INTRODUCTION

This is the period of discovery when researchers are focusing upon enumeration of global microbial diversity placing it around 1 trillion \((10^{12})\) inhabiting the earth (Locey and Lennon, 2016). At the same time significance of such findings in understanding the role of microbial communities in ecosystem functioning is also expanding. The huge number of microbial communities present on earth sets a challenge to find links between diversity and function.

Microbial diversity on earth includes bacteria, archaea, viruses and eukaryotic microbes which together compose a microbiome although this term is synonymously being used largely for bacteria. Therefore, the term mycobiome coined by Ghannoum et al. (2010) is used to represent the underrepresented component of microbiome, the fungus. Despite ubiquitous presence of bacteria and fungi in all ecosystems, domain bacteria predominate more than fungi in abundance (5.1 million species; Blackwell, 2011) and the amount of total DNA (~1.7×10^27 Mb; Landenmark et al., 2015) in the biosphere. Relative to mycobiome, patterns and processes in understanding microbiome are better documented (Dietert and Dietert, 2015) not only in humans but also in plant system (Berendsen et al., 2012) and other biomes. However, many researchers are currently exploring fungi which have been largely ignored as an integral part of microbiome (Cui et al., 2013). Fungi are widely distributed across all ecosystems as single celled or mycelial form, dominating more so under stressful conditions; they also show hyphal lifestyle wherein they are mainly involved in decomposition processes (Fig. 1). Mycobiome includes microscopic forms as well as world's largest and oldest organism, *Armillaria solidipes* (previously known as *Armillaria ostoyae*). This humongous fungus encompasses an area 3.7 sq miles (9.6 sq km) and is considered to be 1,900 to 8,650 year old (Ferguson et al., 2003). Fungi possess unique physiological, morphological characteristics and ecosystem function therefore it becomes reasonable to study how these organisms contribute to ecosystem dynamics.

Our current knowledge in characterizing mycobiome has improved by the development of next generation sequencing (NGS). Furthermore, use of modern bioinformatics tool has helped in discovering novel lineages thereby reshaping the tree of life (Hug et al., 2016). Growing interest in studying mycobiome is supported by several reasons. First, as the role of fungi towards ecosystem processes, driving nutrient cycling and as causative agent in many infectious diseases is extensively studied (Treseder and Lennon, 2015) which has further evoked the curiosity to investigate the functions encoded by the microbial genes and how they largely influence the overall health of the host (Qin et al., 2010). Secondly, growing evidence for significant role of fungus in host fitness and disease progression leads to investigate abiotic factors which shape distinct mycobiome (Fig. 2). Also, knowledge of mycobiome becomes essential in making deeper understanding of how microbiome affects ecosystem processes (Oever and Netea, 2014).

In this review we present a brief overview of our present knowledge on the diversity of fungi in major earth biomes.
with a focus on how their communities shift with slight perturbation, thus, suggesting outlook to improve our understanding on the role of mycobiome in regulating ecosystem processes.

**DIVERSITY AND ABUNDANCE OF FUNGI IN MAJOR BIOMES**

**I. Human System**

The magnitude with which fungi colonize different body sites is much smaller than bacteria (Underhill and Iliev, 2014). The composition of mycobiome varies between the different body sites and thus is believed to play an important role in the state of both health and disease. Since they are a minor part in microbiome, it faces many challenges such as lower abundance constituting 0.1-1 % of total microbiome and second isolation of fungal DNA may be difficult (Qi et al., 2010; Huffnagle and Noverr, 2013). As reported even ancient oral microbiome is conserved (Warinner 2014).

(a) Gut mycobiome: The human microbiome in our body is of the same order (updated revised ratio 1:1; Sender et al. 2016). Human gut contains 66 genera and 184 species of fungi (Underhill and Iliev, 2014). Hoffmann et al. (2013) have identified Saccharomyces (89%), Candida (57%) and Cladosporium (42%) in fecal samples from 98 healthy individuals as most prevalent genera in human gut. However, more research is required to establish that certain genera are exclusively found in gut or are influenced by dietary intake.

