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Growth modeling for prediction of cotton leaf curl disease (CLCuD)

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ABSTRACT: Plant diseases are the major threats for crops around the world, because they causes losses in yield, environmental and social problems. Therefore, it is necessary to have a description of the dynamics of plant disease in order to have sustainable strategies to prevent and diminish the impact of diseases on crops. Various mathematical models have been employed to create model which give a description of epidemic dynamics. In this study an attempt have been made by using three models *viz.,* Monomolecular, Logistic and Gompertz models. from the results it was observed that the Gompertz model performed better for cotton leaf curl disease (CLCuD) index for the year 2016 and 2017 with lowest mean square error (MSE) 6.84 and 7.47 with high coefficient of determinations (R^2) 0.989 and 0.987, respectively. The predicted values were also calculated on the basis of the above models. Similarly, it is revealed that the Logistic model is the best fitted model for the cotton leaf curl disease incidence for the year 2016 and 2017 with lowest mean square error (MSE) 11.45 and 3.04 and high coefficient of determinations 0.995 and 0.998, respectively. The predicted values were calculated on the basis of the above fitted models.

Key words : Cotton leaf curl disease, growth modelling, prediction

The mathematical modesl have been employed to create models which give a description of epidemic dynamics. The commonly used mathematical tools used are disease progress curves, linked differential equation, area under disease progress curve and computer simulation.

Today the Mathematical modelling of crop disease is a rapidly expanding discipline within plant pathology. Since plant diseases, weeds and environmental factors are the major threats to agriculture production. It is estimated that 14.1 per cent of crops are lost due to plant disease alone. The total crop loss from plant disease is about million US $/year through the world (Leke *et al.,* 2015). The first models of the temporal development of epidemics were developed by Van der Plank (1963) and have since formed the basis for disease modelling (Campbell and Madden, 1990). Singh *et al.,* (2019) studied the development of growth model for *Ziziphus mauritiana* for powdery mildew disease.). Pardeep *et.al.,* (2019) studied on annual compound growth rates of guava (*Psidium guajava* L.) fruit in Haryana using non linear model.

A model is a simplification of reality and attempts to summarise the main processes, to put forward hypothesis and to verify their coherence and consequences. It also represents a trial to determine the minimal hypothesis which would allow minimal mathematical representation of real processes. In epidemiology, modelling aims to understand the main determinants of epidemic development in order to develop sustainable strategies for strategic and tactical management of diseases.

Epidemiological models can be classified into three types – descriptive, predictive and conceptual according to their main objective.

Keeping in view of the importance of mathematical modelling, an attempt has been made to fit the mathematical model to cotton leaf curl disease data. This data has been taken during the crop seasons 2016-2017 and 2017-2018 in Cotton Research Area, Department of Genetics and Plant Breeding CCS HAU Hisar. Data have been recorded weekly during the crop season. The three models namely monomolecular model, Gompertz and Logistics model were studied to know the behaviour of disease and best fit model were found out using the R software out.

MATERIALS AND METHODS

Cottn Leaf Curl virus susceptible cultivar HS 6 was sown on 10.5.2016 during *kharif* 2016 and on 11.5.2017 during 2017 crop season with a spacing of 67.5 x 30 cm in Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. All the recommended agronomical practices were followed for raising the crop. The observations on disease progress *i.e.* disease incidence and disease intensity were recorded at an interval of 7 days till first week of October under field conditions. R software was used to analyse the data.

