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Modelling of Population Growth for a Seasonal Incidence of Mustard Aphid, Lipaphis erysimi

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SUMMARY

In the present study a method of fitting a nonlinear growth model to the data of mustard aphid population is discussed. It shows the appropriateness of the aphid population growth model to the data set. The highest aphid population is predicted in the first standard meteorological week by the fitted

Keywords: Nonlinear, Growth model, Population, Productivity, Pest.

1. INTRODUCTION

Mustard (Brassica juncea) is the major edible oilseed crop in India. It is extensively grown in many parts of the country mainly during cool moist climate of winter months which is the major factor for the favorable growth and productivity of mustard. Productivity of mustard is highest (1559 kg per ha) in the state of Haryana and lowest (524 kg per ha) in Assam. Further, an overall national average of harvested yield is in the range of 900-1150 kg per ha which is just a fraction of the attainable yield of 2500-3000 kg per ha. The yield loss due to aphid infestation in mustard ranged from 87.16 to 98.16% (Anonymous 1995). Amongst the various insect pests invading mustard crops, mustard aphid, Lipaphis erysimi is considered the most serious. Thus, the current productivity can be increased manifold particularly in the North-Eastern Region of India, if adequate management practices for major diseases and pests at different phenological stages of the crop are taken up in time. It is also reported in many studies for its various health benefits. However, many researchers opined that seed yield as well as seed quality of mustard are adversely affected

following equations:

by major insect pests. Keeping in view of these points, population growth study of the most important pest for mustard namely, mustard aphid, Lipaphis erysimi is presently considered. Moreover, nonlinear models are extensively used to study the population growth of many organisms in agriculture. Different forms of nonlinear models are usually fitted to the available data. In the present study, an aphid population model is fitted to describe the growth of mustard aphid population using a data observed at College of Post Graduate Studies, CAU, Umiam, Meghalaya.

2. METHODOLOGY

Prajneshu (1998) developed a deterministic model for aphid population growth explaining the relationship between aphid population density (Y) at time (t) and the form of the model, is given below:

$$Y(t) = ae^{bt} \left(1 + de^{bt}\right)^{-2},$$

where a, b and d are the descriptive parameters which are related to the interpretative parameters by the

$$\gamma = 2b^2 \frac{d}{a}$$
, $Y_0 = \frac{a}{(1-d)^2}$ and $\lambda = (b^2 - 2\gamma Y_0)^{1/2}$,

where λ is the intrinsic birth rate per capita, γ , the death rate divided by the cumulative population density and Y_0 , the initial population density at time 0.

To examine model performance, it is desirable to use some of the summary statistics like root mean square error (RMSE) and mean absolute error (MAE):

$$RMSE = \left[\sum_{t=1}^{n} \left(Y_t - \hat{Y}_t \right)^2 / n \right]^{1/2}; \text{ and }$$

$$MAE = \sum_{t=1}^{n} \left| \left(Y_{t} - \hat{Y}_{t} \right) \right| / n,$$

where

- *Y*, Observed aphid population at time *t*;
- \hat{Y} , Predicted aphid population at time t;
- n Number of observations, t = 1, 2, ..., n.

The better model will have the least values of these statistics. It is, further, recommended for residual analyses to check the model assumptions such as independence or the randomness assumption of the residuals and the normality assumption. To test the independence assumption of residuals, run test procedure is available. However, the normality assumption is not so stringent for selecting non-linear models because their residuals may not follow normal distribution.

3. RESULTS AND DISCUSSION

The average data of mustard aphid, *Lipaphis erysimi* at different stages of crop growth recorded at College of Post Graduate Studies, CAU, Umiam, Meghalaya, India at weekly intervals during November, 2009 to February, 2010 (Bhutia *et al.* 2011) is considered for the present study and the same dataset is reproduced in Table 1 along with its predicted values. The first (zero) observation is included for model fitting although no aphids are observed during the initial period as suggested by some authors. The growth model is fitted to the above aphid population data using the Statistical Package SAS 9.3 version. The summary of the model fitted is presented in Table 2. The low values of RMSE, MAE show an appropriateness of the fitted model to the data. The graph of fitted model

along with observed aphid population is also depicted in Fig 1. The highest aphid population predicted by the fitted model lies in the first standard meteorological week which coincides the first week of the January month. The residuals are plotted against time in Fig 2, shows no pattern. Further, it is clear from the residual analyses that the randomness assumption follows since the run test |Z| value (0.52) is less than 1.96 of normal distribution at 5% level of significance. Also, the normality assumption regarding the error term is met for the model since Shapiro-Wilk's test p-value of the fitted model is 0.49. Thus, it can be concluded that the above nonlinear model is suitable to explain the growth of the given dataset of aphid population.

Table 1. Observed and predicted average number of aphids

Time (in weeks)	Average Number of aphids per plant	Predicted Average Number of aphids per plant
Nov.week1	0.47	0.98
Nov.week2	2.12	2.05
Nov.week3	5.48	4.23
Dec.week4	17.78	8.60
Dec.week5	18.65	16.85
Dec.week6	20.18	30.83
Dec.week7	55.30	49.79
Jan.week8	70.48	65.95
Jan.week9	55.07	67.48
Jan.week10	62.03	53.03
Jan.week11	39.01	33.77
Feb.week12	15.36	18.77
Feb.week13	0.43	9.66
Feb.week14	0.00	4.77

Table 2. Results of fitted model

	Aphid population growth model		
A) Parameter Estimation along with asymptotic standard error			
а	0.470 (0.25)		
b	0.743 (0.06)		
d	0.001 (0.0009)		
B) Goodness of Fit			
RMSE	6.51		
MAE	5.20		
C) Residual Analysis			
Run test $ Z $ Value	0.52		
Shapiro-Wilk's Test p-value	0.49		

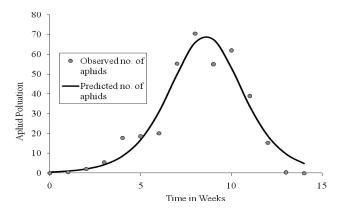


Fig 1. Observed and predicted values

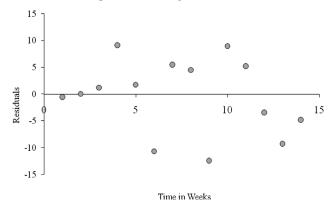


Fig 2. Residual plot against time

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