

The impact of land use change on the diversity and emergence of fungal pathogens

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Abstract

Fungal pathogens challenge the integrity of natural environments while threatening global food security and forestry industries. The occurrence of new and emerging plant fungal infections is on the rise, particularly in the context of land use change, but has gone largely unnoticed because of inadequate detection methods. To effectively address existing knowledge gaps relating to the emergence of fungal pathogens associated with land use change, an interdisciplinary approach to research is required. Such research should bridge gaps between the fundamental studies of taxonomy, ecology and distribution modelling, as well as the applied sciences related to land use management, agricultural production and plantation forests. Without a cohesive plan linking these disciplines and sectors, it would be impossible to fully understand how fungal pathogens enter an ecosystem and how to mitigate the resultant damage in the future. There is a need to develop sustainable plant protection strategies, requiring fresh insight into the biology and evolution of the corresponding pathogens. Currently, there are very few early warning systems or mechanisms for predicting a fungal pathogen outbreak in agricultural or tree-based systems; it is thus imperative that, as a first step, we generate a fundamental understanding of how these outbreaks occur. In the following chapter, we aim to discuss these issues and make suggestions on how to better research and manage land use change and the related fungal pathogens. We suggest that in order to better predict how or when an outbreak might occur, scientists should begin by studying the natural reservoirs of fungal pathogens before determining stable states in fungal communities and associated communities of fungal pathogens. Next, it is important to determine how these communities change as they are exposed to external pressures, such as land use conversion. Finally, it is crucial to better understand what environmental triggers lead to increased pathogenicity in fungal pathogens and related shifts in life mode strategies, causing beneficial fungi to shift into a pathogenic mode.

Keywords

Agriculture, environment, fungal community, infectious diseases, life mode shifts, public health, saprobes

Introduction

Fungal pathogens impart multiple risks and represent a threat to various phylogenetically distant hosts, including members of the plant and animal kingdoms (Gnat et al., 2021). About 8,000 species of fungi and fungi-like taxa are linked with diseases in plants (Fisher et al., 2020; Horst, 2008). It has been established that plant-infecting fungi and oomycetes challenge the integrity of natural environments and threaten global food security (Fisher et al., 2012; Savary et al., 2019). Pathogenic fungi can infect plants at any phase of development under natural environmental conditions (Narayanasamy, 2011). Opportunistic fungal pathogens affect a plethora of hosts such as humans, fish, and insects, as well as wild and domestic animals (Daszak et al., 2011; Kirkland and Fierer, 2018; Konopka et al., 2019; Lorch et al., 2015; Martel et al., 2014; Nguyen et al., 2013; Turner et al., 2011). Such invasive fungal infections, which are emerging rather alarmingly worldwide, have been linked to a high rate of morbidity and mortality among the hosts (Fisher et al., 2012; Ghoyounchi et al., 2017). All in all, infections caused by fungal

pathogens raise concern since this leads to significant losses in biodiversity and affects the conservation of organisms (Daszak et al., 2011; Turner et al., 2011; Martel et al., 2014). Despite the devastating effects of fungal pathogens and the far-reaching impacts of diseases they cause, several knowledge gaps regarding these culprits remain to be elucidated.

Many new pathogenic fungi associated with diseases of economically important plants have been discovered in recent years, predominantly from the phylum Ascomycota. Interestingly, several of these pathogenic taxa may not have been properly described or identified until after the occurrence of the diseases (Bleher et al., 2009; Farrer et al., 2011). As an example, over 220 new species have been introduced in the pathogenic genus *Fusarium* solely during the last five years (Species Fungorum, 2023). As a result of plenteous taxa being introduced in a short space of time, the exact ecological role of these taxa is poorly understood, and their precise taxonomic resolution remains debatable. Notably, one of the *Fusarium oxysporum* strains (formerly known as Tropical Race 4), responsible for Panama Disease that is devastating banana plantations worldwide, was recently recognized as the species, *Fusarium odoratissimum* (Cheek et al., 2020).

