

<https://soilfun.org/>, a web-based platform for soil-inhabiting *Ascomycota* species

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Abstract

Soil covers a large area of the earth's crust and supports a high level of bio-diversity. This diversity is influenced by numerous geobiological variables, which impact soil fungal distribution worldwide. The taxonomy of soil-associated fungi has been investigated over the years using various approaches. To recover below-ground fungal species, researchers currently use culture-dependent and culture-independent approaches such as high-throughput techniques. As a result, a significant amount of taxonomic information is being generated and scattered throughout many publications. Most recent publications and databases of soil *Ascomycota* are derived from high-throughput techniques mainly focused on higher taxonomic ranks; however, information of the genera and species identified from soils are not conglomerated into a single database. Therefore, the Soil Fungi website aims to create an online platform to compile the soil-associated fungal species with comprehensive taxonomic descriptions and continuously update them following the most recent classifications. The scattered information will be obtained from publications and conglomerated on the website where users have quick and user-friendly access. This paper introduces the <https://soilfun.org/> website with its objectives and functions and provides a guideline for accessing and retrieving information. The website will serve as a central database of soil-associated fungal species, including their taxonomic descriptions and other relevant information. Users will be able to access and retrieve information from the website easily. The Soil Fungi website will be an essential tool for researchers, students, and other interested parties in soil mycology.

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Introduction

Soil is a remarkably complex substrate that provides various niches for microbial communities. In this environment, fungi are the main biotic component and mediate many below-ground functions. However, their distribution is variable due to inconsistencies in resource levels (nutrition, soil, water, and air)^[1,2]. Besides, most fungi spend at least one stage of their life in the soil, showing different trophic modes such as pathogenic, saprobic, or mutualistic^[3,4]. Studies have shown that *Ascomycota*, *Basidiomycota*, *Chytridiomycota*, *Glomeromycota*, *Mortierellomycota* and *Rozellomycota* are widely distributed in edaphic habitats^[5–7].

Culturing and high-throughput sequencing (HTS) methods are currently applied for detecting belowground *Ascomycota* groups^[5,7–9]. *Ascomycota* is represented by dominant classes in soil, including *Arthoniomycetes*, *Dothideomycetes*, *Euro-*

tiomycetes, *Leotiomycetes*, and *Sordariomycetes*^[5–7,10,11]. Of them, some genera, such as *Fusarium*, *Penicillium*, and *Phoma*, are prevalent^[7,12], while others, such as *Ambrosiella*, *Arcopilus*, *Didymocyrtis*, *Kionochaeta*, and *Parathyridaria* have rarely been isolated^[13–15]. This is because exclusive adaptations to below-ground environments and a lack of isolation techniques make it difficult to recover *Ascomycota* species. Most soil ascomycetes are identified at higher taxonomic ranks through HTS, which led to many recent publications and databases showing the taxonomy and distribution patterns of belowground fungi only up to the genus level^[16].

High-throughput sequencing has impacted the estimation of the number of fungi and the endemism of soil taxa in different parts of the world^[8,17,18]. Some databases have attempted to gather information on soil fungal diversity based on HTS. For example, the GlobalFungi (<https://globalfungi.com/>) provides information on taxonomy, ecology, and reference sequences of

taxa from different habitats, including soil^[17]. The Global Soil Mycobiome consortium dataset, a global soil study recovered 722,682 fungal Operational Taxonomic Units (OTUs), representing 62.4% of the total OTUs^[7]. Among them, 330,054 OTUs were assigned to *Ascomycota*. The total number of fungi is estimated as 6.28 million species^[9] and found the highest diversity from soil and litter samples, revealing that soil fungal sequences have 75% overlap with previously known species. In addition, some studies have recovered unculturable fractions representing several new lineages at the phylum level^[4–6,10,19].

