Ecology and Epidemiology

Detecting Patterns of Wheat Stripe Rust Pandemics in Time and Space

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ABSTRACT

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Pandemics of wheat stripe rust from 1950 to 1990 were analyzed with data from five key regions in different geographical areas in northern China. Epidemics in one region were correlated with epidemics in other regions. Spatial correlation coefficients increased as spatial distance decreased. The epidemic time series of the source region, where rust occurs year round, was not correlated with lagged epidemic series of regions in the dispersion area. Average epidemic indices of one region were associated with distance from the source region and latitude of the region. Time series analysis also was used to determine temporal pattern. An epidemic time series of each region was identified as the autoregressive integrated moving average (ARIMA) (3,1,0) for the source region and ARIMA (2,2,0) for regions in the dispersion area, which indicate that the epidemic value in a given year is related to epidemics of the previous 4 yr. There was a downward trend in the 41-yr pandemic series, except in Gangu. Mean epidemic indices from northern China were greater for the period of 1950–1969 than for the period of 1970–1990. Less frequent and less destructive pandemics were noted in the second period; this may be due to improved disease management by advanced agricultural techniques.

Additional keywords: epidemiology, forecast, Puccinia striiformis.

Wheat stripe rust (*Puccinia striiformis* Westend.) is the most important pandemic wheat disease in China (16). There are three independent pandemic systems of this disease (12,16); the largest and the most important one is in northern China (Fig. 1). There, wheat is grown on 16 million hectares, which accounts for more than 60% of the total wheat production in China. Previous studies (9,12) showed that the pathogen source area of the system is in the mountainous region of Gangsu Province, where wheat is grown year round and where *P. striiformis* can overwinter and oversummer. In the fall, northwest air currents carry uredinio-spores to the Yellow River Basin (the dispersion area) as far south as Xinyang and as far east as the eastern coast; the uredinio-spores cause infection on winter wheat seedlings. In the dispersion area, pathogen survival to the following spring on infected leaves depends on latitude and severity of winter (12). In some years, the disease can cause yield losses as high as 65% (10).

The Chinese Plant Pest Monitoring and Forecasting Station has given the study of wheat stripe rust number one priority, and agents have monitored the disease in provinces, legislative

regions, and counties. Other important plant pests that develop on a continental scale have been monitored systematically with standardized pest indices by this network every season for decades. Vast amounts of pest development data on a continental scale have accumulated. Similar data are collected by government agencies in different countries, such as the Animal and Plant Health Inspection Service, United States Department of Agriculture. However, to our knowledge, these data have not been used with quantitative analysis. The present study mainly examines disease development in fields; periods are limited to growing seasons. Quantitative analysis of long-term disease pandemics on a macroscale is needed. Interest in the study of disease epidemics on meso- and macroscales is increasing, and a few studies to model interregional spread (14) and to predict pandemic race-cultivar interaction (15) have been reported. Such information will be useful for the development of sustainable agriculture.

A pandemic record over decades is a time series. Analysis of time series is a well-developed branch of statistics. It has been widely applied to many ecological disciplines as a powerful tool to detect a long-term pattern of population dynamics (5). Some methods from time series analysis have been used to detect disease spatial patterns in fields (4,8). Time series analysis should be useful in modeling long-term dynamics of plant disease. In this study, we analyzed wheat stripe rust pandemics in northern China over the period of 1950–1990; we used a time series approach.

MATERIALS AND METHODS

Pandemic data. The northern China pandemic system of wheat stripe rust covers the Yellow River Basin (Fig. 1). Ecology and epidemiology of the pandemic system have been well-documented (12,16). Data from five regions representing different geographical

areas of the system were used (Table 1). In brief, the Gangu region, where wheat is grown in the valley during winter and on the mountain in summer, is the pathogen source area of the system (9,12). *P. striiformis* can overwinter and oversummer in Gangu. Xian, Xinyang, and Zhengzou are regions in the frequent dispersion area of the system (12). In the Xian region, 300 km east of Gangu, the pathogen overwinters in diseased leaves, and epidemics develop in early spring. Xinyang is in the southeast area of the system, where winter wheat is infected in the fall, and the pathogen reproduces slowly during winter (11,12). Zhengzou is near the transitional line for pathogen overwintering. There, winter survival of diseased leaves depends on snow depth and winter temperature. Consequently, the amount of endogenous spring inoculum varies from year to year. Beijing is far north and is in an infrequent dispersion area of the system. Very few diseased leaves are detected in the fall, and the pathogen overwinters only when there is a thick snow cover. Urediniospores from the southern part of the system provide initial inoculum for Beijing in the spring.

