Towards a Decision Support System for Barley Yellow Dwarf Virus: the Role of Modelling

Derek MORGAN, Ian Barker & Keith Walters
Central Science Laboratory, Sand Hutton,
York, YO4 1LZ, UK

Abstract
A computer model has been developed to simulate the temporal and spatial dynamics of barley yellow dwarf virus (BYDV). The model is composed of three sub-models which described aphid population dynamics (incorporating aphid/vector immigration, development, mortality and reproduction), aphid dispersal (of both winged and wingless aphids), and virus epidemiology (incorporating acquisition, transmission and latent periods of virus in both vector and host plant). Output from the model suggested that the latent period of the virus in its plant host and dispersal of aperous vectors had the greatest influence on overall virus incidence. Although at a prototype stage the model appears to provide a sound basis for the development of a practical system for management of BYDV.

INTRODUCTION

Barley yellow dwarf virus (BYDV) is a important disease of cereals and grasses throughout the world causing significant losses to crops. In the UK it is a particular problem of early-sown winter cereals, in particular barley, with infection of newly-emerging crops occurring in September and October. Introduction of the disease (primary infection) into the crop is the result of viruliferous winged (alate) aphids migrating into crops and subsequent spread of the disease (secondary spread) occurs as a result of the dispersal of the infectious wingless (aperous) offspring of the immigrant alates. Infected plants have distinct coloration and high levels of virus infection in fields will result in characteristic yellow patches (foci) of infected hosts.

Traditionally management of the virus has depended upon the application of pesticides to control aphid vector populations. However pesticides tend to be applied routinely and irrespective of the risk of virus infection. An empirical infectivity index has been devised in the UK, based on a combination of alate cereal aphids caught in traps and the proportion carrying virus (Plumb, Lennon & Gutteridge, 1986), which provides an indication of the likelihood of primary infection but has proven unreliable for effective management of the disease as it does not take into account virus infection caused by secondary spread (Kendall & Chinn, 1990).

A reliable forecasting system is needed based upon thorough understanding of the biological processes involved. However, until recently, little was known about the factors which determine the introduction and spread of BYDV (Morgan, Carter & Jepson, 1988) and although computer models describing the epidemiology of the disease have been developed (Morgan, 1989; Kendall, Brain & Chinn, 1992) they have not considered the spatial aspects of virus spread; no attempt was made in either model to investigate the spatial component of vector dispersal and subsequent spread of the virus. The aim of this paper is to describe the development of a computer model which simulates the spread of BYDV both in time and space.

METHODS

The model contains three inter-related sub-models describing aphid population dynamics, aphid dispersal and virus epidemiology. A conceptual flow diagram of the structure of the model is given in Figure 1.

Aphid population dynamics

The submodel consists of three components; (i) immigration, (ii) development and survival, and (iii) reproduction and morph determination. A comprehensive description of the sub-model is given in Morgan (1989). It is assumed that alate aphids land randomly in a cereal field and reproduce asexually. In turn the offspring of these immigrants develop and eventually become reproductively mature and produce offspring. All processes are dependent upon temperature; favourable warm temperatures increase development and reductive rates, whereas detrimental low temperatures cause mortality.
Aphid dispersal

It is assumed that after landing on a plant alate aphids will behave as aperous aphids and move between plants by walking rather than flying (flying).

Aperous aphids are assumed to move to new hosts by walking between plants. Each day the sub-model assumes that 5% of the total number of aphids move from their existing location to a new host. The sub-model assumes that an aphid moves in a random direction and will re-locate to one of the eight potential new hosts surrounding the host from which it moved. Additionally, the model assumes that a re-locating aphid is twice as likely to move to a new host within the same row as its previous host rather than to a new host in adjacent rows. This assumption reflects the fact that plants within rows tend to be sown more closely than the spacing between rows.

Virus submodel

Previously healthy plants become infected with virus as a result of infectious aphid vectors colonizing and feeding on them, whereas previously healthy aphids acquire virus by feeding on an infectious host plant.

Each day, after aphid dispersal has taken place, the virus status of each plant and aphid is updated. A plant/aphid host can be in one of three states; healthy, has no virus; latent, has virus but insufficient titre for either healthy aphids to acquire (from plant) or for healthy plants to be infected (from aphid); or infectious, whereby sufficient virus is present for transmission. The day after a plant/aphid has been infected it enters the latent category and after a latent period it enters the source category. Arrays are used in the sub-model to maintain the virus status and the date they acquired virus if they have become infected of every individual plant and aphid.