Few studies compare the taxa recovered by HTS and culturing methods from the same sample or location. For example, Stefani et al.^[20] compared the fungal diversity from petrochemical-contaminated soils in Canada. They found that the number of OTUs ranged from 153 to 235 depending on the level of contamination (slightly to highly contaminated), and culturing methods yielded 8 to 43, respectively. Based on these results, we can roughly estimate that only around 5%–65% of the soil fungal community can be cultured in any environment and we need to develop methods to approach the rest of the 35%–95%. A study on Antarctic crypto-endolithic fungal communities identified several black fungal species that were only detectable through cultivation and found a 12% overlap of species from both culture-dependent and -independent approaches, which resulted in 4,618 colonies and 1,439,748 sequences^[21]. The successful isolation of these species highlights the importance of using both complementary techniques^[21]. Compared to overall HTS results, the cultured fraction is smaller as they have vast differences between the two approaches. However, HTS results can excel in culturing the soil taxa, for example, to plan on isolating targeted taxa or selecting suitable fungal isolating methods in a particular area^[8,16]. Culturing is essential to obtain molecular and morphological data of species and recover the undetectable ones from HTS.

However, around 80% of all soil-inhabiting taxa are not assigned to species level, and 20% to known orders^[5,19,22]. Thus, the soil can potentially reveal many undiscovered species in the future^[8,9]. Contemporary studies have described and resolved soil-associated *Ascomycota* species from *Dothideomycetes*, *Eurotiomycetes*, *Leotiomycetes*, and *Sordariomycetes* with morpho-molecular support^[23–28]. However, no recently updated study or database shows the total number of species isolated from the soil^[16].

Over the last few decades, several books have been published based on morphology, such as *Compendium of soil fungi*^[29–31], *Manual of soil fungi*^[32], *The Genera of Hyphomycetes from soil*^[33], and *Soil fungi: diversity and detection*^[34], which provided the diversities of worldwide soil species with comprehensive morphological illustrations. The *Atlas of soil ascomycetes*^[35] illustrated anamorphic and teleomorphic (fruit body and hyphomycetes form on cultures) structures, culture characteristics, and keys to the species. Currently, many taxonomists have adopted DNA sequences to determine species boundaries. However, species delineation criteria can differ among groups, such as cryptic species, pathogenic genera, and species complexes that need solid phylogenetic resolution^[36–39]. In this regard, soil-associated species are a highly complex group, and taxonomists have been using the polyphasic approach, combining morphological, physiological, ecological, and molecular methods to determine species^[36,38,40,41].

Precise identification of fungal species/genera is critical for further use in taxonomy and biotechnology research^[8,16,42–44]. For example, pathogens are important in disease management, while soil-borne extremophilic genera (e.g., *Verruconis*) are sources of bioactive compounds^[42,45,46]. Thus a database integrating taxonomy, ecological, and economic information of soil fungi helps to identify these organisms by end-users. The Soil Fungi website aims to collect and provide accurately identified soil fungi and continuously update checklists and notes on genera. This will increase the availability of information in the field and provide a valuable resource for researchers and students studying soil fungi. The website will be a central database of soil-associated fungal species, including their taxonomic descriptions and other relevant information. Users will be able to easily access and retrieve information from the website, such as the distribution of certain fungal species and their ecological roles. The website will also provide a platform for collaboration between researchers and interested parties, allowing information and idea sharing. Furthermore, the Soil Fungi website will help estimate the number of soil genera discovered over time. This information will be useful for understanding the diversity and distribution of soil fungi and for developing conservation strategies for these important organisms.

Why is it important to have a database for soil fungi?

