State of the World’s Fungi 2018

8. Plant-killers: Fungal threats to ecosystems


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PLANT-KILLERS: Fungal threats to ecosystems

The rapid spread of fungal diseases around the world is damaging natural ecosystems

Which fungal diseases pose the greatest threats to global ecosystems? Why are these threats on the increase and what biosecurity is urgently needed to reduce their global spread?

stateoftheworldsfungi.org/2018/plant-killers.html
1. Describing the world's plant diversity

Plant-killers: Fungal threats to ecosystems
Fungi and plant–fungal interactions provide great benefits to humans. However, they also provide some of the greatest threats.

In *State of the World’s Plants 2016*[^1], we reported the devastating impacts of the top ten fungal diseases globally. These all reduce the yields of crops and are a major challenge to food security. This year, we explore the threats that fungi pose to non-crop plants and especially plants in natural ecosystems. We discuss how and why these threats emerge and their broad impact on the natural environment.

**Fungal diseases as a worldwide threat to ecosystems**

The impact of fungal diseases on plants and animals is increasing worldwide[^2-^11], and detrimental effects on plants in natural ecosystems are an important part of this worrying global trend[^4]. These fungal pathogens have wide-ranging effects due to the large number of species they affect directly as hosts or indirectly via ecological interactions. The impacts can be long term and can severely affect ecosystem functions such as carbon sequestration[^6]. Long-established pathogens cause ongoing impacts, such as northern hemisphere species of *Armillaria* (e.g. honey fungus) and *Heterobasidion* that cause root rots of many tree species. However, much of the global increase in fungal impacts is driven by newly emerging pathogens, of which we now give some key examples (see also Boxes 1–3).

Until 2010, myrtle rust (*Austropuccinia psidii*) was mainly known as a problem in plantations of introduced plants in South America[^7]. However, in 2010 it was detected in Australia where it has the potential to infect over 1,000 different native species in the Myrtaceae family, including eucalyptus (*Eucalyptus* spp.) and paperbark/tea trees (*Melaleuca* spp.)[^10]. It has now escaped eradication attempts and has spread along the entire east coast, where it has had severe effects on native forests[^7]. The spread of myrtle rust has continued; in 2013 it was detected in South Africa and New Caledonia, and it was found in New Zealand for the first time in 2017 (see Figure 1).

The ash dieback fungus (*Hymenoscyphus fraxineus*) is more restricted in its host range than myrtle rust, with severe effects only known from ash trees (*Fraxinus* spp.). However, ash trees are abundant in continental Europe and a key component of native woodlands. Ash dieback was first found in Poland in the early 1990s and over the subsequent years has spread rapidly east to west across Europe. However, it is not just the ash tree itself that is at risk. There are around 955 other species, including 68 fungal species, that live in association with ash[^9] and are thus also under threat. A recent study has reported the presence of *H. fraxineus* on three new species outside the ash genus (but still within the same family, Oleaceae); these are *Chionanthus virginicus*, *Phillyrea angustifolia* and *Phillyrea latifolia* (N. Spence (Defra), pers. comm., 19 July 2018). It remains to be seen whether these new hosts will develop the disease or contribute to its spread.

**Box 1: Dogwood anthracnose**

Dogwood anthracnose is a lethal disease of native dogwoods (*Cornus* spp.) in the USA and is caused by the fungus *Discula destructiva*. Dogwoods are found in the understorey of woodlands and are important for their fruits, which provide autumn food for many birds and mammals[^37].

**Box 2: Beech bark disease**

Beech bark disease is caused by *Neonectria* fungal species and an insect pest. Modelling suggests that replacement of American beech (*Fagus grandifolia*) by another tree species would lead to 13% less carbon storage in plants and the forest floor after a century as compared to a healthy beech stand[^38].
Plant-killers: Fungal threats to ecosystems

FIGURE 1: THE SPREAD OF MYRTLE RUST GLOBALLY
Myrtle rust (*Austropuccinia psidii*) is native in South America, from where it has spread across the globe. Each orange dot is a record of myrtle rust, with the year it was first reported shown alongside (where known).

