# Mathematical Models of Host Plant Infection by Helper-Dependent Virus Complexes: Why Are Helper Viruses Always Avirulent?

X.-S. Zhang, J. Holt, and J. Colvin

Natural Resources Institute, University of Greenwich, Central Avenue, Chatham Maritime, Kent, ME4 4TB, United Kingdom.
Accepted for publication 17 September 1999.

## ABSTRACT

Zhang, X.-S., Holt, J., and Colvin, J. 2000. Mathematical models of host plant infection by helper-dependent virus complexes: Why are helper viruses always avirulent? Phytopathology 90:85-93.

Interactions between viruses in plants are common, and some viruses depend on such interactions for their survival. Frequently, a virus lacks some essential molecular function that another provides. In "helper-dependent" virus complexes, the helper virus is transmitted independently by a vector, whereas the dependent virus depends on molecular agents associated with the helper virus for transmission by a vector. A general mathematical model was developed of the dynamics of host plant infection by a helper-dependent virus complex. Four categories of host plants were considered: healthy, infected with helper virus alone, infected with dependent virus alone, and infected with both viruses. New planting of the host crop was constrained by a maximum abundance due to limitation of the cropping area. The ratio of infection rate to host loss rate due to infection is proposed as an important epidemiological quantity, $A$, that can be used as a measure of the mutual adaptation of the virus and host. A number of alternative equilibria of host infection could occur and were determined exclusively by parameter values; it was informative to display their distribution in the parameter plane: $(1/A)_{\text{helper}}$ versus $(1/A)_{\text{dependent}}$. A simple analysis of the distribution of the final equilibria illustrated that the dependent virus could affect the survival of the helper virus, so facilitation between the two can be reciprocal. The distribution of the final equilibria also indicated that a well-adapted helper virus increases the opportunity for a dependent virus to evolve and survive, and the model, therefore, explains why infection with a helper virus usually causes no or little damage to plants, whereas infection with a dependent virus or mixed infection with both often causes very severe damage.

*Additional keywords*: epidemic, evolution, groundnut rosette virus disease, plant virus, rice tungro virus disease, vector transmission.

Mixed infections of plant viruses are common in nature, and several economically important plant virus diseases involve interactions between causative agents (18,34). Broad categories of virus interaction can be distinguished epidemiologically, although the underlying mechanisms are diverse. An interaction between two viruses can be synergistic or antagonistic, complete or partial, and bilateral or unilateral, as explained below. In a synergistic interaction, the presence of one virus in some way facilitates the other virus, and in an antagonistic interaction, infection by one virus decreases infection by another virus, a feature that is sometimes termed cross-protection (32). The interaction may be complete or partial, e.g., infection by one virus may completely prevent or merely reduce infection by another virus. The effects may operate in both directions, when viruses facilitate infection by each other (bilateral), or in only one direction, when virus 1 facilitates infection by virus 2 but not vice versa (unilateral). The situation also may be more complicated, e.g., a mixture of antagonism and synergism, in which virus 1 may facilitate virus 2 but virus 2 may reduce infection by virus 1.

To survive and spread, most plant viruses have evolved specific associations with animal vectors that allow them to be transmitted from plant to plant. In some cases, interactions between viruses can occur only through associations with vectors (31). The virus properties responsible for vector transmissibility have been elucidated by comparative studies with vector-specific strains and vector-nontransmissible variants of certain viruses. Evidence that the dependent transmission phenomenon, first described by Clinch et al. (14), is more common than previously thought is accumulating. Some viruses rely on helper components for transmission by vectors but lack the ability to produce them. With some noncirculative viruses, for instance, vector transmission depends on virus-encoded factors that are not constituents of the virions and can be provided only by another virus (40). Helpers are required for transmission of some potyviruses and caulimoviruses by their aphids vectors. The helper and dependent viruses exist in a "helper-dependent" virus complex in which there is a complete unilateral facilitation of the dependent virus by the helper. The natures and origins of the helper mechanism may be quite diverse (32,34,39,41). Here we focus on the helper-dependent type of virus interaction, because of its great importance in many viral crop diseases. In such complexes, virus 1 (helper) can be transmitted independently by the vector, but virus 2 (dependent) is totally dependent on virus 1 for its transmission by the vector. Virus 2 is commonly the principal disease agent, with virus 1 alone causing few or no disease symptoms. Some examples of these complexes are shown in Table 1.

We take as examples two economically important diseases: *Rice tungro virus* disease (RTD) and *Groundnut rosette virus* disease (GRD). RTD is a major problem in Southeast Asia. There are two viruses involved in RTD (26,44): *Rice tungro spherical virus* (RTSV) and *Rice tungro bacilliform badnavirus* (RTBV). They are both transmitted in a semipersistent manner by several leafhopper species. Infection with RTBV alone causes severe symptoms, whereas infection with only RTSV causes almost no symptoms in tropical rice varieties. Severe leaf yellowing and stunted growth occur when a plant is infected with both viruses. New infections

Corresponding author: J. Holt; E-mail address: hj30@gre.ac.uk

Publication no. P-1999-1103-01R

may be initiated in a crop by the immigration of viruliferous vectors or by transplantation of seedlings that were infected by vectors in the seedbed. There is complete unilateral facilitation of RTBV by RTSV: RTSV can be acquired by the vector and transmitted independently to new plants, but acquisition and inoculation of RTBV requires the presence of a helper component associated with RTSV (22).

GRD is caused by a complex of three agents: *Groundnut rosette virus* (GRV), its satellite RNA (satRNA), and *Groundnut rosette assistor luteovirus* (GRAV). The satRNA depends entirely on GRV for its replication (7,27,35), and GRV must be associated with its satRNA to be transmitted by vectors. The satRNA has been found in all naturally occurring GRV isolates. GRAV alone causes no obvious symptoms. Disease symptoms are associated with the presence of the GRV-satRNA complex, in which the satRNA is largely responsible for different symptom types. Plants with either green or chlorotic rosette symptoms are severely stunted and bushy in appearance due to shortened internodes and reduced leaf size. GRAV replicates autonomously in plants and is transmitted only by aphids, of which the most important is *Aphis craccivora* Koch (Homoptera: Aphididae). GRV-satRNA depends on GRAV for its packaging in the GRAV coat protein and subsequent transmission by the aphid vector (33). In nature, all three agents must be present together for transmission by the aphid vector to occur. Through the ability to utilize the coat protein of GRAV, GRV and its satRNA gain epidemiologically by acquiring a persistent relationship with the aphid vector.

Most models of plant virus disease spread have considered a single infectious agent only (10,25,28,42,45). We are not familiar with other dynamic models of plant virus disease with multiple infection agents, except for a model by Burrows (8) who derived expressions for disease progress curves corresponding to different categories of virus-virus interaction. Competitive exclusion has been examined in the long-term dynamics of models of human virus disease (3). Here we look at long-term infection dynamics of helper-dependent virus complexes in cropping systems in which new planting of the host occurs over the course of time. Our objective is to develop simple dynamic models to investigate some of the general principles of the epidemiology of diseases caused by helper-dependent virus complexes and to consider potential constraints in their evolution.

## MODELS

**General case of unilateral facilitation.** Four categories of host plants are considered: healthy, infected with virus 1 alone, infected with virus 2 alone, and infected with both viruses together, designated $X$, $Y$, $Z$, and $U$ (per square meter), respectively. Infection is assumed to occur as a result of vector activity. Assuming that once infected a host plant does not recover, there are eight possible sequences of transmission among the four categories (Table 2). Some assumptions have been made about the sequences of transmission. For direct transition from a healthy plant to one infected with both viruses (mixed infection), for example, it is assumed that infection is proportional to a contact rate between healthy hosts and hosts with mixed infections—a product of the number of healthy plants, number of mixed-infected plants, and a transmission rate parameter, $p_1$. This process occurs when vectors viruliferous with both viruses feed on a healthy plant. Thus, although no attempt is made to model the vector population, it is implicitly assumed that vector infectivity mirrors host infection.

