathogenicity (O'Connell et al. 2012, Kubo & Takano 2013). New species have been introduced and some species have been renamed, based on well-defined morphological characters and support of molecular data (Sharma et al. 2013, 2015, Liu et al. 2014, 2015, Yan et al. 2015).

Every year there are numerous publications on *Colletotrichum*. A Google search of *Colletotrichum* reveals that there were 5400 scientific articles in 2015, 25,700 in the last five years and 32,200 in the last 10 years. *Colletotrichum* papers are also highly cited, for example Hyde et al. (2009a), Cannon et al. (2012) and Weir et al. (2012). In contrast to other important plant pathogenic genera such as *Diaporthe*, *Phomopsis* and *Bipolaris*, *Colletotrichum* papers are more numerous and highly cited. A similar trend can be found in the Web of Science revealing 4556 hits.

When a species of *Colletotrichum* is studied we use its name. All information on a species, such as its taxonomy, systematics, hosts, collection details, morphology (such as spore and cultural characters) and molecular data (especially genetic sequences and phylogenetic information) are linked to the scientific name (Jayasiri et al. 2015).

### **Importance of naming *Colletotrichum* species with regard to species identification and diversity**

Naming species enables scientists and ecologists to estimate the diversity and the number of fungi, as well as to predict their ecological role. Misidentification of species results in inaccurate records. The name of a species is used to convey association with a host, history, origin, properties and substrate.

*Colletotrichum* comprise several cryptic species complexes, and identification of species within these complexes are important (Cannon et al. 2012, Hyde et al. 2014). If all the species that 'look alike' are assumed to be a single species, then we assume that this single species has a wide range of biological traits. Therefore, the name influences how we interpret the species ecology and evolution. If cryptic species are mistaken for a single species, then understanding of the species becomes inaccurate. *Colletotrichum* species complexes or aggregates are described by the name and characteristics of the most well-known or important representative species in the group (Cannon et al. 2012, O'Connell et al. 2012, Crouch et al. 2014, Hyde et al. 2014). Presently, eleven species complexes, based on universally accepted phylogenetic clades, have been recognized (Damm et al. 2009, 2012a, b, 2013, 2014, Cannon et al. 2012, Weir et al. 2012, Crouch 2014, Hyde et al. 2014, Liu et al. 2014). Morphological characters and habitats of these species complexes differ. For example, species of the gigasporum complex have long straight conidia, while those of the caudatum complex have falcate conidia that have apical filiform appendages (Crouch 2014, Liu et al. 2014). Species of the gloeosporioides and acutatum complexes are known to cause fruit rots and post-harvest diseases in many economically important crops (Damm et al. 2012b, Peng et al. 2013, Yan et al. 2015). It is therefore possible to name the complex by observing its morphological characters. Species can then be further identified by using molecular data.

Knowing the name of the species of this genus is very important when conducting a study to assess species diversity/richness of *Colletotrichum* on a specific host. Not only correct naming of species of *Colletotrichum* is important in ecology and evolutionary studies, but also has significance in biodiversity assessment and conservation, host relationships and in applied science. Accurate naming is needed for mycologists and taxonomists, to avoid naming the same species twice and to identify the diversity and species richness in the genus.

### **Importance of naming *Colletotrichum* species with regard to plant pathology and quarantine**

Species with similar morphology may have a considerable physiological and pathogenic variation. Therefore, recognition of these species is particularly important for bio-security.

### *Plant pathology*

Scientific names of fungi are important as they allow us to identify the pathogens, saprobes and endophytes that exist in a single genus (Crous et al. 2015). Species of *Colletotrichum* are well-known as anthracnose pathogens on various plant hosts (Than et al. 2008a, b, Cannon et al. 2012, Hyde et al. 2014). Formulation of effective management strategies depends on proper identification of the disease and the causal agent (Wingfield et al. 2012) and examples for this are elaborated below.

Research in plant pathology mainly relies on accurate communication of pathogens. Names allow pathologists to understand lifestyles and modes of infection of a genus or a species, in order to implement proper control strategies. Species of *Colletotrichum* were, thought to be host-specific in earlier studies (Cannon et al. 2012). However, most of these pathogens are not host-specific and occur on many different hosts. For an example, *C. fructicola* was initially reported from coffee berries from Thailand (Prihastuti et al. 2009), but now it is known from many hosts, such as, apple, avocado and grapes (Weir et al. 2012, Peng et al. 2013). Species belonging to caudatum, graminicola and spaethianum species complexes are however, restricted to grasses (Damm et al. 2009, Cannon et al. 2012, Crouch 2014). Therefore, naming of *Colletotrichum* species helps in identifying pathogenic species on different hosts.