There is growing evidence that many fungal pathogens are emerging after their habitats are disturbed. These pathogens can grow and survive as benign forms of fungi, such as saprobic fungi, but alter their life modes to become pathogenic when they are disturbed or stressed. As such, the effects of land use change, which is happening at the global level, has the potential to cause increases in the number of fungal pathogens found in these disturbed systems, impacting agricultural crops, wildlife, and humans. In this chapter, we aim to discuss the issue of how land use change causes an increase in the diversity and abundance of fungal pathogens and why this is an issue that should not be ignored.

What is land use change?

Even though the terms 'land cover' and 'land use' are sometimes used synonymously, they are fundamentally different. Land cover refers to the physical elements that cover the earth's surface, including crops, forests, grassland, water, snow, open soils, or populated areas. Any activities, especially anthropogenic, taking place within a landscape could be considered land use. Such activities could include farming, recreational, industrial, or transportation. The alteration of the landscape and associated land cover for these activities results in land use change. Land management practice is generally directed towards managing the properties of the land cover without altering its land use type. While the latter change may result from natural occurrences, the effect of human intervention is more pronounced, either directly or indirectly. Specifically, land use change is the process whereby land is directly managed or used in different ways by humans (Keenan et al., 2015; Mastel et al., 2018; Wirsenius et al., 2010). Examples include irrigation, afforestation, ploughing, integrated farming, intercropping, and increasing the yield of a crop by applying organic or chemical fertilizers and pesticides. The intricate connection between land cover and land use may be exemplified by situations where a single land cover is managed in different ways or subjected to several land uses at the same time; for instance, when a forest area is used for recreational activities as well as wood production purposes. Land use pressures have reduced terrestrial biodiversity and imposed stress on the organisms within the land use system. The biodiversity impact of land-use pressures can vary among biomes; grasslands are most affected, and tundra and boreal forests are least affected (Newbold et al., 2016).

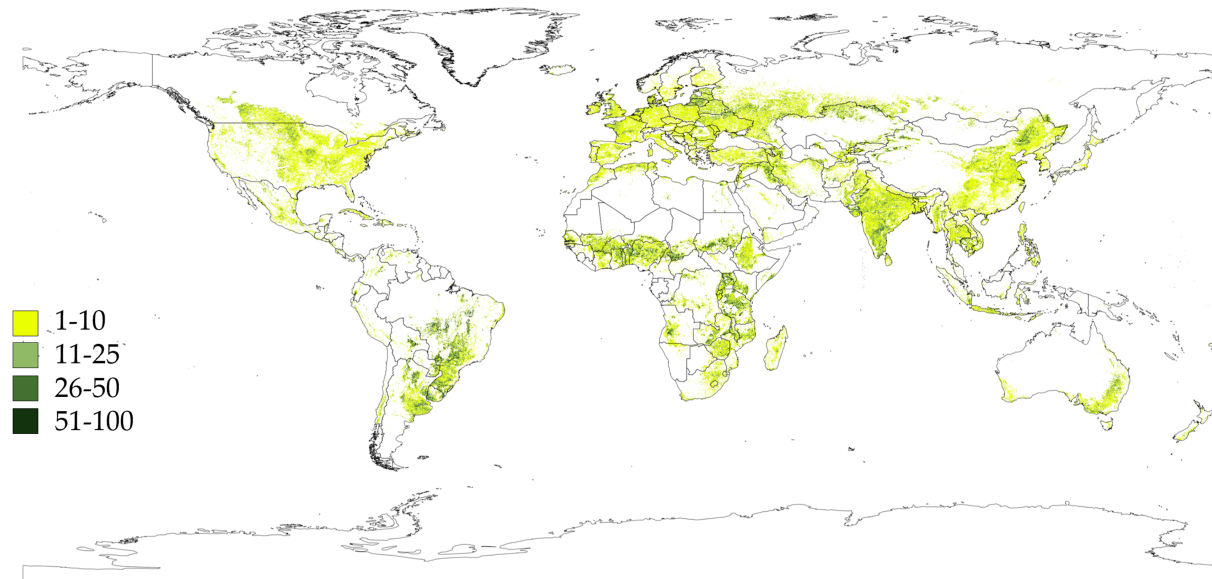


Figure 1. Cropland percentage gain in 2000–2020 within a $1 \times 1^\circ$ grid cell. The dataset derived from Landsat Analysis Ready Data (Potapov et al., 2020) produced by the Global Land Analysis (<https://glad.umd.edu/ard>).