The current information on soil fungal taxonomy is available as HTS and culture-dependent data^[4,6,8,47–50]. These two forms of data can cause contradictions in species identifications and seem unstable and affect studies. Moreover, the number of fungal species in the soil has been estimated from HTS methods, but there is no updated account for recently identified or recorded species from the soil. In addition, morpho-molecular identifications also face shortfalls as some genera are well-studied, while some have phylogenetic ambiguities^[51–53]. For example, specious genera, such as *Aspergillus*, *Cladosporium*, *Fusarium*, *Mucor*, *Penicillium*, and *Trichoderma* are common in soil. Due to the similar morphologies resulting from hybridization, cryptic speciation, and convergent evolution, their species delineation is difficult^[54]. Therefore, compiling updated phylogenetic and morphological data of the genera/species present in the soil are essential. It is also important to gather data on the type of soil ecosystem, locality, identification method, and economic impact of the species or genera. Since most of the information is scattered among various publications and databases, compiling them into a single database is beneficial for mycologists, ecologists, clinical studies, and the general public.

Even though information about soil fungi is available in online databases e.g., Fungal Genera^[55], GlobalFungi^[17], UNITE^[56], and Global Soil Mycobiome consortium (GSMc)^[7], they lack specific information on fungal species and relevant morpho-molecular data. Further, in other databases like 'Faces of Fungi' (www.facesoffungi.org)^[57], 'Dothideomycetes' (www.dothideomycetes.org/)^[58], 'Sordariomycetes' (<https://sordariomycetes.org/>)^[59], GSM microfungi (www.gsmmicrofungi.org/)^[60], and 'Coelomycetes' (<https://coelomycetes.org/>)^[61] information about *Ascomycota* studies are commonly found. However, a website compiling morpho-molecular data of soil fungi has not been developed. Therefore, we developed and

A web-based platform for *Ascomycota* in soil

implemented a web-based platform as the information hub for soil fungi research. The website provides a checklist of all the soil-associated *Ascomycota* genera. These generic notes include taxonomic descriptions, phylogenetic data, and other hosts/-substrates for each species, accompanied by photographic plates or drawings and detection methods. It also provides a list of novel or existing species of soil fungi for each genus, which will be updated over time. The data from previous studies will be periodically included to disseminate information in a holistic approach, enhancing the in-depth understanding of the soil-inhabiting fungi and resource for retrieving multiple data.

Soil Fungi website

The website provides a comprehensive checklist of all the soil-associated genera in *Ascomycota* essential for identifying and classifying soil fungi. The generic notes contain morphological descriptions, information on phylogenetic analyses such as gene regions, a summary of the latest phylogenetic revisions, ecological and economic impacts and the distribution. For each genus, a list of novel or existing soil-inhabiting species is provided, which will be uploaded and updated over time. Each species is accompanied by taxonomic descriptions, photographic plates or drawings, and detection methods. Each species/genus description is linked to the original publication(s), thus, users have real-time access to further details (Fig. 4). The website ensures that researchers can access the latest information about soil fungal taxonomy and keep up with the latest research developments. The data from previous studies are rearranged, and future studies will be periodically included to disseminate information in a holistic approach. Therefore, the website remains an up-to-date resource for researchers, providing them access to the latest research on soil fungi. These data will enhance an in-depth understanding of the soil-inhabiting fungi and will be important for future research. We encourage all the taxonomists and interested parties who work on soil fungi to contribute their published data to this website which will enhance the information availability and ensure that the website becomes an invaluable resource for retrieving multiple data, providing researchers a platform to share their research and collaborate with others in the field.

Construction

On the website, taxa are arranged according to the latest classification^[53]. The history of soil taxonomy is briefly described, and links to related literature are provided. All taxonomic entries are checked by the curators prior to uploading and published in a consistent format. The list of curators and their contact details are displayed in Table 1.

Interface and visualization of the database

The website is available at <https://soilfun.org/> and provides a user-friendly interface to retrieve updated information on the classification of soil-inhabiting *Ascomycota*. It is easy to access and navigate. The homepage comprises a navigation bar and a search tool to retrieve information.

Home page

The Home page displays the summary of the project (Fig. 1). A navigation bar is displayed at the top of the page. Below the navigation bar, the main objectives of the webpage are

Table 1. List of curators for the <https://soilfun.org/> website.

