

## Cross-Kingdom Pathogenicity across Plants and Human Beings

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### Editorial

Plants normally harbour microorganisms beneficial to the plants. However, many of these microbes may cause diseases to human beings in form of food-borne infections. Moreover, plant pathogens may also infect human beings, resulting in cross-kingdom pathogenicity. For instance, many members of Enterobacteriaceae which are pathogens to human beings are also known to cause rots and blights in plants. Many microbes found in rhizospheres of plants are also known to cause diseases (*Pseudomonas aeruginosa*, *Serratia marsescens*, etc.). Therefore, many inhabitants of plants (both rhizosphere and phyllosphere) residing in or on plant tissues can be opportunistic pathogens of humans [1]. Despite of the morphological and physiological changes of hosts, microbes have evolved surprisingly to inhabit diverse hosts, thus leading to cross kingdom pathogenicity [2-5]. There are a number of microbial pathogens capable of infecting both plants and humans. This pathogenesis can be taken place by direct or indirect methods. It has been suggested that human pathogens are indirectly transferred to plants through environment or with the aid of any carrier. Plant pathogens can be shifted to humans by direct contact or indirectly through environment [1,2,5].

To cause cross-kingdom infection, pathogens must be evolved to a level that allows them to survive in different hosts. In doing so, a pathogen must be able to find specific target receptors on host, land on those targets and evade host immune systems. Defensive system of hosts, even of different kingdoms, share certain similarities and is evoked by recognizing the same MAMPs (microbial associated molecular patterns) [4,6]. Therefore, the number of pathogens capable of causing cross-kingdom pathogenicity is limited. By residing frequently in the close proximity of the potential host, opportunistic pathogens gain ability to overcome target's defence systems. As the pathogen grows in vicinity of a potent host through generations, it adapts and evolves based on the exudates and environment of the host [3]. This adaptation is crucial to survive in an alternate host, and helps microorganisms to acquire determinants capable to target the pathways common in both hosts. In addition to this adaptation, niche specific virulence factors and host specific determinants are considerably switched by the horizontal gene transfer in both human and plant pathogens and widely spread in the environment. Cross kingdom pathogenicity is also supported by the selective pressure or evolutionary directionality [7-9].

Among human pathogenic bacteria *Enterococci*, *Serratia*, *Enterobacter* and *Salmonella* are more prone to cause disease in plants. Whereas different phytopathogenic species of *Stenotrophomonas* [5], *Burkholderia* and *Pantoea* are evolving as human pathogens [2]. Some plant endophytes e.g. *Cryptococcus gattii* [5] *Streptomyces* spp., *Klebsiella pneumonia*, *Morganella morganii*

and *Pantoea agglomerans* are more often asymptomatic within plants but have clinical significance [2]. *Rhizopus arrhizus*, *Alternaria alternata*, *Fusarium oxysporum*, *Aspergillus flavus* and *Microascus cinereus* are the fungal phytopathogens evolved to infect the humans [5]. Pathogenicity determinants of some pathogens have been recognized for both plants and humans while other are unknown or identified in case of one host only. Kirzinger et al. [2] has elucidated many infection target sites of many cross-kingdom disease (both plants and humans), as well as the disease causing determinants.

Pathogenic molecules involved in cross-kingdom pathogenicity target conserved components of the host, thereby creating potential to infect a wide range of hosts. Baarlen et al. [3] has reported enzymes, secondary metabolites and toxins that target conserved constituents of hosts. Infections are usually caused by the aid of toxins that target the host cell membrane and facilitate necrosis to utilize cellular components as source of nutrients [3,10]. Many homologous target receptors are also found in both animals and plants, thus further facilitating the cross-kingdom pathogenicity. In animals (mammals and insects) target receptors are known as TLRs (toll like receptors) [11,12] while in plants homologous receptors are recognized as RLPs (receptor like proteins) and RLKs (receptor like kinases) [13]. Phytopathogenic determinants in case of *Salmonella* (flagellum proteins) and *Enterococci* (quorum sensing system gene (*fsrB*) and a serine protease (*sprE*)) are almost the same as involved in human infections [2]. Phytopathogen *Burkholderia pseudomallei* exhibits human disease potential as it harbours an operon which shows similarity with signalling molecule of *Pseudomonas aeruginosa* associated to virulence [2,14]. As cross-kingdom pathogenicity involves synthesis of molecular determinants capable of recognition and interaction with (almost) conserved target sites, evasion from host immune system and above all, survival in host environment, therefore, ironically, the characteristics of the host governing the fate and survival of the pathogen lays the foundation and provides the criteria for the evolution of the cross-kingdom pathogenesis.

Many studies have been done to explore the diversity of the plant microbiome. However, the vast repertoire of microbial diversity can only be unveiled by using culture-independent studies. Recent trend has been the studies that come under the vast umbrella of metagenomics; study of total DNA of the microbial community. Major focus has been the rhizosphere of the plants [15] as it is one of the richest habitats of microbes. More recently, metatranscriptomics (study of total RNA of microbial communities) has also been employed to explore rhizospheric microbiota. Turner et al. [16] used this approach to analyze rhizospheres of wheat, oat and pea. They found out that pea plant had a very diverse rhizosphere community as compared to wheat and oat. However, the latter two had much higher abundance of eukaryotic microbes as compared to wheat. They

detected presence of a variety of taxa, many of which are known to contain possible human pathogens. Chauhan et al. used both metagenomics and metatranscriptomics to study rhizospheric microbiome of transgenic switchgrass. Many microbial groups detected by them are also known to house pathogens [17].

Frequency of emergence and re-emergence of infectious diseases is highly influenced by the cross kingdom pathogenesis, as these pathogens have aptitude to uphold the level of their population in variety of niches [4]. The cross-kingdom pathogenicity demands much work to be done in order to explore insights of the mechanisms involved, thus leading to possible recommendations to control and contain this pathogenicity.

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