

Review

Mathematical modeling tendencies in plant pathology

L. M. Contreras-Medina^{1,2}, I. Torres-Pacheco¹, R. G. Guevara-González¹, R. J. Romero-Troncoso², I. R. Terol-Villalobos³ and R. A. Osornio-Rios^{2*}

¹Laboratorio de Biosistemas, División de Estudios de Posgrado, Facultad de Ingeniería, Universidad Autónoma de Querétaro, Cerro de las Campanas s/n, C.P. 76010, Querétaro, Qro., México.

²HSPdigital CA Mecatrónica, Facultad de Ingeniería, Campus San Juan del Río, Universidad Autónoma de Querétaro, Querétaro, Qro. México.

³Centro de Investigación Desarrollo Tecnológico en Electroquímica, Parque Tecnológico Querétaro, Sanfandila-Pedro Escobedo, C.P. 76700-APDO 064, Querétaro, Qro. México.

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Nowadays plant diseases represent one of the major threats for crops around the world, because they carry healthy, economical, environmental and social problems. Considering this, it is necessary to have a description of the dynamics of plant disease in order to have sustainable strategies to prevent and diminish the impact of the diseases in crops. Mathematical tools have been employed to create models which give a description of epidemic dynamics; the commonly mathematical tools used are: Disease progress curves, Linked Differential Equation (LDE), Area Under disease Progress Curve (AUDPC) and computer simulation. Nevertheless, there are other tools that have been employed in epidemiology of plant disease like: statistical tools, visual evaluations and pictorial assessment. Each tool has its own advantages and disadvantages. The nature of the problem and the epidemiologist necessities determine the mathematical tool to be used and the variables to be included into the model. This paper presents review of the tools used in epidemiology of plant disease remarking their advantages and disadvantages and mathematical modeling tendencies in plant pathology.

Key words: Plant disease epidemics, mathematical modeling, disease progress curves, area under disease progress curve, linked differential equation.

INTRODUCTION

Currently plant diseases, weeds and environmental factors are the major threats to agricultural production, mainly in less developed countries because they provoke between 31 to 42 percent of worldwide crop losses (Van den Bosch et al., 2006). Taking into account that 14.1% of crops are lost to plant disease alone, the total worldwide crop loss from plant disease is about \$220 billion dollars, this implies several problems in other important sectors (e.g. health, environmental, social) (Agrios, 2005); these losses are in part responsible for the suffering of 800 million people who lack adequate food (Strange and Scott, 2005). Due to the aforementioned problems it is necessary to have adequate, economic and environmentally acceptable strategies to manage the

epidemic development of plant diseases in order to decrease the crop losses and reduce their consequences (Van Maanen and Xu, 2003; De Wolf and Isard, 2007). Most current practices have been used in order to control epidemics, like the use of chemical control (Blaise et al., 1999) having a direct environmental impact due to its chemical residues (Orlandini et al., 2008). Then, in order to obtain sustainable practices for strategic and tactical management of diseases and also to decrease its environmental impact, it is necessary to understand the determining factors of epidemics (Royle and Ostry, 1995; Jeger, 2004). Mathematical, statistical and other tools have been used to understand these factors by modeling the epidemic dynamics; the objective in modeling is to simplify the reality in order to summarize the process of the epidemic (Van Maanen and Xu, 2003). Mathematical tools have been gaining popularity because they allow knowing a description of the epidemic dynamics and by consequence, to develop optimal forecasting and con-

*Corresponding author. E-mail: raosornio@hspdigital.org. Tel: +52-427-274-12-44. Fax: +52-427-274-12-44.