Dysbiosis of gut fungal mycobiota is associated with various diseases like increased diversity and abundance of Candida sp., Gibberella moniliformis, Alternaria brassicicola and Cryptococcus neoformans. These appear at the site of inflamed mucosa with decreased presence of Saccharomyces cerevisiae in the fecal mycobiome of patients with Crohn’s disease (Li et al., 2014). Similar results have been reported in pediatric patients with IBD and healthy controls (Chehoud et al., 2015). During IBD, pathogenic fungi, Candida and Trichosporon are highly abundant with decrease in non-pathogenic genus Saccharomyces (Iliev et al. 2012). Now more common diseases such as obesity are found to be influenced by mycobiome. For instance, obese people have increased abundance of fungi belonging to the phylum Ascomycota, classes Saccharomycetes and Tremellomycetes, and families Dipodascaceae and Saccharomycetaceae compared with non-obese subjects (Rodriguez et al., 2015).

(b) Oral mycobiome: According to Human Microbiome Project Consortium (HMPC), human mouth is heavily colonized by microbes and in complexity it is second to only colon. Around 50 - 100 bacterial genera have been identified in healthy human subjects (Bik et al., 2014). The first time oral mycobiome of 20 healthy human subjects was characterized through deep sequencing using ITS sequence (Ghannoum et al., 2010) that showed the presence of 85 fungal genera. Among ~15 most prevalent genera, pathogens such as Aspergillus, Cryptococcus, Fusarium and Alternaria were found as a part of resident mycobiome which varied greatly between different individuals. Beside ~15 most prevalent fungal genera, Malassezia and Epicoccum were found as additional fungal forms (Dupuy et al., 2014). Significant link has been established between oral mycobiome and HIV infected individuals where Candida, Aspergillus and Fusarium are most abundant fungal genera; no such pattern changes were observed in the microbiome (Mukherjee et al., 2014). The functional aspect of wide diversity in oral mycobiome and high variability within species could be essential to manage environmental stress.

(c) Lung mycobiome: Investigators are now looking at other body sites for fungal communities like lung which was previously thought to be a sterile organ. Charlson et al. (2012) reported presence of Davidiellaceae, Cladosporium, Eurotium, Penicillium groups in healthy control. Candida, Neosartorya, Malassezia, Hyphodontia, Kluyveromyces are most prevalent genera in diseased condition like cystic fibrosis (Delhaes et al., 2012). Exclusive dominance of Candida is also reported in lung transplant patients (Charlson et al., 2012) which is most likely due to immunocompromised condition and long term antibiotic use. Respiratory tract and oral cavity are exposed to environmental pathogens like Aspergillus which is commonly found in healthy lung and shares other genera of oral mycobiome (Ghannoum et al., 2010). In immunocompromised condition commensal forms may turn into pathogen causing aspergillosis (Underhill and Iliev, 2014)

(d) Skin mycobiome: Malassezia, Rhodotorula, Debaromyces, Cryptococcus and Candida are common skin commensal fungal genera identified based on culture based approach (Roth and James, 1988). With use of high throughput sequencing, Findley and colleagues (2013) have characterized healthy skin mycobiome wherein genus Malassezia dominated 11 torso and arm sites and plantar heel, toenail and toe web. Mycobiome is altered in dandruff afflicted scalps and has been reported to be dominated by Acremonium, Filobasidium, Penicillium, uncultured soil fungus, Malassezia, Cryptococcus, Didymella, Rhodotorula, Eupenicillium, Coniochaeta and an uncultured Ascomycte (Park et al., 2012). Malassezia is generally most common...
form in healthy and diseased state and is ecologically hyper-diverse fungus on earth (Amend, 2014).

