

Host Shifts by Plant Pathogens: An Issue of Concern

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SUMMARY

An increasing in the number of disease epidemics have been associated with pathogen host species jumps. Although pathogens often infect closely related species, there are also many cases in which the original and new hosts are taxonomically diverse. With the upcoming reports of host jumps by plant pathogens the management of the emerging diseases is also a serious concern, thus continuous speculation of pathogen population is the need of the hour.

INTRODUCTION

With the upcoming cases of shifts of the plant pathogens from the usual host crops to non-host crops, the concern for crop losses is also raising. It is already a challenging task to manage prevailing deadly plant pathogens and yet some more pathogens have started lining up to cause severe losses to host crops. Host jump is emerging issue and requires attention of plant pathologist for successful management of plant disease and to minimise crop losses. Due to complex host pathogen interaction is very difficult to conclude the exact mechanism of host jump but still some conclusion can be drawn on the basis of existing theories and the ongoing studies related to it.

The concept of Host Jump

Host jumping is defined as a process by which pathogens settle in new host groups. It forms the base of evolution of pathogens, as it leads to pathogen diversification. There are two fundamentally different kinds of host jump: those that occur within the life cycle of a pathogen – among plant pathogens, the rust fungi are the most widely known example that falls into this category– and those that occur in the course of evolution. Both forms have a fundamentally different setting and influence the evolution of pathogens in different ways. It is very common phenomenon to be observed in facultative pathogens, as they can reproduce even if they kill their hosts. Host range expansion and host jumps are two different terms, however the exact differentiation between host range expansions and host jumps is bit difficult because the borders between those two categories are often ill-defined. The prevailing definitions states that host range expansions are to species closely related to the original host, while host jumps are to distantly related hosts. Instead, any expansion of the host range by an organism that leads to isolation from the original gene pool, leading to genetic differentiation and finally speciation, should be considered a host jump, irrespective of the phylogenetic distance of the hosts. Host jumps are likely to start through an evolutionary process, with a suboptimal interaction of a pathogen with a new host and proceed by relative increases in efficiency of infection. The process of host jumping is concluded when the new host can be colonised with a similar efficiency to that of the original pathogen on the original host. During the initial phase of suboptimal interaction, either defence reactions of the new host halt the pathogen before a large quantity of spores for new infections have been formed, or the host individual is killed after a fast initial colonisation. This initially unbalanced interaction with the host will lead to a substantial reduction in fitness. It can be assumed that the vast majority of host jumps will almost immediately end with the removal of the pathogen from the newly colonised host due to the inability of the pathogen to sustain the disease cycle. Pathogens that are also able to obtain nutrients from dead plant tissue have an evolutionary advantage over obligate biotrophs at this stage, as necrotrophy is part of their pathogenic nature. They can absorb nutrients from dead tissue, enabling the formation of propagules even if the establishment of a biotrophic interaction fails.

Probable reasons of Host Jumps

Entry of pathogens to non native areas: Pathogens, when invade new areas along with their cultivated hosts have probabilities to jump to new hosts in that area. Hosts that are brought to new geographic areas are prone to infection by the pathogens that prevail in that area and become host to them. An example of an alien pathogen

species performing host jumps is the rust fungus *Puccinia psidii* which after introduction from North America to Australia colonised a variety of native Myrtaceae.

Higher mutation rate: A high mutation rate together with short life cycles that is more number of cycles per season (and asexual reproduction, as this will make selection of somatic mutations possible) enables the pathogen to out run the host, which is important especially in the initial phases of host jumps.

Pre-adaptations in the pathogen: There must be pre-adaptations in the pathogen that is jumping hosts – the pathogen needs to be able to suppress defence reactions in the new host, at least to some degree. It is conceivable that effective manipulation of only a few hubs in plant defence pathways is sufficient to allow some colonisation.

Selection pressures: When the selection pressure on the pathogen population exceeds a limit, that is the host plant can no more sustain a pathogen population for very long durations it will lead to development of such strains which might try to infect the non host species just to retain their progeny and prevent the chances of extinction.

CONCLUSION

Host jumping is a fundamental process by which pathogen groups are able to persist over long evolutionary time scales. By jumping from one host to another they are trying to escape their extinction on a particular group of hosts that they colonised after a previous cycle of host jumping, radiation and speciation. Host jumps are enabled by several factors, as evolution is a natural phenomenon, it will happen what we can do to deal with it is to have sufficient knowledge about the pathogen and keeping an eye on the changing pathogen populations so that effective management measures can be taken to minimise the crop losses.

REFERENCES

- Kemler M, Lutz M, G€oker M, Oberwinkler F, Begerow D. 2009. Hidden diversity in the non-caryophyllaceous plant-parasitic members of Microbotryum (Pucciniomycotina: Microbotryales). *Systematics and Biodiversity*, 7: 297–306.
- Sharma R, Mishra B, Runge F, Thines M. 2014. Gene loss rather than gene gain is associated with a host jump from monocots to dicots in the smut fungus *Melanopsichium pennsylvanicum*. *Genome Biology and Evolution*, 6: 2034–2049.
- Thines, M. 2019. An evolutionary framework for host shifts –jumping ships for survival. *New Phytologist*, 224: 605–617doi: 10.1111/nph.16092