In addition to the process of virus transmission, it is necessary to model the dynamics of the host plant itself. If the host is a crop, there are cycles of planting and harvesting. In most dynamic models of plant disease (10,25,28,45), it is assumed that new planting occurs as a continuous process. This simplifying assumption can be justified for some annual (45), as well as perennial, cropping systems (10). In areas of tropical irrigated rice cultivation in southeastern Asia, where RTD occurs (44), two or three crops are grown per year. Planting continues throughout the year, with rice crops at different growth stages always present (6,12,21,43). Within a locale, therefore, planting is often continuous, although there may be some seasonal patterns in planting frequency. In a spatial model of RTD spread between fields, planting patterns must deviate considerably from a continuous pattern to cause major changes to the simulation of a RTVD epidemic (24). Planting of groundnut crops is usually less continuous than that of irrigated rice, but in areas of bimodal annual rainfall, two crops are grown per year, volunteers and escapees occur, and a continuous groundnut presence is possible (36). In the model of Jeger et al. (28), a constant host population was assumed by exactly balancing mortality and new planting. In the model of Holt et al. (25), new planting was constrained by the availability of cuttings used for vegetative propagation and by a maximum plant density, leading to a planting term of logistic form. Here we use the planting assumptions of Chan and Jeger (10): to replace losses, new planting of healthy material occurs at a rate constrained by a maximum plant population, $K$ (per square meter), giving a regulating term of monotonic form. New planting was assumed to take place at a net rate, $r(K - P)$, where $r$ is the planting rate and $P$ is the current plant abundance ($P = X + Y + Z + U$). Planting is, therefore, most rapid when plant abundance is lowest and declines asymptotically to zero as $P$ approaches $K$.

Virus infection may cause host damage and death. Host plant losses due to infection may take the form of actual plant mortality or simply the presence of reduced amounts of host biomass due to reduced growth of diseased plants. Net reduction due to infection is given by $q_1Y$, $q_2Z$, and $q_3U$, where $q_1$, $q_2$, and $q_3$ are the loss rates associated with infection by virus 1 alone, infection by virus 2 alone, and mixed infection (per day), respectively. These relationships are depicted in Figure 1, and the model is specified by

$$dX/dt = r(K - P) - p_1XU - p_2XU - p_3XU - p_6XY$$
$$dY/dt = p_2XU + p_6XY - p_4YU - p_8YZ - q_1Y$$
$$dZ/dt = p_3XU - p_5ZU - p_7ZY - q_2Z$$
$$dU/dt = p_1XU + p_5ZU + p_4YU + p_7ZY + p_8YZ - q_3U$$

There are two possible ways for transmission of the dependent virus to occur: (i) when the recipient host is already infected with the helper, and (ii) when the helper and dependent viruses are simultaneously transmitted to the recipient host (18,32). For non-

TABLE 1. Examples of helper-dependent virus complexes

| Host plant | Helper virus (genus) | Dependent virus (genus) | Transmission | Reference |
|---|---|---|---|---|
| Potato | *Potato virus Y* (*Potyvirus*) | *Potato aucuba mosaic potexvirus* (*Potexvirus*) | Nonpersistent | 29, 30 |
| Parsnip | *Anthriscus yellows virus* (*Waikavirus*) | *Parsnip yellow fleck virus* (*Potyvirus*) | Semipersistent | 17 |
| Rice | *Rice tungro spherical virus* (plant *picornavirus*) | *Rice tungro bacilliform virus* (plant pararetrovirus, badnavirus group) | Semipersistent | 4 |
| Lettuce | *Beet western yellows virus* (*Luteovirus*) | *Lettuce speckles mottle virus* (*Umbravirus*) | Persistent | 19 |
| Carrot | *Carrot red-leaf virus* (*Luteovirus*) | *Carrot mottle virus* (*Umbravirus*) | Persistent | 46 |
| Tobacco | *Tobacco yellow vein assistor virus* (*Luteovirus*) | *Tobacco yellow vein virus* (*Umbravirus*) | Persistent | 1 |
| Pea | *Pea enation mosaic virus* RNA-1 (PEMV group) | *Pea enation mosaic virus* RNA-2 (PEMV group) | Persistent | 16 |
| Groundnut | *Groundnut rosette assistor virus* (*Luteovirus*) | *Groundnut rosette virus* (*Umbravirus*) | Persistent | 36 |

persistent and semipersistent viruses, both i and ii are possible, and all eight transmission processes, $p_1,\ldots,p_8$, can occur. For persistent viruses, only ii is possible, and transmission processes $p_7$ and $p_8$ cannot occur.

**Parameter estimation.** All parameters, $p_1,\ldots,p_8$, are transmission rates that are measurable, at least in relative terms, in transmission experiments.

In the field, transmission rates are determined by many factors, including the number and life stages of vectors, crop variety and age, intensity of cropping, and other environmental conditions. Here, to obtain a simple approximation, the transmission rate was assumed to be a constant and was estimated by comparing simulated with observed disease progress curves. To approximate parameter $p_1$, the model used to simulate disease progress was specified as

$$dU/dt = p_1U(K - U)$$

where $K$ is the maximum abundance of the host plant (25 $m^{-2}$ for rice, 14 $m^{-2}$ for groundnut) and $K - U$ is an approximation of the abundance of healthy plants. The transmission rate has the unit per plant per day. Using the data from Holt and Chancellor (23) for RTD and the data from Olorunju et al. (38) for GRD, the transmission rates, $p_1$, were estimated as 0.0044 $plant^{-1}$ $day^{-1}$, with a range of 0.002 to 0.008, for RTD, and 0.009 $plant^{-1}$ $day^{-1}$, with a range 0.0045 to 0.02, for GRD.

For RTD, the experimental data concerning the relative values of the eight transmission rates are cited by Holt and Chancellor (23), and using the above estimate of $p_1$, the other transmission rates were estimated relative to it (Table 3). Using the data from Naidu et al. (37), the other transmission rates for GRD also were estimated. Clearly, the larger the value of the transmission rate, $p_i$, the more important the corresponding transmission process in the dynamics of the system. For RTD and GRD, not all possible transmission processes are equally important. Table 3 indicates estimates of the rates associated with each.

TABLE 2. Possible transitions between host infection categories

| Host transition | Transmission by infected vectors | Transmission rate | Contact rate |
|---|---|---|---|
| $X \rightarrow U$ | $U$ | $p_1$ | $p_1XU$ |
| $X \rightarrow Y$ | $U$ | $p_2$ | $p_2XU$ |
| $X \rightarrow Z$ | $U$ | $p_3$ | $p_3XU$ |
| $Y \rightarrow U$ | $U$ | $p_4$ | $p_4YU$ |
| $Z \rightarrow U$ | $U$ | $p_5$ | $p_5ZU$ |
| $X \rightarrow Y$ | $Y$ | $p_6$ | $p_6XY$ |
| $Z \rightarrow U$ | $Y$ | $p_7$ | $p_7ZY$ |
| $Y \rightarrow U$ | $Z$ | $p_8$ | $p_8YZ$ |

The loss rate of infected plants due to disease, $q$ with appropriate subscript, depends on the degree of varietal tolerance of infection. The mean period from infection to death or removal can be considered $1/q$. Infection with the helper virus alone causes no or few symptoms, hence $1/q$ can be regarded as equal to the crop period. Therefore, $q_1(m)$ = 1/(100 days) = 0.01 $day^{-1}$ for rice plants infected with RTSV alone, and $q_1(m)$ = 1/(150 days) = 0.0067 $day^{-1}$ for groundnut plants infected with GRAV alone (100 and 150 days, respectively, are taken as crop durations for rice and groundnut). The single infection by a dependent virus causes much more severe damage to host plants (reflected by parameter $q_2(l)$) than infection by a helper virus alone, and mixed infection also results in severe damage to host plants (reflected by $q_3(n)$). For RTD, it is assumed that $n = 2l$ (23), whereas $n = l$ (20) for GRD.