II. Aquatic System

Fungi in marine ecosystem are both non-diverse and low in abundance as compared to fungal isolates found in terrestrial or other environments (Peay et al., 2016). This could be related to the fact that very low fraction (0.6%) of documented fungi are derived from marine environment. Several reports show the dominance of Ascomycetes and Basidiomycetes forms in deep marine sediments, hydrothermal vents, mangroves, corals and anoxic marine waters (Bass et al., 2007, Simoes et al., 2015, Amend et al., 2012). Yeasts and some unknown fungal forms are dominant in these environmental conditions (Le Calvez et al., 2009; Tisthammer et al., 2016). Phylogenetic analysis based on unique fungal SSU rDNA sequences analyzed Neospora, Aspergillus, Cordyceps, Fusarium, Ustilago like lineages, Coprinus, Antrodia Exidia which were found to be more diverse in marine habitats (Richards et al., 2012). For the first time members of Chytridiomycota was reported by Le Calvez and colleagues (2009) in deep vent ecosystem. They used SSU rRNA to determine fungal diversity in two deep sea hydrothermal vents. Out of 20 different phylotypes, nine were unsuspected phylotypes in vent ecosystem and five were new at genus level, two from Chytridiomycota and three from Basidiomycota. The species matching 97.7% similarity was found to be a pathogenic fungus, Chytridium polysiphoniae. However, diversity of fungi was high in deep sea hydrothermal vents as compared to surface water samples (Massana and Pedr’os Ali’o, 2008). Freshwater ecosystems show presence of members of Cryptomycota which plays a significant role in the microbial loop of freshwater ecosystem (Jones et al., 2011).

Edgcomb et al. (2011) reported high frequency of Basidiomycete yeast resembling closely Malassezia and Cryptococcus by targeting both RNA and DNA based diversity profiles. Especially, Malassezia a diverse and important group in marine environment (Amend, 2014; Gao et al., 2008) shows that marine taxa are interlinked with human and terrestrial genera and do not form a single monophyletic clade. Fungi from marine and terrestrial habitats are capable of making transition to deep sea where they can withstand deep saline conditions due to their membrane composition and structure.

In contrast to a study by Tisthammer et al. (2016) distinct mycobiome was observed between sediments and water column where Ascomycota and Basidiomycota were most abundant datasets whereas Chytridiomycota and Cryptomycota were present infrequently; only 15.4% of OTUs were shared between water column and sediment samples.

Mangrove fungi are second largest group dominated by Ascomycota (76% - 85%) and Basidiomycota (14% - 24%) in the rhizosphere sediments. In Avicennia marina (gray mangrove), fungal genera Aspergillus, Schizosaccharomyces, and Gibberella dominate the rhizospheric region; also, the rhizosphere harboured distinct mycobiome as compared to bulk soil (Simoes et al., 2015).

Fungi are also associated with corals and believed to be mutualistic, commensal to opportunistic pathogen depending upon environment and overall coral health. Metabolically active and diverse resident marine fungal community is dominated by Basidiomycetes and Ascomycetes in this environment. Sordariomycetes and Dothideomycetes (Ascomycota), and Agaricomycetes and Ustilaginomycetes (Basidiomycota) are the most species rich groups. Symbiodinium genotype and water temperature had no discernible impact on the fungal community (Amend et al., 2012). However, much more work needs to be done to unravel functional and nutritive relationship between fungi and coral hosts.

III. Plant System

Microbial communities associated with plants help in nutrient acquisition, growth and increased stress tolerance. Microbe-plant interaction occurs in three regions of plants, viz., rhizosphere, phyllosphere and endosphere. A single tree individual may host as many as 200 species of fungi (Bahram et al., 2010). Rhizosphere microbiome has gained considerable attention and this information has been recently reviewed (Berendsen et al., 2012). A study by Bai et al. (2015) analyzed the fungal community using 454 pyrosequencing targeting ITS region and reported presence of Ascomycota and Basidiomycota as a dominant phylum in the soil sample. Thelebolus and Mortierellales increased abundantly in the rhizospheric soil as a result of continuous cropping of soybean. Thanatephorus, Fusarium and Alternaria were predominant fungal pathogens. Another study by Ambardar et al. (2016) for the first time reported the dynamics of major fungal phyla in the rhizosphere of Crocus sativus and among these the members of phylum Zygomyctota were most dominant. An interesting fact about microbial dynamics depicted in this investigation was that the cornosphere in flowering and dormant stage was dominated by Basidiomycota and Zygomyctota, respectively clearly implying that fungal diversity is niche and growth stage specific.