Inaccurate identification or characterization of a species may result in inappropriate or insufficient control measures being taken for a devastating pathogen (Crous et al. 2015). For an example, *C. kahawae* subsp. *kahawae* is a coffee pathogen present only on the African continent and is considered as a quarantine pest in Australia. However, *C. kahawae* subsp. *ciggario* is already present in Australia, but the latter is not pathogenic on coffee (Weir et al. 2012). Therefore, accurate naming of this taxon is crucial.

### *For Quarantine*

It is important to know the host distribution of a particular *Colletotrichum* species. Host-specific taxa may have a limited distribution, which may lead to important bio-security implications.

In order to have effective quarantine policies, accurate nomenclature is essential. It is important to maintain accurate records of pathogens, through a pest risk assessment process. This will help to determine whether those pathogens are present or have a potential threat of introduction to a country or a region (Hyde et al. 2010). Having names for pathogenic fungi allows scientists to construct quarantine databases such as Q-bank ([www.q-bank.eu](http://www.q-bank.eu) 2016), Invasive Species Compendium ([www.cabi.org](http://www.cabi.org) 2016) and share the knowledge on potential pathogenic species. These databases provide data on morphology, hosts, distribution, symptoms, biology and ecology, detection and inspection, plant trade and impact, prevention and control and are linked with sequence data available in GenBank.

Some plant pathogenic *Colletotrichum* species are important quarantine species, as they can be introduced to countries where they may not occur (Lubbe et al. 2004). For example, *Colletotrichum acutatum*, which is an important pathogen on strawberry, is absent in Chile, Estonia and Scotland (Sreenivasaprasad & Talhinas 2005, Damm et al. 2012b, CABI 2016). *Colletotrichum gossypii* which is pathogenic only on cotton plants is reported to have quarantine significance as it is seed dispersed (Hyde et al. 2009b, EPPO 2014). This species has been included into the quarantine pest list in Sudan (IPPC 2016). However, the status of this name is uncertain and new collections and epitypification is necessary (Salustiano et al. 2014). *Colletotrichum higginsianum* is also considered as a quarantine pest in Sudan (IPPC 2016). *Colletotrichum kahawae* subsp. *kahawae*, the pathogen causing coffee berry disease has a quarantine concern in Australia and in China as it is presently only known from the African continent (Cooke et al. 2009, Ministry of Agriculture of the People's Republic of China 2015, Q-Bank 2016). *Colletotrichum acutatum*, *C. circinans*, *C. coccodes*, *C. theobromicola* (syn *C. fragariae*), *C. linicola* and *C. trifolii*

are considered as quarantine pests in Belgium (BBS 2016). *Colletotrichum theobromicola* (syn *C. fragariae*), *C. horii*, *C. truncatum* is declared as a prohibited pest in Western Australia (DAFWA 2016). *Colletotrichum panicola* is considered as a regulated pest in Canada (CFIA 2016). *Colletotrichum camelliae*, *C. caudatum*, *C. curcumae* and *C. lilli* are considered as regulated pests in New Zealand (MPI 2016). *Colletotrichum coccodes*, *C. kahawae* and *C. musae* are considered as a quarantine pest in Nepal (IPPC 2016). There are major concerns, however, in connection to names given to some existing pathogenic species. Identification and naming by non experts and plant pathologists with no appropriate mycological knowledge can lead to improper disease management strategies. In addition, some of the species names listed in these databases are out of date and in need of urgent revision. In order to take suitable phyto-sanitary measures, accurate identification of species is therefore critical. However, identification of *Colletotrichum* sp. in imported consignments is difficult, because these species cannot be accurately identified using morphology alone. Therefore the best method to control the introduction of *Colletotrichum* species to countries that are free from certain anthracnose diseases is to include them in a list that requires a certification scheme. This would ensure that pathogen-free planting materials, fruits and vegetables are traded nationally and internationally.

