

**Population Biology of Plant Pathogens: The Synthesis of Plant Disease
Epidemiology and Population Genetics**Vineeth M¹, MD Thabrez²**Abstract**

It is no secret that much of the effort in plant pathology has shifted over the last 50 years from practical problem-solving to studies of more specialized academic interest. Our fundamental knowledge of plant disease and host–pathogen interactions has increased enormously, while at the same time the shift in emphasis has not been so extreme that practical disease management is ignored entirely. Granted, some practical problems still remain unsolved, but not always because of lack of attention by problem-solvers; some plant diseases are intractable, given current constraints, despite the relatively large inputs of energy and research activity (e.g., potato late blight, rice blast). Equally important, new disease problems continue to arise as old ones are solved (or not), in an ongoing dynamic.

Keywords- Epidemiology, Population biology, Genetics

Introduction

One needs only to look at the attention given recently to emerging pathogens, antimicrobial resistance, biotechnology, and most recently, crop bioterrorism (Crop biosecurity and countering agricultural bioterrorism: Responses of the American Phytopathological Society. October 2002. Published online) to see examples of the ever-changing problems facing plant pathologists

Population biology

We propose the use of the term population biology to describe a relatively

holistic perspective of the ecological and evolutionary dynamics of plant and pathogen populations—and their interactions. Despite previous claims that epidemiology alone is a holistic discipline (80), population biology explicitly integrates ecological, genetic, and evolutionary principles within a population context (Fig. 1). As such, it is even broader and more encompassing than either epidemiology or population genetics alone (Dobzhansky., 2014). Brinjal, *Solanum melongena* L., is a common, popular and extensively grown vegetable crop in the

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subtropics and tropics. Insect pest infestation is one of the major bottlenecks in increasing the yield potential in brinjal crop. The crop is susceptible to the attack of various diseases in different stages with varying degree of damage which causes considerable losses by reducing potential yield and quality of the produce. In view of the lucrative returns from brinjal, farmers with limited land holdings and resources are forced to follow monoculture and intensive cultivation, which also exacerbates the survival of various pathogens from one season to another.

Synthesis of Epidemiology and Population Genetics

concepts- Plant disease epidemiology is a discipline concerned with understanding the dynamics of disease in time and space. It is a holistic science in terms of being concerned simultaneously with populations of pathogens and host plants within an environmental context, i.e., the classic disease triangle. The interdisciplinary nature of epidemiology extends further because of the need to understand (Groth, 1987) environmental complexity, including a variety of abiotic and biotic factors. Moreover, epidemics must often be analyzed within an environment strongly shaped by human activity, especially disease management. Among the temporal aspects of epidemiology, one might ask questions such as whether pathogens are monocyclic or

polycyclic; and disease progress curves are analyzed to quantify the temporal development of epidemics. Spatial aspects are typically focused on the patterns of inoculum and disease, and the processes that form patterns, especially dispersal. Analysis of the dynamic changes in spatial patterns, e.g., focus expansion, is the attempt to integrate temporal and spatial aspects of epidemics simultaneously (Hulbert and Mitchelmore., 2018).

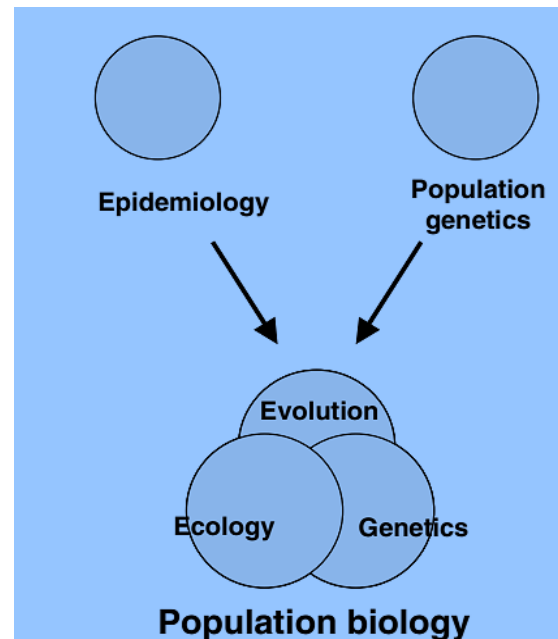


Fig 1- The synthesis of epidemiology and population genetics: population biology

Tracking genotypes-

The first two examples highlight a relatively simple application of genetic markers to track specific genotypes in space and time. This type of study does not depend on an understanding of evolutionary or genetic concepts beyond those needed to develop

markers for distinguishing among different genotypes (Iott *et al.*, 2017).