Implementation

The model was developed in FORTRAN 77 and runs on a IBM PC-compatible. With a daily iteration the model takes approximately 145 minutes on a 80486 PC 66 MHz to simulate 60 days of virus epidemiology.
RESULTS

Simulations

Figure 2 is a typical spatial representation of output from the model. On the first day of the simulation very few immigrant alates have landed into the crop and subsequently few plants have been infected with virus (Figure 2a) but after 10 days some plants have become infected and sufficient time has elapsed for some of them to become infectious (Figure 2b). After 30 days infectious apterous aphids have spread the virus from the original source of the disease and distinct foci of virus infection are visible (Figure 2c). After 60 days the foci are pronounced and approximately elliptical in shape (Figure 2d). Figure 3 summarises the temporal spread of virus spread in Figure 2. Virus incidence gradually increases from zero on the first day of the simulation to a final virus incidence of approximately 4% of all plants infected.

As a result of the stochastic nature of the model it is necessary to carry out many simulations to determine mean incidence of virus spread. Fifty simulations were made with the model. Mean incidence was approximately 5.3%, with minimum and maximum incidence of 3.7 and 6.9%, respectively.

Sensitivity Analysis

The effect of small changes to the proportion of infective alate immigrants, the proportion of aphids dispersing, latent period of the virus in the plant host and total number of aphids were investigated through a sensitivity analysis of the model. Table 1 summarises the results.

The largest build up in virus incidence resulted from increase in dispersal of aphids (increasing the daily proportion of moving aphids by 5% increased virus spread by approximately 65%), although increasing the proportion of alate immigrants carrying virus resulted in smaller increases in virus spread (10% increase in proportion of viruliferous immigrants increased virus incidence by about 50%).

The greatest reduction in virus incidence occurred by increasing the latent period of the virus in the host plant (increasing the latent period by 2 days reduced virus spread by about 60%), while increasing aphid mortality resulted in similar suppression of virus spread (5% increase in aphid mortality reduced virus incidence by about 50%).

Figure 2. Spatial dynamics of BYDV epidemiology on day 1 (Fig. 2a), 10 (Fig 2b), 30 (Fig 2c) and 60 (Fig 2d)
Figure 3. Temporal dynamics of BYDV epidemiology

Table 1. Effect of variable changes on virus incidence

<table>
<thead>
<tr>
<th>Process</th>
<th>Change</th>
<th>Mean</th>
<th>se</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Infectious immigrants</td>
<td>+10%</td>
<td>5.3</td>
<td>0.82</td>
<td>3.7, 6.9</td>
</tr>
<tr>
<td>Mortality</td>
<td>+5%</td>
<td>7.8</td>
<td>0.45</td>
<td>1.4, 13.3</td>
</tr>
<tr>
<td>Apteræ dispersal</td>
<td>+5%</td>
<td>2.7</td>
<td>0.34</td>
<td>2.3, 3.2</td>
</tr>
<tr>
<td>Latent period</td>
<td>+2 days</td>
<td>8.1</td>
<td>2.69</td>
<td>3.8, 15.9</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.3</td>
<td>0.45</td>
<td>1.4, 3.3</td>
</tr>
</tbody>
</table>

DISCUSSION

The computer model described in this paper has provided useful insights into understanding the complex interactions of the various biological processes involved in BYDV epidemiology. In addition, the predicted spatial dynamics and incidence development curves of the virus resemble those observed in cereal fields.

Computer modelling provides a method for assessing the relative contributions of biological processes interacting in a biological system and have been used in crop breeding programmes to highlight characteristics which could confer resistance/tolerance to pests and diseases (Campbell, Darby & Morgan, 1994). The model has highlighted the significance of several processes on epidemiology of BYDV. The greatest reduction in BYDV incidence occurred as a result of extending the latent period of the virus in its plant host. Several studies have shown that it takes about 4-5 days before BYDV can be acquired from newly infected plants (Gill, 1969; Plumb, 1974) and extending the latent period to 6 days would reduce overall incidence of the virus by 60%.

Conversely, the model showed that if the likelihood of aphids dispersal was increased by only 5% virus incidence would increase by over 65%. Hence it is imperative to be aware of the variables which facilitate aphid dispersal. Several factors have been shown to initiate aphid dispersal, including overcrowding (Ito, 1960), abiotic conditions (Bailey, et al., 1995) and natural enemies (Roitberg, Myers & Fraser, 1979). Although some can be manipulated, e.g. overcrowding, the relative economic importance of these measures have yet to be considered.

Although the model is at an early prototype stage, it provides a sound basis for extension as a system for practical management of BYDV. Such a system could be developed to provide regional forecasts of the potential spread of the disease and to recommend suitable control strategies for virus and vector.

ACKNOWLEDGEMENTS

DM wishes to thank the MAFF and the HGCA for financial assistance and the CSL for the opportunity to attend the symposium.
REFERENCES