Stripe rust epidemic data of the above five regions (Fig. 1; Table 1) from 1950 to 1990 were used. Annual epidemics of stripe rust in each region were recorded as epidemic indices in five classes (Table 2). Based on the five classes, epidemics between two classes were also recorded (Table 2). The epidemic index reflects prevalence and severity of disease in a region. For quantitative analysis, the five classes were assigned values of 0–4 (Table 2). Epidemic index values of each region were plotted against time to examine the trend over 41 yr. The overall pandemic series in northern China was the mean index value calculated from the five regions.

Spatial analysis. Epidemic trends over the 41 yr were compared among different regions. The frequency of each epidemic index ≥ 3.0 was counted for each region over the 41 yr, and average epidemic indices were compared among the five regions. Spatial relationships among the five regions were determined by calculating a spatial correlation coefficient matrix from the 41 yr of epidemic data.

We also determined correlations between the epidemic series of the source region (Y_t) and the lagged epidemic series of dispersion regions (Y_{t+i}, $i = 1, 2, \ldots 10$ yr) to check for a lagged relationship between source region and dispersion regions of the epidemic.

Temporal analysis. There are four types of time series: (1) white noise (WN), which is a purely random process; (2) autoregressive (AR), in which a current value is related to the past values; (3) moving average (MA), in which a current value is related to current and past random variations; and (4) autoregressive moving average (ARMA), which is the linear combination of AR and MA processes (1,6).

An output signal of a system is a combination of input, regular, and irregular (WN) signals. A pattern exists in the sequential records of a system output (time series) if a regular signal has been input. Generally, a time series is composed of WN series and other regular signal series. Components of regular signals usually include trend and cyclic behavior (oscillation). A series having cyclic pattern shows attributes of an AR series. By using different techniques, one can decompose a series into regular and irregular signals to find out the patterns. For this analysis, time series approach was used, and a computer package, Timeslab (6), was employed. The method is briefly described here, but details can be found in texts by Chatfield (1) and Newton (6).
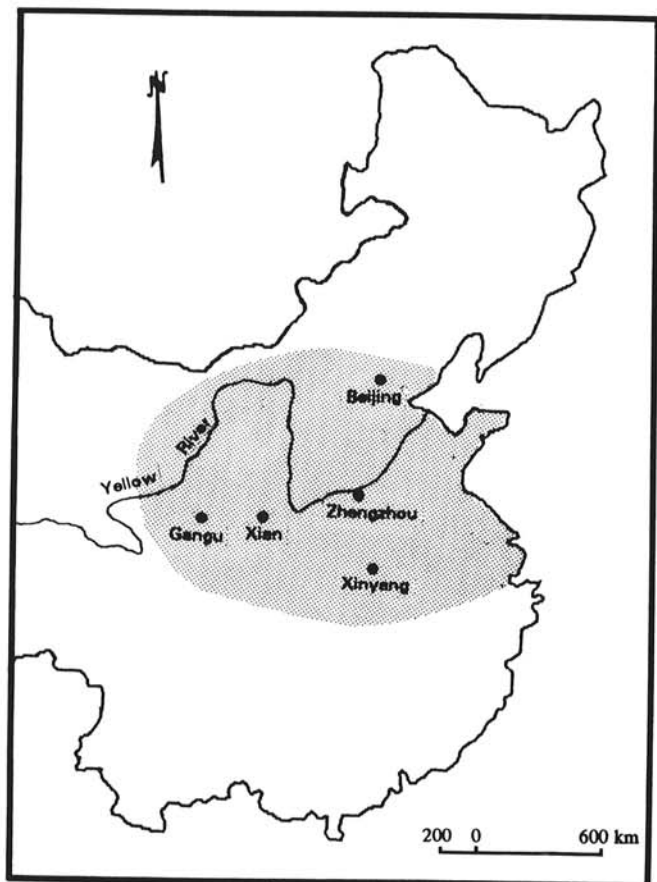

Fig. 1. Pandemic system of wheat stripe rust (*Puccinia striiformis*) in northern China (shaded areas). Gangu is the source region of the system, and the other regions are in the dispersion area. The prevalent currents are eastward in fall and northward in spring.

