

REVIEW ARTICLE

Emerging plant diseases under a changing climate scenario: Threats to our global food supply

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ABSTRACT

This review highlights the impact of emerging diseases; emerging diseases and pathogen dispersion; disease spread; and possible causes contributing to the emergence of pathogens. Some plant diseases are caused by potentially dangerous pathogens that have led changes in humanity. Despite our efforts in the fight against these dangerous pathogens; the influences of natural phenomena such as hurricanes or strong winds that disperse pathogens remain. However, some actions such as investment in research priorities that are focused on quarantined pathogens and official regulations can help in disease prevention. We discuss emerging diseases as a threat to crops, identify future research areas, and encourage the establishment of research networks focused on quarantine pathogens to address the problem and minimize risks.

Keywords: Emerging diseases; Quarantine, Plant pathogens; Climate change

INTRODUCTION

Food security is necessary to feed the growing human population. According to FAO (2006), Food Security is achieved with four components: availability of food, food access, food use, and food stability. Yield losses in agricultural production due to plant pathogens directly affects these components.

Food stability has been affected many times as a result of sudden food crises (Gregory et al. 2005). Some of these crises led to major disease epidemics affecting plants that were caused by agents such as arthropod pests and pathogens of plants (or a combination thereof). Many

historical and contemporary diseases have emerged and threatened crops; by default, these diseases affect food security. Emerging plant pathogens can be devastating for cultivated crops, hence, they have been included in global lists as quarantined pathogens. Abiotic (e.g., strong winds, hurricanes, global trade, climate change) and biotic factors (i.e., human migration, translocation of afflicted plants by humans) are increasing the risk for pathogens to spread.

In effect, plant pathogens can affect food security. Because of the growing need to feed the global population, research on plant pathogens primarily focuses on their effects upon agricultural productivity and crop protection.

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Received: 13 February 2018; **Accepted:** 21 May 2018

The objective of the review is to highlight some of the most recent destructive diseases attributed to plant pathogens and discuss potential factors affecting their emergence. Also, because of the global distribution for some plant pathogens, we propose that researchers build international networks in coordination with competent authorities, to address with public policies, the most destructive diseases, those that are classified as quarantine diseases.

Impact of historical emerging diseases

An emerging disease is an original case or group of cases that are newly recognized or newly appeared in an area and can increase fast in incidence and severity (Daszak et al., 2003). It represents the initial presence of a disease in a crop and, if left unchecked, can result in disease epidemics of disastrous proportions.

The introduction, or arrival, of potentially hazardous plant pathogens to a new cropping area generates risks in food production. Indeed, a large number of registered plant epidemics have reduced the production of various crops in the world throughout history (Strange and Scott, 2005). Crops epidemics have long been associated with human hunger and suffering. Among the most devastating cases affecting humanity were the famines in Ireland and Bengal in which at least three million people died. The arrival of a new strain of *Phytophthora infestans* (Mont.) de Bary in Ireland and the practice of a potato monoculture caused the death of one million people (Andrivon, 1996; Forbes, 2004; Agrios, 2005). Similarly, the shocking epidemic of leaf blight of rice caused by the fungus *Cochliobolus miyabeanus* (S. Ito & Kuribayashi) Drechsler ex Dastur brought serious repercussions on the population in Bengal. Because of the epidemic, two million people died, especially in the cities of Calcutta and Dhaka (Padmanabhan, 1973). There are many other cases about the arrival of new pathogens to a new area that, when added to monoculture practices and favorable environmental conditions, facilitated the occurrence of devastating diseases, causing human deaths for starvation and economic losses (Ullstrup, 1972; Strange and Scott, 2005).

Continual evolution of emerging pathogens presumably leads to the emergence of new, dangerous strains for plants produced in conditions favorable to spread of these strains. New crop species are constantly introduced in different countries, and typically grown in large monoculture fields. Further, many varieties and cultivars are selected mainly by their productivity, without consideration for their susceptibility to pathogens. These favorable conditions suggest some plausible reasons why new diseases might emerge and flourish (Oliver and Solomon, 2008).

Emerging diseases and pathogen dispersion

In many countries or regions, incidence of emerging diseases increases quickly over a few months with higher emergence rates in some countries than others. This feature may be due to the combination of favorable conditions (Daszak et al., 1999).

