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The Genues *Trichoderma*: Ecologicological Diversity, Taxonomic Classification and Its Agricultural, Human Health, Industrial and Environmental Applications

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Abstract

The genus Trichoderma is a diverse group of free-living fungi in the family Hypocreaceae (class Ascomycetes), that are living at different ecosystems in a wide range of climatic zones and that can be found all over the globe. The common ecological nich of the genus Trichoderma includes Natural soils, Decaying wood, Agricultural Habitats, Endophytes and mushroom related substrates. Trichoderma classified base on their morphological and cultural characteristics, conidiophore structure as well as the size of conidia. Now adays, molecularmethods including DNA fingerprinting and sequence analysis of multiple genes (ITS1-5.8 rDNA-ITS2 and genes encoding translation-elongation factor 1-alpha (tef1) as well as some specific molecular databases have been used for taxonomic classification of this fungi. Trichodermahave been used agriculture biological control of plant diseases and as plant growth promoter, in industry as sources of cellulolytic and hemicellulolytic enzymes used in different industries, in human health producer of secondary metabolites that have clinical importance and in enviromt they are as a potential biodegrader of toxic compounds and soil bioremediation.Therefore, this review article presented the ecological diversiy, taxonomic classification and application of genus Trichoderma.

Keywords: Agricultural; Diversity; Enviromental; Industrial; Taxonomic; Trichoderma

Abbreviations: ITS: Internal Transcribed Spacer; BLAST: Basic Local Alignment Search Tool; MDPM: Multilocus Data Base of Phylogenetic Markers; RTL: RefSeq Targeted Loci Database; NCBI: National Center for Biotechnology Information; UNITE: User-friendly Nordic ITS Ectomycorrhiza Database; ISHAM: International Society for Human and Animal Mycology; BCA: Biocontrol Agents; IAA: Indole-3-acetic Acid; IAAld: Indole-3-acetaldehyde; IEt: Indole-3-ethanol.

Introduction

The genus Trichoderma is a diverse group of free-living fungi in the family Hypocreaceae, commonly present in all soils [1]. These ascomycetes fungi are opportunistic, non-virulent plant symbionts that colonzing the root ecosystems of the plant and intracted with another groups of fungi by parasitism relationshipe [2]. *Trichoderma* spp. occurs worldwide and is present in different geographic regions

and climatic zones of the Globe [3,4]. Several species reveal high association with plants and are often isolated from different soils as the predominant species in the plant root ecosystem [4]. They have an ability to use different substrates as carbon sources by decomposing woody and herbal materials and other organic matter [3]. There are ways in which *Trichoderma* benefit plant cultivation, such as enhancing root system and plant development, inducing resistance, and increasing the availability of nutrients [2,5]. Different species of *Trichoderma* are effectively used for the control of large number of soil-borne plant pathogens like *Phytophthora, Rhizoctonia, Sclerotium, Pythium, Fusarium, Sclerotini, Macrophomina and Gaumannomyces* [6,7]. They are also known to increase crop productivity, resistance to biotic and abiotic stresses, and uptake of nutrients, root growth and development [8].

Trichoderma colonizes several ecological niches where they play a vital role; they are not only biocontrol agents of plant-pathogenic fungi, but also producers of secondary metabolites with medical values [9] and involved in environmental protection as agents of bioremediation [10]. Similarly, *Trichoderma* has vital rol in different industries since it is a major source of large quantities of hydrolytic enzymes like cellulases and hemicellulases [11,12]. Thus, this review paper presents the ecological diversity and taxonomic classification of Trichoderma and its apllications in detail.

Ecological Diversiy of Trichoderma

Trichoderma species are cosmopolitan soil fungi, colonizing a wide range of soil niches from cool temperate to tropical climates including agricultural, orchard, forest, pasture and desert soils [13-15]. The high versatility of the genus *Trichoderma* species have also been recovered in extreme environments like mangrove swamps, salt marshes and estuarine sediments where adverse osmotic potential conditions pose a real challenge for fungal survival [13]. Among the common ecological niches of trichoderma includes Natural soils, Decaying wood (Plant material), Agricultural Habitats, Endophytes and mushroom related substrates.