TABLE 1. Characterization of five epidemic regions in the northern China pandemic system of wheat stripe rust (*Puccinia striiformis*)

Region	Over winter	Over summer	Reproduction in winter	Position in the system
Gangu	Yes	Yes	Variable	Source
Xian	Yes	No	No	Frequent dispersion
Xinyang	Yes	No	Yes	Frequent dispersion
Zhengzou	Variable	No	No	Frequent dispersion
Beijing	Rare	No	No	Infrequent dispersion

Analysis of a time series requires that the series be stationary, because most of the probability theory of time series is concerned with stationary time series (1). A stationary series has a mean and a variance that are unchanged in time and a frequency that is normally distributed. If there is a trend in a series, the series is not stationary, and it must be stabilized by transformation. For our epidemic series ($Y_1, Y_2, \ldots Y_{41}$), we transformed the time series by differencing to stabilize the process. The first order difference was $X_t = Y_t - Y_{t-1}$. The second order difference was $W_t = X_t - X_{t-1}$, or $W_t = Y_t - 2Y_{t-1} + Y_{t-2}$. Generally, order of difference should not be greater than two to avoid overdifferencing (1).

Patterns in a stationary time series were identified with a procedure called ID.MAC (6). We used the following methods in time domains to examine patterns: AR correlation (correlogram), which measures the correlation between observations at different time lags; and partial AR correlation, which measures the correlation between observations at different time lags after the common linear effect of the data has been removed. If a correlogram is within the 95% simultaneous confidence band and the partial autocorrelation coefficients are close to 0 over lag time, there may be no pattern. The process is considered WN (random). A pattern may exist if the above situations do not occur, and the type of the pattern can be determined based on plots of correlogram and partial autocorrelation. Generally (6), for an AR process with order p, AR(p), the correlogram decays exponentially to 0. The partial autocorrelation function also is 0 for lags greater than p. For an MA process with order q, MA(q), the correlogram is 0 for lags greater than q (cut off at q), and the partial autocorrelation decays exponentially to 0. For an ARMA process, neither the correlogram nor the partial correlogram is 0 past some lags; rather, they each decay exponentially to 0. Data were examined by individual location.

An ARMA model was constructed with the ARMASEL procedure as:

$$X_t = a_1 X_{t-1} + \ldots + a_p X_{t-p} - b_q Z_{t-q}$$
$$- \ldots - b_1 Z_{t-1} + Z_t \qquad (1)$$

in which $a_1, \ldots, a_p$ and $b_1, \ldots, b_q$ are unknown parameters to be estimated from the data. Equation 1 expresses X_t as a linear combination of AR term $a_i X_i$, in which the current value is related to past values, and of MA term $b_j Z_j$, in which the current value is related to current and past shocks. ARMASEL is a stepwise regression procedure used to determine the values of parameters. The selected parameters are expected to be consistent with the order of a process. We examined the residual process to determine if it was WN (6). If a nonstationary series is stabilized with dth order difference before regression, the model constructed would be called an integrated ARMA model, ARIMA(p,d,q). We used the Akaike Information Criterion (AIC; 6) to determine the fit of a model.

RESULTS

Wheat stripe rust fluctuates in the five regions and appears erratic in time (Fig. 2). There were five severe pandemics in northern China from 1950 to 1990 (Fig. 2). Pandemics in 1950, 1964, and 1990 attained a destructive epidemic index of 4, whereas pandemics in 1957 and 1959 reached 3.5 (Table 2). The 1959 pandemic resulted from the breakdown of resistance in a dominant cv. Bima-1 (13). In terms of epidemic frequency, the series in northern China can be divided into two periods, 1950–1969 and 1970–1990. The disease occurred more frequently in the first period. The average epidemic indices were 2.15 and 1.33 for the first and second periods, respectively.

Spatial relationship. Generally, values of spatial correlation coefficients decreased as the spatial distance between two regions increased (Fig. 1; Table 3). The greatest value of r was 0.84 for Beijing-Zhengzou, and the smallest value was $r = 0.56$ for Gangu-Beijing.