Source of primary inoculum of potato late blight has been searched for the sources of primary inoculum of *Phytophthora infestans* that caused late blight epidemics in potato fields in The Netherlands. They combined a traditional epidemiological approach of studying disease gradients and the locations of disease foci in relation to potential sources (cull piles, organic farms, or volunteers) with a population genetics approach of studying the spatial distribution of pathogen genotypes. The obvious application of this information in disease management is to eliminate the source of inoculum, if possible, by sanitation.

Diversity and spatial patterns of genotypes-

The combination of assessing pathogen genetic diversity and spatial patterns of genotypes and disease has proven to be a powerful combination for inferring the reproductive biology of pathogens in the field. For many organisms, all else being equal, sexual populations have more genotypic diversity because of recombination. Moreover, for many fungal plant pathogens, sexual and asexual inoculum differ in their dispersal characteristics, e.g., wind versus splash dispersal, which often affect the spatial patterns of disease and genotypes.

Genetic Drift

The random sampling of gametes

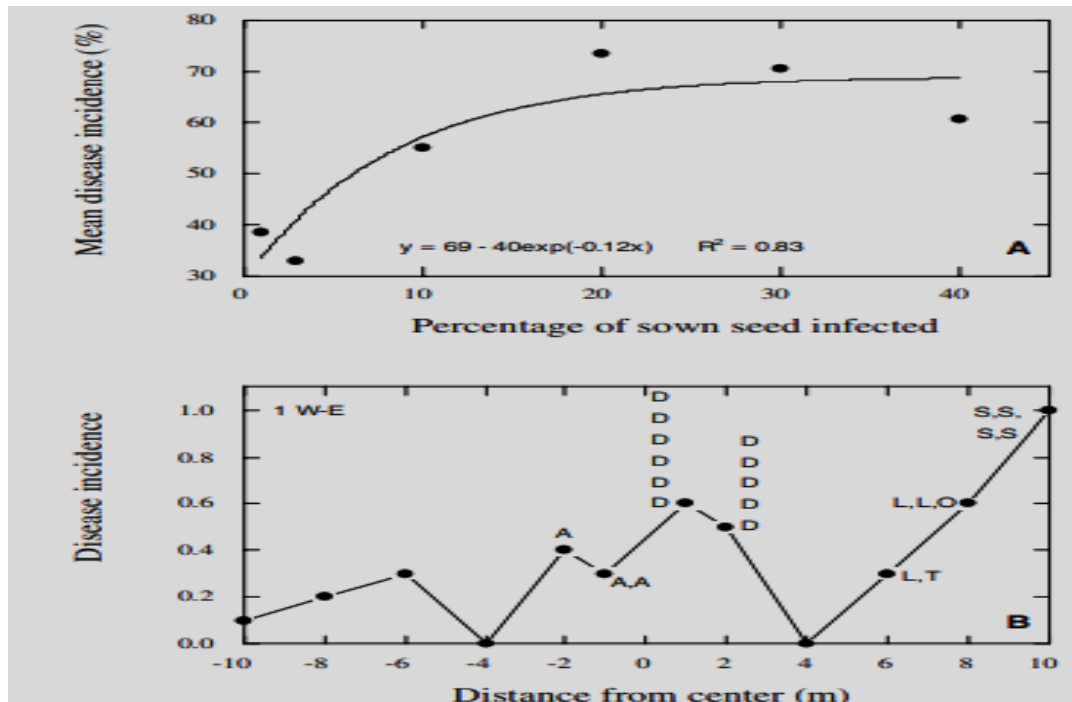


Fig 2- Epidemiology and genotype tracking of *Stagonospora nodorum* on wheat. A, Disease incidence in foliar epidemics as a function of percentage of infected seed sown, B and C, Disease incidence and multilocus restriction fragment length polymorphism (RFLP) genotypes in two perpendicular transects

between generations in finite populations results in random fluctuations in gene frequencies. This process, termed random genetic drift, is considered to be generally a weak force which acts to decrease genetic variation within populations through fixation of alleles. The effect is large in small populations and small in large populations (Moseman., 2016).

Selection

Selection can be a strong force in establishing and maintaining local differences. Host populations can act as powerful selective forces on pathogen populations and vice versa.

Recombination

Recombination increases genetic diversity in populations by breaking up existing combinations of genes and allowing the formation of novel combinations.

