The Current State of *Trichoderma* **Taxonomy and Species Identifcation**

Feng Cai, Kai Dou, Ping Wang, Komal Chenthamara, Jie Chen, and Irina S. Druzhinina

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1 Introduction

Molds from the genus *Trichoderma* (*Hypocreales*, *Ascomycota*) are among of the most common fungi; they are easy to isolate and handle in a pure culture (Migheli et al. [2009](#page-31-0); Zachow et al. [2009](#page-32-0); Chen et al. [2021](#page-29-0)). Consequently, the taxonomy of

Fungal Genomics Laboratory (FungiG), Nanjing Agricultural University, Nanjing, China

Institute of Chemical, Environmental, and Bioscience Engineering (ICEBE), TU Wien, Vienna, Austria e-mail: caif8@mail.sysu.edu.cn

K. Dou \cdot J. Chen (\boxtimes) School of Agriculture and Biology, Shanghai Jiaotong University, Shanghai, China e-mail: jiechen59@sjtu.edu.cn

P. Wang Ausliva International, Suzhou, China

K. Chenthamara Institute of Chemical, Environmental, and Bioscience Engineering (ICEBE), TU Wien, Vienna, Austria

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F. Cai $(\boxtimes) \cdot$ I. S. Druzhinina

School of Ecology, Sun Yat-sen University, Shenzhen, China

Trichoderma started with the beginning of the modern fungal taxonomy in the eighteenth century (Persoon [1794\)](#page-31-1). Similar to other fungi, it was in the descriptive stage for two centuries and before entering a period of turbulence caused by molecular methods (Bissett [1984](#page-28-1); Bissett [1991a,](#page-28-2) [b,](#page-28-3) [c](#page-28-4); Kuhls et al. [1997](#page-30-0); Kindermann et al. [1998;](#page-30-1) Kullnig et al. [2000](#page-30-2)). Ideally, taxonomy should refect the nature of the organism and help its investigation. The biology of *Trichoderma* offers a convenient example to illustrate this relationship. Many *Trichoderma* strains have properties of environmental opportunism meaning that they are capable of fast colonization of a great variety of natural and artifcial substrates, are highly competitive in microbial communities, are resistant to xenobiotics including chemical fungicides, and are potent producers of various metabolites such as enzymes, secondary metabolites, or surface-active proteins (Druzhinina et al. [2011;](#page-29-1) Sun et al. [2019;](#page-31-2) Gao et al. [2020;](#page-29-2) Druzhinina and Kubicek [2017;](#page-29-3) Pang et al. [2020\)](#page-31-3). Some *Trichoderma* species can survive in soil and colonize rhizosphere possessing almost no harm to plants but stimulating their growth and development (Druzhinina et al. [2011](#page-29-1); Harman et al. [2004;](#page-30-3) Marra et al. [2019;](#page-31-4) Rivera-Méndez et al. [2020](#page-31-5)). Being mycoparasitic, a growing number of *Trichoderma* species are proposed as biofungicides for plant protection in agriculture (Ding et al. [2020](#page-29-4); Wu et al. [2018](#page-32-1)). However, the same property also makes *Trichoderma* species causative agents of the green mold disease on mushroom farms (Komoń-Zelazowska et al. [2007](#page-30-4); Kredics et al. [2010\)](#page-30-5) (see Kredics et al. in this book). Finally, some *Trichoderma* strains also have clinical signifcance as causative agents of nosocomial mycoses in immunocompromised humans (Chouaki et al. [2002](#page-29-5); Myoken et al. [2002;](#page-31-6) Kredics et al. [2003](#page-30-6)). These versatile, largely benefcial, but also harmful properties of *Trichoderma* make the taxonomy of this genus a high priority task because the correct identifcation of a species can predict its properties and thus facilitate applications. The taxonomy of *Trichoderma* has been intensively studied over the last two decades resulting in a hundred-fold increase in the species number from a few "species aggregates" of Rifai [\(1969](#page-31-7)) to several hundred molecularly defned species enumerated in several recent reviews (Druzhinina et al. [2006;](#page-29-6) Atanasova et al. [2013](#page-28-5); Bissett et al. [2015;](#page-28-6) Cai and Druzhinina [2021\)](#page-29-7). Thus, today *Trichoderma* comprises the genus of very common fungi with most species that have been characterized using modern molecular techniques.

The large number of species in *Trichoderma* appears to be reasonable: Whole genomic investigations of this genus and other hypocrealean fungi have estimated the origin of the genus at the edge of Cretaceous-Paleogene mass extinction event 66–67 million years ago (Kubicek et al. [2019](#page-30-7)). The most recent phylogenomic tree (Kubicek et al. [2019\)](#page-30-7) indicates that the formation of the major infrageneric clades such as Sections *Trichoderma* and *Longibrachiatum* recognized by John Bissett in the 1990s or the *Harzianum* Clade (Bissett [1984;](#page-28-1) Chaverri et al. [2003\)](#page-29-8) was formed somewhat 20–25 million years ago, while some closely related species such as *T. reesei* and *T. parareesei* shared a common ancestor 4–8 million years ago. This vast evolutionary time and the relatively high evolutionary rates (compared to, e.g., vertebrates) offer the genus *Trichoderma* tremendous possibilities for the adaptation to the environmental conditions and speciation. However, similar to other fungi, many evolutionary different strains of *Trichoderma* still share remarkable

morphological and ecophysiological similarities. It appears that many traits suitable and accessible for direct examination by taxonomists are homoplasious and appeared due to convergent evolution. Thus, the most diffcult task of modern taxonomy of *Trichoderma* is to retrieve the traits that would allow one to distinguish a great number of species.