Experiment details : Plant disease epidemics are investigated according to variables of interest which are formulated as functions of external factors, such a disease progress curves show the epidemic dynamics over time (Agrios 2005). The mathematical tools can be used to obtain the information about the appearance and amount of inoculums, change in host susceptibility during growing period, weather events and the effectiveness of cultural and control measures. Growth models provide a range of curves that are often similar to disease progress curves (Van Maanen and Xu,2003) and represent one the most common mathematical tools to describe temporal disease epidemics. In growth modelling, data are usually collected over time. In general, growth models are mechanistic in nature, rather than empirical. A mechanistic model usually arises as a result of making assumptions about the type of growth, writing down differential or difference equations that

Table 1. Parameter estimation of various growth model for cotton leaf curl disease index for *kharif*, 2016

Model	a	B	c	R^2	MSE
Logistic	0.495	1.36	57.24	0.978	12.91
Gompertz Model	**0.305**	**1.05**	**60.410**	**0.989**	**6.84**
Monomolecular	0.041	0.00	131.46	0.966	20.415

Table 2. Parameter estimation of various growth models for cotton leaf curl disease index for *kharif*, 2017

Model	a	B	C	R^2	MSE
Logistic	0.349	4.49	66.132	0.978	13.273
Gompertz Model	**0.207**	**2.05**	**72.163**	**0.987**	**7.47**
Mono molecular	0.043	0.00	132.34	0.987	7.75

represent these assumptions and then solving these equations to obtain growth model. The utility of such model is that, on one hand, they help to gain insight into the underlying mechanism of the system and on the other hand they are of immense help in efficient management. Some well known nonlinear growth models are Monomolecular, exponential and Logistic and Gompertz models. A brief description of the above growth models is given as :

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

This model describes the progress of a growth situation in which it is believed that rate of growth at any time is proportional to resource