In order to formulate, effective quarantine policies, the ability to accurately distinguish between closely related species is essential. However, due to morphological plasticity, taxonomic problems in *Colletotrichum* identification are well known. Even though the use of DNA barcode or combination of sequences from different loci for the recognition of species of quarantine importance requires moderately skilled personnel, it has several advantages. It does not require fruiting bodies or mature life stages that facilitate morphological examination and has a high yielding probability. Many plant pathogens can also exist predominantly in their asexual, latent or sterile endophytic phase and therefore go undetected through traditional methods of identification. In many cases, taxonomic experts fully conversant with *Colletotrichum* taxonomy are scarce and therefore availability of rapid molecular tools enables simple and cost effective detection of specific species. If there is a validated reference database library available, this method also allows us to identify taxa to species level (Quaedvlieg et al. 2012). Tao et al. (2012) developed a real-time PCR assay for the detection of *C. kahawae* subsp. *kahawae* based on DNA sequence analyses of the GAPDH gene region. Therefore, development of markers to detect species easily is important in quarantine. Knowledge and accurate *Colletotrichum* names will allow governments and scientists to formulate policies in trade quarantine and determine funding priorities for research of specific species of economic importance. Plant breeding programs and disease control provide good examples for this (Cai et al. 2011).

### **Importance of naming *Colletotrichum* species with regard to human infections**

A few species of *Colletotrichum*, namely *C. coccodes*, *C. dematium*, *C. gloeosporioides* and *C. graminicola* are known to cause keratitis and subcutaneous phaeohyphomycosis in humans (Shiraishi et al. 2011, Shivaprakash et al. 2011, Natarajan et al. 2013). Three separate cases of keratitis caused by *C. coccodes*, *C. crassipes* and *C. dematium* have been reported in India (Natarajan et al. 2013). *Colletotrichum truncatum* has been reported to cause keratitis and endophthalmitis in India (Shivaprakash et al. 2011). *Colletotrichum crassipes*, *C. dematium*, *C. gloriosporioides* and *C. graminicola* have been listed as the clinically important species in Spain by Cano et al. (2004). *Colletotrichum gloeosporioides* has been reported to cause a deep tissue mycosis following a penetrating injury with a lemon tree thorn in Australia (Figtree et al. 2013). *Colletotrichum gloeosporioides* is also known to causes severe corneal infection (Rodriguez 2014). Lin et al. (2015) reports a case of *C. gloeosporioides* causing cutaneous infection, which potentially can lead to life-threatening systemic dissemination. Therefore, early recognition and intervention are required to reduce the morbidity and mortality. However, the identification of these species has to be revised and updated.

In order to treat these diseases, a physician does not need to know the species names or even the genus name. As long as they know that the disease is caused by a fungus, and that the fungus

has not developed resistance, they can prescribe antifungal drugs or any other treatment depending on the nature of the infection. However, knowing the names of species will allow mycologists to predict whether a species can be an emerging human pathogen. This will also enable hospitals and mycologists to take necessary preventive measures to avoid infection by these species.

Emergence of novel pathogens due to climate change is becoming quite common nowadays. Species can build up resistance to survive the occurring climate change and thus resulting in the evolution of novel strains. Knowing the names of the *Colletotrichum* species is fundamental in identifying the species correctly as well as to find better treatment.

### **Importance of naming *Colletotrichum* species in agriculture**

Controlling the diseases caused by species of *Colletotrichum* is very important to obtain a high yield in economically important crops. In order to achieve this, the causal agents of the diseases need to be identified. However, generally farmers do not need to know the names of species that cause diseases. As long as they know the common name or the widely used name of the pathogen that causes diseases, as well as the main symptoms of the disease, it is generally adequate for them to take the necessary actions to mitigate the diseases (Everett 2014). However, they need to know the organism well. Knowing the difference between the organisms that cause diseases will allow them to use the exact controlling methods in mitigating them. For an example, the farmers should be able to recognise different symptoms of different pathogens, as *Phytophthora* may need different control strategies than *Colletotrichum*.

Once a disease occurs on the field proper control strategies should be taken. However, the need to name the species depends on the control strategy. Managing anthracnose can be done with fungicides, where we do not need to know the names of the species, but only if it is an ascomycete. However, identification of the species causing anthracnose in a field is useful when we want to implement specific control strategies.

### **Importance of naming *Colletotrichum* species in bio-control**

Some *Colletotrichum* species are potential bio-control agents. In order to use these taxa as bio-control agents, it is necessary to understand the population data on the potential bio-control species. Also, identification of its taxonomic rank and interactions with its hosts will provide a better understanding.