The phyllosphere, the habitat provided by the leaves of living plants, is one of the largest microbial habitats on Earth, with an estimated global surface area of more than 4×10^8 km² (Morris and Kinkel, 2002). It is mainly colonized by phylum Ascomycota followed by Basidiomycota (Eusemann et al., 2016). Genotype of plant is a major factor in shaping the mycobiome in phyllosphere than does the geographical distance (Cordier et al., 2012).

IV. Soil System

Soil is a reservoir of thousands of fungal and bacterial species that play an important role in natural and managed agricultural soils (Tardy et al., 2015). Fungi are widely distributed in all terrestrial environments and previously detailed understanding of major groups of fungi, the extent of diversity in unique habitats in India, are well documented (Manoharachary et al., 2005). Saprotrophic taxa are more abundant in surface of the forest floor whereas mycorrhizal fungi predominate at soil depth where they show symbiotic association with roots of plants (Lindahl et al., 2007). Unlike
other soil fungi which are not influenced by plant-soil feedbacks, ectomycorrhizal fungi are positively related with host plant and high soil pH. Both groups are actively involved in major function of decomposition therefore variation in their community structure affects the ecosystem processes eventually changing plant productivity and diversity. A comprehensive study of 365 global soil samples from natural ecosystem using pyrosequencing revealed presence of Basidiomycota (55.7%), Ascomycota (31.3%), Mortierellomycotina (6.3%) and Mucoromycotina (4.4%) (Tedereso et al., 2014).

A culture-independent survey of the soil mycobiome in 600 soil samples found 20 most abundant families; predominant families were Atheliales, Corticiaeae, Cortinariaceae, Inocybaceae, and Russulaceae. Like animal and plant system, soil fungi exhibited geographic endemic (Talbot et al., 2014). Fungal communities were found to be divergent but functionally redundant across different biogeographical regions. It is likely due to the involvement of fungi in decomposition process of organic matter. Most importantly a vertical stratification of fungal diversity exists in soil (Lindahl et al., 2007; Voriskoova et al., 2013). The diversity in L horizon is influenced more by season than those present in the deeper horizon. In L horizon dominant fungal genera are Mycena, Sistotrema and Cryptococcus while in H and Ah horizon Russula and Lactarius are present. Abundance of fungal community declines with depth owing to the properties of soil i.e., organic matter content and pH (Voriskoova et al., 2013).

**ROLE OF METAGENOMICS AND NEXT GENERATION SEQUENCING**

Traditional approaches to cultivate fungi in agar medium and classifying based on morphological features cannot predict complete diversity in natural environment. Undoubtedly, advances in sequencing methods have revolutionized our understanding of fungal diversity. Unculturable fungi constitute a major proportion of species like unculturable bacteria which go undetected through traditional methods. It could be best exemplified by the study of Dellahe et al. (2012) who found that around 60% of fungi remain undetected through culture based methods. Out of 247 species found in the digestive tract, only 59 were identified by *in vitro* culture and 207 by molecular techniques (Gouba and Drancourt, 2015). With the advent of metagenomics and NGS platforms a great deal about fungal diversity even in unexplored ecosystem like marine and animal is now known with greater resolution (Chen et al., 2011; Table 1).

Metagenomics is a shotgun sequencing based method widely adapted to sequence DNA isolated from the environment and draft genomes are reconstructed from genome fragments (Dick et al., 2009). Through this technique organisms can be classified using phylogenetic information and metabolic capability. Besides being a powerful sequencing technique certain drawbacks associated with metagenomics study are the expenses involved and computational challenges (Morgan and Huttenhower, 2012). Furthermore, a major problem associated in assessing fungal diversity is that they constitute a minor component in microbiome samples.