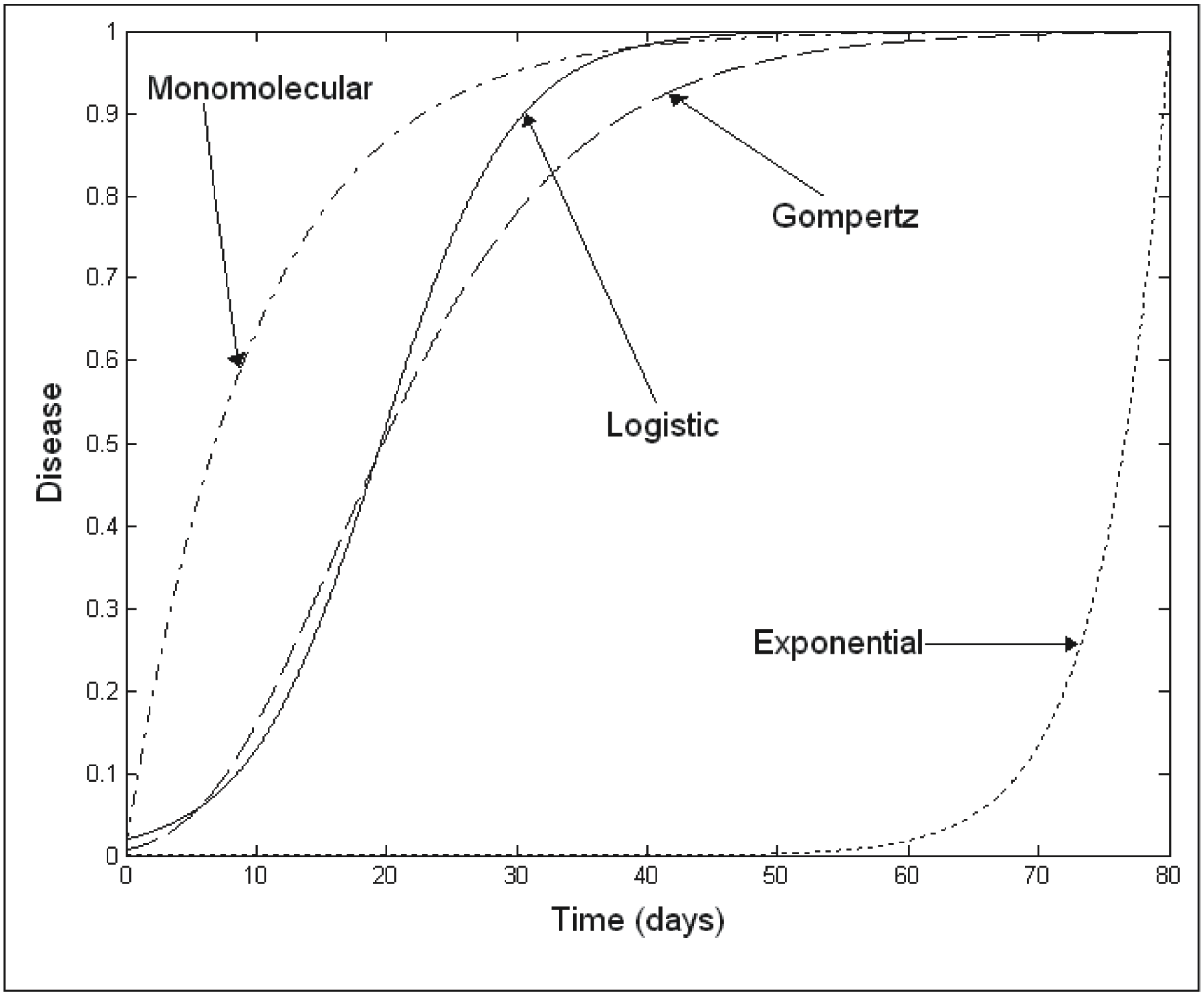

Fig.1. Examples of disease progress curves represented by monomolecular, exponential, logistic and Gompertz models

yet to be achieved, *i.e.*

Y(t) = c-(c-b)*exp(-a*t) + e(t)

Where c is the carrying size of the system. On integration, we get the model.

(ii) Logistic model: A second type of logistic model was proposed by Van der Plank (1963), being more appropriate for most polycyclic diseases, meaning thereby that there is a secondary spread within a growing season (Forrest, 2007). This growth model is the most widely used for describing epidemics of plant disease (Jamadar *et al.,* 2009).

It is given by the $\frac{dy}{dt} = a`y(1 - \frac{y}{c})$, on integration, we get
Y(t) = c/(1+b*exp(-a*t))

The graph of Y(t) versus t is elongated. S-shaped and the curve is symmetrical about its Inflexion.

(iii) Gompertz model: This growth model is appropriate for polycyclic diseases as an alternative to logistic models. Gompertz model has an absolute rate curve that reaches a maximum more quickly and declines more gradually than the logistic models (Forrest, 2007). This is another model having a sigmoid type of behavior and is found to be quite useful in biological work. However, unlike the logistic model, this is not symmetric about its point of inflexion. The differential equation for this model is
Integration of this equation yields
Y(t) = c*exp(-b*exp(-a*t)) + e(t),

where
Y(t) denotes the variable under study at time t,
'a' denote the intrinsic growth rate,
'c' the carrying capacity of the environment,
b = [b-Y(0)]/Y(0) and Y(0) is the value of Y(t) at t = 0 and **e(t)** is the error term.

In general the parameter 'a' is the coefficient of external influence emanating from outside system

Fig. 1 shows the example of disease progress curves represented by growth models where it can be seen that Gompertz and logistics models have a characterstics sigmoid form and an inflection point meaning secondary

RESULTS AND DISCUSSION

The five descriptive statistics (Minimum value, first quartile, second quartile, third quartile and maximum value) for the disease index and disease intensity for the year 2016 and 2017 are shown by the Box Whisker Fig. 1 and 2. From the Fig. 1 the range of the disease index was found to be 0 -63 and 0-73 for the year 2016 and 2017, respectively. It was also observed that half of the disease index is lying below 40 and half of the disease index lying above 40 for the year 2016. Similarly, median for the year 2017 was found to be 42.

From Fig. 2 the range of the disease intensity was found to be 0 100 and 75-100 for the year 2016 and 2017, respectively. It also showed that second quartile coincide with the third quartile for both the year. The observations recorded from weeks 20-23 showed outlier.