Natural Soils, Decaying Wood and Plant Material

According to the survey conducted by Vajna [16] survey *Trichoderma species* from dead wood of apple twigs, oak and cork wood samples collected from Hungary, identified isolates as *Trichoderma aueroviride*, *T. koningii*, *T. harzianum*, *T. longibrachiatum*, and *T. viride* based on morphological and cultural characteristics. Similarly, Vasanthakumari and Shivanna [17] reported the isolation, morphological and cultural characteristics based identification of *Trichoderma asperellum, T. koningii, T. harzianum* and *T. viride* from the rhizospheric plane of grasses of the subfamily *Panicoideae*. Isolates of Trichoderma obtained from forest soil of China have been identified as 12 taxa (*T. asperellum, T. atroviride, T. brevicompactum, T. citrinoviride, T. erinaceum, T. hamatum, T. koningiopsis, T. harzianum, T. reesei, T. spirale, T. stromaticum, T. vermipilum* and *T. virens*) Based on the ITS barcoding [18].

Agricultural Habitats

In agricultural ecosystem *Trichoderma* species can be isolated and showing positive effects on cultivated plants such as biological control of phytopathogens, increasing nutrient availability and uptake, inducing systemic resistance, promotion of plant growth, improving crop yields and degrading xenobiotic pesticides [19]. It has reported that the diversity of *Trichoderma* species was very high in wheat fields of China [20]. In another investigation, 11 *Trichoderma* species were identified by ITS barcoding from wheat rhizhospheric soil of winter season in Hungary comprising *Trichodema atroviride, Trichodema brevicompactum, Trichodema gamsii, Trichodrma harzianum, Trichodema koningiopsis, Trichodema longibrachiatum, Trichodema pleuroticola, Trichodema rossicum, Trichodema spirale, Trichodema tomentosum* and *Trichodema virens* [21]. Based on molecular approaches and morphological characteristics, Yuang and coworkers found2078 strainsof Trichodermaisolated from agricultural fields of east chinaand theseisolates were identified to 17 known speciesas: *Trichodema* harzianum*Trichodema* asperellum, *Trichodema* hamatum, *Trichodema* virens, *Trichodema* koningiopsis, *Trichodema* brevicompactum, *Trichodema* atroviride, *Trichodema* fertile, *Trichodema* longibrachiatum, *Trichodema* pleuroticola, *Trichodema*erinaceum, *Trichodema* oblongisporum, *Trichodema* polysporum, *Trichodema* spirale, *Trichodema* capillare, *Trichodema* velutinum, and *Trichodema* saturnisporum, *Trichodema* harzianum, *Trichodema* asperellum, *Trichodema* hamatum, and *Trichodema* virens [22]. Recently it has reported that about thirty four isolates have obtained from different crop fields identified as *Trichoderma species* by using ITS-5.8s region sequence analysis [23]. Nawaz and his coworkers suggested that different Trichoderma species were unevenly distributed in different chili farms of the Punjab province of Pakistan.

Endophytes

There are several research evideces about endophytic Trichoderma, for example:*Trichoderma amazonicum* as a novel isolate from rubber tree (*Hevea* spp.) [24]. Six different banana endophytic *Trichoderma* species reported by *TrichO*KEY identification, among which four species: *Trichodema asperellum, Trichodema brevicompactum, Trichodema harzianum* and *T. virens* found inside the

roots while two species: *Trichodema atroviride* and *Trichodema koningiopsis* were detected on root surface. Also it has described by Samules, et al. Trichodema *solani* as an endophyte in tubers of *Solanum hintonii* in Mexico. Trichoderma isolates also were recovered from tomato rhizosheraccording to morphology and based on the translation elongation factor 1-α gene sequence similarity, andwere designated as Trichoderma harzianum, *Trichodema* koningii, *Trichodema* asperellum, *Trichodema* virens and *T. viride* [25].