Another feature of emerging pathogens is their ability to infect a broad number of plants as well as new hosts altogether. For instance, human pathogens have been recorded affecting plants. *Enterobacter cloacae* (Jordan) Hormaeche and Edwards is a clear example of a human pathogen exploring new hosts. The bacterium has been linked to nosocomial outbreaks (Gaston, 1988; Van den Berg et al., 2000) but was reported as a plant pathogen causing disease on onion (*Allium cepa* L.) in the USA (Bishop and Davis, 1990). Later, this bacterium affected many hosts including, but not limited to: mulberry (*Morus* L.) in China (Wang et al., 2010); dragon fruit (*Hylocereus* spp.) in Malaysia (Masyahit et al., 2009); macadamia (*Macadamia integrifolia* Maiden & Betche) in Hawaii (Nishijima et al., 2007); lucerne (*Medicago sativa* L.) seeds in China (Zhang and Nan, 2013); cassava (*Manihot esculenta* Crantz) in Venezuela (Santana et al., 2012); and chili pepper (*Capsicum annum* L.) in Mexico (Garcia-Gonzalez et al., 2018, to be published). These events indicate this bacterium has emerged as a plant pathogen in three continents: North America, South America, and Asia.

Xylella fastidiosa Wells et al., 1987 typically affects grape (*Vitis vinifera* L.) but is another example of a bacterium affecting a new plant host, causing mulberry leaf scorch in California (Hernandez-Martinez et al., 2007). To find a genetic explanation, a genetic typing study performed by Almeida and Nunney (2015) showed that mulberry isolates clustered together, and their relation with the other subspecies was dependent marked. This ambiguity revealed about equal mix of genes from subsp. *fastidiosa* and subsp. *multiplex*. So, seven inspected loci showed three alleles from subsp. *fastidiosa*, three from subsp. *multiplex*, and one chimeric allele containing sequences of both subsp. (Almeida and Nunney, 2015). Additionally, there are two other key factors that can aid the introduction and spread of pathogens (e.g., *X. fastidiosa*) causing new diseases: natural host plants of *X. fastidiosa* and insects (Hopkins and Purcell, 2002, and references therein). Natural host plants can serve as reservoirs for the bacterium and insects feeding upon these plants can become infected, thereby transmitting the bacterium to subsequent plants fed upon by infected insects (Hopkins and Purcell, 2002, and references therein).

Other novel plant pathogens listed in EPPO quarantine/alert list, and their recent worldwide distribution

Thekopsora minima (Artur) Sydow & P. Sydow is a rust that causes premature defoliation on blueberries (*Vaccinium*

corymbosum L.) and also affects *Azalea* spp. (Schilder and Miles, 2011). The pathogen was recorded in North America and Japan (Sato et al., 1993) and has been introduced on blueberries in other countries (e.g., in South Africa in 2006 [Mostert et al., 2010], Australia in 2012 [McTaggart et al., 2013], and Germany in 2015 [NPPO of Germany, 2016]). In 2012 in Tasmania all infected plants were eradicated (Tasmanian government, 2014). In Mexico the disease is listed as economically damaging (McTaggart et al., 2013; EPPO, 2016). The risk in Mexico is high because the market for berries is very important for the country's economy. Rust spores are spread over longer distances by wind and hurricanes besides trade.

Raffialea lauricola sp. nov. T.C. Harr. Fraedrich & Aghayeva is a fungus that causes mortality of redbay (*Persea borbonia*). The fungus and its vector, the ambrosia beetle *Xyleborus glabratus* Eichhoff, are originated from Japan and Taiwan (FAO, 2006). The disease has been observed in the Southeastern USA since 2003 (Rabaglia et al., 2006); more recently, the disease was reported in Florida causing avocado wilt disease (Ploetz et al., 2012). The risk for the Mexican avocado is high because it is one of the most important exportation fruit, and the domestic consumption is high.

Candidatus Phytoplasma phoenicium sp. nov. is a bacterium that causes almond witches' broom and was reported for the first time in almond in Lebanon in the 1990s (Choueiri et al., 2001). Later, symptoms of almond witches' broom were observed in Iran, although some genetic variability was observed among the strains (Verdin et al., 2003; Zirak et al., 2009). In 2001, this disease was added to the EPPO Alert list, but was removed from the list in 2006. However, because the new phytoplasma species *Candidatus* Phytoplasma phoenicium was later found in several major stone fruit trees in Lebanon and Iran, it was added again to the EPPO alert list (Abou-Jawdah et al., 2009). Perhaps its genetic variability led the pathogen to be more aggressive to its host and even to extend its pathogenicity to a larger number of hosts. These latter hypotheses represent the current major risk around the world. *Asymmetrasca decedens* Paoli is reported as the vector of this pathogen (Abou-Jawdah et al., 2009).