trolling mechanisms. Descriptions of temporal disease progress were used prior to 1960s when Ware et al. (1932) and Ware and Young (1934) presented curves to illustrate the effects of crop resistance and fertilizer treatment for the dynamics of cotton, Wilt and Large (1945, 1952) proposed disease progress curves to demonstrate the benefits of fungicide applications on the development of potato late blight. Nevertheless, the first temporal development model of plant disease epidemic was proposed by Van der Plank (1960, 1963), which has been the base of many epidemiological models created so far. The mathematical tools employed in plant disease epidemiology use several variable values as inputs; these variables are considered according to the nature of the problem and the questions to be answered (Van der Plank, 1982). Schoeny et al. (2007) proposed a predictive model of *Ascochyta* blight where an important variable in the model was the airborne inoculum. The variables used by the mathematical tools summarize the key characteristics in the epidemic dynamics. The most common mathematical tools used in plant disease epidemiology are: disease progress curves, linked differential equations, area under disease progress curve and computer simulations. Nevertheless, there are other tools to evaluate the disease progress. This paper presents an updated review about mathematical tools used in plant disease epidemiology. The paper is divided in five sections, the first one presents the mathematical tools used for modeling plant disease epidemics, the second section shows an analysis of variables commonly utilized by mathematical tools, the third section presents an analysis about the advantages and disadvantages of mathematical tools used in plant disease epidemiology, the fourth section shows tendencies in epidemiology of plant disease and finally the fifth section presents conclusions.

MATHEMATICAL TOOLS USED IN PLANT DISEASE EPIDEMIOLOGY

Plant diseases epidemics are investigated according to variables of interest which are formulated as functions of external factors, for instance temperature and rain (Van Maanen and Xu, 2003). The problem nature and epidemiologist specific questions determine the mathematical tool to be used for modeling plant disease epidemics (Kranz and Royle, 1978; Sutherst, 1993; Van Maanen and Xu, 2003; Xu, 2006). Next, the most common mathematical tools to describe epidemic dynamics are presented.

Disease progress curves

Disease progress curves show the epidemic dynamics over time (Agrios, 2005). This mathematical tool can be used to obtain information about the appearance and

amount of inoculum, changes in host susceptibility during growing period, weather events and the effectiveness of cultural and control measures. Growth models provide a range of curves that are often similar to disease progress curves (Van Maanen and Xu, 2003) and represent one of the most common mathematical tools to describe temporal disease epidemics (Xu, 2006). The growth models commonly used are: Monomolecular, Exponential, Logistic and Gompertz (Zadok and Schein, 1979; Nutter, 1997; Nutter and Parker, 1997; Xu, 2006). A brief description of each growth model is presented as follows:

Monomolecular

This growth model is appropriate for modeling epidemics where there is not secondary spread within a growing season, meaning that the plant disease has a single cycle during growing season (Forrest, 2007). This model is also called negative exponential model (Campbell and Madden, 1990).

Exponential

This model is also known as the logarithmic, geometric or Malthusian model. This growth model is appropriate when newly diseased (infected) individuals lead to more diseased (infected) individuals and has been used to model changes in disease prevalence on a geographic scale, it can be applied to describe the very early stages of most polycyclic epidemics (Forrest, 2007).

Logistic

Was proposed firstly by Veshulst in 1838 to represent human population growth. A second type of logistic model was proposed by Van der Plank (1963), being more appropriate for most polycyclic diseases, meaning that there is a secondary spread within a growing season (Forrest, 2007). This growth model is the most widely used for describing epidemics of plant disease (Segarra et al., 2001; Jeger, 2004).

Gompertz

This growth model is appropriate for polycyclic diseases as an alternative to logistic models. Gompertz model has an absolute rate curve that reaches a maximum more quickly and declines more gradually than the logistic models (Forrest, 2007).

Figure 1 shows examples of disease progress curves represented by growth models, where it can be seen that Gompertz and logistic models have a characteristic sigmoid form and an inflection point meaning secondary