Mushroom-related Substrata

Thefindingof[26]demonstratedthatgreenmouldaffected oyster mushroom in Hungary were *Trichodemaasperellum, Trichodema atroviride, Trichodema longibrachiatum* and one undescribed species *Trichoderma* sp. DAOM 175924, which represented 90% of the isolates.*Trichoderma harzianum* was found to cause deleterious infections of green mold on Polish mushroom farms [27]. In Poland, seven mushroom associated *Trichoderma* species (*Trichodema aggressivum, Trichodema atroviride, Trichodema citrinoviride, Trichodema harzianum, Trichodema longibrachiatum, Trichodema virens,* and *Trichodema viride*) were identified with *Trichodema aggressivum* as most abundant species (60% of the isolates) [28]. *Trichoderma mienum* was found as a new species of the *Semiorbis* clade isolated from *Pleurotus ostreatus* and shiitake bed logs in Japan [29].

Taxonomic Classification of *Trichoderma*

The genus *Trichoderma* first describedby Persoon in 1794 until Rifai made the first real attempt to produce a workable classification system of the genus that was based on species morphology and on the concept of species aggregates classification of Trichoderma remained obscure and contradictory. The genus *Trichoderma* possesses key morphological characteristics like: - highly branched conidiophores with a conical or pyramidal outline [30].

Classification Based on Morphological Characteristics

The genus *Trichoderma* possesses key morphological characteristics that are still used to identify *Trichoderma species*. It is a septate fungus and produces highly branched conidiophores with a conical or pyramidal outline [30]. Identifications based on morphology characters (lask-shaped structures called phialides are found at the tip of the conidiophores, conidia, are produced at the end of the phialides where they accumulate to form a conidial head [31] remain the primary method for identification and verification of species in Trichoderma. Like all deuteromycetes, Trichoderma species can only reproduce asexually through intense sporulation or clonal growth from hyphae fragments [31]. However, the genus *Trichoderma* also has a sexual (teleomorph) stage known as Hypocrea which is in the ascomycete order Hypocreales [32]. *Trichoderma* teleomorphs possess all the key characteristics of Trichoderma anamorphs and can reproduce sexually to form ascospores. *Trichoderma species* form floccose or tufted colonies of various colours (white, yellow, green), which in the past were used to identilfy species [30]. Today, the use of morphological characteristics for identifying Trichoderma species is being progressively replaced by molecular tools, which provide a more robust and reliable form of species identification.

Molecular Classification

Primarly identification of *Trichoderma/Hypocrea in* the species level was performed based on their morphological and cultural characteristics [31]. Based on previous taxonomic classification identification of species was performed by morphology, conidiophore structure as well as the size of conidia [31,33]. However, the likeness in form or structure as a result of environmental condition or parallel evolution but not from common ancestry orgin,is common in *Trichoderma*, which affects the validity of species identification and without professional expertise this may often lead to incorrect diagnoses, therefore the results of early studies must be handled with special care [34]. In order to get around such problems and give precise species-level diagnoses, the use of molecular methods is recommended.

Using of molecular techniques and tools for the *Trichoderma* identification and biodiversity study gets a focus. These molecular methods includes DNA fingerprinting and sequence analysis of multiple genes (ITS1-5.8 rDNA-ITS2 and genes encoding translation-elongation factor 1-alpha (*tef1*), RNA polymerase II subunit (*rpb2*), calmodulin (*cal1*), endochitinase (*chi18-5*,), it is now possible to identify every *Trichoderma* isolate and/or recognize it as a putative new species [34,35]. Several studies have consistently shown that *tef1* introns provide the highest power of resolution within clades [33]. In recent years, the development of an oligonucleotide barcode (*Trich*OKEY) and a customized similarity search tool (*Tricho*BLAST) facilitated identification of new species, both tools are based on ITS, *tef1*and *rpb2* sequences of vouchered specimens and provides more reliable identification of *Hypocrea/Trichoderma* than GenBank [35,36]. The advantage of this system is that this database does not contain the substantial number of sequences in GenBank originating from wrongly identified species. *Tricho*MARK is updated version of *Tricho*BLAST which is available on www.isth.info and *Tricho*CHIT (www.isth.info), an online barcoding programme for the screening and identification of the excellent chitinase producer strains

of *Hypocrea lixii/Trichoderma harzianum* was developed by Nagy, et al. [37].