The general fungal taxonomy is regulated by the Code, i.e., CN International Code of Nomenclature for algae, fungi, and plants (Turland et al. [2018\)](#page-32-2), that now contains an advanced section for fungi in Chapter F, San Juan Chapter F (May et al. [2019\)](#page-31-8). Even though the Code strictly regulates nomenclatural acts, it assumes a heterogeneity of approaches to defne species (Turland et al. [2018\)](#page-32-2). This can be explained by the complexity of lineage-dependent evolutionary processes (Steenkamp et al. [2018;](#page-31-9) Inderbitzin et al. [2020](#page-30-8)) or numerous pragmatic criteria used by the taxonomists for the classifcation of particular fungal groups. Lücking et al. [\(2020](#page-31-10)) found that the best practice depends on the group in question and the required level of precision. Some fungi can be grouped based on phenotype characteristics; however, most fungi, especially asexual forms such as *Trichoderma*, require timeconsuming and labor-intensive methods that include culturing, DNA barcoding, and phylogenetic analysis as well as discipline- or taxon-specifc approaches such as physiological profling (Lücking et al. [2020](#page-31-10)). Therefore, it is common for species concepts determined by the taxonomy providers to vary even within one genus. However, taxonomy users expect that the identifcation of species should be precise and accurate. For *Trichoderma*, this collision of possibly vague species delimitation and the need for the exact species identifcation was recently addressed in Cai and Druzhinina [\(2021](#page-29-7)). This topic requires a thoughtful discussion that will also be presented in this chapter and continued elsewhere.

The biology of *Trichoderma* offers a number of exclusive opportunities to the taxonomists. Fungi from this genus are ubiquitous and relatively simple to recognize and collect in natural and human-made habitats. They are easy to isolate directly from specimens and from a broad range of substrates based on the characteristic genus-specifc features. Most strains have fast growth in vitro on all common laboratory media and do not require demanding cultivation conditions such as temperature, illumination, or humidity. Importantly, and as it will be described in most chapters of this book, many *Trichoderma* spp. have highly valuable properties for industry and agriculture. Respectively, *Trichoderma* has attracted the attention of classical mycologists and people focusing on applied microbiology and developmental applications. Therefore, all collections of microorganisms have numerous *Trichoderma* isolates. Public depositories of gene sequences contain thousands of *Trichoderma* DNA barcodes, and the number of the whole genome sequences has grown exponentially. However, the identifcation of *Trichoderma* is also considered to be extremely diffcult. Fungal taxonomists including experts working with this genus for many years now frequently fail to determine the species (Cai and Druzhinina [2021](#page-29-7)).

In this chapter, we investigate the theoretical background of these collisions in *Trichoderma* research aiming for a concise review of the taxonomic state of the genus. We present a brief synopsis of *Trichoderma* taxonomy through January 2021,

list all *Trichoderma* species names, and explain the latest identifcation protocol for *Trichoderma* species.

2 The Numerical State of *Trichoderma* **Taxonomy and Species Identifcation**

After the implementation of the "One fungus – One name" concept of fungal nomenclature (Taylor [2011\)](#page-31-11)—and based on the voting organized by the International Commission on *Trichoderma* Taxonomy (ICTT) (formerly www.isth.info, now www.trichoderma.info) of the International Commission on the Taxonomy of Fungi (ICTF, [www.fungaltaxonomy.org\)](http://www.fungaltaxonomy.org)—*Trichoderma* was selected as a single generic name that should be used for all stages such as holo-, ana-, and teleomorphs. Consequently, the taxonomy of the genus *Trichoderma* was updated to include the species names previously attributed to teleomorphs from such genera as *Hypocrea*, *Sarawakus*, and *Protocrea* (Jaklitsch [2009a](#page-30-9); Jaklitsch et al. [2014\)](#page-30-10). The formal transfer of a few species of *Hypocrea* to *Trichoderma* is still pending (Cai and Druzhinina [2021\)](#page-29-7); nevertheless, these species are valid names of the genus (Table [1](#page-4-0)).

As of January 2021, the genus *Trichoderma* contains 468 species epithets, among which 379 names are currently in use, while 89 names (19%) are synonyms of different categories (abandoned names, orthographic variants, synonyms) (Cai and Druzhinina [2021\)](#page-29-7) updated with materials from Gu et al. ([2020\)](#page-29-9). Forty names were introduced before the twentieth century. Of these, only five are currently in use including such important species as *T. viride* and *T. atroviride*. Sixty species were introduced in the twentieth century based on their morphology, (sometimes) ecophysiological properties, and biogeography (Rifai [1969;](#page-31-7) Bissett [1984,](#page-28-1) [1991a,](#page-28-2) [b](#page-28-3), [1992\)](#page-28-7). The end of the century coincided with the introduction of molecular methods in *Trichoderma* taxonomy and the proposal of the genealogical concordance phylogenetic species recognition concept (GCPSR) as the most powerful approach to distinguish fungal taxa (Taylor et al. [2000](#page-32-3); Lücking et al. [2020](#page-31-10)). These changes resulted in a rapid increase in the number of taxa adding the majority of modern *Trichoderma* species names (364, 78%) delineated in the first two decades of the twenty-frst century. Consequently, only 14 (4%) currently valid *Trichoderma* species have not been characterized by molecular markers (Cai and Druzhinina [2021\)](#page-29-7), while 365 species (96%) have been DNA barcoded. This makes the genus *Trichoderma* a suitable model for DNA barcoding and molecular evolutionary studies in fungi.