Influence of land use change on fungal communities

Fungi are one of the largest groups of heterotrophic eukaryotes, comprising exceptional degraders, symbionts, endophytes, and pathogens (Pölme et al., 2020; Rokas, 2022). Thus, fungi not only help maintain biogeochemical cycles but also contribute towards plant growth and biodiversity maintenance within various ecosystems (Bahram and Netherway, 2022; Frac et al., 2018; Lara-Capistran et al., 2021; Pölme et al., 2020). It has been established that fungal communities are sensitive to and influenced by environmental changes (Morrison-Whittle et al., 2017; Tedersoo et al., 2014). Importantly, fungi are also able to shift their life modes, for example, changing from a decomposer to a pathogen depending on environmental conditions or available resources (Allen et al., 2001; Williamson et al., 2007). However, the impact of land use change on the diversity and life modes of fungi remains poorly studied and most of these studies have solely focused on soil fungi (Ontivero et al., 2022; Romdhane et al., 2022; Rutten et al., 2021; Shi et al., 2019; Sui et al., 2019).

Several studies have documented the impact of land use change on fungal communities (Balami et al., 2020; Fracetto et al., 2013; Lupatini et al., 2012; Oehl et al., 2010; Rillig and Mummey, 2006; Romdhane et al., 2022; Sui et al., 2019; Verbruggen et al., 2010; Wilson et al., 2009; Xu et al., 2017), and these studies help highlight the impact that land use change has on the fungal species found within those landscapes. For example, the conversion of forest to pasture and agriculture did not reduce the fungal diversity of these systems, but it did change the population level of species that make up the ecosystem, thereby indicating changes in fungal niches in the soil (Fracetto et al., 2013). In addition, agricultural intensification, application of fertilizers, crop rotation, tillage or compaction may equally influence fungal diversity in soil systems (Babin et al., 2019; Banerjee et al., 2019; Degruene et al., 2017; Hartmann et al., 2015; Piazza et al., 2019). Although the majority of evidence for the impact of land use change on fungal communities is not specific to fungal pathogens, it does provide strong support for the extent to which land use change can impact the fungi found within these systems. Below we will discuss in more detail how fungal pathogens are influenced by land use change and which factors are more likely to cause a shift in fungal life modes. We will look at which studies have found that land use change causes an increase in pathogen diversity.

Impacts of land use change on fungal pathogens

How land use change can cause a shift in the life mode of fungi

Fungi do not create their own food; they obtain their nutrients from existing organic matter in the environment. Fungi can behave like endophytes, saprobes, parasites or mutualistic organisms in accordance with their response to internal host signals or environmental factors (Rai and Agarkar 2016). The saprotrophic lifestyle is characterized by retrieving nutrition from, and growing on, organic matter. Mutualistic fungi partake in a symbiotic relationship with their hosts, whereby both parties derive some benefits. Endophytic fungi are examples of mutualistic organisms; they internally colonize living plant tissues without causing any visible symptoms of disease and live in mutualistic association with plants for at least a part of their life cycle. Alternatively, fungal pathogens evidence three major lifestyles, namely, (i) the necrotrophic lifestyle (e.g., *Botrytis cinerea*), which is characterized by killing the host cells before feeding on its dead tissue; (ii) the biotrophic lifestyle (e.g., *Erysiphe necator*), which is characterized by retrieving nutrition from and growing on the living tissue of hosts by evading the plant defense mechanisms; and (iii) the hemibiotrophic lifestyle (e.g., *Colletotrichum gloeosporioides*), which is characterized by an initial biotrophic infection mode, followed by a transition to the necrotrophic stage.