History of DNA Sequence-based Fungal Identification

Routinely use of PCR and DNA sequencing in the mid-1990s, in biology laboratories for fungal strain and species identifications, contributed to the rapid expansion of fungal DNA sequences of several DNA fragments of the ribosomal RNA gene cluster to public databases. For example, the first comprehensive dataset of the variable D1/D2 domain of the nuclear large subunit (nLSU or the 28S) ribosomal DNA for about 500 species of ascomycetous yeasts generated by Kurtzman and Robnett. They found that the sequence divergence in this domain was generally sufficient to differentiate closely related species, and comparison of phylogenetic trees derived from the D1/D2 domain and the nuclear small subunit (nSSU or the 18S) ribosomal DNA sequences for selected members of the Saccharomyces clade showed that the two trees were highly concordant, with similar statistically well-supported branches. Subsequently a similar dataset for basidiomycete yeasts established by Fell, et al. and Scorzetti, et al. [38,39]. They found that most basidiomycete yeast species could also be distinguished using the D1/D2 domain sequences of nLSU rRNA. However, they showed that, in general, the ITS region was better at distinguishing closely related species than the D1/D2 domain.In addition, they found that the intergenic spacer (IGS, situated between the 3'-end of the 28S rRNA gene and the 5'-end of the 18S rRNA gene) region of the ribosomal gene cluster could also be used for additional differentiation of species and even among strains within the same species. Because the ITS sequences typically show greater variation and have better discriminating power than the D1/D2 domain between closely related taxa [38,39], in most descriptionsof new filamentous fungal taxa, the ITS sequences are often obtained and analyzed, contributingto the expansion of ITS sequences in the public domain.

In 2007, a group of mycologists organized a workshop in Virginia, USA, to discuss various genes that could be used for fungal barcoding [40,41]. These discussions set the stage for a multinational consortium of mycologists to meet in Amsterdam in 2011 to evaluate six DNA regions (SSU, LSU, ITS, RPB1, RPB2, MCM7) and nominate the official fungal barcode, the ITS region, which was later approved by the Consortium for the Barcode of Life [42]. The resulting paper (coauthored by >100 mycologists) included taxa sampled from all major fungal phyla, including the Ascomycota and Basidiomycota, the largest phyla within the kingdom fungi [43]. These two phyla include the fungi from which the greatest numbers of secondary metabolites have been isolated [44]. The recognition of ITS as the official DNA barcode marker for fungi represents a noteworthy advance, which has greatly benefited the research community.

Schoch with his coworkers found the ITS region to be among the markers with highest probability of correct identifications for a very broad group of sampled fungi [42]. Additional fungal investigations have provided support for the ITS region as a suitable fungal barcode [45-47]. Protein-coding genes are often difficult to amplify and sequence, since they occur as a single copy within the genome rather than as multiple copy tandem repeats as with the ribosomal genes. Moreover, most environmental surveys (metagenomic studies) of fungi are using the ITS region in their studies [48-52] to identify fungi using modern sequencing technology, such as next-generation sequencing, which can aid in rapid identification of fungi without the need to clone the amplicons. This sequencing approach has therefore created a surge in the number of ITS sequences that are available in GenBank [40]. Therefore, the practicality and broad kingdom-wide taxonomic applicability make ITS a useful tool for fungal barcoding for most (~70% of all fungi tested) [42].

Even though the ITS region performs well as a suitable fungal barcoding marker, it has been subject to debate [53]. Now a days there are research findings that indicated defficiency of the ITS region in some highly speciose genera, such as *Aspergillus, Cladosporium, Fusarium*, *Penicillium*, and *Trichoderma*, as these taxa have narrow or no barcode gaps in their ITS regions [42,54-56]. To over come the ITS problem, protein-coding genes are utilized for species identifications via barcoding due to the presence of intron regions, which sometimes evolve at a faster rate compared to ITS and are employed in phylogenetic analyses due to their better resolution at higher taxonomic levels compared to rRNA genes [57]. Moreover, these genes allow for an easy recognition of homology and convergence, as they are believed to occur as a single copy in fungi. Protein-coding genes in fungal systematics have been used widely for constructing molecular phylogenies to aid in the identification and classification of taxa, largely due to the landmark studies in systematic and taxonomic mycology supported by the National Science Foundation, such as Assembling the Fungal Tree of Life [43,5758,59]. These efforts among fungal systematists lead the way to a safer classification of the fungal kingdom and impart knowledge regarding gaps in our understanding of evolutionary relationships among fungi.