**Reductions of the general model.** The general model can reflect all possible transmission processes, but it is difficult to analyze due to the complexity of the interactions that exist among the four categories of host plant. To derive results concerning possible equilibria, we concentrate on the three specific situations in which only the main processes of transmission are considered. We initially consider the simple single virus case and then three reductions of the general model.

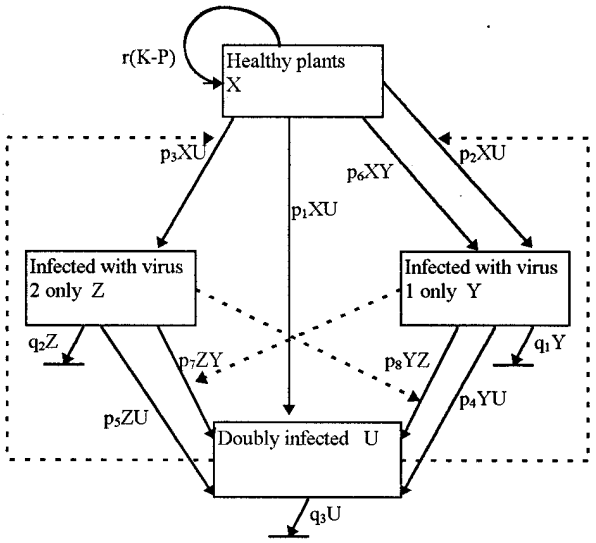


**Fig. 1.** Flow chart of the general model of host infection by a helper-dependent virus complex. Virus 1 is a helper virus; virus 2 is a dependent virus. Solid arrows indicate transitions; dotted arrows indicate influences. Variables and parameters are explained in text.

TABLE 3. Estimated parameter[a] values taken from Holt and Chancellor (23) for *Rice tungro virus* disease (RTD) and from Olorunju et al. (38), Farrell (20), and Naidu et al. (37) for *Groundnut rosette virus* disease (GRD)

| Parameter | Estimated value (RTD) | | Estimated value (GRD) | | Unit |
|---|---|---|---|---|---|
| | Standard value | Range | Standard value | Range | |
| $p_1(b)$ | 0.0044 | 0.002–0.008 | 0.0090 | 0.0045–0.02 | $plant^{-1}$ $day^{-1}$ |
| $p_2$ | 0.0011 | 0.0005–0.002 | 0.0058 | 0.0028–0.012 | $plant^{-1}$ $day^{-1}$ |
| $p_3(d)$ | 0.0022 | 0.001–0.004 | 0.0061 | 0.0030–0.013 | $plant^{-1}$ $day^{-1}$ |
| $p_4(c)$ | 0.0044 | 0.002–0.008 | 0.0090 | 0.004–0.02 | $plant^{-1}$ $day^{-1}$ |
| $p_5(e)$ | 0.0044 | 0.002–0.008 | 0.0090 | 0.004–0.02 | $plant^{-1}$ $day^{-1}$ |
| $p_6(a)$ | 0.0044 | 0.002–0.008 | 0.0125 | 0.006–0.026 | $plant^{-1}$ $day^{-1}$ |
| $p_7$ | 0.0005 | … | … | … | $plant^{-1}$ $day^{-1}$ |
| $p_8$ | 0.0022 | 0.001–0.004 | … | … | $plant^{-1}$ $day^{-1}$ |
| $q_1(m)$ | 0.01 | 0–0.02 | 0.0067 | 0–0.014 | $day^{-1}$ |
| $q_2(l)$ | 0.03 | 0.02–0.06 | 0.05 | 0.02–0.1 | $day^{-1}$ |
| $q_3(n)$ | 0.06 | 0.04–0.12 | 0.05 | 0.02–0.1 | $day^{-1}$ |
| $r$ | 0.01 | … | 0.0067 | … | $day^{-1}$ |
| $K$ | 25 | … | 14 | … | $m^{-2}$ |
| $m/a$ | 2.27 | 0–10 | 0.74 | 0–2.3 | $m^{-2}$ |
| $n/b$ | 13.62 | 5–60 | 5.56 | 1–20 | $m^{-2}$ |

[a] Parameters explained in text.

The single virus case has been studied previously (10,25,28,42, 45). During virus-host evolution, infection of a host with a single virus that is a potential helper probably forms the starting point for the evolution of a helper-dependent virus complex.

The first reduced model for infection by two viruses considers only three categories, *X*, *Y*, and *U*, in which infection with the dependent virus alone does not occur. For both RTD and GRD, when a vector carries both viruses, inoculation of both together seems to be relatively common. Inoculation of virus 1 alone (RTSV or GRAV, respectively) is far less common when the vector carries both viruses. When the vector is viruliferous only with virus 1 (RTSV or GRAV), the inoculation probability of this virus appears to be higher (13). Given these considerations, only transitions $p_6$, $p_1$, and $p_4$ from Figure 1 are considered in reduction 1. This model is applicable to the special case of some RTD-resistant varieties that are seldom infected with RTBV alone, e.g., Balimau Putih (9).

The second reduced model, which also has only three categories, *X*, *Z*, and *U*, is considered where infection with the helper virus can only occur together with infection by the dependent virus. In some cases, infection with helper virus 1 alone seems rare, e.g., in rice varieties TN1, Choron Bawla, and Goria (9,22). Moreover, pea enation mosaic virus (PEMV) RNA-1 has not been shown to infect plants on its own and depends on the presence of PEMV RNA-2 to establish a fully systemic infection (16). In these special cases, there are only three categories, *X*, *Z*, and *U*, of host plant, and the general model can be reduced by deleting category *Y* and its associated transmission processes.

In most cases, reductions 1 and 2 are over-simplifications, but a combination of the two reduced models provides a model that incorporates the main transmission processes of RTD and GRD in typical host varieties. The four reduced models are illustrated in a flow chart (Fig. 2), and the equations are given in Table 4.

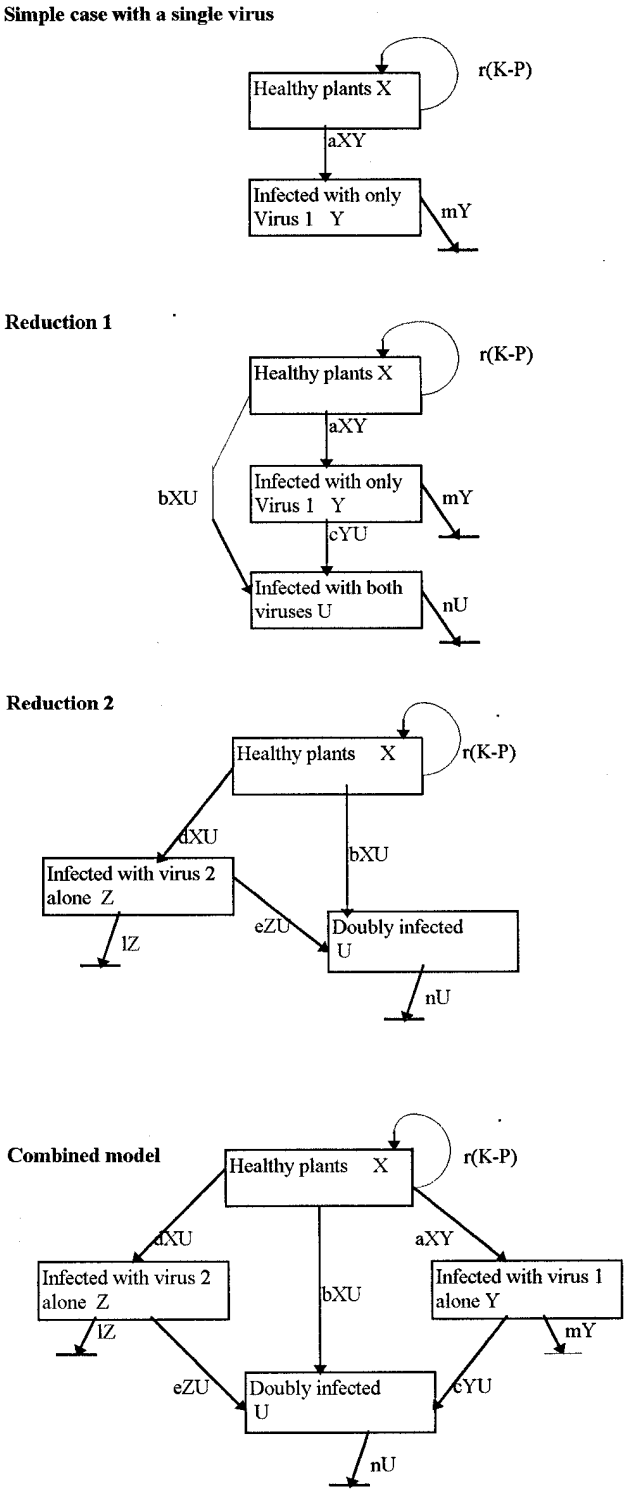


**Fig. 2.** Flow charts of the simple case with a single virus, reduction 1, reduction 2, and combined models. Variables and parameters are explained in text.