Position	Name	Contact details
Head curator	Dr. A. Roberto G. Farias	rfariasagro@gmail.com
Expert curator	Prof. Dr. Rasoul Zare	simplicillium@yahoo.com
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	Prof. Dr. Sajeewa Maharachchikumbura	sajeewa83@yahoo.com
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displayed in the left column, while the right column displays the search tool and the recently updated entries. The bottom of the page shows the publisher details, copyright information, and contact details. The navigation bar consists of eight menu items (Home, Outline, Archives, Reference, Curators, History, Reference, Notes, and Contact). These menu items facilitate easy navigation throughout the website, allowing users to access the information they need, quickly and efficiently.

Outline

Under this navigation menu item, the website presents the latest taxonomic representation of genera that are recorded from soil obtained from peer-reviewed publications (Fig. 2). The user can scroll down to find any taxa or the search bar is optional, where the user can type preferred taxa, and be directed to the exact location. Each taxon is linked to its corresponding taxonomic description, which can be accessed by clicking on the relevant name.

Archives

The orders to which different fungi isolated from soil belong are listed alphabetically under this menu item (Fig. 3). When the user clicks on a preferred order, a dropdown list containing its families and a 'Read more about...' link to the description of each hierarchical taxonomic level is displayed. Similarly, when the user clicks on a family, it shows the related genera and a 'Read more about...' link to the family description. When the user selects a preferred genus, a 'Read more about...' link to the description of the genus and a list of soil-associated species linked to their taxonomic descriptions and illustrations are shown (Fig. 4). Each taxonomic description includes a web source link, enabling the reader to access the original publication directly. This information is continuously updated according to the latest publications, ensuring user access to the most up-to-date and accurate information on soil-inhabiting *Ascomycota*.

Curators

Curators and contact details are provided under this menu item (Fig. 5). These curators are expert fungal taxonomists who continuously monitor the webpage and suggest improvements.

History

Under this menu item, the evolution of soil fungal taxonomy is briefly discussed, together with the available culture-dependent and independent approaches (Fig. 6).

References

References used in the entries are provided under this menu.

Notes

Important events, information, and the latest trends in soil fungal taxonomy are provided here.

Contact

Under this menu item, a dialogue box is provided for the users to exchange information directly or share their suggestions and/or comments. Furthermore, the email and the address of the publisher are also given.