It has been shown that fungi are capable of expressing different lifestyles (from mutualism to parasitism) with their hosts, and the relationship can be described as a continuum, ranging from symbiotic to parasitic (Rai and Agarkar, 2016). In other words, the same fungus can be isolated in different forms. For example, the genus *Epichloe* comprises species which express both mutualistic and parasitic lifestyles (Schardl and Leuchtmann, 2005). In another instance, when an endophytic fungus is isolated from asymptomatic plant tissues and re-inoculated on the original host species, the fungal species is revealed to have either a mutualistic, commensal, or parasitic lifestyle (Schulz et al., 1999). Thus, both mutualistic and pathogenic fungi may remain in dormant states inside the host plant tissue.

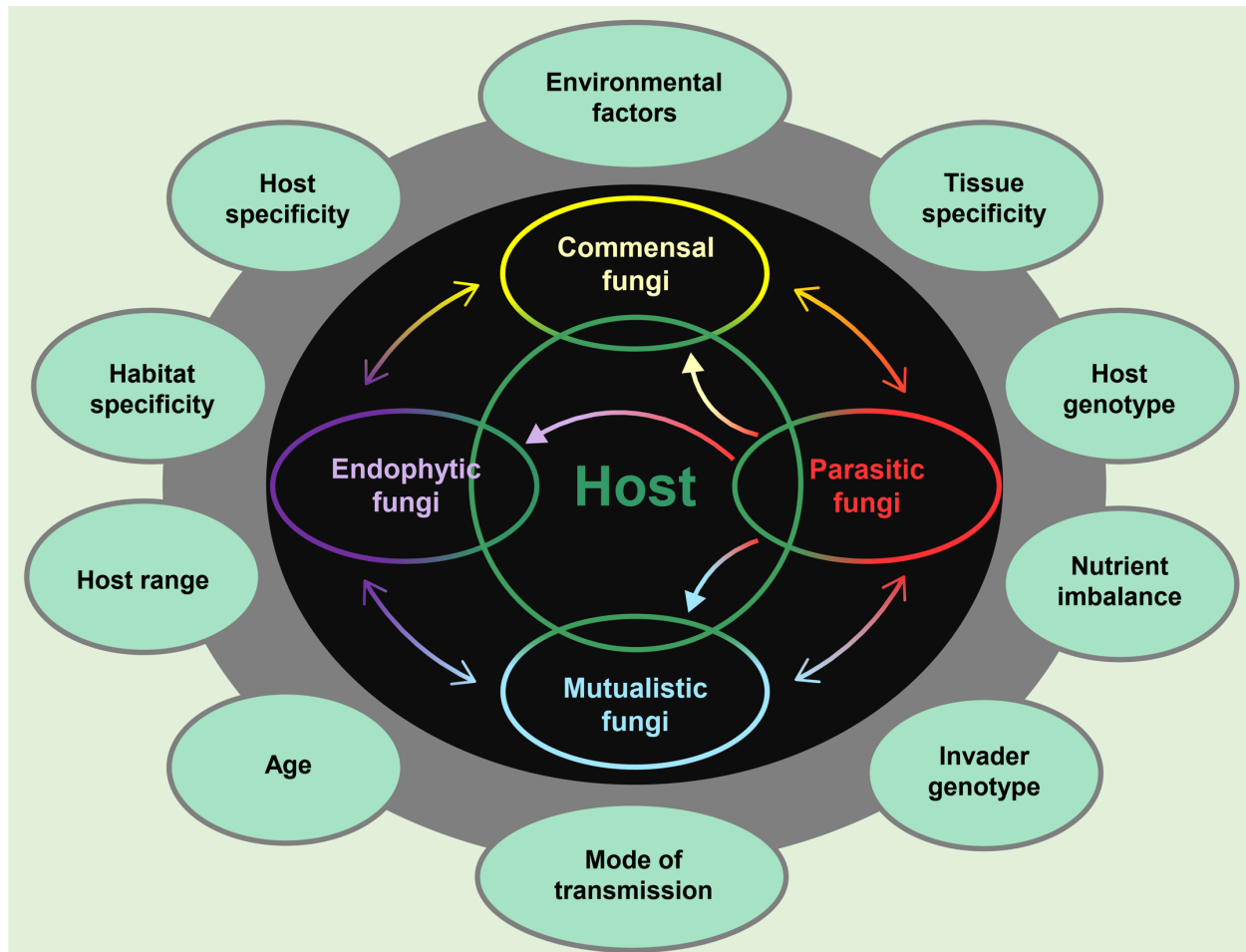


Figure 2. Various fungal interactions and the factors affecting these interactions (adapted from Rai and Agarkar, 2016)

Table 1. Examples of fungi that shift their life modes as a result of disturbance or environmental stress

Fungus	Previous life mode	Previous host	Current life mode	Current host	References
<i>Colletotrichum musae</i>	Pathogenic	Banana	Mutualistic	Pepper	Redman et al. (2001)
<i>Colletotrichum acutatum</i>	Pathogenic	Strawberry	Commensal	Watermelon	Redman et al. (2001)
<i>Epichloe festucae</i>	Mutualistic	<i>Lolium perenne</i>	Pathogenic	<i>Lolium perenne</i>	Tanaka et al. (2006)
<i>Diplodia mutila</i>	Endophytic	<i>Iriarte deltoidea</i>	Pathogenic	<i>Iriarte deltoidea</i>	Alvarez-Loayza et al. (2011)
<i>Neurospora crassa</i>	Endophytic	<i>Pinus sylvestris</i>	Pathogenic	<i>Pinus sylvestris</i>	Kuo et al. (2014)

Dimorphism is another scenario that refers to the ability of certain fungi to switch between two morphologies, such as unicellular yeast and multicellular filamentous growth forms, in response to changes in environmental conditions (Nadal et al., 2008). These changes are the result of the fungus responding to different environmental cues or signals. Dimorphic fungi can detect these signals and shift their morphologies as an adaptation to the new prevailing conditions. This switch alters host-microbe interactions, and the fungus, in its new life mode, can be pathogenic to mammals, plants, and insects