## ANALYSIS AND RESULTS

The objective was to examine the likely long-term outcome for host infection and its relationship to the characteristics of the virus-host plant interaction. All the results obtained were based on models that incorporate continued new planting of the host and, therefore, relate to cropping systems in which this occurs. New planting was constrained by a maximum host abundance, *K*, which was an important quantity in the solution of the models; such a constraint is reasonable given that cropping area is always limited. Analytical and numerical techniques were used to analyze the properties of the reduced models. Equilibrium population levels for

TABLE 4. Model equations and assumptions for further reduction

| Linked differential equations | Assumptions |
|---|---|
| Simple case with a single virus | |
| $dX/dt = r(K - P) - aXY$<br>$dY/dt = aXY - mY$ | The host is infected only with a single virus<br>$a = p_6$, $m = q_1$, $P = X + Y$ |
| Reduction 1 | |
| $dX/dt = r(K - P) - aXY - bXU$<br>$dY/dt = aXY - cYU - mY$<br>$dU/dt = bXU + cYU - nU$ | Probability of vectors infective with both viruses feeding on healthy plants and causing infection with only virus 2 is so low that plants infected with only virus 2 can be omitted (i.e., $p_3 = 0$, $P = X + Y + U$)<br>Probability of a healthy plant becoming directly infected with both viruses is not so low it can be omitted ($b = p_1$)<br>Probability of healthy plants becoming infected with virus 1 by vectors infective with both viruses is very low (i.e., $p_2 = 0$)<br>$c = p_4$, $n = q_3$ |
| Reduction 2 | |
| $dX/dt = r(K - P) - bXU - dXU$<br>$dZ/dt = dXU - eZU - lZ$<br>$dU/dt = bXU + eZU - nU$ | Infection with only helper virus 1 is so rare it is assumed that $Y = 0$<br>$P = X + Z + U$, $l = q_2$, $d = p_3$, $e = p_5$ |
| Combined model | |
| $dX/dt = r(K - P) - aXY - bXU - dXU$<br>$dY/dt = aXY - cYU - mY$<br>$dZ/dt = dXU - eZU - lZ$<br>$dU/dt = bXU + cYU + eZU - nU$ | Includes only transmission processes that appear in reductions 1 and 2<br>$P = X + Y + Z + U$ |

different plant categories were obtained analytically and numerically by setting each of the equations to zero. Sensitivities of the equilibria to parameter changes were analyzed, and the distribution of all possible final equilibria was examined graphically in the parameter space. Numerical simulation was performed over a range of parameter values (Table 3) and initial states using the software package Modelmaker, version 3.0 (Cherwell Scientific, Oxford). All numerical experiments for the simple single virus case, reduction 1, and the combined model confirmed the following results. After some transitions following the starting state, the system will monotonically or cyclically evolve to an equilibrium that is independent of the initial conditions but determined exclusively by the parameters. The results are shown in Table 5 and Figure 3.

In the simple case with a single virus ($Z \equiv 0$, $U \equiv 0$), the damage rate/infection rate ratio has a clear epidemiological meaning. Where there is close mutual adaptation between host and virus, the $m/a$ ratio is low, i.e., infection of the host occurs readily, but the virus causes little damage to the host. This ratio appears independently in the expression of the equilibria and has the unit of categories $X$ and $Y$, and its value determines the long-term survival of the virus. The virus can survive only when the $m/a$ ratio is less than the maximum host abundance, $K$, which is a constraint of planting. Maximum plant abundance, $K$, is a critical value for the ratio. The reciprocal of the ratio can be interpreted as a measure of the mutual adaptation between the virus and host, which we designate $A$ ($=a/m$); a high value of $A$ means that the host and virus are well adapted to each other. For the single virus case, there is a clear relationship between $A$ and the basic reproductive number, $R_0$, because $(m/K)/a[=1/(AK)]$ is equivalent to $R_0$. The conclusion about the threshold value for disease persistence has been described previously in theoretical studies of epidemics caused by single disease agents (28,45).

The ability of a single virus to survive in a particular interaction can be reduced by decreasing $K$ or increasing $m$ ($m$ also can be considered a roguing rate and, as such, can be manipulated). In the single virus case, the persistence of the virus is independent of the new planting rate, $r$, although the abundance of diseased plants depends on $r$. This model has a disease-free equilibrium, $P^* = K$, whereas in the model of Chan and Jeger (10) $P$ approaches an asymptote strictly less than $K$ due to disease-independent mortality.

In reduction 1, in which the dependent virus can exist only as a mixed infection with the helper virus, there are four types of equilibria. As in the single virus case, the reciprocal of the $m/a$ ratio can be regarded as the mutual adaptation of the helper virus and host, $A_{\text{helper}}$. Due to the strong connection between $Z$ and $U$, which becomes clear later, the reciprocal of the $n/b$ ratio can be regarded as the mutual adaptation of the dependent virus and host, $A_{\text{dependent}}$. The distribution of the four alternative equilibria are displayed in Table 5 and Figure 3 (reduction 1) in the parameter plane $(1/A)_{\text{helper}}$ versus $(1/A)_{\text{dependent}}$. There are four critical curves: $(1/A)^{\text{low}}_{\text{dependent}}$, separating equilibria IV and III; $(1/A)^{\text{up}}_{\text{dependent}}$, separating equilibria II and IV; $(1/A)_{\text{dependent}} = K$, separating equilibria I and III; and $(1/A)_{\text{helper}} = K$, separating equilibria II and I. In equilibrium III, the helper can survive even if the helper-host interaction is poorly adapted (i.e., $(1/A)_{\text{helper}} > K$) if the mutual adaptation of the dependent virus and host is high (i.e., $(1/A)_{\text{dependent}}$ is low). Compared with the single