The largest database of *Trichoderma* names is available in MycoBank [\(http://](http://www.mycobank.org/) www.mycobank.org/) followed by Index Fungorum ([http://www.indexfungorum.](http://www.indexfungorum.org) [org](http://www.indexfungorum.org)). Most species names are recorded in both taxonomic depositories, but MycoBank still has 14 and Index Fungorum has 8 unique records. Therefore, none of the offcial depositories of fungal taxonomy has the full list of *Trichoderma* species names (Fig. [1](#page-19-0)). To date, the most complete list of *Trichoderma* species can be found in Table [1](#page-4-0) (sorted alphabetically for convenience). Alternatively, the newly

Table 1 The alphabetic list of all species names deposited for *Trichoderma* in Index Fungorum ([http://www.indexfungorum.org/\)](http://www.indexfungorum.org/), MycoBank [\(https://www.mycobank.org/\)](https://www.mycobank.org/), NCBI Taxonomy Browser [\(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi\)](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi), and scientifc literature as of February 2021

Species name	Author(s)	Year	Reference strain
Trichoderma acremonioides	Zhang & Zhuang	2018	HMAS 279611
Trichoderma adaptatum	Chen & Zhuang	2017	HMAS 248800
Trichoderma aeroaquaticum	Yamag., Tsurumi, Chuaseehar. & Nakagiri	2012	NBRC 108034
Trichoderma aerugineum	Jaklitsch	2009	CBS 120541
Trichoderma aeruginosum	Link	1816	not in use
Trichoderma aestuarinum	Gonçalves & Alves	2019	MUM H-19.05
Trichoderma aethiopicum	Mulaw, Kubicek & Samuels	2012	CBS 130628
Trichoderma afarasin	Chaverri & Rocha	2015	CBS 130755
Trichoderma afroharzianum	Chaverri, Rocha, Degenkolb & Druzhin.	2015	CBS 124620
Trichoderma aggregatum	Chen & Zhuang	2017	HMAS 248863
Trichoderma aggressivum	Samuels & Gams	2002	DAOM 222156
Trichoderma albocorneum	(Doi) Jaklitsch & Voglmayr	2014	G.J.S. 97-28
Trichoderma albofulvopsis	Qin & Zhuang	2016	HMAS 273760
Trichoderma albofulvum	(Berk. & Broome) Jaklitsch & Voglmayr	2014	CBS 114787
Trichoderma albolutescens	Jaklitsch	2011	CBS 119286
Trichoderma alboviride	Chen & Zhuang	2017	HMAS 247224
Trichoderma album	Preuss	1851	not in use
Trichoderma alcalifuscescens	(Overton) Jaklitsch & Voglmayr	2014	CBS 122303
Trichoderma alni	Jaklitsch	2008	CBS 120633
Trichoderma alpinum	Chen & Zhuang	2017	HMAS 248821
Trichoderma alutaceum	Jaklitsch	2011	CBS 120535
Trichoderma amazonicum	Chaverri & Gazis	2011	CBS 126898
Trichoderma americanum	(Canham) Jaklitsch & Voglmayr	2014	CBS 976.69
Hypocrea ampulliformis	Doi & Yamat.	1989	JCM 11982
Trichoderma andinense	(Samuels & Petrini) Samuels, Jaklitsch & Voglmayr	2014	CBS 345.97
Trichoderma angustum	Qin & Zhuang	2017	HMAS 273784

Species name	Author(s)	Year	Reference strain
Trichoderma chlorosporum	Chaverri & Samuels	2003	CBS 114231
Trichoderma christiani	Jaklitsch & Voglmayr		2015 CBS 132572
Trichoderma christianii	Jaklitsch & Voglmayr		2015 not in use
Trichoderma	Chaverri & Samuels	2003	CBS 114577
chromospermum			
Trichoderma cinnabarinum	Wallr.	1833	not in use
Trichoderma cinnamomeum	Chaverri & Samuels	2003	G.J.S. 97-237
Trichoderma citrinella	(Ellis) Zhuang & Zeng	2017	
Trichoderma citrinoviride	Bissett		1984 CBS 258.85
Trichoderma citrinum	(Pers.) Jaklitsch, Gams & Voglmayr	2014	CBS 894.85
Trichoderma collae	(Schwein.) Sacc.		1886 not in use
Trichoderma compactum	Yu & Zhang	2007	CBS 121218
Trichoderma composticola	Samuels & Jaklitsch		2013 CBS 133497
Trichoderma concentricum	Chen & Zhuang		2017 HMAS 248833
Trichoderma confertum	Chen & Zhuang	2017	HMAS 248896
Trichoderma confluens	Qin & Zhuang		2016 HMAS 244993
Hypocrea coprosmae	Dingley		1952 PDD 10453
Trichoderma cordobense	Speg.		1926 not in use
Trichoderma corfecianum	Sacc.		1911 not in use
Trichoderma corneum	(Pat.) Jaklitsch & Voglmayr		2014 CBS 100541
Trichoderma cornu-damae	(Pat.) Zhu & Zhuang		2014 G.J.S. 06-03
Trichoderma corrugatum	(Doi, Liu & Tamura) Liu, Zhu &		2014 not in use
	Zhuang		
Trichoderma costaricense	(Chaverri & Samuels) Chaverri,		2014 P.C. 21
	Jaklitsch & Voglmayr		
Trichoderma crassum	Bissett	1992	CBS 336.93
Trichoderma cremeoides	Jaklitsch & Voglmayr		2015 S112
Trichoderma cremeum	Chaverri & Samuels		2003 CBS 111146
Trichoderma croceum	Bissett		1992 not in use
Trichoderma crystalligenum	Qin & Zhuang		2017 not in use
Trichoderma crystalligenum	Jaklitsch		2006 CBS 118980
Trichoderma cuenisporum	Chaverri & Samuels		2003 not in use
Trichoderma cuneisporum	Chaverri & Samuels		2003 not in use
Trichoderma	Li & Chen	2018	not in use
cyanodichotomus			
Trichoderma dacrymycellum	Jaklitsch		2009 WU 29042a
Trichoderma danicum	(Jaklitsch) Jaklitsch & Voglmayr	2014	CBS 121273
Trichoderma decipiens	(Jaklitsch, Põldmaa & Samuels) Jaklitsch & Voglmayr	2014	G.J.S. 97-207