The best fit growth model amongst the Gompertz, Logistic, and Monomolecular was found on the basis of the experimental data. It

Table 3. Forecasting of cotton CLCuD index for *kharif*, 2016 by using the different growth models

Standard week	Actual	Logistic model	Gompertz model	Mono Molecular model
22	**0**	1.36	0.05	-
23	**0**	2.19	0.34	-
24	**0**	3.51	1.32	2.97
25	**1.33**	5.54	3.61	8.12
26	**5.99**	8.56	7.57	13.06
27	**10.99**	12.82	13.06	17.81
28	**21.49**	18.39	19.53	22.36
29	**30.48**	25.02	26.28	26.73
30	**33.32**	32.06	32.7	30.93
31	**37.15**	38.71	38.42	34.95
32	**45.81**	44.31	43.27	38.82
33	**46.48**	48.6	47.24	42.53
34	**48.14**	51.64	50.39	46.09
35	**48.81**	53.7	52.85	49.52
36	**52.31**	55.03	54.74	52.8
37	**54.48**	55.87	56.17	55.95
38	**56.31**	56.4	57.26	58.98
39	**60.88**	56.73	58.07	61.88
40	**63.8**	56.93	58.68	64.67

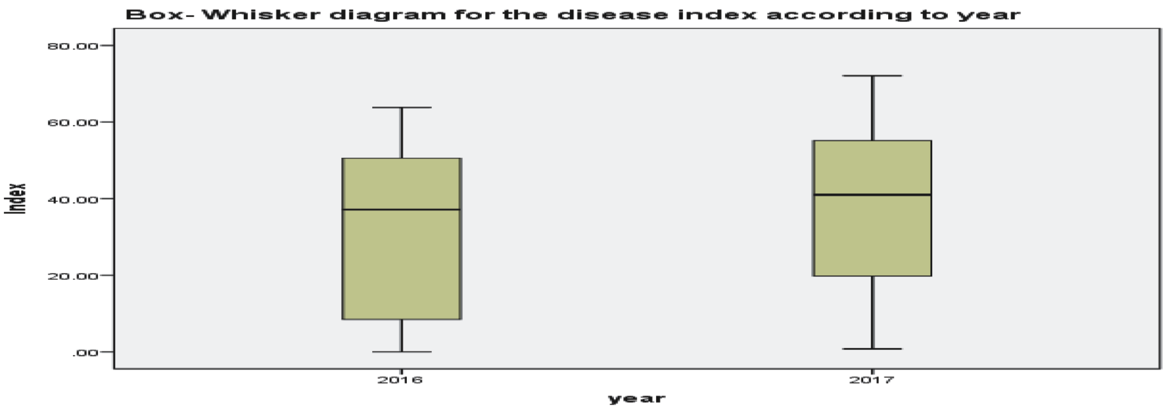

Fig 1. Box whisker diagram for the disease index according to year 2016 and 2017

Box Whisker diagram for the disease incidence according to year

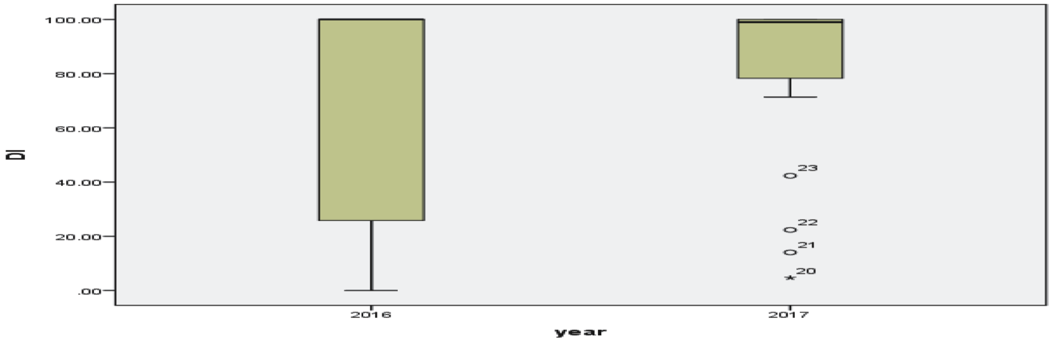

Fig 2. Box whisker diagram for the disease incidence according to year 2016 and 2017