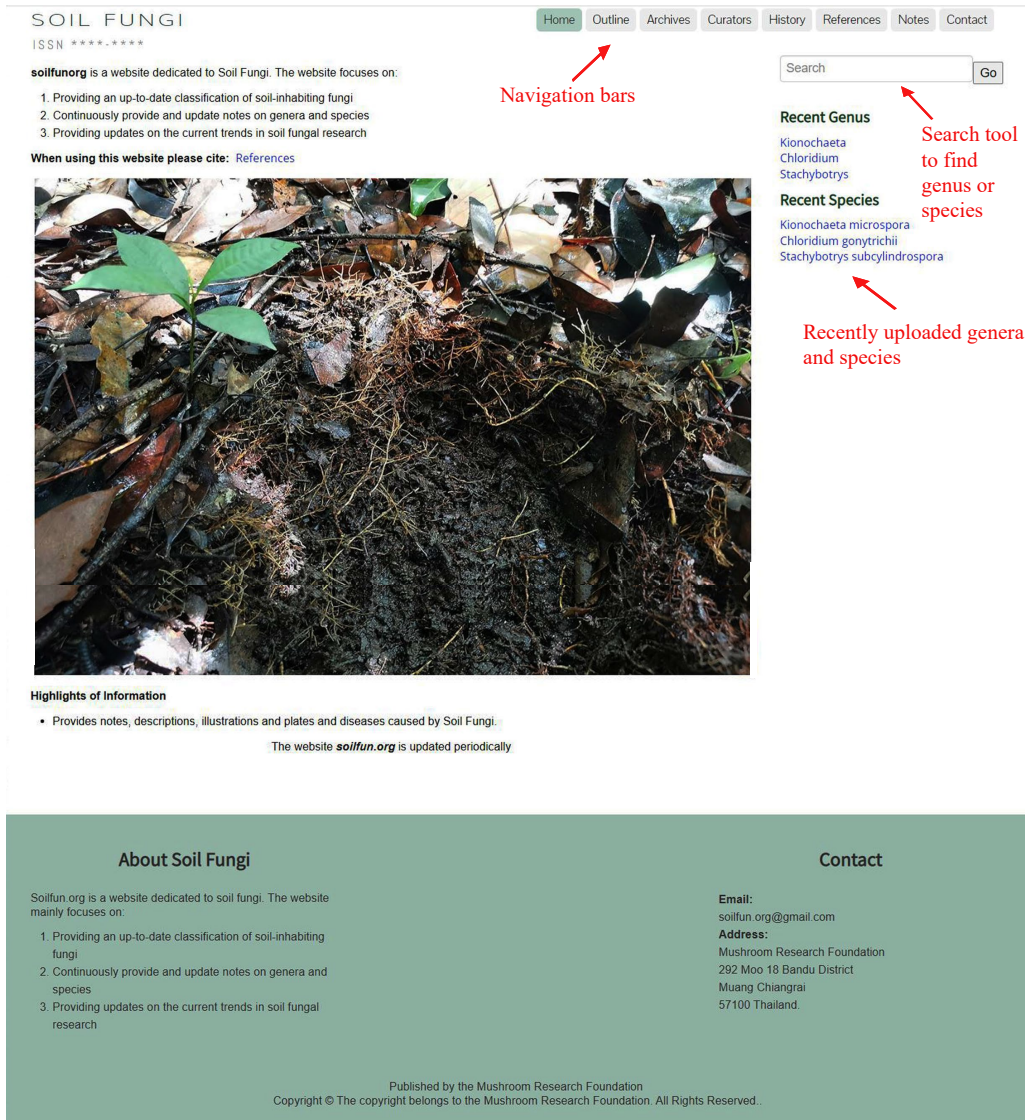


Fig. 1 Home page of the Soil Fungi website.



Fig. 2 'Outline' contains soil inhabiting *Ascomycota* taxa according to the latest classification.

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Soil Fungi Heirarchy

Amphisphaeriales
Calosphaeriales
Chaetosphaeriales
Hypocreales ← Order
[Read more about Hypocreales orders »](#)
Cordycipitaceae ← Family
[Read more about Cordycipitaceae family »](#)
Flavocillium ← Genus
[Read more about Flavocillium genus »](#)
Flavocillium primulinum ← Species
Flavocillium subprimulinum

Gamszarea
Lecanicillium
Simplicillium
Stachybotryaceae
Microascales

Search Go

Recent Genus
Jattaea
Wardomycopsis
Scopulariopsis

Recent Species
Jattaea reniformis
Wardomycopsis fusca
Wardomycopsis dolichi

Fig. 3 'Archives' configured with a dropdown list of taxonomic hierarchy with links to order, family, genera, and species descriptions.

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Amphisphaeriales » Beltraniaceae » Beltraniella

Beltraniella fertilis ← Species name

Beltraniella fertilis Heredia, R.M. Arias, M. Reyes & R.F. Castañeda, Fungal Diversity 11: 100 (2002) Fig. X

Index Fungorum number: IF489903; Faces of fungi number: FoF 0363z ← IF and FOF numbers