TABLE 5. Equilibria of models and conditions

| Equilibrium | Condition |
|---|---|
| Case with a single virus | |
| (I) Virus dies out (virus extinction)<br>$X^* = K$, $Y^* = 0$ | (I) $(1/A)_{\text{helper}} \geq K$; virus is too badly adapted to survive |
| (II) Virus persists (virus exists)<br>$X^* = m/a$, $Y^* = [r/(r+m)][K-(m/a)]$ | (II) $(1/A)_{\text{helper}} < K$; virus is mutually well adapted with the host |
| Reduction 1 | |
| (I) Both viruses die out<br>$X^* = K$, $Y^* = U^* = 0$ | (I) $(1/A)_{\text{helper}} \geq K$ and $(1/A)_{\text{dependent}} \geq K$; both viruses are too badly adapted to survive |
| (II) Mixed infections die out<br>$X^* = m/a$, $Y^* = [r/(r+m)][K-(m/a)]$, $U^* = 0$ | (II) $(1/A)_{\text{helper}} < K$ and $(1/A)_{\text{dependent}} \geq (1/A)^{\text{up}}_{\text{dependent}}$; helper virus is well adapted but dependent virus is still too badly adapted |
| (III) Infection with virus 1 alone dies out<br>$X^* = n/b$, $Y^* = 0$, $U^* = [r/(r+n)][K-(n/b)]$ | (III) $(1/A)_{\text{dependent}} < \min[(1/A)^{\text{low}}_{\text{dependent}}, K]$; dependent virus is mutually well adapted with the host |
| (IV) All categories remain<br>$X^* = [rcK + r(m-n)]/[rc + a(r+n) - b(r+m)]$<br>$Y^* = (n - bX^*)/c$<br>$U^* = (aX^* - m)/c$ | (IV) $(1/A)_{\text{helper}} < K$ and $(1/A)^{\text{low}}_{\text{dependent}} < (1/A)_{\text{dependent}} < (1/A)^{\text{up}}_{\text{dependent}}$; helper virus is well adapted and dependent virus is neither too well adapted nor too badly adapted [a,b] |
| Reduction 2 | |
| (I) Both viruses die out<br>$X^* = K$, $Z^* = U^* = 0$ | (I) $(1/A)_{\text{dependent}} \geq (1/A)_{\text{cr}}$; dependent virus is too badly adapted |
| (II) Both viruses can coexist<br>$Z^* = (n/e) - (b/e)X^*$<br>$U^* = [erK - (r+l)n]/[e(r+n)] + \{[(r+l)b - re]/[e(r+n)]\}X^*$ [c] | (II) $(1/A)_{\text{dependent}} < (1/A)_{\text{cr}}$ and outside the cycle region; dependent virus is well adapted; $(1/A)_{\text{cr}}$ is a critical line dividing two equilibria and can only be obtained by numerical calculation |
| Combined model | |
| (I) Both viruses die out<br>$X^* = K$, $Y^* = Z^* = U^* = 0$ | (I) $(1/A)_{\text{helper}} \geq K$ and $(1/A)_{\text{dependent}} \geq K$; both viruses are too badly adapted to survive |
| (II) Only helper virus persists<br>$X^* = m/a$, $Y^* = [r/(r+m)][K-(m/a)]$, $Z^* = U^* = 0$ | (II) $(1/A)_{\text{helper}} < K$ and $(1/A)_{\text{dependent}} \geq (1/A)^{\text{up}}_{\text{dependent}}$, helper virus is well adapted but dependent virus is still too badly adapted |
| (III) Infection with virus 1 alone dies out [d]<br>$Y^* = 0$ | (III) $(1/A)_{\text{dependent}} < \min[(1/A)^{\text{low}}_{\text{dependent}}, K]$; dependent virus is mutually well adapted with the host |
| (IV) All four categories remain [e] | (IV) $(1/A)_{\text{helper}} < K$ and $(1/A)^{\text{low}}_{\text{dependent}} < (1/A)_{\text{dependent}} < (1/A)^{\text{up}}_{\text{dependent}}$; helper virus is well adapted and dependent virus is neither too well adapted nor too badly adapted; $(1/A)^{\text{up}}_{\text{dependent}}$ and $(1/A)^{\text{low}}_{\text{dependent}}$ are only calculated numerically |

[a] $(1/A)^{\text{up}}_{\text{dependent}}$ is given by $(1/A)^{\text{up}}_{\text{dependent}} = (n/b)^{\text{up}}(m/a) = (m/a) + (rc/b)[K-(m/a)]/[r + a(m/a)]$.

[b] $(1/A)^{\text{low}}_{\text{dependent}}$ is given by $(1/A)^{\text{low}}_{\text{dependent}} = (n/b)_{\text{low}}(m/a) = (1/2)(m/a) - [r/(2b)](1+c/a) + \sqrt{\{(1/2)(m/a) - [r/(2b)](1+c/a)\}^2 + [(r/b)(m/a)] + [rc/(ab)]K}$.

[c] $X^*$ is determined by $[(r+l)b - re]X^{*2} + \{[erK - (r+l)n] + [rK/(d+b)](ne - nb + bl)\}X^* + [rK/(d+b)][erK + n^2 - nl - e(r+n)] = 0$.

[d] $X^*$, $Z^*$, and $U^*$ are determined by $r(K - X^* - Z^* - U^*) - bX^*U^* - dX^*U^* = 0$; $bX^* + eZ^* - n = 0$; $dX^*U^* - eZ^*U^* - lZ^* = 0$.

[e] Values are determined by $r(K - X^* - Y^* - Z^* - U^*) - aX^*Y^* - bX^*U^* - dX^*U^* = 0$; $aX^* - cU^* - m = 0$; $dX^*U^* - eZ^*U^* - lZ^* = 0$; $bX^* + cY^* + eZ^* - n = 0$.

virus case (Fig. 3, single virus case), the helper can exist over a larger parameter space in the mixed infection than when alone, and in this sense, the helper virus benefits from mixed infection with the dependent virus.

The fact that only two equilibria (virus extinction and virus coexistence) exist for reduction 2 reveals the strong connection between *Z* and *U*: if mixed infection does not occur, there is no opportunity for single infection with the dependent virus to occur either. If mixed infection persists, single infection with the dependent virus can always persist. In reduction 2 there is a region in the parameter plane where the dynamic system evolves into a limit cycle rather than a fixed point, i.e., no stable equilibrium exists, and there is a Hopf bifurcation. The stable limit cycle, an explicitly nonlinear feature, also is found in models of other pathosystems (25,42). The limit cycle is unlikely to occur in nature, however, because its location on the parameter plane implies a poorly adapted complex but a well-adapted dependent virus when present as a single infection, i.e., either the dependent virus would have to cause much more damage when associated with the helper virus than it does alone, or the infection rate of the dependent virus on its own would have to be much greater than that for both viruses together. Such extreme situations have not been found but could exist if the helper virus has a less mutually well-adapted relationship with the host than with the dependent virus.