Table 1 (continued)

* *T. brevipes* was transferred from *Cordyceps* (Hypocreales) to *Trichoderma* (Bissett et al. [2015\)](#page-28-6). No DNA barcoding information is available for this species.

** The name of *Trichoderma viride* is presented diferently in the three databases, namely the NCBI Taxonomy Browser contains *T. viride* Pers. 1832, while MycoBank and Index Fungorum refer to *T. viride* Pers. 1794.

re-established website of the ICTT [\(www.trichoderma.info\)](http://www.trichoderma.info) contains the other copy of the complete list of species and is designed to be regularly updated. The interactive, updated, and searchable version of the complete list of *Trichoderma* species is available as a supplementary tool in the species identifcation protocol

Fig. 1 The numerical representation of *Trichoderma* taxonomy. The left Venn diagram shows the number of *Trichoderma* species deposited in the major depositories of fungal taxonomy such as Index Fungorum ([http://www.indexfungorum.org/\)](http://www.indexfungorum.org/), MycoBank ([https://www.mycobank.org/\)](https://www.mycobank.org/), and NCBI Taxonomy Browser [\(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi\)](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi). The right Venn diagram shows the numbers of species that have one or several of the three DNA barcode sequences required for the molecular identifcation of *Trichoderma*. The bar plot illustrates the alarming situation related to identifability of *Trichoderma* species. Numbers near the bars show the numbers of species (based on the estimates updated from Cai and Druzhinina [2021](#page-29-7), www.trichokey.com and www.trichoderma.info)

[\(www.trichokey.com](http://www.trichokey.com)) (Cai and Druzhinina [2021](#page-29-7)). However, as the number of species grows rapidly (Cai and Druzhinina [2021\)](#page-29-7), it has been suggested to screen the most recent taxonomic literature and compare it to the data on recent website updates.

The introduction of molecular methods in *Trichoderma* taxonomy not only resulted in the rapid growth of the species number but it also ended the morphological identifcation of *Trichoderma* (Kullnig-Gradinger et al. [2002;](#page-30-11) Druzhinina and Kubicek [2005;](#page-29-10) Druzhinina et al. [2005](#page-29-11)). Regardless of the experience and training of the taxonomist, the analysis of many morphological features cannot lead to unambiguous diagnosis of *Trichoderma* taxa even at the level of clades or sections. Thus, identifcation can only be achieved via analysis of DNA barcodes.

Even though 96% of *Trichoderma* species are characterized molecularly and the sequences are preserved in public databases, the Taxonomy Browser of NCBI [\(https://www.ncbi.nlm.nih.gov/taxonomy](https://www.ncbi.nlm.nih.gov/taxonomy)) contains only 340 species names (89% from all and 93% from molecularly characterized) meaning that sequence records for at least several dozen described species were not updated; however, these are still deposited as taxonomically undefned records (i.e., *Trichoderma* sp. strain ID). Consequently, these species will not appear in the results of the sequence similarity search using NCBI BLAST. The vouchered sequences can be retrieved based on sequence accession numbers provided in the publications.

Due to the high number of cryptic and closely related species, the accurate molecular identifcation of *Trichoderma* species requires analysis of at least three DNA barcodes (Cai and Druzhinina [2021](#page-29-7)) (see below). Considering the updated records for early 2021, the largest number of species have been DNA barcoded for *tef1* (86%) followed by *rpb2* (82%) and ITS (78%); only 270 (71%) have all 3 DNA barcodes (Fig. [1\)](#page-19-0). Other commonly provided DNA barcodes (*chi18-5*=*ech42*, *cal1*, *act*, *acl1*, 18S rRNA=SSU, and 28S rRNA=LSU) are sequenced for less than onehalf of the species; therefore, they currently have limited or no suitability for molecular identifcation regardless of their properties.

We notice that the number of species suitable for accurate species identifcation based on molecular markers is even lower than the estimate provided above (71%, Fig. [1](#page-19-0)). Our analysis showed that the identifcation of at least 50 recently described species is compromised by either incomplete reference sequences or sequences indistinguishable from the sister species (Cai and Druzhinina [2021\)](#page-29-7). Thus, we counted only 224 (60%) of *Trichoderma* species that can be potentially identifed based on available DNA barcodes (ITS, *tef1*, and *rpb2*). Still, this number appears to be an overestimate because the individual analysis of species frequently reveals further taxonomic collisions and leads to ambiguous results.