Tomato leaf curl New Delhi virus (ToLCNDV) was first described on tomatoes in 1995 in India (EPPO, 2016) then other countries in Asia found the virus on a wide range of crops. ToLCNDV was observed on courgette (*Cucurbita pepo* var. *giromontiina*) in 2012 in Spain (San Ambrosio and Fernández, 2014). After Spain, it was detected in Tunisia in January 2015, causing high severity on cucumber (*Cucumis sativus* L.), melon (*Cucumis melo* L.) and courgette (*C. pepo* var. *giromontiina*) (Mnari-Hattab et al., 2015). Draws attention

that in Italy it was reported in autumn the same year (Panno et al., 2016). The virus is transmitted in a persistent mode by the whitefly *Bemisia tabaci* (Gennadius) (San Ambrosio and Fernández, 2014). The insect vector migration could be the reason for the spread of the disease in Spain, then in Tunisia and in Italy. The alert of this disease is by its rapid dispersion and wide range of crops can affects.

Euwallacea sp., a pest of tea (*Camellia sinensis* (L.) Kuntze) associated with *Fusarium ambrosium* (Gadd and Loos) Agnihotr. and Nirenberg, was reported in Sri Lanka since the mid-2000s. Currently, the complex has been reported in Africa (i.e., Comoros, Madagascar, and Reunion), in America in Costa Rica, Guatemala, Panama, and in the USA (California, Florida, and Hawaii) and many countries in Asia. It affects woody plants, such as avocado (*Persea americana* Mill.). Euwallacea sp. and *Fusarium euwallaceae* sp. nov. (S. Freeman et al.), its obligate symbiotic fungi, is causing mortality on several trees in California (USA) and Israel. It is still unknown the way both were introduced into these countries. Although, transport of diseased plants likely contributed to the introduction and movement of infested plant material is likely to ensure broad dispersion (Eskalen et al., 2012; Freeman et al., 2013; Jones and Paine, 2015; Carillo et al., 2015).

Puccinia graminis f. sp. *tritici* Ug99 is present in Uganda, Kenya, Ethiopia, Sudan, Yemen, Iran, Tanzania, Eritrea, Rwanda, Egypt, South Africa, Zimbabwe and Mozambique. It affects wheat causing losses of 70% or more. A new virulent strain was identified in wheat fields in Uganda, in 1999, it was designated Ug99. This new race broke the resistance conferred by the gene Sr31. Transmission, as other rusts, has been carried by wind or the movement of people carrying the fungus (e.g., contaminated clothing) (Singh et al., 2011).

The list of invasive or emerging pathogens is increasing. In addition to the above mentioned pathogens, new and emerging pathogens include *Neofusicoccum parvum* (Pennycook & Samuels) Crous, Slippers & A.J.L. Phillips 2006 (Molina-Gayosso et al., 2012), *Emaravirus* sp. (Rose rosette virus) (Dobhal et al., 2016), and *Pantoea stewartii* (Smith, 1898) Mergaert et al., 1993 (EPPO, 2016).

Possible causes of emerging pathogens

Some hypotheses for the emergence of new pathogenic organisms (i.e., bacteria and fungi) are: 1) the organism may be endemic in the crop regions but the new host discovered recently; 2) after being endemic the organism became pathogenic, due to an increase in the organism's virulence, or due to a decrease in the host's defenses; 3) the organism may have been recently introduced into a new area and previously unexposed hosts and the organism is

pathogenic to novel plants (e.g., chili pepper); or 4) insect vectors exploit (i.e., feed upon) new plants harboring the pathogenic organism and transmit the organism to subsequent plants.

The emergence of diseases is thought to be the result of various factors such as interactions among other pathogenic organisms, plant-pathogen interaction, plant-insect-pathogen interaction, and adverse environmental conditions (i.e. irregular water regime and prolonged droughts). Many authors mention that adverse factors can interact and “help” to subsequently cause complex diseases. For example, Deberdt et al. (2014) proposed that climatic factors could change the nature of microorganisms turning them into opportunistic pathogens.

Climate change (or global warming), reflected by changes in average temperatures, reduction of annual rainfall, irregular distribution of rainfall and extended drought periods, may modify the growth or quality of crops, and potentially cause plant mortality (Carnicer et al., 2011; Besson et al., 2014). Some authors agree that when plants become weakened or stressed by environmental factors, microorganisms can easily colonize plants thereby causing plant death (Moricca and Ragazzi, 2008; Moricca et al., 2016). Indeed, global warming has contributed to the decline of trees and plants worldwide (Allen et al., 2010). While some researchers hypothesized that emerging diseases are caused solely by the effects of environmental factors, no strong evidence has been presented to support these hypotheses.