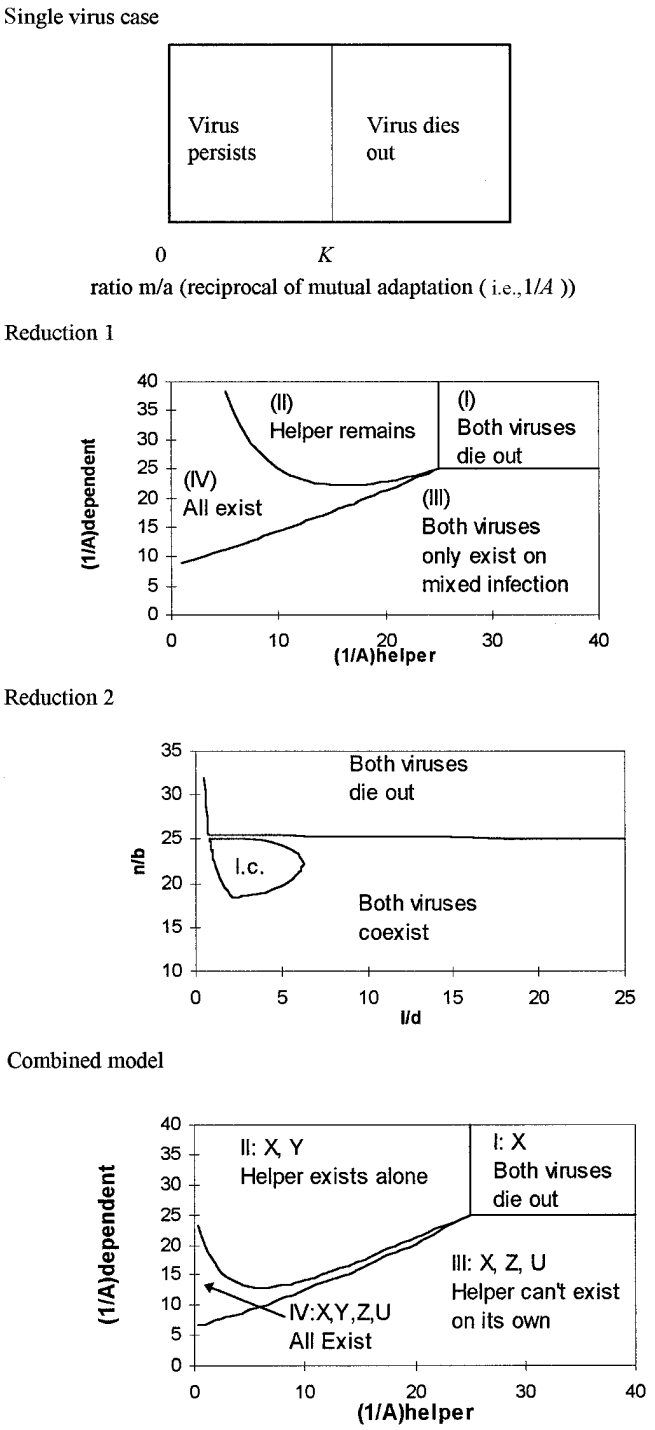


**Fig. 3.** Distribution of equilibria in the parameter plane for the simple case with a single virus; reduction 1 model, where $a = 0.004$, $b = 0.006$, $c = 0.003$, $r = 0.01$, and $K = 25$; reduction 2 model, where $l = 0.05$, $n = 0.08$, $e = 0.025$, $r = 0.01$, $K = 25$, and l.c. denotes limit cycle; and combined model, where $a = b = c = e = 0.0044$, $d = 0.0022$, $r = 0.01$, $K = 25$, and $l = n/2$. In the reduction 1 and combined models, mutual adaptation is in its reciprocal form, which appears in the solutions of the models. Thus, when (1/*A*) is low, mutual adaptation is high, and when (1/*A*) is high, mutual adaptation is low. Variables and parameters are explained in text.

The combined model presents an equilibrium distribution similar to that found in reduction 1, and there are four types of equilibria in the parameter plane $(1/A)_{helper}$ versus $(1/A)_{dependent}$ (Fig. 3, combined model). It also becomes apparent that categories *Z* and *U* are closely connected: category *Z* relies on category *U* to survive, as for reduction 2. The combined model, therefore, integrates two important features of the reduced models and also confirms the main results of the two models. It is suggested that the combined model reflects the primary characteristics of the helper-dependent virus complex. Four trajectories of the combined model over time (Fig. 4) show typical dynamics as the system evolved to each of the four equilibria. Figure 4 shows the typical trajectory of the combined model as it evolves into equilibrium IV. During the progress of an epidemic caused by a helper-dependent virus complex, initially there are many more plants infected with the helper virus alone, next mixed infection increases, and, finally mixed infections predominate but single infections persist (equilibrium IV). This theoretical result is consistent with the experimental field data on RTD (11). We now focus on the combined model to discuss the helper-dependent virus complex.

## DISCUSSION

A number of important results emerged from the analysis of the combined model. When $c > b$, i.e., it is easier for infection with virus 2 to occur if the host was previously infected with virus 1, the critical value of $(1/A)^{up}_{dependent}$ may be even larger than the maximum abundance, *K*, if the mutual adaptation of the helper and host, $A_{helper}$, is very high, i.e., $(1/A)_{helper} << K$. This indicates that as long as the helper virus is extremely mutually well adapted with the host, the helper-dependent virus complex can persist even if the dependent virus causes considerable loss. Further, as the transmission rate, *c*, increases, so does the critical value of $(1/A)^{up}_{dependent}$ and, concurrently, the critical value of $(1/A)^{low}_{dependent}$ decreases, and the area of the region occupied by equilibrium IV in the parameter plane increases. This implies that the larger the transmission rate, *c*, the greater the opportunity for the helper-dependent virus complex to exist. This theoretical result allows some exploration of possibilities for virus disease control. The term $-nU$ in the combined model can be considered the deliberate removal of diseased plants (roguing). If the transmission efficiency, *c*, is not excessive, an increase in the roguing rate, *n*, such that the *n*/*b* ratio remains high, will cause the system to stay at final equilibrium II, in which virus 2, the principal pathogen, is eliminated. For RTD, loss due to infection with RTBV (virus 2) is quite high, whereas loss due to RTSV (virus 1) is relatively low. With an acceptable amount of roguing, it can be expected that severe losses due to RTD would be alleviated. However, where the transmission efficiency, *c*, is large, an impractically high roguing rate, *n*, would be required to keep the system at equilibrium II. Numerical simulation also shows that the critical curve, $(1/A)^{up}_{dependent}$, will move up as the maximum

plant abundance, $K$, increases, which can be easily seen in reduction 1. Thus, intensification of cropping increases disease incidence and makes roguing less effective. For GRD, infection with only GRAV causes no obvious symptoms, infection with GRV-satRNA causes symptoms, and mixed infection with GRAV and GRV-satRNA together causes severe symptoms and considerable damage to groundnut. Analogous comments also apply to GRD.

If the dependent virus (virus 2) is itself very well adapted (high value of $A_{\text{dependent}}$), the system will remain in equilibrium III or IV. It is perhaps surprising that this phenomenon is independent of the value of $A_{\text{helper}}$. Therefore, if the dependent virus is very well adapted, the two viruses (helper and dependent) can coexist even if the helper is poorly adapted, i.e., given $(1/A)_{\text{dependent}} < \min[(1/A)^{\text{low}}_{\text{dependent}}, K]$, doubly infected plants can occur even when $(1/A)_{\text{helper}} > K$, so the helper virus can exist in the mixed infection. Thus, a benign dependent virus can provide the conditions for a badly adapted helper virus to survive and facilitate the helper in the helper-dependent virus complex, and therefore, it is possible under some circumstances for the benefit between the helper and dependent viruses to be reciprocal and mutual.

As the mutual adaptation of the helper and host, $A_{\text{helper}}$, decreases the length of the interval of $A_{\text{dependent}}$ (range of adaptation levels of the dependent virus) for the existence of equilibrium IV decreases. In other words, a badly adapted helper virus reduces the parameter space available to the dependent virus. Once $(1/A)_{\text{helper}}$ exceeds the maximum plant abundance, $K$, there are only two possible equilibria: I or III, depending on whether $(1/A)_{\text{dependent}}$ is greater than $K$.

In the two pathosystems considered here, $m$ is small, and $n$ is large. From the distribution of equilibria in the parameter plane (Fig. 3, combined model), it is expected that these pathosystems would be most likely to exist in equilibrium II or IV. For both RTD and GRD, assays of host plants in infected fields indicate that all infection types usually occur (i.e., equilibrium IV) but that mixed infection predominates (11,37). If we consider the evolution of virus interactions, it is apparent from Figure 3 (combined model) that there is a clear selective advantage for dependent viruses to evolve to utilize helper viruses that cause little or no damage. However, if the dependent virus is itself very well adapted (high $A_{\text{dependent}}$ value), then even a badly adapted helper virus should, according to Figure 3 (combined model), allow the dependent virus to persist. Once a complex has evolved, the helper virus could subsequently become less well adapted. That such cases have not been found in nature is notable. Dependent viruses are always found with low or nondamaging helpers. Such circumstances are most likely to lead to equilibrium IV, and the model offers a rigorous explanation of why this is so.

Two strategies for noncirculative virus transmission are currently recognized: capsid and helper strategies (41). In the former, virions are considered to interact directly with the vector. Viruses with the helper strategy no longer interact directly with the vector but interact through the mediation of a helper protein. This strategy is found in a diverse group of noncirculatively transmitted viruses. If transmission can be accomplished by the seemingly more straightforward capsid strategy, why did the helper strategy evolve? Pirone and Blanc (41) have suggested that the helper strategy may be more robust in adapting to evolutionary changes in the host and vector populations.