Among protein-coding markers the translation elongation factor 1-alpha (tef1) and beta-tubulin (tub2/BenA) have been most commonly used for inferring phylogenetic relationships among fungi [55,57,59]. Using the ITS marker alone for identification might not sufficient in certain fungal clades, and it may be necessary for the user to sequence one or more single-copy protein-coding genes

for certain fungal genera and/or lineages to obtain a more precise identification at the species level (e.g., Aspergillus, Penicillium, and Trichoderma). Due to the limitations of a single-marker barcoding system in fungi, a group of mycologists recently completed a study testing >1500 species (1931 strains or specimens) of Dikarya (Ascomycota and Basidiomycota) for different ribosomal and single-copy protein-coding markers [56].

Molecular Databases used for Trichoderma Sequences Barcoding

Druzhinina and co-workers was introduced DNA Barcoding for Trichoderma identification and integrated it with a TrichOkey program [35]. There are several curated databases that are dedicated to the identification of ITS and other ribosomal and protein-coding sequences that have been established for different groups of fungi [60]. Internal transcribed spacer (ITS) sequence fragment is subjected to an individual Basic Local Alignment Search Tool (BLAST) in GenBank to verify identity [61]. Basic Local Alignment Search Tool search is usually employed using nucleotide collection (BLASTn), where curated RefSeq records, as well as their GenBank duplicates, are included by default in BLAST [62,63]. The original version of TrichOKey made use of several species-, clad- and genus-specific oligonucleotides sequences (named as hallmarks) derived from ITS (nuclear ribosomal internal transcribed spacer) region for a quickidentification of75 single species, 5 species pairs and 1 species triplet [35]. Another identification tool box, TrichoBLAST, for Trichoderma identification had also been developed, which is a combination of a multilocus data base of phylogenetic markers (MDPM), a diagnosis program of phylogenetic markers (TrichoMARK) and a local BLAST server [36]. TrichOKey and TrichoBLAST are Trichoderma-specific identification tools and had promoted Trichoderma-related studies during an earlier period with the classification system in genus Trichoderma containing only species. However, the current taxonomy of Trichoderma has changed dramatically and a recent report listed accepted Trichoderma names Bissett J [64] that has not been updated into the databases of TrichOKey and TrichoBLAST. Thus, there are no Trichoderma-specific identification tools currently applicable.

Apart from the mentioned identification databases, there are numerous databases with a broad diagnostic scope not only dedicate to Trichoderma [65,66]. The Genbank database contains the largest number of nucleotide sequences including multilocus barcodes. However, identification of Trichoderma spp., similar to other fungi, via BLASTn program in Genbank was advised to be cautious due to the non-curated association of sequences with the species name [35,67]. Aware of this issue, a curated sequence database was created especially for Trichoderma, referred to as RefSeq Targeted Loci database (RTL), with a joint effort between the National Center for Biotechnology Information (NCBI) and fungal taxonomy experts. Besides, among the numerous curated databases involving fungi sequences, the UNITE (User-friendly Nordic ITS Ectomycorrhiza Database) could also be adopted to identify Trichoderma species within a limited number of species. For a comprehensive learning of the identification tools and databases, it is advised to refer to the latest publications [65]. Taken together, the most suitable identification system currently available for Trichoderma is RTL-based BLASTn search due to its consistency with the up-to-date taxonomy of Trichoderma. The International Society for Human and Animal Mycology (ISHAM) working group for DNA barcoding have recently established a database, with special focus on the majority of human and animal pathogenic fungi [60].