| Table 1: Reported diversity of fungi in different biomes |
|---|---|---|---|---|
| No. | Sample and specimen type | Sequencing used, sample size, health status | Dominant fungal composition | Reference |
| 1 | Gut mycobiome, fecal samples | Pyrosequencing 454, n = 69, Healthy individuals | Candida, Saccharomyces, Geotrichum, Paecilomyces, Penicillium, Aspergillus, Flavobacterium, Debaryomyces, Pichia, Torula, Rhodotorula, Trichophyton, Trichophyton, Phoma, Talaromyces, Acremonium, Filobasidium | Ittali-Adams et al. (2015) |
| 2 | Oral mycobiome, oral rinse samples | Pyrosequencing 454, n = 20, Healthy individuals | Candida, Cladosporium, Aspergillus, Fusarium, Penicillium, Alternaria, Dothiorella, Cryptococcus, Phoma, Sclerotinia, Aureobasidium, Chrysogaster, Hormodendrum | Oliveira et al. (2010) |
| 3 | Skin mycobiome, scalp swabs | Pyrosequencing 454, n = 5, Healthy individuals | Alternaria, Penicillium, Fusarium, Uncultured soil fungi, Malassezia, Cryptococcus, Daldinia, Rhodotorula, Eszophilicum, Coniothyrium, Uncultured dermatophytes | Fink et al. (2012) |
| 4 | Skin mycobiome, skin swabs | Roche 454, n = 10, Healthy individuals | Malassezia (globosa, restricta, sympadialis), Penicillium (chrysogenum, ananosis), Aspergillus (fulvus, terreus, vermiculosus), Alternaria, Candida, Chrysosporium, Cladosporium, Mucor, Rhodotorula, Trichophyton | Finkley et al. (2013) |
| 5 | Lung mycobiome, bronchoalveolar lavage and oropharyngeal wash | Pyrosequencing 454, n = 4 (Paulege and Finkley sample) | Candida, Daldinia, Cladosporium, Paecilium, Aspergillus | Chabot et al. (2012) |
| 6 | Marine mycobiome, water and sediment sample | Pyrosequencing 454, n = 456 (Palige and Finkley sample) | Penicilium, Acremonium, Exophiala, Aureobasidium | Schumann et al. (2016) |
| 7 | Soil mycobiome, seasonal sampling of three parcels of Picea glauca (Quercus petraea) forest soil | Pyrosequencing 454, n = 4 seasons | Amanita, Myxomphalia, Mucor, Talaromyces, Talaromyces, Leucosporidium, Leptosphaeria, Pratia, Sclerotinia, Monilia, Alternaria, Penicillium, Aspergillus, Filobasidium, Phoma, Talaromyces, Rhiococcus, Debaryomyces, Phoma, Pichia, Torula, Rhodotorula, Aspergillus, Penicillium, Cladosporium, Pichia, Debaryomyces, Phoma, Talaromyces | Voriskova et al. (2013) |
| 8 | Plant mycobiome, wheat heads from two seasons of field | Illumina sequencing n = 10 | Gliocladium, Penicillium, Aspergillus, Pichia, Debaryomyces, Phoma, Talaromyces | Heit et al. (2011) |
| 9 | Rhizosphere mycobiome, Crocus annus | Pyrosequencing 454, n = 4 seasons | Rhizopus, Penicillium, Aspergillus, Pichia, Debaryomyces, Phoma, Talaromyces | Ambuhl et al. (2016) |
| 10 | Needle mycobiome, Picea glauca | Roche 454, n = 94 (3 samples from each season site) | Coniophora, Phialocephala, Dothidiales, Helotiales, Tricholoma | Turrioni et al. (2016) |

Microbial communities are mostly dominated by bacteria and there is relatively less amount of fungal DNA. Secondly, paucity of reference database for complete fungal genome is also a drawback. A second method is the targeted amplicon sequencing in which highly variable taxonomic marker ITS (Internal Transcribed Spacer) region is targeted and amplified and then compared with reference databases. For culture independent studies ITS region is amplified using PCR for mycobiome profiling. There are two ITS regions, ITS1 is located between 18S and 5.8S genes while ITS2 is located between 5.8S and 28S genes. Use of ITS marker for taxonomic classification is much similar to 16S rDNA region amplified to study bacterial community but differs in some respects. First, fungal ITS sequences of different species can differ widely in size and sequence content (Santamaria et al., 2012). The ITS RNAs are degraded shortly after transcription and are not incorporated into the ribosome (Allmang et al., 2000). Thus these regions are not conserved making it highly difficult to classify fungi to the species level. Second, there is no well established reference database of ITS sequences in fungi like 16S sequences for bacteria. Furthermore, ITS region generally provides insufficient taxonomic marker since known biological species are seldom grouped together within the same OTU (Schoch et al., 2012). Whole genome sequencing is far beyond possibilities delivered currently.
through sequencers like Illumina NextSeq and HiSeq since detecting fungi at species or even at subspecies level (10^{-10}-10^{-14} nucleotides per run) capacity is required (Zoll et al., 2016).

