

Evolutionary forces in plant pathogen population: empirical prospects

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The genetic structure of pathogen population is affected by the complex interactions among the pathogen, its host plant and other variables. As the main part of this interaction, plants have an innate ability to recognize the potential invading pathogens and mount successful defenses. The pathogen on the other hand strives to evade the recognition by the host or suppress the host defense mechanisms. This is a dynamic evolutionary process, explained by a Zigzag Model as an evolutionary arm races between the two hostile organisms. The form of interaction and a specific evolutionary force responsible for the change in the amount and distribution of genetic variation within and among pathogen population varies in natural or human guided ecosystem. The central idea of this presentation is to discuss the various forms and interactions of evolutionary forces in these two settings.

In natural ecosystem, variation in the genetic structure of pathogen population and the respective host is determined by a specific gene-for-gene coevolution. It is a form of reciprocal genetic change occurring in the two ecologically interacting species: the pathogen and its host. Mutation, sexual recombination and selection are important evolutionary forces acting at various stages of the interaction. Invasion and attack by a pathogen results in reduced plant fitness. Within the diseased plant population, mutation or recombination produces new receptor allele that can recognize the pathogen elicitor. In the presence of constant disease pressure, plants with the new resistance allele will be favorably selected (produce more offspring) and increase in frequency. The increase in the resistance allele in plant population will in turn reduce pathogen's fitness. Consequently, the overall level of disease in the plant population decreases. Mutation or sexual recombination in the pathogen causing the loss or alteration of the avirulence allele will help the pathogen evade or suppress the plant resistance system. Since this increases the fitness advantage of the new variants, selection will favor and increase their frequency in the pathogen population. In addition, those pathogens with both sexual and asexual life cycles have evolutionary advantage as the former has variation maximization effect while the later boosts the frequency of new variants.

Purposeful manipulations in agricultural system are routinely practiced in order to minimize the impact of plant pathogens on the agricultural commodity. These practices include development and preferential deployment of resistance genes in plant genome, management of alternative host, chemical applications and other cultural practices. In response, the relative efficiency of evolutionary forces and subsequent genetic structure of pathogen populations in agro-ecosystem differ from the basic models that are aforementioned. Directional selection, population size, gene flow and mating system are well studied evolutionary forces responsible for the emergence and spread of new genetic variants or loss of defeated alleles (i.e mutations). Part of this presentation will evaluate how these forces operate in the agricultural systems and how they impose evolution risks. The models will also be implicated to the breeding strategies and resistance gene management practice.

One may also be righteously concerned on the development of efficient diagnostic tools to track these evolution risks in relation to both human interventions and natural phenomena. Since the advent of molecular techniques, it is possible to generate comprehensive information on the pathogen diversity, evolvability and distribution patterns. The presentation will briefly highlight some of these molecular techniques along with their relative merits in inferring genetic diversity and ecosystem stability.

Reference

Bruce A. McDonald and Celeste Linde (2002). The population genetics of plant pathogens and breeding strategies for durable resistance *Euphytica* **124**: 163–180