Application of Trichoderma

Trichoderma in Human Health

Trichoderma species are possible source of important antimicrobial agents against gram negative and positive bacteria, fungi and yeast" [68]. Earlier in 1995, isolated peptides from Trichoderma strains showed antibacterial activity against S. aureus [69]; *Trichoderma harzianum* produced 44.06 µg/mL of the well-known antifungal drug, cyclosporine [70]. Similarly, Trichodermanins C–E (1–3), new diterpenes with a rare fused 6-5-6-6ring system, have been isolated from a fungus *Trichoderma harzianum*"Cytotoxicity assay using three cancer Cell lines showed significant activity in Yamada, et al. [71]. Broth extracts of *Trichoderma* species (*Trichoderma harzianum, Trichoderma longibrachiatum, And Trichoderma koningii*) showed antifungal and antibacterial Activity against Paecilomyces variotii, Penicillium notatum, Nematospora coryli, Mucor miehei, Bacillus brevis, Bacillus subtilis, Enterobacter dissolvens and Sarcina lutea using agar disk diffusion method [68].

Trichoderma species Displays antimicrobial activity against many important bacteria, yeasts, and filamentous fungi [72], in which numerous and varied secondary metabolites, such as peptaibols, gliotoxin, gliovirin, polyketides, pyrones, and terpenes may be involved [73]. As a natural product, terpenes constitute the largest group of secondary metabolites with important pharmacological activities such as antiviral, antibacterial, antimalarial, and anti-inflammatory actions, inhibition of cholesterol synthesis, and anticancer activity. A large series of these compounds are produced by the filamentous fungi like Trichoderma [74,75]. Sesquiterpenes from Trichoderma have demonstrated

antibacterial, antifungal and neuroleptic activities. There are different species of Trichoderma producing bioactive compound that act as a mycotoxin such as Trichothecene the secondary metabolite synthesized mainly by Fusarium and fungal genera such as Trichoderma, Trichothecium, and Stachybotrys [76].

Enviromental Role of Trichoderma (Bioremediation)

The genus Trichoderma is genetically very diverse with a number of capabilities among different strains with agricultural and industrial significance [77,78]. There are several reports indicating, potential application of *Trichoderama* remediation of soil and water pollution [10]. Its use has also been demonstrated in preparation of biofilms in the field of nanotechnology [79,80]. Heavy metals like cadmium, copper, mercury, manganese, zinc, and arsenicare increasingly being released into the environment from geochemical and industrial wastewater, their uses in pes-ticides, fertilizers, wood preservatives, tanning, and other anthropogenic activities; are among the most difficult contaminants of the enviroment [81]. Fungal strains grouped in the genus Trichoderma possess very effective soil colonization, with high biodegradation potential [10,78].

Industrial Significances of Trichoderma

The genus Trichoderma is a good source of several hydrolytic and industrially important enzymes. In addition to their role as natural plant protection agents (biofungicides) and bioremediation practices, Trichoderma Sppecies are utilized in several industrial purposes—mainly in the large-scale production of antibiotics, enzymes, and biofuels [82]. The extracellular enzymes produced by *Trichoderma* species are frequently used in the food and textile industries [83]. Enzymes from Trichoderma are applied to improve the brewing process (β-glucanases), as macerating enzymes in fruit juice production (pectinases, cellulases, hemicellulases), as feed additive in livestock farming (xylanases) and for pet food. Cellulases are mainly applied in baking, malting, and grain alcohol production [84] the genus Trichoderma is also potential source of bioenergy production. The enzymes like cellulases or hemicellulases produced by Trichoderma species, e.g. T. reesei mainly used in the production of the second generation biofuels that obtained from the agricultural waste [84]. The Genus Trichoderma are sources of mycotoxins and more than 100 metabolites with antibiotic activity including polyketides, pyrones, terpenes, metabolites derived from amino acids, and polypeptides. Trchoderma have been also employed in production of nanoparticles, for example silver nanoparticles (AgNPs) use T. reesei [80] and synthesis of extracellular gold nanoparticles using T. koningii [79].