Thus, we conclude that while the taxonomy of *Trichoderma* attracted considerable attention over the last two decades, the taxonomic situation in the genus is alarming and requires urgent improvements (Fig. [1](#page-19-0)). The reasons for this unfortunate state of *Trichoderma* taxonomy and possible measures that can be taken for its improvement will be discussed below.

3 Three Stages of *Trichoderma* **DNA Barcoding**

The development of DNA barcoding of *Trichoderma* went through three pronounced stages: First, the species could be identifed based on the combination of diagnostic oligonucleotide sequences in specifc areas of ITS sequences of the rRNA gene cluster when the total diversity of the genus did not exceed 100 taxa (Druzhinina et al. [2005\)](#page-29-11). This method was implemented in the web-based tool *TrichO*KEY and was supported by the public database of the reference sequences. At least for a decade, the *TrichO*KEY tool was appreciated by users of *Trichoderma* taxonomy because of its simplicity. For most species recognized at that time, a pasting of an ITS sequence in the web form provided an unambiguous and fnal identifcation result that did not require further analyses (reviewed at Druzhinina et al. ([2006\)](#page-29-6)). The identifcation could be performed by people having no experience in fungal taxonomy or molecular phylogeny. However, there were already several pairs of species that shared the same phylotypes of ITS and therefore were not distinguishable. Upon subsequent introduction of more and more new species, insuffcient variability of ITS was demonstrated for many infrageneric groups especially for the clades within Section *Trichoderma* and Section *Longibrachiatum* as well as the *Harzianum* Clade*.* Therefore, ITS started to lose its reputation as the diagnostic marker for *Trichoderma* species (Druzhinina et al. [2012;](#page-29-12) Atanasova et al. [2010\)](#page-28-8).

A new effort was focused on a search for the so-called "secondary" DNA barcode loci that would aid in unambiguous species identifcation. At that stage, the suitability of various loci was tested based either on the random use of recently cloned and characterized genes (e.g., $ech42 = ch18-5$) or more commonly following the practices used for the large DNA barcoding initiatives such as the Fungal Tree of Life project (Lutzoni et al. [2004](#page-31-12)). Thus, *rpb2* (Liu et al. [1999\)](#page-31-13), *cal1* (Carbone and Kohn [1999](#page-29-13)), *act* (Carbone and Kohn [1999\)](#page-29-13), 18S rRNA=SSU (White et al. [1990\)](#page-32-4), and 28S rRNA=LSU were sequenced for a broad range of species, but only *tef1* locus received broad support by the community (Cai and Druzhinina [2021\)](#page-29-7). Therefore, the second phase of *Trichoderma* DNA barcoding was associated with the use of the large intron of *tef1* gene (Kopchinskiy et al. [2005](#page-30-12)) for sequence similarity search. The sequences of *tef1* were sufficiently polymorphic and allowed species identifcation with quite high precision versus the curated database of vouchered sequences using such tools as *Tricho*BLAST or (with more caution) NCBI BLAST. At that stage, we estimated that intraspecifc variability of *tef1* large (4th) intron could be as high as 4–5% meaning there was a 95% similarity threshold for most of the species in BLAST.

Rahimi et al. [\(2021](#page-31-14)) recently offered a way to identify *T. reesei* strains by searching for the long (400 bp) sequence of *tef1* fragment that they postulated to be diagnostic for this species. However, no such hallmarks were reported for other *Trichoderma* spp. This "*tef1*" stage ended with the so-called species boom that occurred in *Trichoderma* in 2014–2015 when more than 100 new species were added mainly due to the taxonomic studies in Europe and China (reviewed in Cai and Druzhinina [2021](#page-29-7)). Dou et al. ([2020\)](#page-29-14) were the frst group to realize that the single secondary barcode—the partial *tef1* sequence—was no longer sensitive enough for the identifcation of *Trichoderma* species. For this purpose, they programmed MIST (The Multiloci Identifcation System for *Trichoderma* [\(http://mmit.china](http://mmit.china-cctc.org/)[cctc.org/](http://mmit.china-cctc.org/))) that relied on the gradual application of sequence similarity search for the three loci: ITS, *tef1*, and *rpb2*. This started the third stage of *Trichoderma* DNA barcoding. This program offered a reasonable replacement to *TrichO*KEY that was consequently shut down (Cai and Druzhinina [2021](#page-29-7)). The strength of MIST was the most complete database of the reference sequences for *Trichoderma* and included the tree DNA barcoding loci for many type strains; it also contained numerous unverifed records and thus could not result in highly accurate or precise

identifcation. Interestingly, the two secondary DNA barcodes (the partial sequences of *tef1* and *rpb2*) have unequal levels of polymorphism. Therefore, no single value of the similarity threshold could be used for either markers. To overcome this issue, we recently collected all DNA barcoding records for all contemporary valid *Trichoderma* species and proposed the species identifcation protocol (Cai and Druzhinina [2021](#page-29-7)). There, we reviewed the interspecifc polymorphism of ITS, *tef1*, and *rpb2* sequences of closely related *Trichoderma* species to fnd the most reasonable sequence similarity values for each of the three DNA barcoding loci. This allowed us to formulate the sequence similarity standard:

$$
Trichoderma \ \left[\text{ITS}_{76} \right] \sim \text{sp} \exists! \ \left(rpb2_{99} \cong \text{tef} 1_{97} \right).
$$

Here, "Trichoderma" means the genus *Trichoderma*, "sp" means a species, "~" indicates an agreement between ITS and other loci, " \cong " refers to the concordance between "*rpb2*" and "*tef1*," and "∃!" indicates the uniqueness of the condition (only one species can be identifed). Subscripts show that the similarity per locus is suffcient for identifcation based on the assumptions of the protocol. This standard was then implemented in the molecular identifcation protocol (Cai and Druzhinina [2021\)](#page-29-7) that required a manual analysis of every set of sequences per individual strain. Still, due to the high number or poorly characterized reference taxa, this protocol would also result in some ambiguous identifcations. Moreover, the application of the identifcation procedure requires training in sequence analysis and can be diffcult for inexperienced people. However, no "easy" solution appears to be feasible at this phase of *Trichoderma* taxonomy.