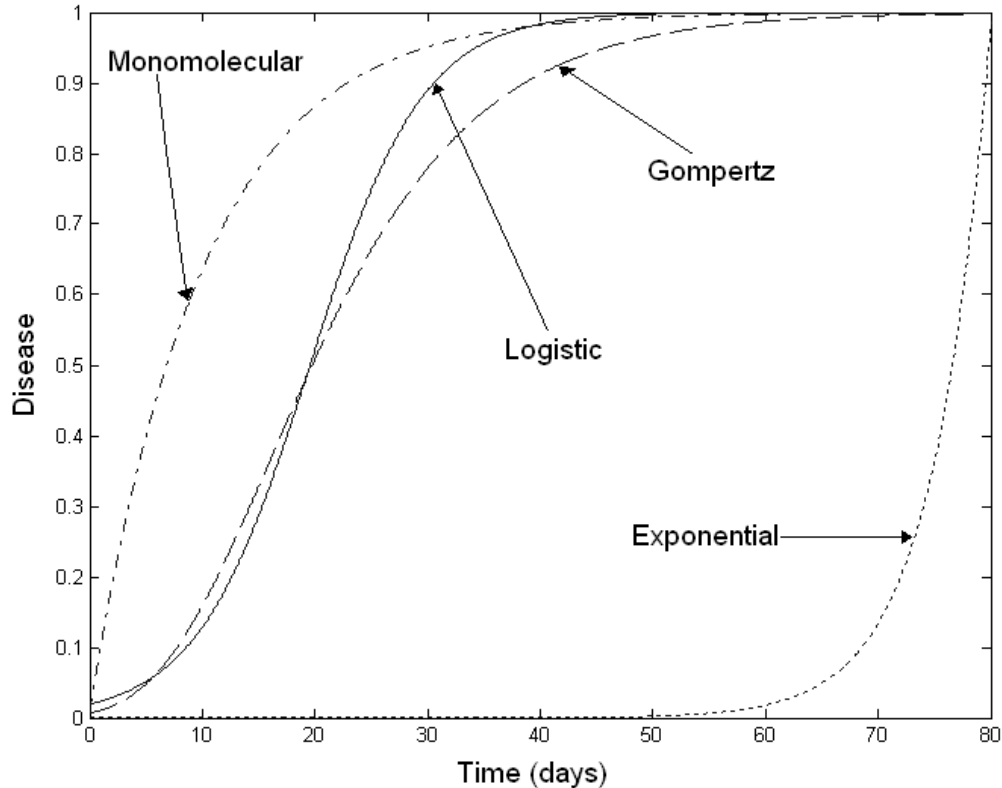


Figure 1. Examples of disease progress curves represented by monomolecular, exponential, logistic and Gompertz models.

inoculation or plant-to-plant spread within the crop in contrast to monomolecular model, which does not have inflection point. The exponential model presents a very small value at the beginning comparing with the other models and latter it increases exponentially.

In general, growth models that incorporate few variables to describe temporal disease dynamics have a good performance; however, this kind of models sometimes do not satisfy the acquiring process of key characteristics because they frequently ignore relevant variables that affect the epidemic development (Xu, 2006), e. g. host growth, fluctuating environmental condition, length of latent and infectious period, etc. Nevertheless, advances in statistical and computing technologies have allowed incorporating several of these kinds of characteristics in order to obtain a more reliable model. It is important to mention that the researchers should be aware of some violations presented in these models by checking if some assumptions about the epidemic are not met and if there are some inevitable violations; they must try to find means to reduce such violations in order to diminish the bias and to correctly interpret results (Xu, 2006). Van der Plank (1960) used exponential, monomolecular and logistic models to describe the development of epidemics. Xu (1999) used a logistic model to forecast and model the apple powdery mildew provoked by *Podosphaera leucotricha*. The work presented by Mersha and

Hau (2008) uses logistic and Gompertz models to study the effects of rust bean on host dynamics of common bean in controlled greenhouse experiments with and without fungicide sprays. A deep description of these growth models can be found in the book written by Campbell and Madden (1990).

Linked differential equations (LDE)

This mathematical tool achieves the description of plant disease epidemics by modeling each of the variables considered to be determinant in epidemic development and latter making the link between them. LDE allows the inclusion of new terms into the model as needed (Madden, 2006). When this technique cannot be easily integrated to obtain an analytical solution, it needs numerical methods to provide a numerical solution (Xu, 2006; Madden, 2006); nowadays, the advances in computational technology have permitted that numerical solutions could be easily obtained through mathematically-oriented software like MATHCAD or MATHEMATICA (Madden, 2006).