*Colletotrichum* species were predicted to become highly important as bio-herbicides (Askew et al. 2011). Some of the successful examples are the biological control of *Arceuthobium tsugense*, an obligate parasitic plant with the use of *Colletotrichum gloeosporioides* (Askew et al. 2011), as well as on *Clidemia hirta* which is an invasive plant in Hawaiian forests (Trujillo et al. 1986). *Colletotrichum truncatum* has been successfully used as a myco-herbicide against *Sesbania herbacea*, which is an introduced plant species except in the USA (Boyette 1991). However, given that *Colletotrichum* taxonomy is currently being revised and updated especially with novel species being described, these names allocated should be relooked into and possibly updated. Several studies have shown that endophytic *Colletotrichum* strains (belonging to the gloeosporioides species complex) provide protection to *Theobroma cacao* against *Phytophthora* pathogens, by inducing the plants' intrinsic defence pathways (Arnold et al. 2003, Mejía et al. 2008). However, there are no records identifying these strains accurately. Correct identification and naming them may lead to their use as successful bio-control agents. *Colletotrichum fioriniae* is known to be an entomopathogen, its name being based on its exotic scale insect host, which is a sap-sucker (Damm et al. 2012b). This species can be used to control the scale insect populations. Although the scientific basis of naming species based on host association can be highly subjective, there could be undiscovered strains with potential bio control potential and hence, naming is crucial in bio control disease management.

Biocontrol of *C. gloeosporioides* causing anthracnose of *Rouwolfia serpentine* can be done with the use of *Trichoderma viride* (Ghosh & Chakraborty 2012) as well as the biological control of *C. panacicola* on *Panax ginseng* by *Bacillus subtilis* (Ryu et al. 2014). Grape ripe rot caused by

*C. gloeosporioides* can be controlled with the use of *Chaetomium*, *Penicillium* or *Trichoderma* bio-products or a mixture of the above three (Soytong et al. 2005). *Bacillus amyloliquefaciens* S13-3 can be used as a bio-control agent for *C. gloeosporioides* (Mochizuki 1998). Wang et al. (2014) used *Bacillus cereus* AR156 as a bio-control agent to control the anthracnose on Loquat fruits caused by *C. acutatum*. *Cryptococcus laurentii* acts as a bio-control agent of *C. gloeosporioides* on mango by competing for nutrients as well as for space (Bautista-Rosales et al. 2014). *Saccharomyces cerevisiae* proved to be an efficient biological control agent against *C. acutatum* during pre-harvest of *Citrus* (Lopes et al. 2015). The moss *Physcomitrella patens* can activate defence responses against *C. gloeosporioides* by strengthening the infected cell wall by the inclusion of phenolic compounds and inducing the expression of a Dirigent-protein-like encoding gene as well as *PAL* and *CHS* defence genes (Reboledo et al. 2015). Given the possibility of specific species acting as biocontrols on specific *Colletotrichum* pathogens, accurate identification and species nomenclature is desirable.

### **Importance of naming *Colletotrichum* species in plant breeding**

Species with similar morphology may have a considerable pathogenic variation levels. Therefore, recognition of these species is particularly important for plant breeding and integrated disease management.

Managing anthracnose often requires fungicides, but another option is to breed, resistant host plants (McDonald & Linde 2002). In order to do this, host genotypes resistant to different *Colletotrichum* species and different pathotypes within the species should be identified (Babu et al. 2011, Garg et al. 2013). The inheritance of resistance can then be studied and it will allow locating and mapping quantitative trait loci for resistance (Kim et al. 2008, Lee et al. 2010, Garg et al. 2013). In order to obtain a true pathotype difference, in a set of different genotypes, a qualitative or phenotypic difference in virulence should be observed (Taylor & Ford 2007). Identification of the pathotypes provides important knowledge of intra-specific species of *Colletotrichum* as well as providing new insights to plant breeders (Cai et al. 2009). Insight into best breeding strategies for durable resistance can be obtained with knowledge of the population genetic structure of the pathogen (McDonald & Linde 2002). For example, Than et al. (2008a) identified that *Capsicum baccatum* strain PBC 80 in Thailand is resistant to ten isolates of *C. acutatum*, which is one of the most destructive pathogens causing Chilli anthracnose in Thailand. Wang et al. (2016) reported that tea plant cultivar ZC108 had greater resistance to tea anthracnose caused by *C. camilliae*. According to Prom et al. (2015), SC748 was the only resistant line of Sorghum towards the foliar anthracnose caused by *C. sublineolum*. ‘Tanjil’ cultivar of *Lupinus angustifolius* has been strongly used for breeding resistant varieties against *C. lupini* in Australia (You et al. 2005). Cultivars ‘Tanjil’ and ‘Wonga’ of *Lupinus angustifolius* bear the dominant gene *Lanr1*, conferring resistance to anthracnose of *Lupinus* (Talhinhas et al. 2016). Among the French-American hybrids of grapevine, *V. aestivalis* cv. Cynthiana (Norton) is resistant to grape ripe rot disease (Sutton 2015). The grape cultivars within *V. vinifera*, ‘Beniyamabico’, ‘Flame Seedless’ and ‘Zabalkanski’, are resistant to ripe rot caused by *C. acutatum* (Jang et al. 2011). Intra-specific taxa can be related to their biological reactions with the host through pathotypic differences (Cai et al. 2009).