Alterations in the host-pathogen interaction process and geography are also factors in the occurrence of emerging pathogens. It is well known that pathogens use specialized secretion systems to produce proteins to infect plants or produce specialized structures or secrete toxins to invade plant cells (Doehlemann et al., 2009). To respond to this infection, plants modulate molecules for its defense. This scenario of alterations in the host-pathogen relationship can be seen in the interaction between avocado (*Persea americana* Mill.) fruit and the fungus *Colletotrichum gloeosporioides* (Penz.) Pens. and Sacc. where the flavonoid epicatechin is synthesized by the avocado fruit to protect itself from the laccase protein produced by *C. gloeosporioides*. The influence of geography is evident where the variability in the pathogenicity of genes within the same species is more evident in specific geographical areas. Isolates of *C. gloeosporioides* from Mexico showed increasing capabilities to metabolize epicatechin, when compared with isolates from Israel (Guetsky et al., 2005).

Changes in gene functionality can also contribute to risks of a new pathogen (Friesen et al., 2006). The

occurrence of lateral transfer is well-documented between prokaryotic species and from prokaryotic to eukaryotic species (Zhaxybayeva and Doolittle, 2011). This process is exemplified when isolated incongruent genes are absent in closely-related species and are in species more distantly related. However, the lateral gene transfer argument has some difficulties. For example, Oliver and Solomon (2008) postulate that the orthologous gene could not be detected in organisms that are related. Although it is possible that the genes may not be avowed as similar but may still develop a high rate of homologous relationships. Changes to gene functionality may also be caused by mutations over translocations and gene creep which can be a result of a high number of genes copied. Thus, in a lineage, an incongruent gene can be developed by selective loss of genes. Differences lateral gain and lineage loss would be more discernible if more genome sequences were available.

Additional evidence of gene functionality is that some strains of a species may lack a gene. This could happen when a recently acquired gene or a gene that had marginal evolutionary benefits. These genes are an example where the microorganism possess said genes with functions as avirulence and necrosis-inducing (Schulz and Boyle, 2005).

Almost always, species have a subset of the genetic variation. However this is possible since lateral transfer of ToxA was successfully evidenced by genetic variation (Stukenbrock and McDonald, 2008). Analysis of transferred genes codon may show the bias in the donor organism rather than in the recipient one, when distantly related microorganisms are compared (Azad and Lawrence, 2007). Transposons are mechanisms that mediate chromosomal rearrangements (Loreto et al., 2008). Movement of DNA from a donor organism is more probable when the gene is associated with a transposon (Feschotte and Pritham, 2007), because the tendency of transposons is to insert new sequences or recombination events that lead to new genes (Schaack et al., 2010). For example, *Magnaporthe oryzae* transposons have been shown to generate high recombination rates, resulting in high rates of gene sequence evolution and gene duplications (Thon et al., 2006). Additionally, Oliver and Solomon (2008) indicate that the core of lateral gene transfer must examine the function of supernumerary or b-chromosomes; the former being demonstrated between fungal isolates by Coleman et al. (2009).

In summary, the first opportunity for virus emergence, is the exposure to new susceptible host plant. Successful initial infection of the host plant by a pathogenic organism is critical in establishment of the organism as an emerging

pathogen or virus (Elena et al., 2011). The virus can remain in its initial form but is capable of genetically modifying itself to aid in exploitation of the susceptible host plant. Elena et al. (2011) estimated mutation rates for six virus in different hosts. The principal finding was the homogeneity in rates of mutation among plant RNA viruses. However, in the same study, the mutation rate for the viroid *Chrysanthemum chlorotic mottle viroid* (CChMVd) was more evident than the observed for RNA viruses. Controversies remain regarding the recombination effectiveness and the emergence process. Some authors indicate the recombination may help the cross-species transmission process (i.e., Chare and Holmes, 2006), but others report the association between recombination and virus emergence as not common events (i.e., Holmes, 2008).

Are UV-B, O₃, and CO₂ involved/linked to emergence or pathogenicity?

Pathogens may be reportedly affected by climate change but strong evidence is lacking. Ultraviolet B (UV-B), ozone (O₃), and carbon dioxide (CO₂), are climatic elements that have been commonly addressed relative to climate change and the emergence of pathogens.