The current (third) stage of DNA barcoding of *Trichoderma* is based on the three DNA loci that are considered to be the most reliable. Still the identifcation process remains complex. Even though Cai and Druzhinina [\(2021](#page-29-7)) argue that all three loci are required for the accurate and precise species identifcation, ITS can only be used to identify *Trichoderma* at the generic level. Most species recognition comes from the diagnostic fragments of *tef1* and *rpb2* gene sequences. The choice of these loci is not determined by their particular suitability for the purpose but rather by their availability in public databases for most species (Fig. [1\)](#page-19-0).

The advantage of *tef1* is the high polymorphism of its large (4th) intron sequence that is 250–300 base pairs long. We determined that individual strains within most of the contemporary species share >97% similarity of this fragment meaning that the polymorphism can reach up to 3% or 20–25 single mutations. This "identifcation window" is small versus that during the second stage of DNA barcoding, but it still offers a reasonable resolution and may potentially lead to unambiguous identifcation of strains having *tef1* phylotypes highly similar to that of the type strain for a given species. However, the disadvantage of *tef1* is also linked to its high polymorphism because it prevents combining strains from different infrageneric clades on a single alignment (Jaklitsch [2009a](#page-30-9), [2011](#page-30-13)). Consequently, many *Trichoderma* taxonomy providers keep sequencing *tef1* for newly described species but have largely abandoned the polymorphic fragment and shifted toward the 3′ end of the gene to the highly conserved fragment of the last (6th) exon (Jaklitsch [2009b](#page-30-14), [2011\)](#page-30-13). Consequently, the taxonomic value of this version of the *tef1* DNA barcode locus is neglectable. This shift coincided with the "species boom" and resulted in the description of the large number of species that cannot be distinguished based on existing DNA barcodes (Cai and Druzhinina [2021\)](#page-29-7).

The properties of *rpb2* are the reverse versus *tef1*: The DNA barcoding fragment of this gene covers an area of relatively highly conserved exon sequence. Contrary to *tef1*, these sequences are easily aligned genus-wide and therefore are suitable for the construction of whole genus phylograms (Atanasova et al. [2013;](#page-28-5) Cai and Druzhinina [2021\)](#page-29-7). Consequently, the polymorphism of *rpb2* is essentially lower than *tef1*, and such well-defned pairs of sister species such as *T. asperellum* and *T. asperelloides, T. reesei* and *T. parareesei*, and *T. harzianum* and *T. afroharzianum* differ by only 1% or a few single mutations of *rpb2* (usually less than eight). Unfortunately, we have detected numerous recently described species that share identical or highly similar (>99%) sequences of *rpb2* (Cai and Druzhinina [2021\)](#page-29-7). The consideration of above-described limitations of *tef1* and *rpb2* DNA barcodes is the main but not the only source of identifcation complexity.

The other issue causing the identifcation ambiguity is related to the cases of unconcordant similarities of the three DNA barcoding loci. For example, Cai and Druzhinina [\(2021](#page-29-7)) pointed to the ambiguous taxonomic position of their model whole genome sequenced strain NJAU 4742 (Zhang et al. [2016](#page-32-5), [2019;](#page-32-6) Pang et al. [2020;](#page-31-3) Cai et al. [2020;](#page-29-15) Gao et al. [2020](#page-29-2); Druzhinina et al. [2018](#page-29-16); Kubicek et al. [2019;](#page-30-7) Jiang et al. [2019;](#page-30-15) Zhao et al. [2021\)](#page-32-7). This strain has the *tef1* DNA barcode identical to the type strain of *T. guizhouense*. Therefore, it was attributed to this species at the second stage of DNA barcoding of *Trichoderma*. However, the *rpb2* sequence of this strain is less than 95% similar to that of the type strain of *T. guizhouense* and has most affnity to *T. pyramidale* (97.8%, which is still below the identifcation threshold). Interestingly, we came across several other strains with the same haplotype of *tef1* and *rpb2* as NJAU 4742. These data suggest the existence of a putative new species (*T. shenii* nom. prov., Cai and Druzhinina [2021\)](#page-29-7). This and numerous other cases of incongruent similarities point to the need for phylogenetic analyses of *tef1* and *rpb2* alignments along with the consideration of the similarities. In turn, these data explain why any attempts at automated identifcation of sequences such as *TrichO*KEY and MIST do not appear feasible.

4 Notes on the Identifcation of *Trichoderma* **Species**

The protocol for molecular identifcation of a single *Trichoderma* strain is detailed in Cai and Druzhinina [\(2021](#page-29-7)). That work also contains several dozen practical examples that provide an overview of various situations related to the implementation of this protocol. In this chapter, we do not repeat the description of the protocol but rather comment on it and highlight a few aspects that appear critical for its understanding and correct use (Fig. [2\)](#page-24-0).