(Table 1). Some of these known dimorphic fungal pathogens are reported as sensitive to land use changes.

How different forms of land use change can impact fungal pathogens

Fungi are closely associated with their hosts. Consequently, changes subjected to the host environment will also affect the fungal community. Changes in land use can therefore be accompanied by alterations in the fungal profile, often which include a shift toward an increase of pathogenic fungi (Brinkmann et al., 2019; Loughlin et al., 2021). Such increasing shifts in the composition of soil fungal communities towards pathogenic species in transformed lands may jeopardize the health of the systems and those of neighboring land use systems (Brinkmann et al., 2019). Similarly, in their study vis-à-vis the effects of land use changes on the phylogenetic and functional diversity of soil fungi, Marín et al. (2017) observed that a plot in a pristine forest (old-growth forest) had a lower phylogenetic fungal richness and harbored abundant saprotrophic fungi and low proportions of ectomycorrhizal as well as plant pathogenic fungi. To the contrary, a plot with total removal of vegetation housed a higher proportion of plant pathogenic fungi, a lower proportion of saprotrophic fungi, and almost no ectomycorrhizal fungi. In another instance, the artificial fertilization of soils was reported to increase the disease susceptibility of plants to fungal pathogens (Liu et al., 2017). Nitrogen fertilization may cause a loss of unfavored plant species, which may in turn entail a reduction in the phylogenetic diversity of the remaining pathogenic fungal species. Subsequently, the remaining plant species are exposed to similar fungal pathogens as well as similar intensity of disease pressure (Liu et al., 2017).