Geographical differences in epidemics were found among the five regions. Epidemics in the Gangu region were greater than or equal to index 1 every year; in Beijing, null disease (index 0) was recorded 15 out of 41 yr. The numbers of epidemic indices ≥ 3.0 during the 41 yr were 19, 11, 11, 12, and 4 for Gangu, Xian, Xinyang, Zhengzou, and Beijing, respectively. Depending on latitude and spatial distance from the source region Gangu, the average epidemic index had a gradient. In the east-west direction, average epidemic indices were 2.22, 1.87, and 1.83 for Gangu, Xian, and Zhengzou, respectively. In the south-north direction, indices were 1.93, 1.83, and 0.91 for Xinyang, Zhengzou, and Beijing, respectively.

The absolute values of correlation coefficients between epidemic process of source region (Y_t) and lagged epidemic process (Y_{t+i}, $i = 1,2, \ldots 10$ yr) of any dispersion region were smaller than 0.26, indicating that the epidemic time series of the source region was not correlated with the lagged epidemic series of dispersion regions.

Time series. The epidemic series for Gangu was not stationary as indicated by frequency distribution. First order differencing, however, resulted in a stationary process for Gangu as shown by the plot of differenced epidemic index values (Fig. 3A) and by the approximate normal distribution of frequency of differenced values. Although the correlogram was within the 95% confidence limits, there was a high value at lag 3 (Fig. 3B). The partial autocorrelation had a high value at lag 3; after which, values were close to 0 (Fig. 3C), indicating an AR(3) process. The result of stepwise regression with a procedure for ARMA selection (ARMASEL.MAC) was an ARIMA(3,1,0) model, in which $p = 3$, $q = 0$, and $d = 1$ (Tables 4,5).

Epidemic series over years had a noticeable downward trend for the dispersion regions (Fig. 2). The series were not stationary. Patterns among dispersal regions were similar. Complete results from Beijing are given as a representative of dispersal regions (Fig. 4); for other regions, only correlograms are shown (Fig. 5). For Beijing, a second order differencing resulted in a stationary process as shown by the plot of differenced index values (Fig. 4A) and by the approximate normal distribution of frequency of differenced values. In the correlogram, there was a significant negative value out of the confidence bands at lag 2 for each region except for Xinyang, which almost reached the lower band (Figs. 4B,5). The partial autocorrelation had a high value at lag 2; after which, values were cut off to 0 (Fig. 4C), indicating the differenced arrays were AR(2). Models for the four dispersal regions were ARIMA(2,2,0), in which $p = 2$, $q = 0$, and $d = 2$ (Tables 4,5).

TABLE 2. Epidemic index of wheat stripe rust (*Puccinia striiformis*) and its numerical values used in analysis

Index	Description	Numerical value
Null	Disease rarely detected in a region	0
Trace	Disease prevalence less than 5% in a region	0.5
Light	Light disease epidemic in a region	1
Light to moderate	Disease more than light in a region	1.5
Moderate	Moderate epidemic in part of a region	2
Moderate to severe	Severe epidemic in <50% of a region	2.5
Severe	Severe epidemic in >50% of a region	3
Severe to destructive	Destructive epidemic in >50% of a region	3.5
Destructive	Destructive yield reduction in a region	4

Residuals from the five regions were WN.

By substituting difference equations into the ARIMA models, we found a common model for the pandemic system:

$$Y_t = a_1 Y_{t-1} + a_2 Y_{t-2} + a_3 Y_{t-3} + a_4 Y_{t-4} + Z_t \qquad (2)$$

in which $a_1, \ldots, a_4$ are coefficients and are different for different regions (Tables 4,5). The model shows that an epidemic of a given year was related to epidemics of the previous 4 yr.
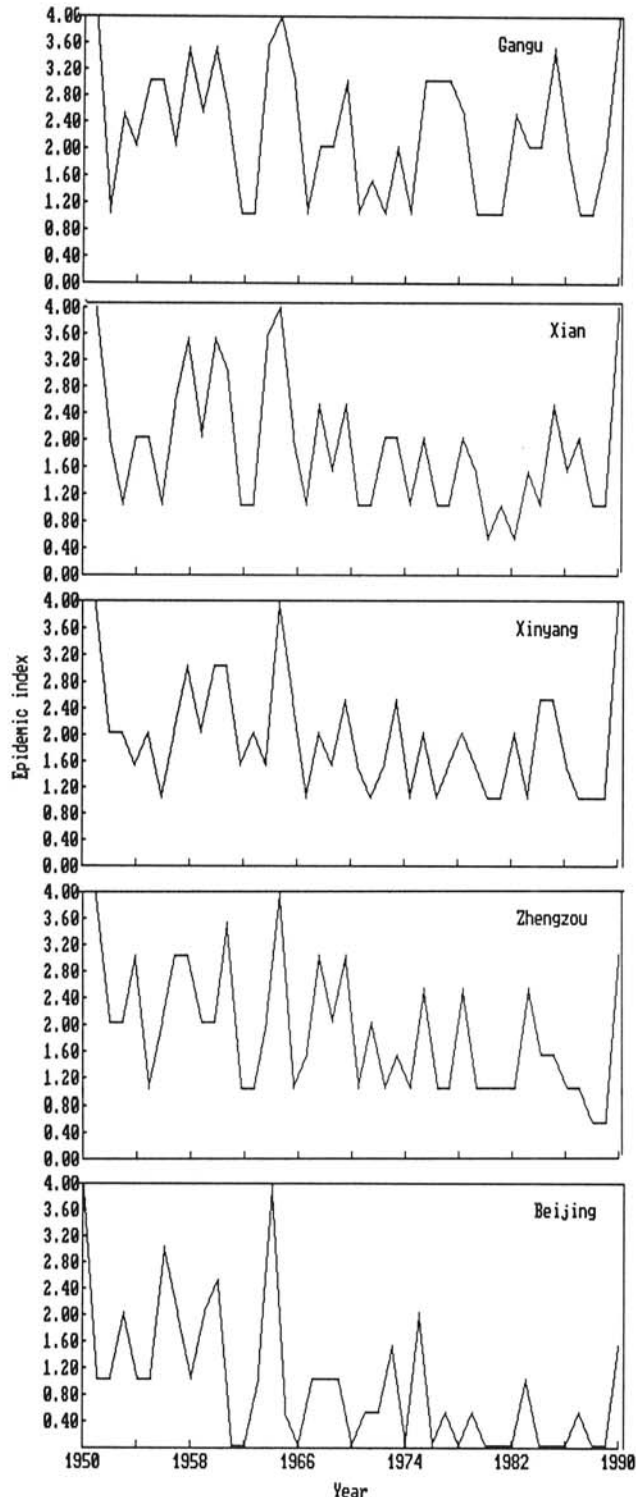
DISCUSSION

Our study showed that the five regions are in one pandemic system, which is consistent with the previous conclusion from historical observations (9,12,16). An epidemic of one region was closely correlated to epidemics of other regions; r increased as spatial distance decreased. There may be a 4-yr cycle of stripe rust pandemic in northern China as shown by the common model (Eq. 2) for the five regions.

Quantitative analysis can effectively outline the spatial pattern of a pandemic system. In our study, the epidemic index and spatial correlation coefficients indicated an epidemic gradient in the

TABLE 3. Correlation coefficient matrix of disease epidemics among the five regions in the northern China pandemic system of wheat stripe rust (*Puccinia striiformis*)[a]

	Region				
Region	Gangu	Xian	Xinyang	Zhengzou	Beijing
Gangsu	1.00	0.68	0.68	0.56	0.56
Xian		1.00	0.78	0.74	0.74
Xinyang			1.00	0.67	0.65
Zhengzou				1.00	0.84
Beijing					1.00

[a]Spatial distances between regions (Fig. 1) are reflected by the relative positions in the table.