Fig. 2 The summary of the current molecular identifcation protocol for *Trichoderma* species (Cai and Druzhinina [2021\)](#page-29-7)

First, it is important to bear in mind that neither the choice of DNA barcode markers nor the sequence similarity threshold values were selected based on their properties or particular suitability for the species recognition in *Trichoderma*. The decision to use these loci was merely pragmatic because these were the only three DNA barcoding markers that were available in public databases for the majority of species (Fig. [1](#page-19-0)). Accordingly, the similarity values were picked such that they could distinguish most of the contemporary species (Cai and Druzhinina [2021\)](#page-29-7). We admit that the whole genome sequences for *Trichoderma* (Druzhinina et al. [2018;](#page-29-16) Kubicek et al. [2019](#page-30-7)) could be used for the detection of essentially more powerful DNA barcoding loci in a hypothetical situation of a taxonomic revision of the entire genus. However, it is important to understand that no such revision appears to be envisioned in the near future for nonscientifc reasons. The comparison of closely related *Trichoderma* strains is impeded by the strain exchange barriers between countries.

For instance, at least 100 *Trichoderma* species have been recently described in China, and this number will likely keep growing (Cai and Druzhinina [2021\)](#page-29-7). Due to the quarantine rules, sending strains across the borders between some specifc countries for examination in other laboratories appears to be diffcult. Thus, at this stage of DNA barcoding of *Trichoderma*, the selection of diagnostic loci and criteria for the identifcation were determined by the availability and other practical considerations.

Second, the protocol largely relies on the sequence similarity values, and its successful implementation requires precisely defned sequence fragments per each locus. Consequently, preparation of the protocol by trimming the sequences is an essential step that must not be omitted (Fig. [2](#page-24-0)). Every DNA barcoding locus can be PCR amplifed using a variety of primer pairs (Jaklitsch et al. [2005](#page-30-16); Carbone and Kohn [1999;](#page-29-13) Liu et al. [1999\)](#page-31-13) resulting in fragments of different lengths. Therefore, the base pairs fanking the diagnostic regions must be removed either manually following the instructions in Cai and Druzhinina ([2021\)](#page-29-7) or using online support such as www.trichokey.com (Fig. [2\)](#page-24-0).

Third, sequencing ITS is compulsory for the identifcation of *Trichoderma* species and the analysis of infrageneric diversity. Unfortunately, to date, the database of vouchered ITS sequences is smaller compared to *tef1* and *rpb2* (Fig. [1\)](#page-19-0) because sequencing of ITS was abandoned by some providers of *Trichoderma* taxonomy after this locus lost its power in distinguishing many pairs or groups of closely related species. However, ITS still has an exceptional value in fungal taxonomy (Schoch et al. [2012\)](#page-31-15). Even in *Trichoderma*, many species have unique phylotypes of ITS and can therefore contribute to the identifcation precision. More critically, ITS is highly diagnostic at the generic border of *Trichoderma* where the limited polymorphism of the protein-coding genes appears to be less informative (Cai and Druzhinina [2021\)](#page-29-7). It is also necessary to determine ITS sequences for all new fungal taxa because it is the main locus used for fungal metagenomic studies and has a vast database of environmental records (reviewed in Lücking et al. ([2020\)](#page-31-10)).

Fourth, it is important to specify that the protocol allows one to identify some species through the analysis of sequence similarity values with no need to run phylogenies. For example, it might be common when a certain strain has the trimmed ITS and *rpb2* phylotypes identical to that of *T. asperelloides* CBS 125938 (type) and the trimmed *tef1* phylotype having one or two SNPs different from that of the above strain. In this case, the application of the *Trichoderma* $[ITS_{76}] \sim sp\exists! (rpb2_{99} \cong tef1_{97})$ standard is unambiguous and leads to the molecular identifcation of the query strain as *T. asperelloides*. Many other cases require phylogenetic analysis. This is in particular necessary when *tef1* and *rpb2* are not concordant or the reference DNA barcoding material is incomplete. The quality of phylogenetic analysis is also strongly infuenced by the taxonomic completeness of the reference materials. The dataset suitable for phylogeny should have no gaps, i.e., it should include all species reported for this infrageneric group. The protocol of Cai and Druzhinina [\(2021](#page-29-7)) offers a list of *Trichoderma* species and reference strains sorted based on their phylogenetic relation (PhyloOrder in Table 2 there and on [www.trichokey.com\)](http://www.trichokey.com). This

should assist people searching for a taxonomically complete set of sequences required for their analysis.

The ffth note on the implementation of the molecular identifcation protocol for *Trichoderma* species refers to the validation and verifcation steps (Fig. [2\)](#page-24-0). These steps were not considered important at the frst and second stages of *Trichoderma* DNA barcoding but now appear critical.

In Cai and Druzhinina [\(2021](#page-29-7)), validation refers to the quality control step in the reference materials for DNA barcoding. The most common issue leading to ambiguous identifcations is the deposition of the reference *tef1* sequences that contain only a portion of the last large intron (Jaklitsch [2009a\)](#page-30-9) that is diagnostic for *Trichoderma* DNA barcoding. One or another end of this sequence is the mission (more frequently the 5′ end of the intron sequence). The taxonomically relevant map and the structure of the *tef1* gene were provided in Rahimi et al. [\(2021](#page-31-14)). As mentioned above, many taxonomists sequence the 3′ end of the *tef1* gene spanning over the last large exon that can be aligned for across the genus, but it has limited or no suitability for DNA barcoding. This refers to numerous new species introduced from Europe and China in prior and over the recent "species boom" in 2009–2015. The missing diagnostic *tef1* DNA barcodes should be provided on the frst instance because with the current high number of taxa, even a single incomplete reference sequence per species will result in ambiguous identifcation.