Amendments of grassland and cropland soils with residues such as wheat straw have been known to significantly influence the soil bacterial and fungal diversity of those particular plots, as reported by Tardy et al. (2015). Of particular interest is that the fungus *Rhizopus* was found to be strongly stimulated by the introduction of wheat residue in the cropland soil as compared to the grassland or control soils. It was hypothesized that such selective stimulation by the fungus could represent a risk for successive crops as *Rhizopus* accommodates some plant pathogenic taxa (Tardy et al., 2015). Inversely, the introduction of wheat straw in the grassland soil promoted higher stimulation of *Fusarium* than in the cropland soil. In addition to being known for its role in decomposing organic matter, *Fusarium* may also represent a risk to subsequent crops as many species of this genus are pathogenic (Tardy et al., 2015). A study conducted by Shi et al. (2019) showed that an increasing forest disturbance was accompanied by a decline of the saprotrophic fungi in the soil, accompanied by an increase of facultative pathogenic fungi. Replacement of grassland with willow and poplar plantation leads to the enrichment of putative pathogenic and ECM fungi associated with trees (Xue et al., 2016). Compared with forestland, tea planting decreased the relative abundance of saprotrophs (e.g., soil saprotrophs and undefined saprotrophic fungi), whereas they increased the relative abundance of pathogenic and pathotrophic-saprotrophic fungi (Wang et al., 2023).

Land use change mostly showed significant shifts in fungal community composition (Balami et al., 2020). The maintenance of fungal dynamics could be attributed to the changes in plant diversity, density/coverage, as well as abiotic factors among land uses that promote diversity even in intensive land use systems. Plant density is known to be a major driver of plant pathogens because different plants provide a range of habitats for different pathogens (Eldridge et al., 2018). The increase in abundance of facultative pathogenic fungi may be related to reduced competition with saprotrophic fungi, changes in microclimate, or increased spore rain (Shi et al., 2019). García-Guzmán and Heil (2014) provided more reports on diseases of annual plants rather than perennial, and light-demanding rather than shade-tolerant plant species. This suggests that plants with rapid growth could be susceptible to plant pathogens (Endara and Coley, 2011). Plant life strategy could also be one of the attributes explaining the low observed plant pathogen alpha-diversity in natural forests where few ephemeral plant species are present (Makiola et al., 2019). A higher plant pathogen alpha-diversity was observed in conventional

compared to organic farming practices (Hartmann et al., 2015). Hence, the land use types with higher disturbance frequency could suppress plant beneficial micro-organisms and thereby promote plant pathogen diversity (Hartmann et al., 2015). Irrigation and fertilizer input could result in a higher pathogen diversity in managed agricultural systems, possibly by lowering the functions of arbuscular mycorrhizal and so the loss of their impact on reducing pathogens (Hong and Moorman, 2005; Makiola et al., 2019). Excess amounts of fertilizer or an unbalanced nutrient supply can also weaken the plant immunity that usually benefits plant pathogens (Anderson, 2002; Hartmann et al., 2015; Makiola et al., 2019). The factors that underlie how different forms of land use change can impact fungal pathogens are described in Figure 3.



Figure 3. Diagrammatic representation of how land use change can lead to an increase in fungal pathogens. When land use change occurs, such as through deforestation or agricultural expansion, natural habitats and ecosystems are disturbed. This disruption can lead to changes in the composition and diversity of fungal pathogens.

Examples of threats associated with land use change and fungal pathogens

There are numerous studies showing how land use change results in an increase in the number of fungal pathogens found in that specific environment. These pathogens can have devastating effects on the plants, humans, and animals associated with these landscapes. If left unchecked, these pathogens can