Usually LDE is employed to investigate relationships of the plant disease dynamics in relation to the host, environment and human intervention (Mannen and Xu, 2003). A relatively simple linked differential equations for

polycyclic disease involve variables like healthy tissue, latently infected, infectious and removed individuals (leaves, roots, plants) (Madden, 2006). Zhang et al. (2001) used four linked differential equations to illustrate the effect of synergism between plant viruses where each differential equation represents one of the following four categories: healthy host plant, infected host plant with a virus kind A alone, infected with a virus kind B alone, and infected with both viruses A and B, the obtained results were used to understand an epidemic that has been ongoing in Uganda since the late 1980s and the information about the development of Cassava Mosaic Disease (CMD) epidemic in Uganda and neighboring countries supports model results.

Area under disease progress curve (AUDPC)

This technique is very useful when the observed patterns cannot be fitted by progress disease curves (Van Maanen and Xu, 2003; Xu, 2006). AUDPC is the amount of disease integrated between two times of interest and it is calculated regardless the curve shape (Shaner and Finney, 1977). Disease progress data is summarized into one value by AUDPC; it is suited when host damage and the amount and duration of the disease are proportional (Xu, 2006).

If a model fits satisfactorily the disease patterns, AUDPC can be obtained from the model by integrating over certain interval of time (Jeger and Viljanen-Robinson, 2001). AUDPC, percentage disease index (PDI) and apparent infectious rate (r) were used to measure the resistance to early blight of tomato with respect to several variables of disease epidemics; these variables were: tomato variety, plant age, artificial and natural inoculation; the obtained values served as indicators to classify the tomato variety into one of the six scales of resistance (highly resistant, resistant, moderately resistant, moderately susceptible, susceptible and highly susceptible) (Pandey et al., 2003). AUDPC is generally used to make comparison between treatments (Jeger, 2004; Xu, 2006) and to evaluate the resistance of plant species to the pathogens (Jeger and Viljanen-Rollinson, 2001; Pandey et al., 2003; Mikulova et al., 2008; Irfaq et al., 2009).

Computer simulation

This tool, jointly with LDE, is used to determine the key dynamic features of the pathosystem. Several models have been used to simulate dynamics of plant diseases in order to prevent and control disease epidemics. One of the first programs was the EPIDEM written by Wagoner and Horsfall (1969) and it was designed to simulate epidemics of early blight of tomato and potato caused by the fungus *Alternaria solani* and it resulted from modeling each stage of the life cycle of the pathogen as a function

of the environment. Subsequently, several kinds of computer programs were created like MYCOS for *Mycosphaerella* blight of chrysanthemum (McCoy, 1976), EPIMAY for southern corn leaf blight (Waggoner et al., 1969), EPIVEN for apple scab caused by *Venturia inaequalis* (Kranz et al., 1973) and a more general and flexible plant simulator called EPIDEMIC (Shrum, 1975) because it could be easily modified for another plant-pathogen system. Improvements of previously developed computer models continue being made and used for new applications (Jeger, 2004), for instance epidemic model EPIMUL has been used to simulate the efficacy of various mixtures in relation to a range of different pathogen characteristics (Lannou et al., 1994). Nowadays, computer programs are used to support other techniques for predicting plant disease and to measure the impact of pathology over certain plant species based on particular variables like leaf wetness, duration of leaf wetness, primary inoculum, temperature, rainfall and moisture. One example of this is PLASMO which is used to measure the impact on the quality of *Plasmora viticola* due to leaf wetness duration (Marta et al., 2005; Orlandini et al., 2008).

Visual evaluation, pictorial assessment and statistical tools

All the previously mentioned mathematical tools display descriptions of the disease dynamics and also give important characteristics about the epidemics as output (e.g length of different infectious event, severity and infection intensity during growing season, etc). Several works, when measuring plant resistance to certain kind of pathogens use scales to evaluate the severity of the plant or usually make the evaluation based on visual inspection. Anaya-Lopez et al. (2003) used a nine-level scale to measure qualitatively the severity of pepper disease provoked by geminiviruses, this scale has been previously used in other works (Hernandez-Verdugo et al., 1998; Godinez-Hernandez et al., 2001). Another kind of evaluation, called pictorial disease assessment, has also been created based on standard diagrams that illustrate the development of the stages in the disease on small simple units (leaves, fruits) or on large composite units such as branches or whole plants (Cooke, 2006); for instance, the modified Cobb scale, which is used to determine the percentage of possible rusted tissue (Roelfs et al., 1992). Holb et al. (2003) investigated the relationship between disease measurement, disease incidence, severity of apple scabs and their implications for the development of predictive models and thresholds levels; the disease assessment based on leave severity and fruit severity are made using a mathematical equation which classifies the fruit and leave severity into a six- and seven-level scale, respectively. Recently, certain works determine visually the severity of infections by evaluating