Resistance cannot be bred for a whole genus to different kinds of diseases. Therefore, naming of *Colletotrichum* species is important in resistant breeding, mainly because they assist in revealing genetic diversity in potential breeding material and provide vital screens for the development of new cultivars.

### **Importance of naming *Colletotrichum* species in whole genome sequencing**

Whole genome sequences allow us to compare genomes of different genera as well as different species in the same genus as well as at the intraspecific level. Analyses of gene datasets provide insights into the adaptations required by a fungus to cause a disease. This enables researches to find the key genes of the plant to combat plant pathogens, as well as to enhance biological control agents. Whole genomes of *Colletotrichum* species are the raw materials for

research on infection, understanding pathogen variation, evolution and population dynamics. As most of the species of *Colletotrichum* are important plant pathogens, it is vital to understand their life cycle in order to implement effective quarantine measures (Crouch et al. 2009b). Draft genome sequences are available for several *Colletotrichum* species including *C. falcatum*, *C. fiorinae*, *C. graminicola*, *C. higginsianum* and *C. sublineola* (Cannon et al. 2012, Baroncelli et al. 2014 a, b, Viswanathan et al. 2016), which provide new insight into the evolution of pathogenicity (Jaramillo et al. 2015). Therefore, it is important to name these strains accurately at the species level. However, wrong identification of species of *Colletotrichum* has led to mistakes in the whole genome history. Strain Nara-gc5 was considered as *C. gloeosporioides* at the time the genome sequence was published (Gan et al. 2013). However, recent revisions showed that this strain actually belongs to *C. fruticola* (Crouch 2014). Therefore, correct naming of *Colletotrichum* species is needed when it comes to whole genome sequencing.

### **Importance of naming *Colletotrichum* species with regard to creating and maintaining knowledge bases**

It is important to scientifically document and record fungal diversity in order to preserve them as well as for efficient usage. Mycologists and plant pathologists have been documenting fungal species, mainly pathogens and these records have served as the basis for national and international checklists. These checklists have been put into databases including species, hosts, typification details, position in classification and synonyms. With the advances in molecular phylogeny and ecology it is very much needed to tie both correct taxonomic names with clearly annotated data (Schoch et al. 2014). Databases such as Index Fungorum ([www.indexfungorum.org](http://www.indexfungorum.org), 2016), MycoBank ([www.mycobank.org](http://www.mycobank.org), 2016) give taxonomic details about the fungi. Most comprehensive collection of DNA sequenced data is available in GenBank ([www.ncbi.nlm.nih.gov/genbank](http://www.ncbi.nlm.nih.gov/genbank)). Databases such as UNITE (Kõljalg et al. 2013, Nilsson et al. 2014), RefSeq (Schoch et al. 2014) have linked species names with their ITS sequences and have provided reference sequences to be used for various studies. The Faces of Fungi database (Jayasiri et al. 2015) was established to deposit taxonomic data, phenotypic details and other useful data. All these databases attempt to provide the currently accepted scientific name, although for many names an update is unavailable. When we are describing a new species, before giving a name for the taxon, we need to check whether the name that we want to give already exists. These databases are also able to provide us that information. Also, they link the name with the reference specimens and molecular data. Therefore, this also shows us that naming species of *Colletotrichum* is important.