reach epidemic levels, thus we cannot ignore the threat posed by some of these pathogens. A striking example is that of Coccidioidomycosis or Valley fever, caused by *Coccidioides immitis*. This is one of the most virulent of the fungal pathogens, causing a serious, and often fatal disease, in humans, domestic animals, sheep, swine, cattle, horses, wild desert rodents, and other animals (Pearson et al., 2019). Colson et al. (2017) found that incidence of coccidioidomycosis is sometimes associated with land use change, typically with soil disturbances in the San Joaquin Valley, California (Lauer et al., 2020). However, with the increase in land use change taking place within the San Joaquin Valley, the number of cases of Valley fever have increased dramatically in recent years (Gorris et al., 2018, 2019; Kollath et al., 2022; Pearson et al., 2019). Cryptococcosis is a potentially life-threatening infection caused by *Cryptococcus gattii* or *C. neoformans*. Specially the Cryptococcal meningoencephalitis is a major opportunistic fungal infection (caused by *C. neoformans*) in patients with weak immune systems, such as those with AIDS (Bicanic and Harrison, 2004; Casadevall and Perfect, 1998). However, *C. gattii*, now holds the distinction of more frequently causing infection in people who have apparently healthy immune systems (Marr, 2012). Altered land use has been identified as one of the reasons behind the emergence of Cryptococcosis in more recent years (Datta et al., 2009; Gadre et al., 2022). *Histoplasma capsulatum* is a pathogenic fungus that causes histoplasmosis (acquired by inhalation of infectious airborne microconidia), a life-threatening systemic mycosis (Kauffman, 2007). It has been hypothesized that the apparent expansion of histoplasmosis into new regions is a consequence of climate change and human-induced land use change (Bellman et al., 1997; Gnat et al., 2021; Maiga et al., 2018). Like with Coccidioidomycosis, building and construction practices that disturb infected soils are associated with histoplasmosis outbreaks.

Intensive plantation of new species (such as the domestication of forest trees) may also provide an opportunity for the rapid emergence of modified pathogen populations and new diseases (Hessenauer et al., 2021). As an example: the intensification of native *Populus deltoides* in North America resulted in the emergence of a new disease with the rapid change of an innocuous foliar pathogen (*Mycosphaerella populorum*) into a destructive and epidemic canker pathogen (Dhillon et al., 2015). In Southwestern France, the large monoculture tree plantations of *Pinus pinaster* favored the emergence and outbreak of the native root and butt-rot pathogen *Armillaria ostoyae*. Oak wilt is a devastating vascular disease of oak trees, caused by the fungus *Ceratocystis fagacearum* (= *Bretziella fagacearum*). Changes in land use and forest management have been shown to promote the development of oak wilt and subsequent epidemics (Juzwik et al., 2008), devastating oak forests and plantations in certain regions.

How to better manage risks associated with land use change in the future

Fungal plant pathogens are accountable for numerous devastating diseases in economically important forests, crops and tree plantations (Doehlemann et al., 2017). Without a deep understanding of the underlying causes of fungal pathogen outbreaks, it is a challenge to effectively control these natural and managed lands from disease susceptibility. Currently, there are few early warning systems or mechanisms for predicting an outbreak of fungal infections in agricultural and tree-based systems, or, more importantly, when converting natural systems into managed, man-made systems. It is thus imperative to initially not only generate a fundamental understanding of how these outbreaks occur but also to further our own understanding of the dimorphic nature and behavior of fungi which are able to switch between life modes. This can be achieved by first studying the natural reservoirs of fungal pathogens before determining stable states in fungal communities and associated groups of fungal pathogens. Next, it is important to determine how these communities change as they are exposed to external pressures, such as land use conversion from one system to another (e.g. from natural forest to agricultural system). Finally, it is important to acquire a better understanding of the environmental triggers that lead to increased pathogenicity in fungal pathogens or which induce a shift in fungal life mode strategies, thereby causing beneficial fungi to switch into a pathogenic mode. This phenomenon

may have profound effects on plant-fungal interactions and various ecological niches. Therefore, it is necessary to identify the factors that trigger changes in fungal lifestyle and understand whether these different lifestyles are interconnected at some points by physiological, biochemical or molecular routes. Research should be significantly boosted in these directions to inform the planning and management of future agricultural projects as well as to avoid the severe consequences that result from harmful fungal pathogens.