Tang et al. (2015) applied combined sequencing and analysis approach to construct a manually curated reference database optimized for annotation of gastrointestinal fungi of 6-10 week old female C57BL/6J mice; they evaluated the strength and weaknesses of Illumina Miseq advantages over Ion Torrent PGM for analyzing intestinal mycobiomes. Miseq platform enabled identification of even the largest ITS1 fragments whereas Ion Torrent PGM failed to amplify longer amplicons. In order to use optimal primer set which induces least bias in the amplified sequence pool, researchers are therefore targeting regions apart from ITS. A study by Dollive et al. (2012) developed 18S rRNA gene amplicons that avoids mammalian and plant sequences and a flexible software pipeline (BROCC) to classify single cell eukaryotes. Another study by Asemanniedja et al. (2016) used a new set of primers targeting the D1 region of nuclear large subunit (LSU) ribosomal DNA. These workers achieved a greater depth of sequencing and the relative proportion of OTU recovered by LSU primers were more compared to ITS2 primers.

**INTERACTIONS AND FUNCTIONALITY**

I. Intra-kingdom interaction (Mycobiome - Mycobiome): Mycobiome can influence ecosystem responses to the environment by interacting among themselves (Table 2). A recent study illustrated the complex and multidirectional interaction within mycobiome in a common disease like obesity (Rodriguez et al., 2015) where an inverse relationship was observed between the phylum Ascomycota with Basidiomycota and Zygomycota whereas, in non-obese patients a negative association was observed between Pichiaceae and Dipodascaceae. The finding of this study is in accordance with other studies on human subjects (Hoffmann et al., 2013; Mukherjee et al., 2014). The importance of intra-kingdom interaction is associated with decrease in normal flora of skin like Malassezia in HIES patients and increased representation of opportunistic pathogens Candida and Aspergillus (Oh et al., 2013).

II. Inter-kingdom interaction: a) Bacteriome - Mycobiome: Inter-kingdom relationship exists between microbe-microbe as well as with host to modulate the ensuing effect. Though bacteria and fungi share similar niche there are several contrasting characteristics between microbiome and mycobiome (Table 3). The crossstalk between microbes is mediated by metabolic intermediates of anaerobic fermentation such as short chain fatty acids (SCFAs) produced by Lactobacilli which inhibit transition from budding to hyphal growth (Noverr and Huffnagle, 2004). Later, SCFAs are found to be involved in protecting epithelial lining by inducing the production of an antimicrobial peptide, cathelicidin LL-37, which is important in maintaining epithelial integrity (Otto et al., 2009).

*Candida* is a resident of normal healthy mycobiome but transition of commensal form to pathogenic form is controlled by bacterial counterpart of microbiome. Jenkinson et al. (1990) reported intermicrobial binding between *C. albicans* and *Streptococcus* in oral cavity. *Candida albicans* strongly influenced microbiota restoration after cefoperazone treatment after which Bacteroidetes and Synergistetes decreased significantly while Firmicutes remained unaltered (Erb et al., 2013). A positive correlation was reported between *Aspergillus fumigatus* and *Streptococcus* in cystic fibrosis patients where latter produced quorum sensing molecules for interaction between SMG members (Streptococcus milleri group) (Delhaes et al., 2012). A recent study by Hoffmann et al. (2013) extended the association of microbiome-mycobiome with archaea lineages. *Prevotella, Candida* and *Saccharomyces* were positively associated with *Methanobrevibacter* and were further correlated with high carbohydrate intake. Both the fungal genera were negatively associated with *Nitrosospira* and absence of *Candida* with high intake of saturated fatty acids.

Apart from syntrophic association a study using model organism *C. elegans* showed that *Enterococcus faecalis* negatively regulated *Candida albicans* hyphal morphogenesis and biofilm formation (Cruz et al., 2013).