This situation is less frequently noticed for *rpb2* sequences. However, *rpb2* can sometimes contain sequences of poor quality that are also not suitable for references. For the cases when the DNA barcoding sequences for the reference strains are either incomplete or of poor quality, the protocol of Cai and Druzhinina [\(2021](#page-29-7)) suggests using the *T*. cf. [species name] construct. The users of taxonomy (researchers that perform the identifcation) are advised to seek or request the completion of reference materials from their respective taxonomy providers. Alternatively (and as it was practiced at early stages of *Trichoderma* DNA barcoding), the reference strains can be obtained from the respective strain collections and sequenced.

The validation step can also fail when several species share the same phylotype of one or several DNA barcodes. Unfortunately, this is also a common situation in *Trichoderma* taxonomy (Cai and Druzhinina [2021](#page-29-7)). For example, *T. afarasin* and *T. endophyticum* share a highly similar *tef1* phylotype (>99% similarity); *T. yunnanense* and *T. kunmingense* share highly similar phylotypes of *rpb2* with each other and with *T. asperellum* (>99%). In this case, the ambiguity of the final identification can be recorded as *T*. aff. *asperellum* if the query strain was isolated from Europe (for instance). If sampling was performed in the Chinese province Yunnan, then the strains can be identifed as *T*. aff. *yunnanense* or *T*. aff. *kunmingense*, depending on other properties.

After the results of molecular identifcation become validated through the quality control of reference materials, the next important step is the biological verifcation of the identifcation result. Biological verifcation requires critical evaluation of such criteria as morphology, ecophysiology, biogeography, habitat, and occurrence. At this stage, the consideration of micromorphological features appears to be reasonable. For example, the three sister species *T. pleuroti*, *T. amazonicum*, and *T. pleuroticola* have numerous common and sharply different morphological and ecophysiological features verifying their distinct taxonomic statuses. Cai and Druzhinina [\(2021](#page-29-7)) provide a detailed explanation of the verifcation stage of their protocol.

Finally, the "new species hypothesis" can be an unambiguous, accurate, and precise result of molecular identifcation. This case ultimately requires validation of reference materials, phylogenetic analysis, and biological verifcation. In this chapter, we avoid discussing the criteria applicable for the delineation of species in *Trichoderma* as Cai and Druzhinina [\(2021](#page-29-7)) had presented a comprehensive discussion of this topic. However, we would like to stress that the correct implementation of the genealogical concordance phylogenetic species recognition concept (Taylor et al. [2000\)](#page-32-3) requires the analysis of single gene topologies. The common use of the single tree based on a combined multilocus alignment is insufficient for the new species proposal.

5 Conclusions

The identifcation of *Trichoderma* species is an intricate and laborious task that requires a background in mycology, molecular biological skills, training in molecular evolution, and in-depth knowledge of taxonomic literature (Cai and Druzhinina [2021\)](#page-29-7). The contemporary diversity of *Trichoderma* spp. cannot be identifed by automated sequence similarity searches (such as NCBI BLAST or MIST BLAST) or oligonucleotide DNA barcodes. All molecular identifcation results require in silico validation and biological verifcation. Similarly, *Trichoderma* spp*.* cannot be identifed by phylogenetic analysis without considering the sequence similarity values relative to the complete set of closely related species. The complexity of the identifcation process points to the need for close interactions between *Trichoderma* taxonomy experts.

In this chapter, we used *Trichoderma* to address the modern taxonomic collision that can also occur in many other genera of common and well-investigated fungi. The taxonomy of these fungi was visited and revisited many times and seemingly progressed with the introduction of new species. The delineation of the cryptic species is considered to be a useful practice because it increases the accuracy and precision of property prediction. However, many of newly recognized species appear to be diffcult to identify. Ultimately, the failure to identify species leads to ambiguity but, more dangerously, to the description of more new species that further complicate the identifcation. This loop has been already reported before and noticed that every single fungal species has been named 2.5 times on average (Hawksworth and Lucking [2017](#page-30-17)). The good taxonomic practice should include the verifcation of species identifability. Even though this process appears to be implemented as a reverse operation to the species recognition, it is frequently obscured by the application of vague species criteria. In an unfortunate case, a species can be recognized based on a comparison with a taxonomically incomplete set of references or based on species

criteria that do not correspond to the state of the art in this genus. Even now, the Code will allow the application of the morphological species concept or a description of a *Trichoderma* species based on the morphological characters and the analysis of any single locus, i.e., ITS.

In this chapter, we tried to emphasize that such cases will result in a valid species name, but this species will not be possible to identify because most sister species were delineated based on advanced molecular species criteria such as GCPSR or even an integrated polyphasic approach. The example above is an exaggeration, but the taxonomic reality of *Trichoderma* is highly ambiguous. We assume that this turbulent state was caused by the recent introduction of highly powerful molecular techniques in fungal taxonomy, and the situation will get its rational solution. However, we set a further warning related to the introduction of the whole genus genomic data in *Trichoderma* taxonomy. The whole genome sequences have a still unexplored inter- and intraspecifc polymorphism and thus offer essentially more options for taxonomic splitting: Species within the genus may share only 75% similarity genome-wide (Kubicek et al. [2019](#page-30-7)) and genomes of the two strains of the same clonal species *T. harzianum* have up to 1000 unique genes each. Therefore, the discussion of the unifed species concept suitable for such fungi as *Trichoderma* is an urgent task for *Trichoderma* researchers and fungal taxonomists.

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