[Based on data from CABI (cabi.org) and CRC Plant Biosecurity (pbcrc.com.au)]

Fungal diseases can remove keystone tree species from ecosystems, with devastating effects

BOX 3: WHITE PINE BLISTER RUST
Extensive natural stands of white pines (*Pinus strobus*) can be seen in North America that are dead or dying due to white pine blister rust (*Cronartium ribicola*), with severe impacts on local ecosystems and grizzly bear habitat[39].

The fungus *Raffaelea lauricola*, which was first found in the USA in 2002, has a symbiotic relationship with the ambrosia beetle (*Xyleborus glabratus*). Together, the fungus and beetle cause laurel wilt[10] and are now devastating natural stands of redbay (*Persea borbonia*) in the southeastern USA, as well as three Critically Endangered native plant species: pondberry (*Lindera melissifolia*), pondspice (*Litsea aestivalis*) and Florida licaria (*Licaria triandra*)[10].

The long-term devastation that can be caused to ecosystems by emerging fungal diseases is demonstrated by the effects of Dutch elm disease (*Ophiostoma novo-ulmi*) in Europe and chestnut blight (*Cryphonectria parasitica*) in North America. Decades ago, these pathogens effectively eliminated keystone tree species from ecosystems and these trees have so far been unable to return to their former function[11,12]. This has knock-on effects for other organisms; for example, bird communities have shown substantial changes in the ten years since the habitat disturbance that resulted from Dutch elm disease in northern Minnesota[13]. In southern Appalachian riparian forests, the demise of chestnuts due to blight has led to the spread of *Rhododendron maximum* and consequent reduction in the species richness of forest vegetation[14].
WHY ARE FUNGAL THREATS EMERGING?

There are many factors that can lead to the emergence of fungal threats and increase their impact (see Figure 2). A major factor in the recent increase in the impacts of fungal diseases globally is the movement of fungal pathogens around the world, often by humans\(^2\). All of the examples outlined previously owe their emerging impact to accidental introduction into geographic regions where native plants have not been previously exposed to the pathogen and don’t have the tools to combat the infection, allowing rapid spread and severe damage to occur. As we reported in State of the World’s Plants 2017\(^{15}\), this is also true of insect pests of plants. Climate change also opens up new regions for fungal pathogens\(^16\). One study indicates that fungi are now moving towards the poles, following their plant hosts at a rate of 6–7 km/year as the Earth warms\(^17\). The planting of monocultures, producing local ecosystems with high environmental and genetic uniformity, can provide cradles for the evolution of fungal pathogenicity\(^18,19\).

Fungi may be particularly good at invasion for several reasons. They have multiple ways of associating with plants, which means they can easily hitchhike on plant species moving around the globe\(^20\). For example, a fungus could enter a country as a harmless, symptomless endophyte of one host species, then move to another host species on which it is pathogenic. Fungi also have multiple ways of reproducing, including clonally, which allows rapid multiplication of a single invader\(^21\). Rapid dispersal can therefore occur by the production of different spore types (many of which are capable of long-distance airborne dispersal) or by vegetative spread. In addition, some are also associated with insects, which enhance their dispersal and propagation.
HOW DO FUNGAL PATHOGENS EVOLVE?

Fungi are able to recombine genetic information within species through both sexual and parasexual reproduction (see Chapter 1). They can also gain genetic information from other species via hybridisation and horizontal gene transfer. These processes allow new pathogen variants to be continually generated\(^2\). Some fungal pathogens possess ‘two-speed’ genomes, which means that while essential genes evolve slowly, the genes involved in pathogenicity and virulence occupy genomic regions that evolve more quickly\(^2\)\(^3\). This may be accelerated by a process known as repeat-induced point mutation, which appears to be unique to fungi\(^2\)\(^4\).