Agricultural Significance of Trichoderma Speciese

Repeated use of chemical pesticides to manage and control fungal pathogens raises a big concerns like: - destruction of soil structure, soil infertility, and accumulation of toxic compounds on crops. In addition to these, there are reports that indicate "chemical fungicides become ineffective on plant pathogens due to their diversity, adaptability and increasing resistance" [1]. Various microbial biocontrol agents are used for management of the plant diseases to attain a sustainable agriculture for future generations [85]. Knowledge about biocontrol potential of the fungus *Trichoderma* species has been recognized as early as 1920 [19]. There are several reports that indicated the potential of trichoderma in agriculture. Trichoderma harzianum (Th. Azad) and Trichoderma viride (01PP) are used as biopesticides and biofertilizer [86,87], growth promoters, and inducers of disease resistance in plants [87]. *Trichoderma harzianum* (Th. Azad) is the main antagonist utilized in management of plant diseases in agriculture [86,88]. The genus *Trichoderma* has also a great potential in improving vegetative growth of plants and nutrient content of soil through decomposition and biodegradation [87]. Trichoderma-based products are marketed worldwide and applied in fields, nurseries, and horticulture for management of fungal soil-borne pathogens such as Pythium and Rhizoctonia [86,87]. It is a safe and environmentally friendly method to reduce the detrimental effects of chemical pesticides [88]. Various articles reported on the role of Trichoderma speciesas antagonist to plant pathogens such as *Trichoderma harzianum, Trichoderma asperellum, and Trichoderma virens* against Phytophthora capsici in red pepper; *Trichoderma* isolates against Sclerotium rolfsii, Colletotrichum gloeosporioides, C. capsici [86], S. minor and S. sclerotiorum in the in vitro experiments [89]; T. atroviride SY3A and T.harzianum SYN were effective biological control agents of R. solani damping-off of cucumber [90]; *Trichoderma* isolates were antagonist to soil-borne phytopathogenic fungi (*Fusarium graminearum, Rhizoctonia solani, Macrophomina phaseoli, and Phytophtora cactorum*) [91]; *Trichoderma* species was antagonist to anthracnose of strawberry;*Trichoderma* isolates inhibit and control the growth of *Fusarium oxysporum* with *Trichoderma Harzianum* being the most effective [92]; *Trichoderma viride, Trichoderma polysporum, and TrichodrmaHarzianum* inhibit more than 60% growth of *C. Paradoxa* [93]; *Trichoderma hamatum* LU593 and *TrichodermaVirens* LU556 delayed aphids manifestation on cabbage [94]; *Trichoderma* Isolates against Sclerotium Rolfsii.

Trichoderma as Biocontrol Agent: Fungi in genus Trichoderma have been known since 1920s for their capability to function as biocontrol agents (BCA) against plant pathogens [32]. The genus Trichoderma has gained

immense importance in past several decades due to its antagonistic ability against wide range of plant pathogens and growth promotion in crop plants. Some species of Trichoderma viz., Trichoderma harzianum, T. viride, T. virens and T. koningii are well known antagonists and are being utilized to control plant pathogens under field conditions [95-97]. Promising Trichoderma isolates have different mechanisms or combination of direct parasitism, competition for nutrients, stimulators of plant health, or inducers of plant systemic resistance against various pathogens [25,87,98]. Several research findings have been reported that various diseases of different crops controlled by *Trichoderma* species. For instance Trichoderma applied against rice sheath blightdiseas caused by Rhizoctonia solani Biswas andFusarium moniliforme,against wheat leaf blightcaused by Alternaria triticina,chick pea Wilt,wilt complex caused by Fusarium,Sclerotium, Rhizoctonia, Potato Black Scurfcaused by Rhizoctonia solani and tomato Fusarium wilt Fusarium oxysporum f.sp. Lycopersici [99].