### Table 2: Features of mycobiome and their reported functions

<table>
<thead>
<tr>
<th>No.</th>
<th>Characteristic</th>
<th>Function of mycobiome</th>
<th>Reference</th>
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<tbody>
<tr>
<td>1</td>
<td>Mycobiome - abundance and diversity</td>
<td>Fungi derive from initial soil inoculation or saprophytic, parasitic or symbiotic. Abundance varies with the type of ecosystem. Abundances are found to be low and lowest in marine environments. More than 3000 OTUs of fungi were observed in human mycobiome and &gt;80,000 species in soil.</td>
<td>Castan and Dimitriou (2016), Dollive et al. (2014), Malassezia and Streptococcus are commensals of skin, teeth and oral cavity.</td>
</tr>
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<td>2</td>
<td>Metabolism of host immunity</td>
<td>Metabolism in human gut - o-galactosidase recognition (Porrett et al. 2016) and can interact with host cells. Certain fungi have been reported to induce and modulate immune responses (Bang et al., 2014).</td>
<td>Inderhees and Barnes (2014)</td>
</tr>
<tr>
<td>3</td>
<td>Nutritional acquisition</td>
<td>Fungi are essential in recycling of nutrients in all ecosystems because they are dominant decomposers of cellulose and lignin. Fungi can also be used as model systems to study the effects of microbiota on host health (Mukherjee et al., 2014).</td>
<td>Tien and Logan (2013), Dennis et al. (2015)</td>
</tr>
<tr>
<td>4</td>
<td>Prophylactic - colonization</td>
<td>Fungi are essential in recycling of nutrients in all ecosystems because they are dominant decomposers of cellulose and lignin. Fungi can also be used as model systems to study the effects of microbiota on host health (Mukherjee et al., 2014).</td>
<td>Tien and Logan (2013), Dennis et al. (2015)</td>
</tr>
<tr>
<td>5</td>
<td>Interactions between mycobiome and microbiome</td>
<td>Fungi are essential in recycling of nutrients in all ecosystems because they are dominant decomposers of cellulose and lignin. Fungi can also be used as model systems to study the effects of microbiota on host health (Mukherjee et al., 2014).</td>
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### Table 3: A comparative assessment of mycobiome vs. microbiome

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<tr>
<th>Characteristic</th>
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<th>Microbiome</th>
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<tr>
<td>Taxonomy</td>
<td>Fungi can also survive in low pH excluding fungal pH range for optimal growth. Community composition mainly related to pH in soil (Knoluk et al., 2010).</td>
<td>Bacterial distribution in ranges of pH, community structure altered strongly with changes in soil pH (Knoluk et al., 2010). Other factors are more pronounced such as temperature or large spatial scale.</td>
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<tr>
<td>Abiotic factors</td>
<td>Community composition altered with soil variations. Fungi show fungal species with diverse and abundant geographical location. Lack of bias in the amplified sequence pool, researchers are therefore targeting regions apart from ITS.</td>
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<td>Inter-kingdom relationships</td>
<td>Inter-kingdom relationships are mediated by metabolic intermediates of anaerobic fermentation such as short chain fatty acids (SCFAs) produced by Lactobacilli which inhibit transition from budding to hyphal growth (Noverr and Huffnagle, 2004). Later, SCFAs are found to be involved in protecting epithelial lining by inducing the production of an antimicrobial peptide, cathelicidin LL-37, which is important in maintaining epithelial integrity (Otto et al., 2009).</td>
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Similarly, reports on negative correlation are also supported for *Campylobacter* and *Candida* in HIV infected individuals (Mukherjee et al., 2014) and *Candida* sp. *Aspergillus clavatus* and Cryptococcus dominance with decreased presence of *Saccharomyces cerevisiae* during Crohn's disease has also been reported (Li et al., 2014).

