Plant Pathology Seminar Series

"There are current Common characteristics & case studies of cross-kingdom fungal pathogens of plants & humans

By: Kayla Spawton

There are currently seven accepted kingdoms of living organisms: Bacteria, Archaea, Protozoa, Chromista, Plantae, Fungi, and Animalia. Although most symbiotic species depend on one or more hosts from a single kingdom, some species are capable of utilizing hosts from multiple kingdoms. Examples of such cross-kingdom symbionts include fungi that can be plant endophytes or entomopathogens, such as *Metarhizium* spp., or bacteria that can be plant or human pathogens, such as *Pantoea* spp. One emerging group of organisms that utilize hosts across kingdoms are fungi that are pathogenic to both humans and plants.[1,2] In order to be a successful pathogen, an organism must be able to attach, enter, colonize, reproduce, and disperse propagules away from a host to infect other hosts, all while avoiding or counteracting host defenses.[1] The defense systems of plants and humans are very different. Plants have a cuticle, cellulose cell wall, basal immunity, and effector-triggered immunity while humans have an intact epidermis, complex architecture of the respiratory system, a core body temperature of 37°C, innate immune defense, and adapted immunity.[2] Despite the differences in structural and immune defense of plant and humans, some fungal species are capable of bypassing both sets of obstacles.

Many fungal pathogens of humans and plants share common characteristics that contribute to successful infection of hosts from both kingdoms. Most known cross-kingdom fungal pathogens of plant and animals belong to the Ascomycota, produce pigmented spores, and are saprophytic.[1,2] Cross-kingdom fungal pathogens of humans and plants usually require a human host with a compromised immune system or trauma to facilitate entry.[1,2] Transmission is often nosocomial, such as through contaminated syringes.[1] In order to infect a human host successfully, crossover fungi must be able to survive at human body temperatures in addition to the range in temperatures of the plant hosts and are, therefore, considered polyextremotolerant.[1,2,3] In the model system of *Fusarium oxysporum*, studies have shown that conserved pathways play important roles in a pathogen's virulence in both animals and plants. This includes the velvet complex, which is responsible for promoting expression of the mycotoxin beauvericin, and mitogen-activated protein kinases, which mediate cellular responses to initiate infection in both animals and plants.[1,2,4,5]

Perhaps two of the most recent publicized cases of cross-kingdom fungal pathogens of humans and plants are the outbreaks of fungal meningitis caused by *Exserohilum rostratum* in the U.S. in 2012, and fungal keratitis caused by *Fusarium* spp. in the U.S. and Asia in 2005 to 2006.[6,7] With the growing number of immunocompromised individuals in the U.S. and increasing contact of humans with one another and diverse environments and microbes, we can expect the number of cross-kingdom fungal pathogens of humans and plants to increase.[8] In order to combat this phenomenon, it is necessary to recognize that plants, humans, and their ecosystems do not exist exclusively or independently. Therefore, a holistic approach should be taken in which research involves the collaboration of scientists from microbiology, human medicine, ecology, public health, and plant health to generate coordinated solutions.

4:10 pm | October 19th,2020| Plant Pathology 515, Fall 2020

Zoom Link and ID: https://wsu.zoom.us/j/91621814000?pwd=MDVOY1prS0QybDRaMXNvTVNxTS82UT09

Meeting ID: 916 2181 4000 Passcode: 5353 Call in number: 1 253 215 8782

College of Agricultural, Human, & Natural Resource Sciences
Washington State University

References

1. van Baarlen, P., van Belkum, A., Summerbell, R.C., Crous, P.W., and Thomma, B.P.H.J. 2007. Molecular mechanisms of pathogenicity: how do pathogenic microorganisms develop cross-kingdom host jumps? FEMS Microbiol. Rev. 21:239-277.
2. Gauthier, G.M., and Keller, N.P. 2012. Crossover fungal pathogens: the biology and pathogenesis of fungi capable of crossing kingdoms to infect plants and humans. Fung. Gen. Biol. 61:146-157.
3. Gostinčar, C., Grube, M., and Gunde-Cimerman. N. 2011. Evolution of fungal pathogens in domestic environments. Fung. Biol. 115:1008-1018.
4. López-Berges, M.S., Hera, C., Sulyok, M., Schäfer, K., Capilla. J., Guarro, J., and Di Pietro, A. 2013. The velvet complex governs mycotoxin production and virulence of *Fusarium oxysporum* on plant and mammalian hosts. Molec. Microbiol. 87:49-65.
5. Segorbe, D., Di Pietro, A., Pérez-Nadales, E., and Turrà, D. 2017. Three *Fusarium oxysprum* mitogen-activated protein kinases (MAPKs) have distinct and complementary roles in stress adaptation and cross-kingdom pathogenicity. Molec. Plant Pathol. 18:912-924.
6. Sharma, K., Goss, E.M., Dickstein, E.R., Smith, M.E., Johnson, J.A., Southwick, F.S., and van Bruggen, A.H.C. 2014, *Exserohilum rostratum*: characterization of a cross-kingdom pathogen of plants and humans. PL0S ONE 9:e108691.
7. Epstein, A.B. 2007. In the aftermath of the Fusarium keratitis outbreak: what have we learned? Clinic. Opthalmol. 4:355-366.
8. Harpaz, R., Dahl, R., and Dooling, K. 2016. The prevalence of immunocompromised adults: United States, 2013. Poster. Open Forum Infec. Dis. 2016:1 (Suppl 1).