In addition to control of plant diseases, different species of the genus Trichoderma have also capability to enhance plant growth and development, to elevate reproductive ability, to modify the rhizosphere, to grow under adverse conditions, competence in the use of nutrients, strong aggressiveness against phytopathogenic fungi and efficacy in supporting plant growth and enhanced defense mechanisms [100-102]. These properties have made Trichoderma a omnipresent genus able to grow in wider habitats and at high population densities [103]. Endophytic Trichodermaused as biological control agentsuppressedfusarium wilt ofbanana, Induced resistance by increasingperoxidase activity and total phenols of banana plantandstimulate vegetative growth of banana seedling[104]. Trichoderma species (T. harzianum, T. viridiae, T. virens) are being utilized in plant disease control as the bio-pesticide [105]. Trichoderma species possess several control mechanisms to combat against phytopathogenic organisms. These biocontrol mechanisms include competition with plant pathogens, mycoparasitism, antibiosis, and production of lytic enzymes and secretion of secondary metabolites [73].

***Trichoderma as* Plant Growth Promotor:** Positive effect on plant development has been demonstrated for several Trichoderma Secondary Metabolites. Seed biopriming and seed treatment with *Trichoderma* species enhanced the speed of germination and seedling vigor in okra, maize, beans, mustard, chilli, soyabean, chickpea, tomato etc. [86,106-108]. Many seed invading pathogens such as Pythium are unable to attack on host due to faster seed germination and seedling vigor.

Effect of *Trichoderma* on Plant Morphology and Plant Physiology: The rhizosphere microbial populations exert beneficial, neutral, or detrimental effects on plant growth. Trichoderma inoculation enhanced root biomass and increased root hair development in maize plant [2,109]. The root system is important for plant fitness because it provides anchorage, effectively use of water, and facilitates the acquisition of mineral nutrients from the soil. It has been reported that *Trichoderma harzianum* and *Trichoderma virens* has been found for growth promotional activity which was correlated with prolific formation of lateral roots [77]. The phytohormones produced by *Trichoderma* species are vital factors in the increase of rice plant height. *TRichoderma virens* is able to produce auxins as indole-3-acetic acid (IAA), indole-3-acetaldehyde (IAAld), and indole-3-ethanol (IEt), which regulate plant root system architecture and which has been play roles in plant growth and development [77]. Cai and his fellows reported that harzianolide produced by *Trichoderma* species can improve the early stage of plant development through the enhancement of root length. These morphological modifications are due to environmental buffering (against pH, heat, drought, waterlogging, cold) and phosphorus solubilization, organic matter decomposition, chilation and siderophore production ability of the *Trichoderma* species [110-117].

Trichoderma species are not only plant morphological determinants but also able to alter several physiological processes such as: net photosynthetic rate, stomatal conductance, transpiration, internal CO_2 concentration, water use efficiency and nutrient uptake. Better nutrient uptake will enhance the physiological processes within the plants treated with *Trichoderma* species leading to good growth performance. It reported that *Trichoderma harzianum* significantly increased the rice plants drought tolerance ability stress and its water-holding capacity. The rice plants treated with *Trichoderma* have been showed approximately three folds increase in net photosynthetic rate and stomatal conductance and two fold increases in water use efficiency when compared to NPK treated plants. High photosynthetic rates coupled with low transpiration rates in *Trichoderma* treated plants indicate high water use efficiency.

Conclusion

The genuses *Trichoderma* that habitate different ecology and found in all climate zone around the world have potential applications in different areas. Trichoderma sppcies have great potential use in agriculture biocontrol agent against different plant pathologies, improving physiological response to stresses and nutrients uptake in plants, enhancing nitrogen-use efficiency in different crops. The genues trichoderma gained great attention for its industrial enzymes production that are used to improve the brewing process (β-glucanases), for fruit juice production (pectinases, cellulases, hemicellulases) and as feed additive

in livestock farming (xylanases. In the environmental aspect it has a great role in the bioremediation of polluted enviromet.Considering these tremonduase importances of Trichoderma, eploring a suitable and efficient Trichoderma strains that will be suitable for different industrial, agricultural and environmental application is mandatory. For Taxonomy classification and diversity study the integration of molecular methed with morphological characters should be utilized.

Declarations

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- The manuscript does not contain experiments using animals.
- The manuscript does not contain human studies.

Competing interests

Authors declare no competing interests.

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