Fig. 2. Epidemic time series of wheat stripe rust (*Puccinia striiformis*) in five regions of the northern China pandemic system from 1950 to 1990. Epidemic index description is in Table 2.
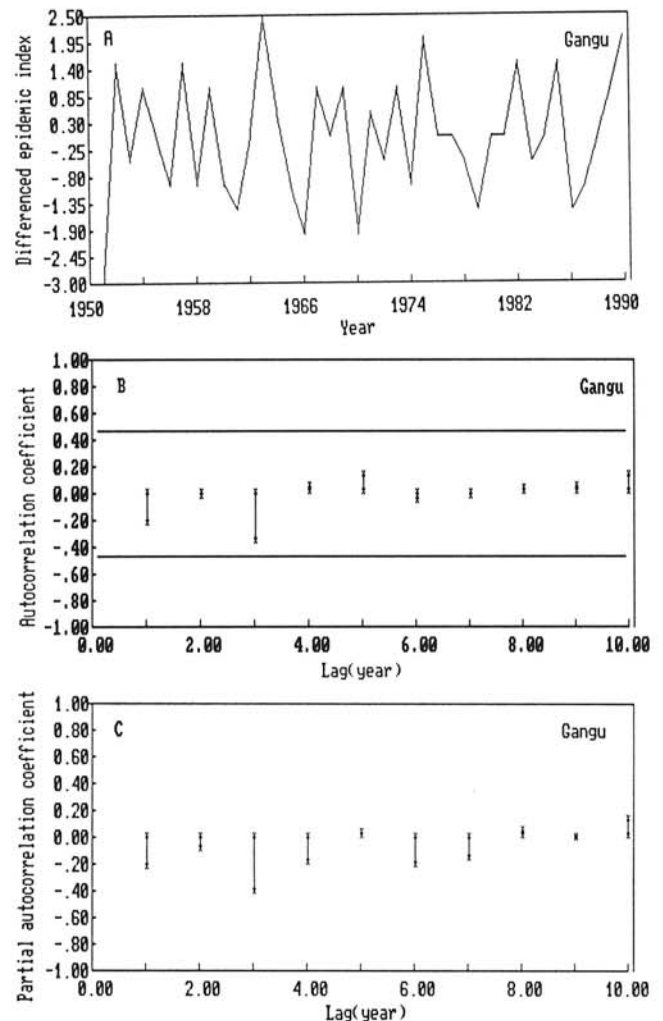

Fig. 3. Identification results of differenced epidemic time series of wheat stripe rust (*Puccinia striiformis*) for source region Gangu. A, Time series after first order difference; **B**, autocorrelation with 95% simultaneous confidence limits; and **C**, partial autocorrelation.

TABLE 4. ARIMA models of wheat stripe rust (*Puccinia striiformis*) for different regions in the northern China pandemic system

Region	Type of model	ARIMA model[a]	WN[b]	AIC[c]
Beijing	(2,2,0)	$W_t = -0.656\,W_{t-2} + Z_t$ (0.118)[d]	1.06	6.52
Zhengzou	(2,2,0)	$W_t = -0.549\,W_{t-2} + Z_t$ (0.131)	1.08	8.31
Xian	(2,2,0)	$W_t = -0.532\,W_{t-2} + Z_t$ (0.132)	1.20	16.92
Xinyang	(2,2,0)	$W_t = -0.408\,W_{t-2} + Z_t$ (0.143)	1.04	5.35
Gangu	(3,1,0)	$X_t = -0.29\,X_{t-1} - 0.195\,X_{t-2} - 0.41\,X_{t-3} + Z_t$ (0.149) (0.153) (0.142)	1.09	12.64

[a] Model from differenced process. The difference was first order ($X_t = Y_t - Y_{t-1}$) for Gangu and second order ($W_t = X_t - X_{t-1}$, or $W_t = Y_t - 2Y_{t-1} + Y_{t-2}$) for other regions.
[b] White noise (random).
[c] Akaike Information Criterion, which measures the fit of a model.
[d] Standard errors of regression coefficients.

TABLE 5. Prediction models of wheat stripe rust (*Puccinia striiformis*) for different regions in the northern China pandemic system

Region	Prediction model[a]	Variance
Beijing	$Y_t = 2Y_{t-1} - 1.656\,Y_{t-2} + 1.312\,Y_{t-3} - 0.656\,Y_{t-4} + Z_t$	1.06
Zhengzou	$Y_t = 2Y_{t-1} - 1.549\,Y_{t-2} + 1.098\,Y_{t-3} - 0.549\,Y_{t-4} + Z_t$	1.08
Xian	$Y_t = 2Y_{t-1} - 1.532\,Y_{t-2} + 1.064\,Y_{t-3} - 0.532\,Y_{t-4} + Z_t$	1.20
Xinyang	$Y_t = 2Y_{t-1} - 1.408\,Y_{t-2} + 0.816\,Y_{t-3} - 0.408\,Y_{t-4} + Z_t$	1.04
Gangu	$Y_t = 0.71\,Y_{t-1} + 0.10\,Y_{t-2} - 0.215\,Y_{t-3} + 0.41\,Y_{t-4} + Z_t$	1.09