Understanding how fungi cause disease in plants has benefitted in recent years from the generation of genetic information provided by the recent sequencing of over 500 fungal genomes (see Chapter 6). This has also helped identify and characterise the fungal pathogen genes that code for so-called ‘effector’ proteins\(^2\)\(^5\). These proteins are transferred by fungal pathogens into their hosts and contribute to virulence by manipulating the host’s immune system. This makes the hosts more susceptible to infection, leading to rapid progression of the disease. Transfer of effector genes between fungal species can lead to the emergence of new diseases\(^2\)\(^6\).

For certain fungal pathogens such as *Fusarium oxysporum* (which causes vascular wilt diseases, such as the devastating Panama disease of bananas (*Musa* spp.)), the ability of different strains to infect specific host plants can be linked to the gain or loss of entire chromosomes\(^2\)\(^7\)\(^\text{,}2\)\(^8\). Hybridisation can also lead to new pathogenic forms; for example, the flow of genes between populations of the fungal pathogens *Ophiostoma ulmi* and *O. novo-ulmi* seems to have contributed to the rapid evolution of Dutch elm disease\(^2\)\(^9\). The ash dieback fungus population in Europe appears to have passed through a bottleneck of just two individuals, but sexual reproduction among their offspring has generated diversity via recombination\(^2\)\(^0\).

WHAT CAN WE DO TO REDUCE THE IMPACTS OF FUNGAL DISEASES?

There is clearly a need for greater biosecurity in global trade. But even with stringent checks, pathogenic fungi can move across borders undetected – for example as spores on clothing, vehicles or packaging, or via birds. It is sobering to reflect that myrtle rust has successfully entered Australia and New Zealand, despite the exceptional vigilance of their biosecurity systems compared to many other countries. Long-term solutions could include a drastic reduction in global trade in live plants, improved detection and removal of contaminated and infected plants and improved decontamination treatments.

Integrated approaches that include risk assessments, surveillance, population genomics, practical epidemiology and climate forecasting are needed, so that effective disease prevention strategies can be developed. Response strategies are also needed for the control, detection and eradication of new outbreaks. Such disease prevention and response strategies are already in place in some countries, including the UK, but they need to be adopted more widely to be effective across the range of problem pathogens.

Improved diagnostic methods may help the situation, particularly DNA-based approaches that can detect asymptomatic infections or provide reliable diagnoses for ambiguous symptoms. For example, an in-field diagnostic process was developed for the ash dieback fungus\(^3\)\(^1\), which allowed accurate diagnoses in the early stages of pathogen spread in the UK.

It is hoped that increased knowledge of the genomes of fungal pathogens will lead to the production of new fungicides\(^3\)\(^2\), including RNA-based fungicides\(^3\)\(^3\). If these are very specifically targeted, deployment may be possible in natural ecosystems without damaging populations of non-pathogenic fungi. Increasing knowledge of the genomes of the hosts of fungal pathogens may also enhance our ability to breed resistance in host plants, as has been done in important crop species. For example, there are several long-term breeding programmes for American chestnut trees resistant to chestnut blight\(^3\)\(^4\) and these are now being enhanced by studies that map resistant genes and allow trees to be scanned for the presence of these useful genes in their genomes\(^3\)\(^5\).

The impacts of fungal diseases on the services provided by natural ecosystems can affect everyone, and increased public awareness is needed if we are to tackle this problem effectively. The willingness of the public to get involved can be seen, for example, in the crowdsourcing of genomic analyses on ash dieback\(^3\)\(^6\) and the fund-raising by organisations such as The American Chestnut Foundation in the USA and Action Oak in the UK. Translating huge public concern into effective citizen action is key to halting the spread of damaging fungal pathogens and reducing their impacts on natural ecosystems.

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**FIGURE 3: WORDCLOUD OF TOP FUNGAL PATHOGENS AFFECTING NATURAL ECOSYSTEMS CONTAINED IN SCIENTIFIC CITATIONS**

[For details of the method, see supplementary material on website: stateoftheworldfungi.org]
References:

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