The helper strategy allows other (dependent) viruses to develop a vector association that would not have been possible by themselves. Facilitation of the dependent virus by the helper, however, may not be unilateral. There is evidence that infection of a plant, particularly with a virulent virus, can make the plant more suitable for insect vector survival and reproduction through changes to the host plant as a food source. Vector crowding on virus-infected plants may cause greater, more rapid vector emigration from severely infected plants than from healthy or mildly infected plants (5,15,31). Thus, if a dependent virus stimulates a change in the host that alters vector behavior, it also may increase transmission of the helper. This raises another question concerning what is meant by a "well-adapted" virus. If we consider the virus alone, an extremely virulent virus might be well adapted due to virulent infection of plants leading to a significant increase in the virus transmission rate. Throughout this paper, the term well adapted refers to the mutual adaptation of virus and host plant.

**Conclusions.** The basic reproductive number, $R_0$ (2,28,45), defined as the number of new infections that arise in a population after the introduction of one infectious diseased plant, is a very important quantity that gives a criterion for persistence of an epidemic involving a single disease agent: the agent persists only if $R_0 > 1$. Because of the complicated situation in a model in which each virus can exist in two categories of host plant, it was impossible to derive an explicit expression for $R_0$ with regard to each virus. Using analyses that were possible and numerical simulations, however, we obtained the distribution of different equilibria in the parameter plane $(1/A)_{\text{helper}}$ versus $(1/A)_{\text{dependent}}$ (Fig. 3, combined model, for RTD), which provides information on the range of outcomes for virus persistence in the helper-dependent virus complex.

The mutual adaptation of the virus and host plant, a quantity that emerged from analysis of the models, was defined mathematically and is important epidemiologically. The host is under selection pressure for greater virus resistance or tolerance (reduced host damage

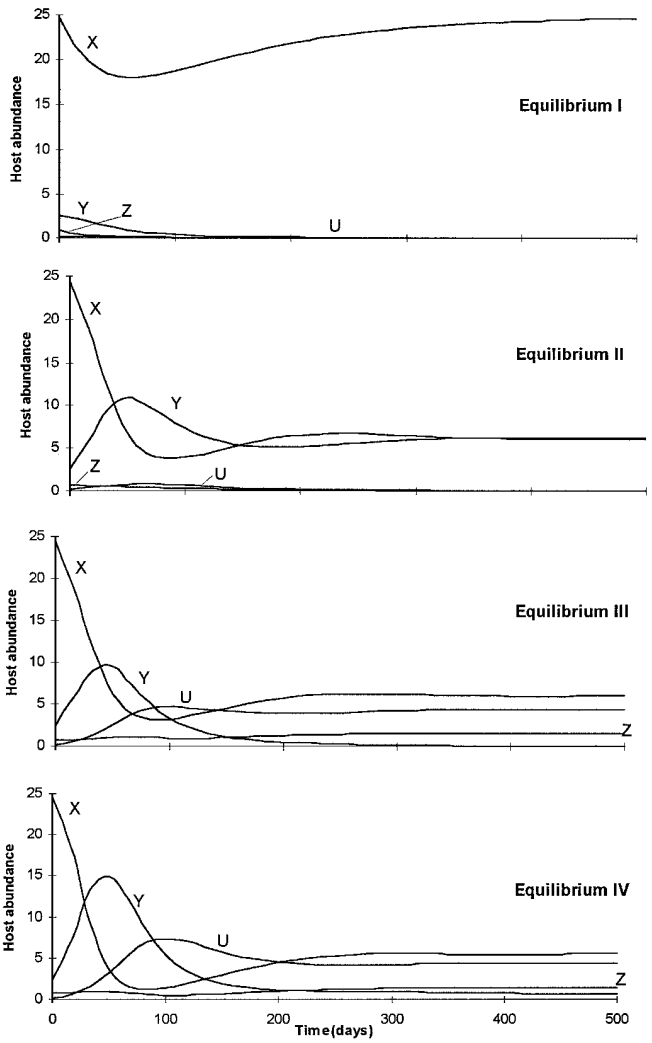


**Fig. 4.** Four typical trajectories of the combined model. The initial conditions are set as $X_0 = 24.6$, $Y_0 = 2.5$, $Z_0 = 0.8$, and $U_0 = 0.2$; the parameters are given as $a = b = c = e = 0.0033$, $d = 0.0016$, $r = 0.01$, $K = 25$, and $l = n/2$. Equilibrium I, $m = 0.083$, $n = 0.085$; equilibrium II, $m = 0.020$, $n = 0.050$; equilibrium III, $m = 0.020$, $n = 0.025$; and equilibrium IV, $m = 0.006$, $n = 0.025$. Variables and parameters are explained in text.

due to infection). The virus has two conflicting adaptation problems: ensuring its survival by preservation of its host plant (minimizing damage) and vector transmissibility (high virus titer and possibly greater damage). In the models investigated here, these two viral properties are approximately represented as loss rate due to infection and infection rate. The parameters appear as a quantity in the solution to the models: ratio of loss rate to infection rate. The reciprocal of this ratio might be regarded as a measure of the mutual adaptation of virus and host.

The models described here incorporate the main transmission processes involved in a helper-dependent virus complex and lead to the conclusion that as the mutual adaptation of the helper and host, $A_{\text{helper}}$, decreases, the biological characteristics necessary for the dependent virus to survive become increasingly constrained. With a well-adapted helper, the dependent virus has an increased chance of evolving to form a helper-dependent virus complex and is also more likely to survive subsequent evolutionary changes. This provides an explanation for the common finding that infection with a helper virus usually causes no or little damage to plants, whereas infection with a dependent virus or mixed infection with both causes very serious damage to plants. Our models also predict a situation in which it is possible for a very badly adapted helper virus to survive if the dependent virus is very well adapted, a situation that has not been found in nature.

## ACKNOWLEDGMENTS

We thank M. Jeger and M. Thresh for their helpful comments. X.-S. Zhang holds a Ph.D. studentship supported by the University of Greenwich.