Colonies on PDA pale white, reaching a diam. of 2–3 cm in 4 days at 25°C, flat and circular-shaped, pale brown, smooth at surface and produce highly branched melanized hyphae with brownish exudates in old cultures, after 16 weeks, with conidiophores forming on the mycelium; reverse light yellow to dark brown. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Mycelium mostly immersed in the substratum, composed of septate, branched subhyaline hyphae. *Setae* numerous, erect, straight or flexuose, unbranched, single or in small groups, thick-walled, verrucose, dark brown at the base, paler at apex, 61.7–149.8 µm long, 2.5–7 µm wide (\bar{x} = 113 × 4 µm, n = 30) at the base, tapering to a pointed apex. *Conidiophores* macronematous, sometimes setiform; single, straight, septate, partly verrucose, thick-walled to smooth-walled, 6.4–91.5 µm long, 2.3–6.5 µm wide (\bar{x} = 37 µm × 3.4, n = 30), sometimes branched at the apical region, dark brown to sub hyaline at the swollen base, paler and slightly tapering towards a pointed apex. *Conidiogenous cells* holoblastic, monoblastic to polyblastic, integrated, terminal. *Conidia* solitary to aggregated, acrogenous, simple, dry, straight, smooth, thin-walled, biconic, turbinate to pyriform, rostrate to pointed at proximal end, rounded at distal end, hyaline to sub hyaline, 5–15 µm long, 2–6.5 µm wide (\bar{x} = 10.11 × 3.97 µm, n = 30) in the broadest part.

Distribution – Atlantic forests, Brazil, Mexico, Thailand ← Host-substrate and distribution

Known hosts – Dead leaves of *Mangifera indica* and *Parinari alvimii*

Material examined – Thailand, Chiang Mai Province, Mae Tang district, Ban Pa Deng, Mushroom Research Center, N 19° 07' 13.7", E 98° 43' 52.9", 905 m, in forest soil (dominated by Dipterocarpaceae), 20th March 2019, Erandi Yasanthika, Erscm11 (MFLU 20-0506), living culture MFLUCC 20-0119.

Notes:
Beltraniella fertilis was introduced by Heredia et al. (2002) based on morphological characteristics. The sequence data for this species was provided by Lin et al. (2017) from strains which was isolated from decaying leaves collected in Thailand.

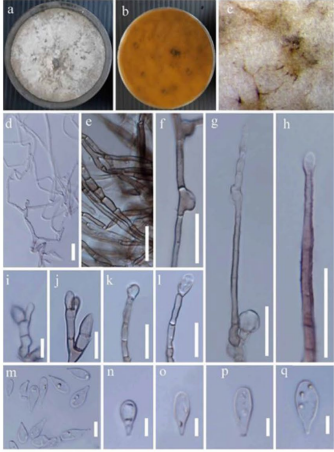


Figure legend

Figure X – *Beltraniella fertilis* (MFLUCC 20-0119) a Mature colony on PDA after 16 weeks with the sporulation, b Reverse of the colonies on PDA after 16 weeks, c Sporulation of the colony with conidial attachments on the mycelium, d Immature aseptate hyphae, e Mature pigmented, septate hyphae, f Chlamydospores on the mycelium, g Verrucose pigmented setae arising from the mycelium, h Conidiogenesis on the setae, i–l Conidiogenesis on the conidiophore, m–q Conidia. Scale bars: g = 25 µm d, h, i = 20 µm, e, f, j, k, l, m = 10 µm, n–q = 5 µm.

References:
Heredia G, Arias RM, Reyes M, Castañeda–Ruiz R. 2002 – New anamorph fungi with rhombic conidia from Mexican tropical forest litter. Fungal Diversity 11, 99–107.
Lin CG, Hyde KD, Lumyong S, Mckenzie EHC. 2017b – *Beltrania*-like taxa from Thailand. Cryptogamie, Mycologie 38, 301–319

Source:
Data and figures were reprinted with permission from:
Yasanthika WAE, Wanasinghe DN, Karunarathna SC, Bhat DJ, Samarakoon SMBC, Ren GC, Monkai J, Mortimer PE, Hyde KD 2020 – Two new Sordariomycetes records from forest soils in Thailand. Asian Journal of Mycology 3(1), 456–472, Doi 10.5943/ajom/3/1/16 -in AJOM ← Web link


Fig. 4 Information provided for the soil-inhabiting species with taxonomic description.