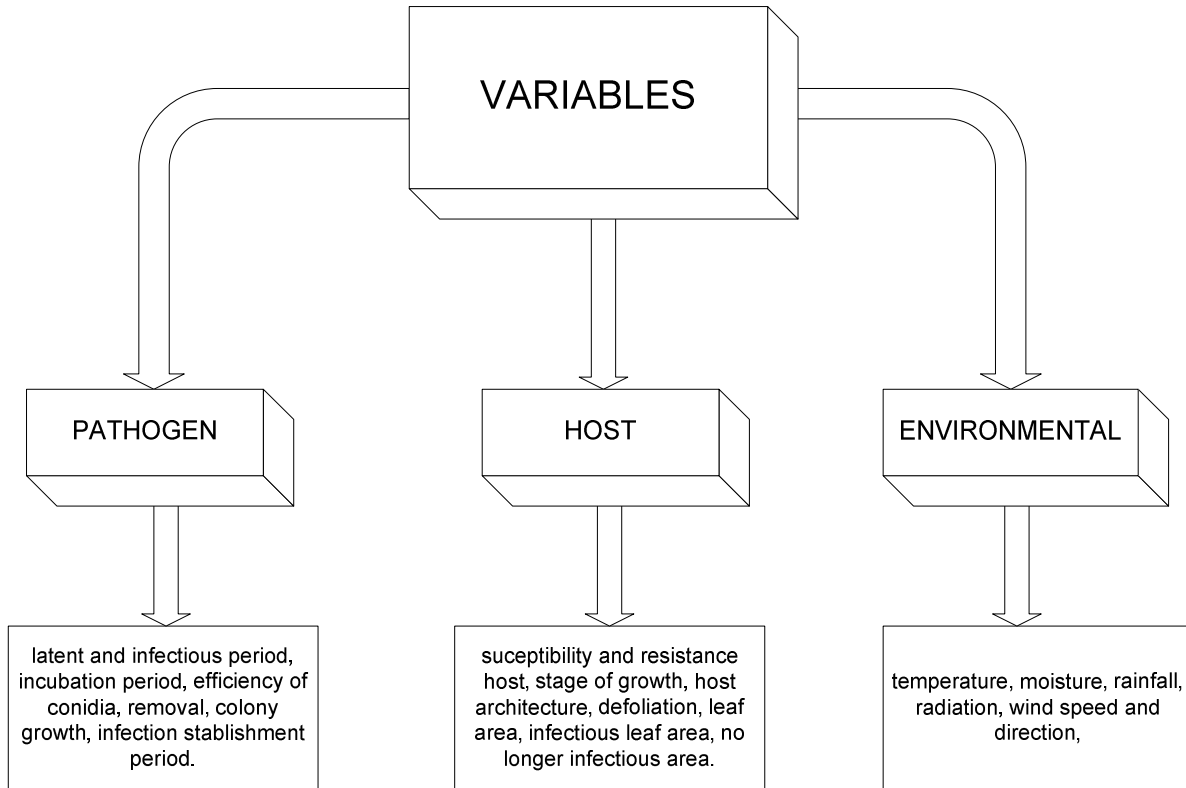


Figure 2. Classification of variables according to pathogen, host and environment.

the leaf area that presents oil spots (Orlandini et al., 2008), where the ability of the surveyors was standardized firstly by mean of cross-tests (Kranz, 1988) and also the severity was classified into a five-level scale.