### LITERATURE CITED

1. Adams, A. N., and Hull, R. 1972. Tobacco yellow vein, a virus dependent on assistor viruses for its transmission by aphids. Ann. Appl. Biol. 71:135-140.
2. Anderson, R. M., and May, R. M. 1982. Directly transmitted infectious diseases: Control by vaccination. Science 215:1053-1060.
3. Anderson, R. M., and May, R. M. 1996. The population biology of the interaction between HIV-1 and HIV-2: Coexistence or competitive exclusion? AIDS 10:1663-1673.
4. Anjaneyulu, A., Satapathy, M. K., and Shukla, V. D. 1994. Rice Tungro. Oxford and IBH Publishing Co., New Delhi.
5. Baker, P. E. 1960. Aphid behaviour on healthy and on yellows virus-infected sugar beet. Ann. Appl. Biol. 48:384-391.
6. Baria, A. R. 1997. Status of rice tungro disease in the Philippines: A guide to current and future research. Pages 76-83 in: Epidemiology and Management of Rice Tungro Disease. T. C. B. Chancellor and J. M. Thresh, eds. Natural Resources Institute, The University of Greenwich, Chatham Maritime, U.K.
7. Block, V. C., Ziegler, A., Robinson, D. J., and Murant, A. F. 1994. Sequences of 10 variants of the satellite-like RNA-3 of groundnut rosette virus. Virology 202:25-32.
8. Burrows, P. M. 1995. Dynamics of unilateral and bilateral protection. Page 50 in: Epidemiological Aspects of Plant Virus Control. B. Raccah, ed. Phytopathological Society of Israeli, Bet-Dagan.
9. Cabunagan, R. C., Daquioag, R. D., Flores, Z. M., and Koganezawa, H. 1990. Identifying tolerance for rice tungro (RTV)-associated viruses in rice varieties using severity index scoring and serology. Int. Rice Res. Newsl. 15:13-14.
10. Chan, M.-S., and Jeger, M. J. 1994. An analytical model of plant virus disease dynamics with roguing and replanting. J. Appl Ecol. 31:413-427.
11. Chancellor, T. C. B. 1995. The ecology of the leafhopper vectors of rice tungro viruses in relation to the dynamics of tungro disease. Ph.D. thesis. University of Reading, U.K.
12. Chowdhury, A. K. 1997. Present status of rice tungro disease in India. Pages 69-75 in: Epidemiology and Management of Rice Tungro Disease. T. C. B. Chancellor and J. M. Thresh, eds. Natural Resources Institute, The University of Greenwich, Chatham Maritime, U.K.
13. Chowdhury, A. K., Teng, P. S., and Hibino, H. 1990. Retention of tungro-associated virus by leafhoppers and its relation to rice cultivars. Int. Rice Res. Newsl. 15:31.
14. Clinch, P. E., Loughnane, J. B., and Murphy, P. A. 1936. A study of the aucuba or yellow mosaics of the potato. Sci. Proc. R. Dublin Soc. 21: 431-448.
15. Colvin, J., Otim-Nape, W., Holt, J., Omongo, C., Seal, S., Stevenson, P., Gibson, G. I., Cooter, R. J., and Thresh, J. M. 1999. Factors driving the current epidemic of severe cassava mosaic disease in East Africa. Pages 76-77 in: 7th Int. Plant Virus Epidemiol. Symp. A. Fereres, ed. International Society of Plant Pathology, Almeria, Spain.
16. Demler, S. A., Rucker, D. C., de Zoeten, G. A., Ziegler, A., Robinson, D. J., and Murant, A. F. 1996. The satellite RNAs associated with the groundnut rosette disease complex and pea enation mosaic virus: Sequence similarities and ability of each other's helper virus to support their replication. J. Gen. Virol. 177:2847-2855.
17. Elnagar, S., and Murant, A. F. 1976. The role of the helper virus, anthriscus yellows, in the transmission of parsnip yellow fleck virus by the aphid *Cavariella aegopodii*. Ann. Appl. Biol. 84:169-181.
18. Falk, B. M., and Duffus, J. E. 1981. Epidemiology of helper-dependent persistent aphid transmitted virus complexes. Pages 161-179 in: Plant Disease and Vectors: Ecology and Epidemiology. K. Maramorosch and K. F. Harris, eds Academic Press, New York.
19. Falk, B. W., Duffus, J. E., and Morris, T. J. 1972. Transmission, host range, and serological properties of the viruses causing lettuce speckles disease. Phytopathology 69:612-617.
20. Farrell, J. A. K. 1976. Effects of groundnut sowing date and plant spacing on rosette virus disease in Malawi. Bull. Entomol. Res. 66:159-171.
21. Hasanuddin, A., Koesnang, and Baco, D. 1997. Rice tungro virus disease in Indonesia: Present status and current management strategy. Pages 94-102 in: Epidemiology and Management of Rice Tungro Disease. T. C. B. Chancellor and J. M. Thresh, eds. Natural Resources Institute, The University of Greenwich, Chatham Maritime, U.K.
22. Hilbino, H., and Cabunagan, R. C. 1986. Rice tungro-associated viruses and relations to host plants and vector leafhoppers. International Symposium on Virus Diseases of Rice and Leguminous Crops in the Tropics. Trop. Agric. Res. Ser. 19:173-182.
23. Holt, J., and Chancellor, T. C. B. 1996. Simulation modelling of the spread of rice Tungro virus disease: The potential for management by roguing. J. Appl. Ecol. 33:927-936.
24. Holt, J., and Chancellor, T.C. B. 1997. A model of plant virus disease epidemics in asynchronously-planted cropping systems. Plant Pathol. 46:490-501.
25. Holt, J., Jeger, M. J., Thresh, J. M., and Otim-Nape, G. W. 1997. An epidemiological model incorporating vector population dynamics applied to African cassava mosaic virus disease. J. Appl. Ecol. 34:793-806.
26. Hull, R. 1996. Molecular biology of rice tungro viruses. Annu. Rev. Phytopathol. 34:275-297.
27. Hull, R., and Adams, A. N. 1968. Groundnut rosette and its assistor virus. Ann. Appl. Biol. 62:139-145.
28. Jeger, M. J., Van Den Bosch, F., Madden, L. V., and Holt, J. 1998. A model for analysing plant-virus transmission characteristics and epidemic development. IMA J. Math. Appl. Med. Biol. 15:1-18.
29. Kassanis, B. 1961. The transmission of potato aucuba mosaic virus by aphids from plants also infected by potato virus A or Y. Virology 13:93-97.
30. Kassanis, B., and Govier, D. A. 1971. New evidence on the mechanism of transmission of potato C and potato aucuba mosaic viruses. J. Gen. Virol. 10:99-101.
31. Kennedy, J. S. 1951. Benefit to aphids from feeding on galled and virus-infected leaves. Nature (Lond.) 168:825-826.
32. Matthews, R. E. F. 1991. Plant Virology. 3rd ed. Academic Press, New York.
33. Murant, A. F. 1990. Dependence of groundnut rosette virus on its satellite RNA as well as on groundnut rosette assistor luteovirus for transmission by *Aphis craccivora*. J. Gen. Virol. 71:2163-2166.
34. Murant, A. F. 1993. Complexes of transmission-dependent and helper viruses. Pages 334-357 in: Diagnosis of Plant Virus Diseases. R. E. F. Mathews, ed. CRC Press, Boca Raton, FL.
35. Murant, A. F., Rajeshwari, R., Robinson, D. J., and Raschke, J. H. 1988. A satellite RNA of groundnut rosette virus that is largely responsible for symptoms of groundnut rosette disease. J. Gen. Virol. 69:1479-1486.
36. Naidu, R. A., Bottenberg, H., Subrahmanyam, P., Kimmins, F. M., Robinson, D. J., and Thresh, J. M. 1998. Epidemiology of groundnut rosette disease: Current status and future research needs. Ann. Appl. Biol. 132:525-548.
37. Naidu, R. A., Kimmins, F. M., Holt, J., Robinson, D. J., Deom, C. M., and Subrahmanyam, P. 1999. Spatiotemporal separation of groundnut rosette disease agents. Phytopathology 89:934-941.
38. Olorunju, P. E., Kuhn, C. W., Demski, J. W., Misari, S. M., and Ansa, O. A. 1992. Inheritance of resistance in peanut to mixed infection of groundnut rosette virus (GRV) and groundnut rosette assistor virus and a single infection of GRV. Plant Dis. 76:95-100.
39. Pirone, T. P. 1977. Accessory factors in nonpersistent virus transmission. Pages 221-235 in: Aphids as Virus Vectors. K. F. Harris and K. Maramorosch, eds. Academic Press, New York.
40. Pirone, T. P. 1991. Viral genes and gene products that determine insect transmissibility. Semin. Virol. 2:81-87.

41. Pirone, T. P., and Blanc, S. 1996. Helper-dependent vector transmission of plant viruses. Annu. Rev. Phytopathol. 34:227-247.
42. Shaw, M. W. 1994. Seasonally induced chaotic dynamics and their implication in models of plants disease. Plant Pathol. 43:790-801.
43. Suzuki, Y., Astika, G. N., Widrawan, K. R., Gede, G. N., Astika, N. S., Suwela, N., Aryawan, G. N., and Soeroto. 1997. Epidemiology-oriented forecasting of rice tungro virus disease in asynchronous rice cropping areas. Pages 30-41 in: Epidemiology and Management of Rice Tungro Disease. T. C. B. Chancellor and J. M. Thresh, eds. Natural Resources Institute, The University of Greenwich, Chatham Maritime, U.K.
44. Thresh, J. M. 1989. Insect-borne viruses of rice and the Green Revolution. Trop. Pest Manage. 35:264-272.
45. Vandermeer, J., and Power, A. 1990. An epidemiological model of the corn stunt system in Central America. Ecol. Model. 52:235-248.
46. Watson, M., Serjeant, E. P., and Lennon, E. A. 1964. Carrot motley dwarf and parsnip mottle viruses. Ann. Appl. Biol. 54:153-166.