Some species present different sensitivity to UV-B radiation; while some may be negatively influenced others may be tolerant. Paul (2000) demonstrated that increased UV-B after inoculation reduced disease in wheat, presumably because direct UV-B damaged the pathogen. Paul (2000) used *Septoria tritici* Rob. apud Desm. to infect wheat and found that *S. tritici* is very sensitive to UV-B rays. Ballare et al. (2011) reported that the effects of ozone depletion in the field will be decreased by changes in UV-B radiation because of the season and possible cloudiness. These event may lead to acclimation and also changes in plants - pathogen interactions. Similarly, bacteria and fungi are commonly more sensitive to damage by UV-B radiation plants (Caldwell et al., 2007). Thus, researchers hypothesize that climate change, via increasing solar UV-B, could predisposed plants to opportunistic pathogens.

Although the potential effect on pathogens of UV irradiation is uncertain, since these pathogens are rarely exposed directly to sunlight.

Ozone (O₃) affects pathogens and host plants differently. According to Manning and Tiedemann (1995) it is unlikely that O₃ has direct adverse effects on pathogens, but they assure O₃ adverse effects are mediated by host plants. Similarly, the same authors have proclaimed that main effects of increased irradiation on diseases would be via alterations in the host plant, and that pathogens are less possibly to be negatively affected by UV-B, CO₂, and O₃, than their corresponding host are.

Climate change has not been inconclusively linked neither to emerging pathogen nor to changes in plant pathogenicity gene mutations. Very little is known regarding the direct impacts of climatic change factors on emerging diseases and we currently have limited knowledge of the way the pathogens manage to adapt to climate change (Desprez-Loustau et al., 2007). Plant pathologists should be encouraged to consider the relationship(s) of CO₂, O₃, and UV-B factors relative to changes in genes affecting pathogenicity of microorganisms.

Disease spread

Once new pathogens emerge the biggest threat is their dispersion into new geographical crops areas. Introduction of new pathogens is a global threat; especially today, with the increasing mobility of people which transport plants, seeds, soil, and raw food (Wilson, 1995; Strange and Scott, 2005).

The spread of plant pathogens take place through short- and long-distance dispersion pathways. Major sources of short-distance dissemination include human practices (i.e., grafting and pruning) and vectors (e.g., insects or humans) (Ashraf et al., 2014). Additionally, sources of long-distance movement include weather (e.g., wind and rain; Grünwald et al., 2012) and inter-regional, domestic, and continental trade (Lamichhane, 2014). For example, spores alone can undertake journeys ranging from a few meters to thousands of kilometers, over land, or through air or water. Additionally, hurricanes can rapidly spread spores long distance as was observed from the Southern hemisphere to the north (Isard et al., 2005), or even from a continent to another, subsequently leading to the establishment of invasive pathogens.

Actions to mitigate pathogen emergence

Countries are making efforts to minimize threats by establishing regulatory measures to prevent, control, or eradicate diseases caused by pathogens potentially dangerous to crops.

National and international organizations for free information about dissemination among scientists, governments, and the public would be crucial to minimize the threat of emergent pathogens.

Phytosanitary regulations are performed worldwide to prevent, combat, and eradicate pests affecting plants. For example, quarantines are an example to prevent or delay the movement of pests from areas where there are not known to exist; conversely, quarantines also enable delayed introduction of pathogens into new areas until risks have been evaluated. Foreign quarantines, prevent the introduction and presence of exotic pests, and domestic

quarantines slow the spread, control, or eradicate any pest that has been introduced to a certain country.

Phytosanitary programs such as those in Mexico include surveillance at ports, airports, and borders and are aided by trained dogs to locate fruit, seeds, and plant products. These programs have generated successful results to stop the introduction of diseases from abroad. Despite similar programs and regulations, pathogens manage to arrive in new crop areas via vectors, humans, or environmental factors.

In this document we encourage researchers globally to focus in the major food threats and cultivate collaborations to establish public policies with competent authorities, design phytosanitary regulations and establish diagnostic protocols which would thereby strengthen government decisions. The protocols are very important to enable accurate detection of pathogens. Morphological analyses, coupled with DNA sequences data currently available, facilitate the identity on new pathogens or variants thereof (Phillips et al., 2013). These kind of diagnostics contribute to a rapid and accurate detection of new pathogens and should be consulted for the development of proper diagnostic protocols.

Conflicts of interest

The authors declare that there is no conflict of interest regarding the publication of this manuscript. This manuscript has not been published and is not going to be considered for publication elsewhere. The authors certify that neither the manuscript nor its main contents have already been published or submitted for publication in another journal.

Authors' contributions

All the authors contributed equally to the writing of this manuscript. They were involved in all sections.

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