It is important to mention that there are other tools used in plant pathology, these are the statistical tools such as: including survival analysis, nonparametric analysis of disease association, multivariate statistical methods, neural networks, meta-analysis, Bayesian statistics, generalized linear models, linear mixed models, decision theory, etc (Garret et al., 2004; Scherm et al., 2006;). These tools use normally distributed ordinal and discrete data, for instance, the linear mixed model, whereas the generalized linear mixed model works with discrete data (Garret et al., 2004). The statistical tools are employed depending on the necessity. For example, Multivariate statistical tools are used to reduce the space of n variables into a low-dimensional space, to assess group differences and variable contribution and to describe and predict the relationship between two sets of variables (Sanogo and Yang, 2004). Survival analysis is a technique for analyzing data sets in which the time until an event occurs is the dependent variable containing censored observations (Scherm and Ojiambo, 2004). Bayesian statistician make use of probability theory to reflect uncertainty; within the Bayesian framework, parameters are treated as if they were random variables and described with probability distributions rather than point esti-

mates (Mila and Carriquiry, 2004).

USING VARIABLES

A proposed model that uses mathematical tools should include the variables that represent the key features in the development of epidemics according with the objective of the investigation; for instance, temperature, moisture, susceptibility and resistance of host, initial inoculum, latent and infectious period and efficiency of conidia are examples of commonly included variables in used models to describe plant disease epidemics (Van der Plank, 1982; Maneen and Xu, 2003; De Wolf and Isard, 2007). The variables that the epidemiologists include depend on the pathosystems, the nature of the problem and the answers to be found (Xu, 2006). The central principle of plant pathology is the disease triangle, where the development of plant disease requires these three equally-relevant components (Parker and Gilbert, 2004).

1. A susceptible host.
2. A virulent pathogen.
3. A favorable environmental condition.

The Figure 2 shows a classification of the variables according to each component of the disease triangle, it mentions some common variables used for modeling

Table 1. Examples of variables included into different kinds of models.

Main variables included	Name of paper	Reference
Initial inoculum, host growth characteristics, and temperature.	Effect of growth stage and initial inoculum level on leaf rust development and yield loss caused by <i>Puccinia recondita f. sp. tritici</i> .	Subba Rao et al., 1989
Rate of lesion increase, conversion rate of infectious into post-infectious tissue, initial proportion of infectious area, initial proportion of disease free-area.	Fungal foliar plant pathogen epidemics: modeling and qualitative analysis.	Kosman and Levy, 1994
Latent infection, visible leaf area, infectious leaf area, no infectious leaf area, infection efficiency of conidia, incubation progress, latency progress, removal, colony growth.	A dynamic simulation model for powdery mildew epidemics on winter wheat.	Rossi and Giosué, 1999
Air temperature, rainfall, relative humidity, leaf wetness duration, initial inoculum, leaf area, spot area, sporulation area, viable spores and incubation.	An agrometeorological approach for the simulation of <i>Plasmora viticola</i> .	Orlandini et al., 2008
Temperature, leaf wetness, rainfall, relative humidity.	Modelling of leaf wetness duration and downy mildew simulation on grapevine in Italy.	Marta et al., 2005
Leaf wetness duration, radiation, rainfall, rainfall amount, temperature, wind speed.	Quantifying and modelling the mobilisation of inoculum from diseases leaves and infected defoliated tissues in epidemics of angular leaf spot of bean.	Allorent et al., 2005
Temperature, relative humidity, vapor pressure deficit, total duration rainfall. Low growth rate, disease carrying capacity, infectious period.	Modelling and forecasting epidemics of apple powdery mildew (<i>Podosphaera leucotricha</i>).	Xu, 1999
Temperature, wind speed and direction, location and onset of primary infection.	A host-pathogen simulation model: powdery mildew of grapevine.	Calonnec et al., 2008
Temperature, humidity, precipitation leaf wetness duration, wind speed and direction.	Assessment of airborne primary inoculum availability and modeling of disease onset of ascochyta blight in field peas	Schoeny et al., 2007
Temperature, rainfall, plant characteristics (stem density, plant geometry, mean distance between nodes, and leaf area).	Effect of pea plant architecture on spatio-temporal epidemic development of ascochyta blight (<i>Mycosphaerella pinodes</i>) in the field.	Le May et al., 2009

plant disease dynamics (Rossi and Giosué, 1999; Xu, 1999; Maanen and Xu, 2003; Orlandini et al., 2008; Le May et al., 2009). Several kinds of variables have been included into certain models which are related in the development of plant diseases. The Table 1 presents some examples of proposed models using mathematical tools here presented and the variables included into the models.