### **Importance of naming *Colletotrichum* species in bioprospecting**

Species of *Colletotrichum* have been utilized for biotechnological applications (García-Pajón & Collado 2003). Endophytic *Colletotrichum gloeosporioides* is used for the purification of large quantities of Huperzine A (Zhao et al. 2013). Use of lipid accumulating *Colletotrichum* strains is a novel source of bio-diesel feedstock (Dey et al. 2011). Purification of novel antimicrobial metabolites from *C. gloeosporioides* against *Staphylococcus aureus* is another example for commercial applications of *Colletotrichum* (Arivudainambi et al. 2011). Genomic studies have revealed that *Colletotrichum* species have large and complex storage of enzymes for ligno-cellulose degradation (Crouch et al. 2014). Knowing the accurate name of the necessary fungus will help to screen promptly for commercial strains, to identify and purify specific metabolites of commercial importance from specific species/strains and to use them in a beneficial way for humans. Pharmaceutical companies need to know species names to be able to correctly select species for screening and manufacture antifungal/antibacterial drugs. Accurate naming is also essential in obtaining patents for products.

### **Importance of naming *Colletotrichum* species with regard to evolutionary history**

Accurate scientific names should be able to communicate as much information such as its classification and phylogeny which are also referred to as evolutionary history. Prediction about



plant associated fungi in connection to its potential pathogenicity and suitable control measures can be done with an accurate name that reflects phylogeny (Rossman & Palm-Hernández 2008). For an example, an isolate determined to be a species of *Colletotrichum* may be pathogenic or endophytic depending on the health of the host. An accurate generic classification implies information about the biological characteristics of the species included in that genus. Today, taxonomists include biochemical, ecological, physiological and molecular data (phylogeny) in order to delineate new species in this genus and these data can provide a better insight into evolutionary history (Zhang et al. 2013). Many fungal names have not been re-assessed since their introduction, and in order to understand the displacement or resurrection of those names, re-examination of the type material or to designate epi- or neo-types is essential (Hawksworth 2015). Sequencing of species has become very common and it helps to clarify evolutionary relationships within this genus, relocate erroneous assignments and identification of new species or complexes (Cannon et al. 2012, Money 2013, Hyde et al. 2014). For an example, Weir et al. (2012) synonymized *C. hymenocallidis* and *C. jasmini-sambac* under *C. siamense*, but the study done by Sharma et al. (2015) showed that there are enough evidence to accept them as distinctive species within the siamense species complex. However, Liu et al. (2016) using GCPSR model showed that, the species which were identified to belong to siamense complex (including the above mentioned two species) are a single species, and siamense is not a species complex. DNA sequence comparisons have demonstrated that most of the traditionally used morphological characters in fungi occur as a result of convergent evolutionary process (Schoch et al. 2014). Another example is that until recently, *C. graminicola* was thought to have a broad host range infecting nearly every grass and cereal in family *Poaceae*, even though physiological specialization and distinct appressorial structures were telling otherwise (Du et al. 2005, Crouch et al. 2006). However, molecular phylogeny revealed that this species is limited to Maize while there are 16 distinct *Colletotrichum* species as endophytes and pathogens of the *Poaceae* (Crouch et al. 2009a,b, Crouch 2014). This shows that with host association, accurate delineation of species boundaries and correct naming of species, correct data on biological, epidemiological, genomic and transcriptomics will be available for a species and this will enable more valid scientific conclusion to be inferred.

Recent studies based on genomics, transcriptomics and molecular phylogeny allows us to see the forces responsible for the evolution of *Colletotrichum* as well as the identification of species boundaries allow us to predict about genome evolution, host adaptation mechanisms and the evolution of key pathogenicity traits (Crouch et al. 2014). Studies done on the host association patterns have shown that, species of *C. graminicola* originate from an ancestral line of non-graminicolous *Colletotrichum* hence, the pathogenic association of *Colletotrichum* with grasses appeared to be of very recent origin and a derived trait (Crouch et al. 2014). Crouch et al. (2014) demonstrated that speciation and host adaptation in *C. graminicola* complex might reflect host diversification. All these developments and applications of genomic data can provide better identification of *Colletotrichum* species and these developments have been possible because all the data are linked to the organisms' scientific name.

## Conclusion

Morphological based naming of *Colletotrichum* species remains at the forefront but DNA sequence based data have also provided adequate insights into different holophyletic groups. However, there could still be misidentification or erroneous names in databases. With regards to fungal species nomenclature, mycologists have some way to go before working out a logical and standardized approach that facilitates species names based on scientific methods and congruent to an International Code of Nomenclature. There are still outstanding nomenclatural problems with *Colletotrichum* species. Is there a need to reconsider how to define and name species? Should mycologists design a scientific and universal nomenclatural framework that would allow a more rational and practical approach towards naming of *Colletotrichum* at both interspecific and intraspecific level? Answers for these questions are yet to be discovered.

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