Establish protocols for screening land use systems ahead of any planned disturbances

Since land-use change affects organisms at several trophic levels, it is essential to properly select land-use systems in order to mitigate any subsequent damage. Therefore, establishing protocols for screening a particular land for suitability before any specific land-use change is effected, becomes imperative. Such protocols should provide methods to assess whether an area of land is suitable or not for a particular use and what risks may be associated with any changes that are brought about. They should also specify ways to identify the kinds of limitations an area of land may have (Driessen and Konijn, 1992; Mohamed et al., 2000). The establishment of these protocols will be more effective if they are evidence-based. The protocols have to be rationally and even politically sound, and should follow an integrated approach, including quantitative, qualitative, ecological, social, and economic aspects (Mohamed et al., 2000; Rossiter and Van Wambeke, 1993). Standardisation of criteria in the protocols may prove to be instrumental in providing meaningful comparisons (Mohamed et al., 2000). Such protocols should include the screening of above- and below-ground fungi present within the given land use system, thus identifying any potential threats from within the fungal communities.

Recommendations on how to predict or mitigate the emergence of fungal pathogens associated with land use change

The accurate identification of fungal taxa inhabiting a particular landscape is key to understanding which fungal taxa are present, and which pathogens are of potential threat within a particular land use system. Screening of fungal taxa needs to be conducted according to their habitat and lifestyle. Rather than just focusing on pathogenic taxa, it is useful to screen for saprophytic and endophytic fungi as well since they can potentially shift life modes and change to pathogens depending on the conditions. Screening should make use of established methods for the isolation and identification of fungal taxa from different habitats and lifestyles (Senanayake et al., 2020). Identification of taxa may be led by different analyses, including an integration of culture-based and molecular analyses, which will ensure maximum coverage of the fungal taxa, as reported in previous studies (Montalvo et al., 2014; Yang et al., 2022).

In addition, we need to improve our understanding of the interactions between hosts, pathogens and the environment across regional and global scales. Integrated approaches encompassing theoretical and practice-based research are needed. Monitoring of fungal inocula in various land use systems must be evaluated with considerable speed. Understanding the relation between host diversity and fungal pathogen infection and infestation can help to develop more effective measures to regulate diseases in agriculture. Before land use systems are changed, consideration should be given to what the future land use systems will be, and this should be considered against the fungi known to be present within the land use system (based on initial screening). Thus potentially avoiding the emergence of pathogens that might infect the plants, trees, or crops within the planned land use system.

Deviations in fungal circulations driven by environmental changes (e.g, habitat loss and changing land use systems) should be further evaluated alongside different fungal groups with distinct geographical distributions in order to identify how this will affect the future distribution of pathogenic fungi and their infections. Small- to large-scale studies should be conducted in different regions, and the obtained data from traditional, small-scale studies should be checked for the appropriateness of being

extrapolated to entire ecosystems or to determine whether or not large-scale pilot studies are required to account for interactions and nonadditive effects in the scaling-up process. Furthermore, there is a strong need to better understand fungi's dimorphic behaviour and what triggers cause a shift in life modes whereby benign fungi becomes pathogenic. All these factors need to be considered to fully appreciate the role that land use change has on the emergence of fungal pathogens within a given land use system, and how best to mitigate the associated risks.

Conclusion

It is important to study where pathogenic organisms occur, instead of where they are simply apparent, in order to better understand their diversity and compositional patterns. Many of them can be asymptomatic or cryptic and can persist in adverse environmental conditions or at hardly discernible levels until the next disease outbreak (Makiola et al., 2019). The triggers or environmental cues that cause fungal life mode shifts remain largely unknown. It is critical to further our understanding of these triggers to better manage and control incidents of fungal pathogenicity and associated damages. One event that has been linked to an increase in the presence of fungal pathogens is land use change, with a number of studies indicating that a shift from natural land use systems to managed agricultural systems (including tree crops and plantations) results in an increase in fungal pathogens (Brinkmann et al., 2019; Rutten et al., 2021). However, the majority of studies have been performed at the plot level, and it is crucial to expand these studies to regional or global scales if we are to truly grasp the potential threats posed by the relationship between land use change and fungal pathogens. Thus, research that can help scientists and practitioners better understand the emergence of fungal pathogens, fungal life mode shifts and more accurately predict how land use change will influence the occurrence of fungal diseases will greatly benefit both scientific and agricultural sectors, allowing for the development of active management strategies, rather than retroactively implementing containment strategies.

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