As it can be seen, the variables are chosen according to the studied pathosystem and the objectives of the epidemiologist. It is generally assumed that the environment is the driven force for disease (Hardwick, 2006). Several works use as driving variables those concerning weather; temperature, rainfall, moisture, leaf wetness, wind direction, radiation, among others (Marta et al., 2005; Orlandini et al., 2008). From this, pathogen variables that are involved directly with epidemic development can be formulated as a function of driving variables

(van Maanen and Xu, 2003) e.g. latent and infectious period, initial inoculation, oil spoil survival (Calonnec et al., 2008). Also, variables relating to host dynamics should be included in order to know how the pathogen dynamics are linked to the host dynamics and how pathogen affects the growth and reproduction of the host (Anderson and May, 1979; Van Maanen and Xu, 2003) e.g. intrinsic and age-related host dynamics (Shtienberg, 2000; Van Maanen and Xu, 2003).

MATHEMATICAL TOOLS USED IN EPIDEMIOLOGY OF PLANT DISEASE: ADVANTAGES AND DISADVANTAGES

The primary objectives of a mathematical tool is to help to understand how the main factors affect the plant disease development in order to prevent disease appearing and

the development of sustainable strategies for disease management. Models have been created using mathematical tools since the apparition of the first model (Van der Plank, 1960; Van der Plank, 1963). Next, some advantages and disadvantages of common mathematical tools are presented:

Disease progress curves that use growth models have the advantage of generally describing the disease progress in a good way by adding few variables (Xu, 2006), but sometimes it is not adequate to describe certain kind of pathologies because it needs to incorporate extra-variables that are determinant in the pathosystem. The disadvantages of these models are the assumptions that the epidemiologist needs to make about the variables used by this mathematical tool. The resulting bias depends on the assumptions made and if a violation of the assumptions is presented, it needs to be reinterpreted in order to obtain a correct result. An example of these disadvantages is presented by Rotem et al. (1988) when disease intensity was masked by the loss of infected leaves and the appearance of new healthy leaves. Kushalappa and Ludwing (1982) showed that ignoring the growth-host effects could conduct to underestimate or even to obtain negative rate values because, may be, the rate of host growth is faster than the disease development rate. If disease increase is not as rapid as plant growth, the proportion of diseased tissue on the plant will appear to decrease (Mersha and Hau, 2008). Analogously, if defoliation occurs as a result of disease, the severity of infected plant will appear to decrease (Waggoner and Berger, 1987; Ojiambo and Scherm, 2005).

LDE is one of the most commonly used mathematical tools in modeling epidemics because it allows that new terms be easily included as needed in order to answer the question about the details of the pathosystem (Madden, 2006). In general, it is too difficult to obtain analytical solutions for this mathematical tool, but numerical solutions can be obtained. An advantage of this mathematical tool is the intrinsic relationship with other tools here mentioned like disease progress curves and computer simulations because important components of disease dynamics can be modeled by using growth models that latter could be linked and simulated using computer programs (Mersha and Hau, 2008). A disadvantage of LDE is that the formulated equations using this tool are extremely troublesome for mathematical analysis, which makes difficult the exploration of different biological properties of host and pathogens or to know the results of different control strategies, on long-term disease development (Madden, 2006).

AUDPC is extensively used in analyzing disease progress curves to make comparisons between treatments, to know the relationship between yield losses and disease, to make a genetic analysis, to evaluate the effectiveness of chemical, biological and cultural controls over disease progress and also for knowing the resistance of

certain species to plant pathogens (Jeger, 2004). A disadvantage of AUDPC is that it depends on a good fitted disease progress curve to obtain correct results; this approach also can yield misleading results when it is summarized over a particular period instead of over a complete period (Xu, 2006).

The computer simulation is a general natural extension of LDE because it depends on computations to obtain a numerical solution. In computer simulation, some model variables in LDE are often assumed to be functions of external factors like temperature, humidity, radiation, wind direction, etc. This mathematical tool can be used to study theoretical and practical problems of certain kinds of pathologies (Agrios, 2005). One disadvantage of computer simulation is that generally each simulator just incorporates one disease to be simulated, restricting its functionality and also, a computer is required to achieve the task, having an intrinsic economical cost.

