



## Mini review

When plants brace for the emerging pathogens<sup>☆</sup>Biswapriya B. Misra<sup>a,\*</sup>, Ratna Chaturvedi<sup>b</sup><sup>a</sup> Department of Biology, Genetics Institute, Plant Molecular and Cellular Biology Program, University of Florida, Gainesville, FL 32610, USA<sup>b</sup> Department of Neurobiology, University of Massachusetts Medical School, Worcester, MA 01605, USA

## ARTICLE INFO

## Article history:

Received 20 November 2014

Received in revised form

23 March 2015

Accepted 31 March 2015

Available online 13 July 2015

## Keywords:

Bacteria

Oomycetes

Fungi

Effector

Genome

Omics

## ABSTRACT

Emerging phytopathogens ranging from viruses, bacteria, oomycetes, and fungi to nematodes have seriously threatened global crop productivity and food security, mostly owing to changing demographic dynamics and geographical movements of crops brought by human beings. An understanding of these new pathogens would allow timely intervention in biological control, phytosanitation, and biosecurity of crops and plants. With the flooding of information in the genomic era and with ensuing advances in other related 'omics', technologies would pave the path to improvement of plants to protect against the pathogens. We introduce the recently reported, emerging repertoire of phytopathogens, from diverse taxa such as fungi, oomycetes, bacteria, viruses, and nematodes, to the re-emerging ones and the cross-kingdom host jumping pathogens.

© 2015 Elsevier Ltd. All rights reserved.

## 1. Introduction

Plants are constantly exposed to and challenged by a realm of biotic factors, many of which many are beneficial while a plethora are pathogens. Plant pathogens belong to viruses, bacteria, fungi, nematodes, protozoa, and insects. In addition, the would-be pathogens are lurking in their immediate environment which, in spite of the presence of a solid innate immunity, fail to provide resistance to the newly faced microbes. Over the course of evolution and agricultural history, pathogens are armored with tools to move and colonize new hosts in the agricultural phase of human civilization, thus changing the plant disease landscape globally. Human population boom, global trade, and co-evolution of both host and pathogens have led to the incremental instances of catastrophic outbreaks from plant pathogens. These exotic pathogens have grown to epidemic proportions. Thanks to the migration, divergence, speciation, recombination events, the intricate interplay of pathogens, newer host availability, susceptibility and abundance, expansion of parasitism protein families within their genomes, and suitability of changing climate conditions, these recent groups of pathogens have evolved to kill in a very efficient manner. Pathogens

secrete proteins among other molecules to modulate plant defense machinery and facilitate colonization of plant tissue, collectively known as 'effectors' [1]. These effectors form a huge part of secretome whose roles are starting to be understood in host-defense modulation, e.g. proteins, toxins and hormones. Of the two major kinds of effectors, apoplastic effectors are released into the extracellular space, while the cytoplasmic effectors are translocated inside the plant cell, thus targeting numerous subcellular compartments [2]. These evolving pathogens show up in a new host species and evolve adaptation to a new host range, owing to mutations leading to increased virulence, or owing to geographic migrations that are mostly human mediated. The behavior of pathogens and their patterns are intriguing. Since the last few decades, these virulent infections have affected both natural populations [3], forests, and managed landscapes, which are subjected to growing systems affected by local practices and economies. This happened in unprecedented proportions, leading to extinction of wild species, loss of biodiversity [4], and affecting crop productivity. Understanding these intensifying disease emergence scenarios is critical to their imminent prevention in a timely fashion, thus the recently known, emergent pathogens are the focus of this commentary.

Historical records for the emerging pathogens are scanty and not available for the majority of the pathogens and possibly many more which have not come under the scanner or stay latent until a catastrophic outbreak. In case of more worrisome emerging

<sup>☆</sup> This article is part of a special section entitled "Molecular Interaction".

\* Corresponding author. Cancer & Genetics Research Complex, University of Florida, Room 437, 2033 Mowry Road, Gainesville, FL 32610, USA.

E-mail address: [biswapriyamisra@ufl.edu](mailto:biswapriyamisra@ufl.edu) (B.B. Misra).

zoonotic viruses, bats are believed to be the reservoirs of such viruses as Hendra, Nipah, SARS and Ebola, in addition to a plethora of unknown viral sequences in their mammalian genomes. This is attributed to their ancient evolutionary origins, while the spread is explained by their flying nature [5]. Although soils and natural resources are also understandably reservoirs for them, by drawing parallels it could be speculated that for plants, similar natural reservoirs are existing in nature in the form of wild species, insect carriers, endophytes, parasites, etc. Both natural and man-made landscapes with cultivated plants represent considerably different habitats for pathogens. A top 10 list of fungal pathogens in terms of their scientific/economic importance was generated that includes *Magnaporthe oryzae*, *Botrytis cinerea*, *Puccinia* spp., *Fusarium graminearum*, *Fusarium oxysporum*, *Blumeria graminis*, *Mycosphaerella graminicola*, *Colletotrichum* spp., *Ustilago maydis*, *Melampsora lini* [6], while a similar list for emerging plant pathogens is imminent. The emerging infectious diseases of plants have been the point of interest of several important reviews here [7], and more recently, here [8].

## 2. Bacterial pathogens

Plants are host to bacterial communities on the phyllosphere and rhizosphere which are best characterized with species chiefly belonging to *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, and *Proteobacteria* [9]. The *Proteobacteria*, *Burkholderia glumae* was recently recognized as an emerging pathogen of rice [10]. *Dickeya* species cause diseases in numerous crops and ornamental plants worldwide. First reported in potato in the Netherlands in the 1970s, the diseases have spread to other European countries. However, since 2004–05 a new pathogen named '*Dickeya solani*' is spreading across Europe, leading to economic losses in potato tuber trade [11]. Bacterial pathosystems underscore a large repertoire of constantly evolving bacterial communities which catch the host defense system off-guard and lead to new colonization events.