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Curators




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Recent Genus
[Pseudophthomyces](#)
[Yunnania](#)
[Eosphaeria](#)

Recent Species
[Eosphaeria uliginosa](#)
[Stellatospora terricola](#)
[Pseudoneurospora amorphoporcata](#)

Fig. 5 'Curators' provides the list of curators with their contact details.

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History

Soil fungi

Fungi have an enormous diversity on earth (Hyde et al. 2020, Liimatainen et al. 2020). Belowground fungal communities have a high diversity compared to other terrestrial ecosystems (Bridge & Spooner 2001, Tedersoo et al. 2022). They are most prominent in soil-biota, accounting for around 90% of the total microbial biomass (Bills et al. 2004). Various edaphic factors can boost or suppress the fungal community assemblage throughout the globe (Fracetto et al. 2013, Frac et al. 2018). Fungi contribute in ecosystem functioning by mediating nutrient cycling of carbon, nitrogen and phosphorus, plant growth and development, and in dead material decomposition (van der Heijden et al. 2008). They can be present as saprobes, mutualistic organisms (mycorrhizal) and/or pathogens in soil.

In the past, taxonomy and detection of soil fungi were based on morphology. Direct inoculation (Waksman 1916), dilution plates method (Warcup 1950), immersion tubes (Chesters 1948), and baiting method (Butler 1907) were commonly used for colony isolation and recovery of *Alternaria*, *Fusarium*, *Mortierella*, *Penicillium*, *Trichoderma*, etc., in different studies (Warcup 1950, Chesters & Thornton 1956). During 1980s molecular methods were introduced; i.e. denaturing gradient gel electrophoresis (DGGE), temperature gradient gel electrophoresis (TGGE), amplified rDNA restriction analysis (ARDRA), cloning and genetic fingerprinting techniques, which helped to picture the unculturable taxa those dwell in soil (Sudhakar et al. 2018, Wu et al. 2019). In recent times, HTS (High throughput sequencing) technologies were developed empowering the taxonomy community and diversity studies of fungi. Currently, 'Next-generation sequencing' (NGS) and 'Third generation sequencing' (TGS), are the most popular in global soil studies (Wu et al. 2019, Tedersoo et al. 2021). This paved the way to recover cryptic taxa, groups in large land areas, studying the family and/or class level, in spite that cultures are important in species identification. Thus, both HTS and culture based morpho-molecular methods are being used for various soil studies (Wu et al. 2019, Chethana et al. 2020).

Aspergillus, *Fusarium*, *Penicillium* and *Trichoderma* are common genera in soil, recovered from many parts of the world by the use of both culturing and HTS methods (Tedersoo et al. 2017, Wang & Zhuang 2022). Recent studies have isolated strains of genera which used to be rare in the soil; i.e. *Calvatia*, *Chloridium*, *Cortinarius*, *Exophiala*, *Juxtiphoma*, *Kionochaeta*, *Kosmitatamycetes*, *Ogataea*, *Phialoparvum*, *Pichia*, *Plectosphaerella*, and *Zygoascus* (Groenewald et al. 2018, Giraldo, et al. 2019, Yasanthika et al. 2022).

Species identification in soil is critical and some of the cultures are sources of biotechnology as HTS methods are still lagged behind (Gutleben et al. 2018, Hyde et al. 2019). Thus, we use culturing and morpho-molecular approaches in their identification. In <https://soilfun.org/> present genera and species introduced or recorded from soils all over the world.

Recent Genus
[Jattaea](#)
[Wardomycesopsis](#)
[Scopulariopsis](#)

Recent Species
[Jattaea reniformis](#)
[Wardomycesopsis fusca](#)
[Wardomycesopsis dolichi](#)

Fig. 6 'History' provides the history and development of studies on soil fungal taxonomy.

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Conflict of interest

The authors declare that they have no conflict of interest.

Dates

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