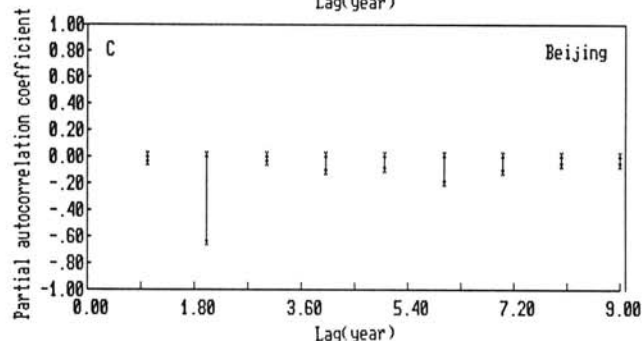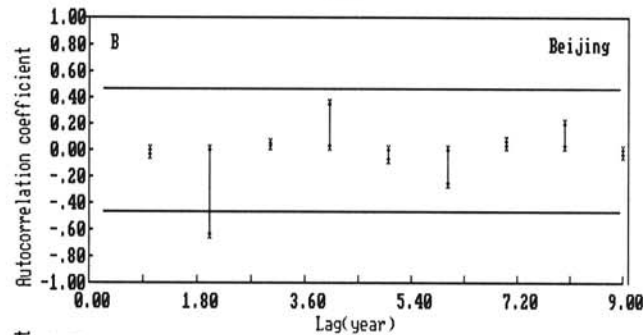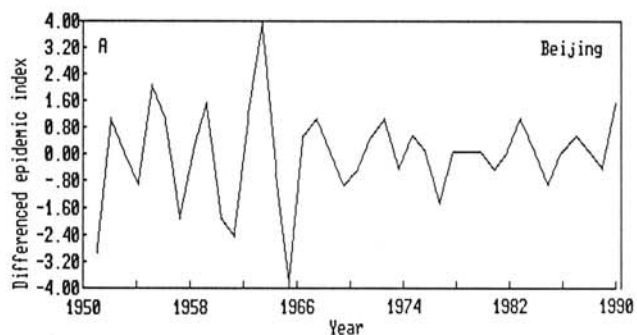[a] Obtained by substituting difference models back to ARIMA models.

Fig. 4. Identification results of differenced epidemic time series of wheat stripe rust (*Puccinia striiformis*) for dispersal region Beijing. **A**, Time series after second order difference; **B**, autocorrelation with 95% simultaneous confidence limits; and **C**, partial autocorrelation.
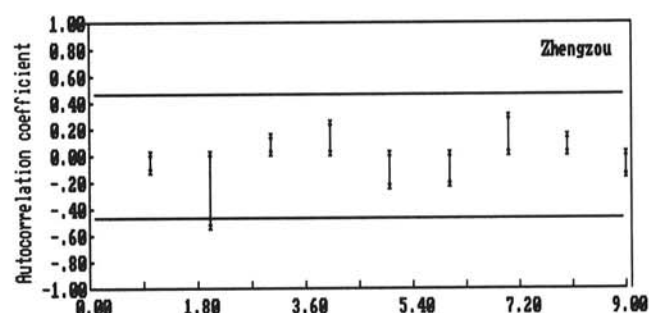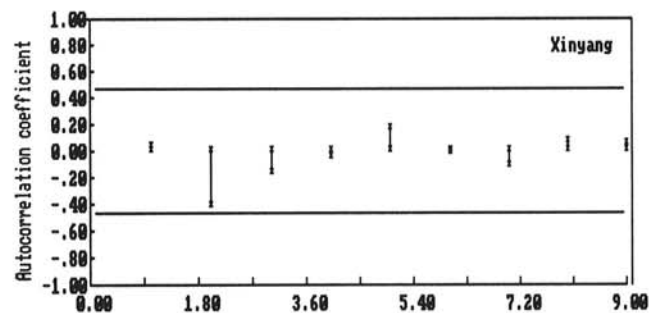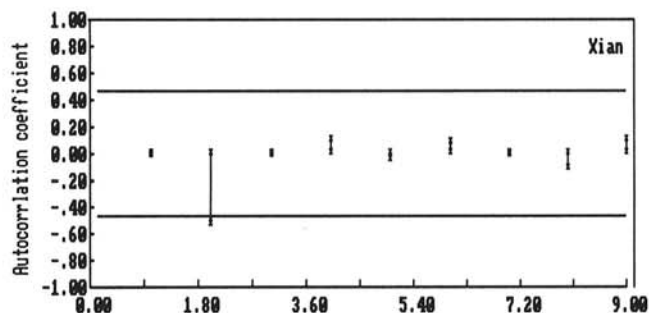