Horizontal gene transfer among bacteria has facilitated not only genome adaptation in bacteria by the transfer of pathogenicity islands (i.e., regions of localized enrichment of pathogenicity-related genes), but the cross-kingdom horizontal gene transfer events that have also helped increase the pathogenicity in the pathogens by using plant host's genes against themselves [8]. Interestingly, analysis of 37 bacterial plant-pathogen genomes revealed 5169 genes of phage origin with approx. 50% with unknown function or relevance to phage biology, suggesting an association between plant diseases and prophage transcriptional modulation in bacteria for these phage lineages [12]. For bacteria such as *Pectobacterium*, *Pseudomonas*, *Ralstonia*, and *Streptomyces*, the prophage is involved in disease symptoms, while in *Xylella* and *Xanthomonas* the prophage activity is associated with genome rearrangements and strain differentiation [12]. A deeper understanding of the shared genes and their encoded proteins among the genomes of these pathogens would provide immense insights into the common evolutionary strategies employed to colonize new hosts. These newer insights into phage-mediated regulation of bacterial pathogenesis holds tremendous potential in understanding of the emergence of these bacterial species.

## 3. Oomycetes in action

The most notorious oomycete known to affect food security in human history is *Phytophthora infestans* that caused the Irish potato famine. A recently emerged plant pathogen, *Phytophthora ramorum* is the causative agent of the sudden oak death epidemic [13]. Invasion of *P. ramorum* and emergence of the sudden oak death disease in forests has caused a severe decline of tanoak (*Notholithocarpus*

*densiflorus*) population in Californian coastal forests [4]. *Phytophthora alni*, a heteroploid hybrid oomycete pathogen, was discovered in 1993 in southern England to be causing lethal root and collar rot in alders and was reported in many European countries. First observed in North America associated with mortality of tanoak (*Lithocarpus densiflorus*) and coast live oak (*Quercus agrifolia*) in coastal forests of California during the mid-1990s, it now has a host range of over 40 plant genera, thus exemplifying the undesirable linkages between horticultural practices and natural forest ecosystems [14]. Hybrid plant pathogens such as *Phytophthora andina*, an increasingly common pathogen in Andean crops such as *Solanum betaceum*, *Solanum muricatum*, *Solanum quitoense*, and several wild *Solanum* spp., has emerged via hybridization between *P. infestans* and a unknown *Phytophthora* species [15]. The secretome of *P. infestans* was recently unraveled [16], while genome sequencing projects on *Phytophthora parasitica* [17] have advanced our understanding of this menacing oomycete. Recently, the analysis of evolutionary dynamics of 10 Stramenophiles yielding 18,459 gene trees constituting the phylome indicated that the genomes of pathogenic oomycetes have constantly gained and lost genes [18]. In particular, *Phytophthora* genus was identified as a major transition point characterized by increased frequency of duplication events that has driven the speciation within the genus. The oomycete specific features of genome evolution include repeat-driven expansions, deletions, gene fusions, and horizontal gene transfer in a landscape organized into gene-dense and gene-sparse sectors and influenced by transposable elements, in addition to gene expression profiles that are highly dynamic throughout the oomycete life cycles that demonstrate striking variation in genome size and content, a plastic set of genes related to pathogenesis, and adaptations associated with obligate biotrophy [19]. Comparing the secretomes of two *Saprolegnialean* oomycetes with that of eight other oomycetes using *de novo* genome and transcriptome sequencing showed novel horizontal gene transfers to the oomycete secretome from bacterial and fungal donor lineages and changes in oomycete secretomes associated with shifts from free-living to pathogenic taxa [20]. The importance of horizontal gene transfers on the emergence of phytopathogens has been shown to be significant for oomycetes and across the bacterial and fungal kingdoms [8]. Comparative genomics and *de novo* genome sequencing of *Hyphochytrium catenoides*, a free-living sister of the oomycetes, indicated that horizontal gene transfers largely converge within the radiation of oomycetes that colonize plant tissues where these transferred genes are implicated in resisting plant defense mechanisms and effector proteins for attacking plant cells [21]. Thanks to the continuing genome sequencing efforts [22–25] and pathogenomics research endeavors in oomycetes, our understanding of plant parasitic oomycete effector repertoire ('effectoromics') function and plant host responses have significantly increased [26]. With several oomycetes species undergoing genome sequencing and annotation, a genome-wide cataloguing of oomycete effectors sounds more realistic [2].

## 4. Fungal invaders

A large number of species of fungi, specifically belonging to ascomycetes, are plant pathogens of great notoriety and economic importance. Gene transfers since 1940s have created a pathogen population with significantly enhanced virulence, thus leading to the emergence of new damaging disease of wheat [27]. Another ascomycete fungus *Ramularia collo-cygni* has elevated itself to an important pathogen of barley in Northern Europe and New Zealand [28]. Similarly, other hybrid plant pathogens include the poplar rust *Melampsora columbiana*, the crucifer pathogen *Verticillium longisporum*, the onion pathogen *Botrytis allii*, and *Heterobasidion* forest pathogens. Furthermore, hybridization and

Download English Version:

<https://daneshyari.com/en/article/2836236>

Download Persian Version:

<https://daneshyari.com/article/2836236>

[Daneshyari.com](https://daneshyari.com)