Agler et al. (2016) demonstrated the effect of pathogenic fungus *Albugo* and *Dioszegia* as hub microbes on stability of microbiome and significant changes in its absence. Hub microbes can influence diversity by acting indirectly via the host or directly through colonization efficiency of other microbes. Hubs are main targets of abiotic factors and transmit direct effect on the microbiome. Similar mechanisms might be controlling mycobiome structure but it remains to be elucidated in human system.

b) Microbiome-mycobiome-viriome: Most recently estimating bacteriophage population of human gut together with its role in inflammatory bowel disease (IBD) and bacterial dysbiosis have been described (Norman et al., 2015). This work shows an inverse correlation between bacteriophage and bacterial diversity in IBD. Contributory role of enteric mycobiome and viriome in IBD provided evidence that the viriome-mycobiome-microbiome and host interaction network exists which must be considered in future studies.

ROLE OF MYCOBIOME IN ECOLOGICAL FITNESS AND DISEASE

In soil ecosystem fungi play an important role in carbon sequestration therefore studying mycobiome becomes important to predict global environment change. Saprotrophic fungi and mycorrhizal fungi are most commonly found where former release extracellular enzymes and decompose organic matter whereas the latter is involved in carbon flow from plant root to soil. (Clenmenson et al., 2013).

Fungi such as, *Saccharomyces boulardii* possesses desirable traits to be used as probiotic as it interacts with resident microflora and protect mucosa as well as against enteric pathogens, neutralizes bacterial toxin and modulates cell signaling pathway (Zanello et al., 2009). Gastrointestinal disease IBD appears in two common forms, Crohn's disease and Ulcerative colitis. In Crohn's disease distinct mycobiome appears at the site of inflamed mucosa (Iliev et al., 2012; Li et al., 2014; Chehoud et al., 2015) with decreased presence of non-pathogenic *Saccharomyces*. These findings could find direct role in attaining healthy state either by supplementing the beneficial fungi or mycobiome manipulation since there is no association of bacteria with this disease. Similarly such interventions can also be applied to other diseases where altered mycobiome is observed such as GVHD (van der Velden et al., 2013), Psoriasis (Paulino et al., 2006), etc. Altered mycobiome can also be used as a biomarker as shown by Chen et al. (2011) in four groups of healthy and diseased patients with different degree of hepatitis B cirrhosis. Increased fungal richness was positively correlated with disease progression or to distinguish between healthy non-healthy obesity (Rodriguez et al., 2015).

In plant system complete community characterization could be helpful to improve the yield and quality significantly (Bai et al., 2015) of agriculturally important crop. Marine environments are relatively poor in nutrition but the diversity, ecology and physiology of fungi has recently been explored and revealed to contain novel lineages and metabolically active community in corals. Uncharacterized fungi could be a source of new drugs and diverse biotechnologically relevant discoveries (Amend et al., 2012).

CONCLUSION

Uncovering the fungal diversity and realizing its importance as an integral part of microbiome is essential to have a broad outlook towards mycobiome. High throughput sequencing has unraveled greater diversity of fungi in previously unexplored ecosystems of earth thus expanding the culture collection of previously unclassified fungi. Fungi are colonizers of diversified habitats such as water, soil, air, litter, plants, etc. However, soil ecosystem is considered to harbour highest diversity of fungi compared to marine environments which contains low diversity. Fungal community exhibits strong biogeographical patterns and is affected by abiotic factors at spatial and temporal scales. At local scales, fungal communities are more diverse and functionally redundant and are least affected by geographical distance owing to the dispersal limitation of fungal spores. To understand whether fungal taxa overlap across habitat is still a matter of speculation. More understanding is needed to uncover the importance of fungi from microbial ecology perspective in terms of cross kingdom interaction (beneficial/ deleterious) and in niche selection. Additionally, functional analysis of mycobiome requires curated reference database and sequenced functional genes. An understanding of cross-kingdom microbial interactions within the context of health and disease holds considerable promise to facilitate the discovery of potential preventative and therapeutic targets.

Mycobiome has indirect implications on ecosystem fitness through interaction between different biomes and within biomes. Therefore, assessing these interactions can help to make personalized medicine, mycobiome manipulation, biomarker for diseases, etc possible in future. Furthermore, variations in mycobiome due to abiotic factors is an area where much more work remains to be done in elucidating the network of mycobiome which it shares with the microbiome. This could only be achieved after assessing the complete fungal diversity in an ecosystem. Thus, it could be concluded that focusing on one without considering the impact of the other could lead us to incomplete understanding of the existence of the networks.

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