Fig. 5. Autocorrelation of epidemic time series (second order difference) of wheat stripe rust (*Puccinia striiformis*) for the regions of Xian, Xinyang, and Zhengzou. The bands are 95% simultaneous confidence limits.

northern China pandemic system. This gradient was consistent with the previous conclusion drawn from historical observations. Historical surveys show that the Gangu region functions as a source of inoculum for northern China (9,12). In the fall, urediniospores are carried to the Yellow River Basin by westerly air currents (12,16). A consistent gradient of rust incidence in early December was detected from Gangu to the east coast in a 4-yr survey (S. M. Zeng, *unpublished*). In our study, the r value for Gangu-Xian was 0.65, which is greater than the 0.54 for Gangu-Zhengzou, indicating a distance dependency. The r value for Beijing-Zhengzou was 0.84 greater than the 0.67 value for Beijing-Xinyang, indicating that the exogenous inoculum of Beijing may be dependent on spores from a closer area such as Zhengzou (12). Zeng (14) demonstrated that interregional disease dispersal is distance-dependent and can be predicted by an interregional dispersal model.

Differences in epidemics among regions may reflect geographical differences. For example, average epidemic indices were 1.93, 1.83, and 0.91 for Xinyang, Zhengzou, and Beijing, respectively. The southern regions of this pandemic system usually are warm and moist in spring and are more suitable for stripe rust development than northern regions. Geographic differences among the regions were also reflected in the trends of pandemic records. The trend for Beijing is steeper than that of other regions, probably because Beijing is in a very developed area of China, where disease management is much improved. In contrast, the trend for Gangu is unremarkable due, perhaps, to a relative slow development of the region where most farms are in remote, mountainous areas. Furthermore, the epidemic difference between source region and dispersal regions was reflected by the ARIMA models identified as ARIMA(3,1,0) for source region and ARIMA(2,2,0) for dispersal regions.

The fluctuation of pandemics can be considered a mixed signal of periodic oscillations and irregular noise and may be explained by the following. First, recent studies (3) show that a pathogen-host interaction can produce very complicated dynamics. Depending on the extent to which pathogens overwinter, a host-pathogen population may vary its oscillation from period cycle to apparently irregular fluctuation (3). The overwintering of the rust pathogen in different regions varies markedly by year and may affect spring epidemics. Second, periodic changes in climate tend to impose oscillations on the internal origin of a biological system (7), which may result in periodic changes in disease epidemics. Third, agricultural activity affects epidemics. Change of host resistance will drive away the pathogen population dramatically, as was true of the epidemic in 1959 (13). The decrease of pandemic frequency in the last two decades also demonstrated the impact of agricultural activity on the disease. Therefore, if oscillations of the three driving forces are not harmonic, the epidemic could fluctuate with a great random shock, $\sigma^2 = 1.04–1.20$ (Tables 4,5).

We considered a time series model as an alternative to regression and simulation in searching for patterns in pest development. Coakley (2) has presented a very good prediction for wheat stripe rust in the Pacific Northwest (United States) by searching for disease-favorable patterns in early spring from historical weather data. A time series prediction model is also a historical pattern. In comparison, Coakley's method presents a pattern from exogenous processes, such as weather variables, and provides a

short-term prediction. The pattern by time series is from the past values of epidemic series (endogenous information) and can be used for long-term prediction. Extrapolation can be done with a time series model but is inadvisable with a conventional regression model.

In this paper, we used the models only to detect pandemic patterns and did not use the model for prediction. Our epidemic indices were categorical variables and were recorded over years. Sequential collection of a categorical variable can be taken as a time series, and an ARIMA model can be developed. However, an ARIMA model for a categorical variable is approximate in comparison with a model for a continuous variable. Furthermore, although the 41-yr data set was very long for plant epidemiology, the record was short in terms of time series, which is also common for ecological time series (5). An observation number ≥ 50 has been suggested for a confident conclusion (1). To unambiguously resolve a cycle component, one must record at least 10 oscillations (5). With the increase of the length of pandemic record, improvement in reliability of our models is expected; and a long-term prediction with the models may be possible.

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