Disease evaluation based on visual estimation has a clear disadvantage, because of the variation between different points of view, given by different evaluators; yet, several works have been developed where visual evaluation of host severity is made and classified into a multilevel scale according to the kind of damage that is presented in the host due to the disease evolution (Anaya-Lopez et al., 2003; Hernandez-Verdugo et al., 1998; Godinez-Hernandez et al., 2001). This also provokes unsuitable strategies to forecast and prevent disease due to the subjectivity of the estimation. Similarly, pictorial assessment presents the disadvantage of subjectivity because it is a tool based on visual evaluation that decreases the reliability of an evaluation.

Statistical tools are attractive because they allow to obtain a model where some drawbacks exist, such as when little is known about the structural form of complex relationships between response variables, when theoretical data presented by other investigation needs to be used or when the calculation probabilities for the parameter of interest needs to be calculated based on empirically derived prior probabilities in conjunction with the conditional probability of each possible outcome (Scherm et al., 2006). The statistical tools have the disadvantage of supposing that the data are normally distributed (Garret et al., 2004) and also the theoretical models proposed by using this tool sometimes have non expected results in practice (Scherm et al., 2006). Table 2 summarizes the advantages and disadvantages of the common tools used to describe the dynamics of plant disease.

TRENDS IN EPIDEMIOLOGY OF PLANT DISEASE

The Mathematical tools used to describe disease dynamics of plants have been and continue being the mainstream of theoretical epidemiology (Scherm et al., 2006). Current works use a combination of the mathematical

Table 2. Advantages and disadvantages of common tools used to describe dynamics of plant disease.

Tool	Advantages	Disadvantages
Disease progress curves.	Often with two or three variables describe satisfactorily the disease.	Needs to make assumption to correct interpretation of results, sometimes ignore key components that affect disease development.
Linked Differential Equation.	New terms can be easily included into the model as needed.	Equation generated are extremely troublesome for mathematical analysis.
AUDPC	Is a very useful alternative to fitting growth models, it can work with growth models.	Needs that the amount and duration of disease be proportional to damage, it may give misleading results when AUDPC is summarized over other period than just over a particular period.
Visual evaluation.	Practical evaluation, does not need a PC, only evaluators are needed.	Subjectivity.
Pictorial assessment.	Practical evaluation, does not need a PC, only evaluators is needed.	Subjectivity.
Statistical tools.	Probability calculation based on empirical knowledge, allows using theoretical data.	Supposes that data are normally distributed, the proposed models are mainly based on theory.

PC: Personal computer.

AUDPC: Area under disease progress curve.

tools here presented in order to obtain a better description of plant disease (Mersha and Hau, 2008), which allows developing better strategies for disease management. Trends in mathematical modeling may continue combining the mathematical tools to model the determinant factors of plant disease. Mathematical and statistical tools employ environmental, pathogenic and host variables, whereas other tools use pictorial assessment and visual estimations. It can be suggested the combination of disciplines to join these tools in order to obtain better fitness than the models so far proposed. The support disciplines can be mathematics to obtain a model to fit the data, image processing to obtain a better visual estimation of variables that can be added to the model, and computer technology to process data coming from sensors and subsequently give a better description about the disease development. Then, by combining the disciplines jointly with an accurate measurement of the variables it is possible to improve the disadvantages of the mathematical and statistical tools and the models so far proposed to describe plant disease epidemic and consequently to obtain a model that better describes the plant disease dynamics.

CONCLUDING REMARKS

The most common mathematical tools used to model plant disease epidemics are: Disease progress curve, LDE, AUDPC and Computer simulations. Nonetheless, there are also other ways to give an evaluation about disease dynamics based on visual, pictorial assessment and statistical tools. The variables used by mathematical tools are chosen by relevance, pathosystem features,

and epidemiologist necessities, which according to the model objective, the epidemiologist can chose the mathematical tool which solely or jointly with other different mathematical tools gives a better description of the reality in order to obtain a more accurate evaluation of the plant disease epidemics. The possible combination of the tools here presented can be made by the conjunction of several disciplines like image processing which could serve to obtain a better objective estimation of variables that can feed to the model allowing obtain a better fitness.

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