When new mutants arise they are necessarily in disequilibrium with other loci. If these mutants are strongly selected, as might be expected with genes for virulence, then alleles at other loci that are associated with the new mutant will also increase in frequency due to linkage or asexual reproduction (Wright, 2021).

Population Biology and Problem Solving

It is interesting to note that for both of these pathogens, genotypic variation in vegetative (or somatic) incompatibility (Fig. 3) was great enough that these relatively simple genetic markers were sufficient to answer the questions being addressed. Although these genetic markers may be perceived by some as old-fashioned (or low-technology), data with as much power as molecular methods for addressing this question could be obtained

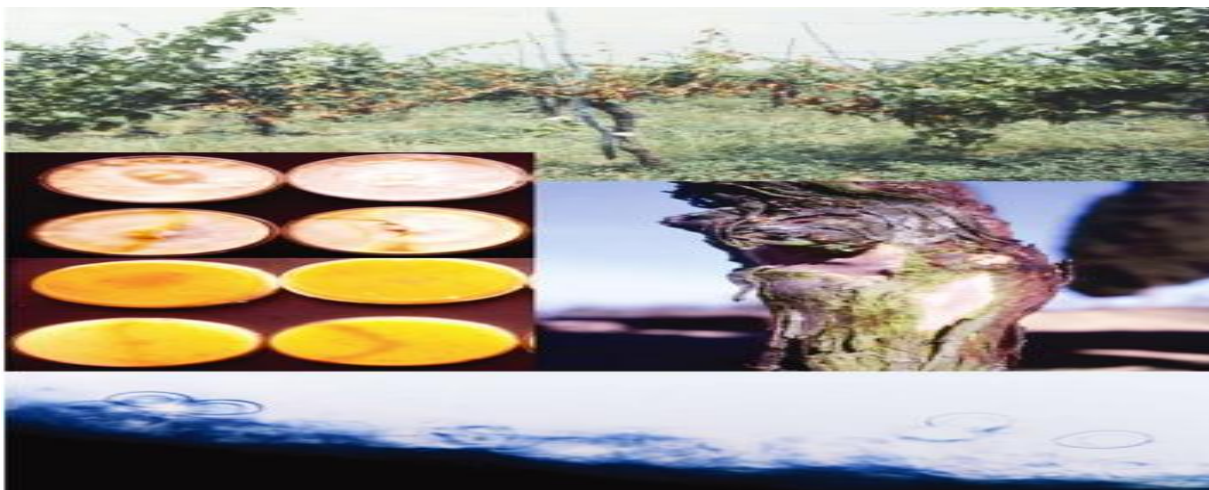


Fig 3- Signs, symptoms, and somatic incompatibility assay in *Fomitiporia punctata*, a causal organism associated with esca disease of grapevine. Clockwise from the top: symptoms of esca in grapevines; fruiting bodies of *F. punctata* (resupinate hymenium) on grapevine; basidiospores from fruiting body of *F. punctata*; somatic incompatibility testing in *F. punctata*. Photographs courtesy of P. Cortesi and G. Minervini

easily and cheaply. These are examples where the simplest methods were used to address specific questions directly. Estimation of population genetic parameters was not necessary for these studies.

Composite Crosses II and V

Composite Crosses II and V (CCII and CCV) are experimental barley populations that have been grown annually at Davis, California, for 60 and 48 years respectively. CCII was created by making all possible crosses between 28 barley varieties representing a diversity of germplasm from major barley growing areas of the world. In 1929, the F1 progeny from these 378 crosses were mixed in equal proportions and propagated under standard agronomic conditions without conscious selection for any trait. In each succeeding year, the population was harvested in bulk, a random sample of seed was saved to advance the next generation and a second sample of seed for genetic analysis (Zhang *et al.*, 1987)

Conclusion

All too often, technical trends or the perceptions of fashion determine the direction of scientific research. The number of papers using genetic markers and describing genetic variation in plant pathogen populations has increased dramatically in the past 10 to 15 years, but often with little contribution to solving real problems. This pattern may be

reminiscent of the trends 20 years earlier when epidemiology went through a method-oriented stage. Research is ultimately dependent on methods,; and the availability of certain technologies makes it possible to address questions that might not otherwise have been feasible. The risk is that methods may drive the questions, not vice versa. Nonetheless, more recent developments are encouraging for population biology, if the kinds of examples described above are any indication of the future direction in this area. It appears that plant pathologists are going beyond the methods and are using genetic and epidemiological tools in the context of population biology to solve problems in agriculture.

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