Table 4. Forecasting of cotton CLCuD index for *kharif*, 2017 by using the different growth models

Standard week	Actual	Logistic Model	Gompertz model	Mono Molecular Model
22	**0.76**	4.49	2.05	-
23	**2.49**	6.19	3.98	2.13
24	**4.33**	8.44	6.84	7.62
25	**8.66**	11.36	10.63	12.88
26	**17.91**	15.02	15.2	17.91
27	**21.65**	19.45	20.34	22.74
28	**24.49**	24.55	25.77	27.36
29	**32.15**	30.13	31.24	31.79
30	**39.98**	35.88	36.53	36.03
31	**40.98**	41.47	41.48	40.09
32	**48.98**	46.59	46.01	43.98
33	**49.31**	51.03	50.04	47.7
34	**51.31**	54.71	53.59	51.27
35	**54.31**	57.64	56.65	54.69
36	**55.98**	59.91	59.27	57.96
37	**58.47**	61.61	61.49	61.1
38	**61.64**	62.88	63.36	64.1
39	**66.97**	63.8	64.92	66.98
40	**72.1**	64.47	66.22	69.74

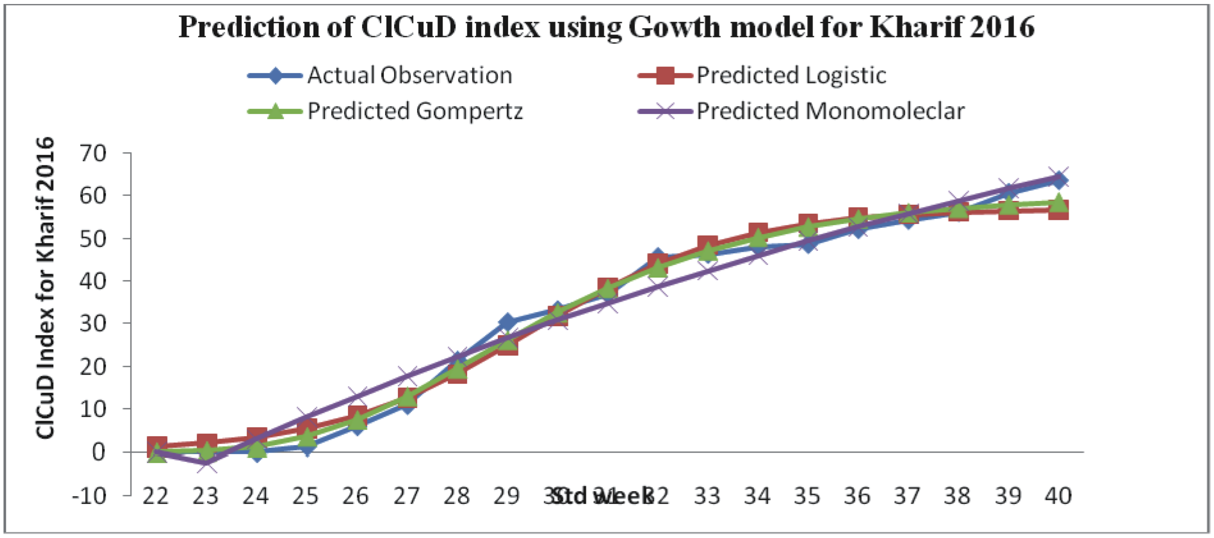

Fig 3. Prediction of ClCuD index using growth model for *kharif* 2016

was observed from Table.1 and 2 that the Gompertz model performed better for cotton leaf curl disease (CLCuD) index for the year 2016 and 2017 with lowest mean square error (MSE) 6.84 and 7.47 with high coefficient of determination (R^2) 0.989 and 0.987, respectively. The predicted value was calculated on the basis of the above model were shown in the Table 3 and 4 and also shown graphically in the Fig. 3 and 4.

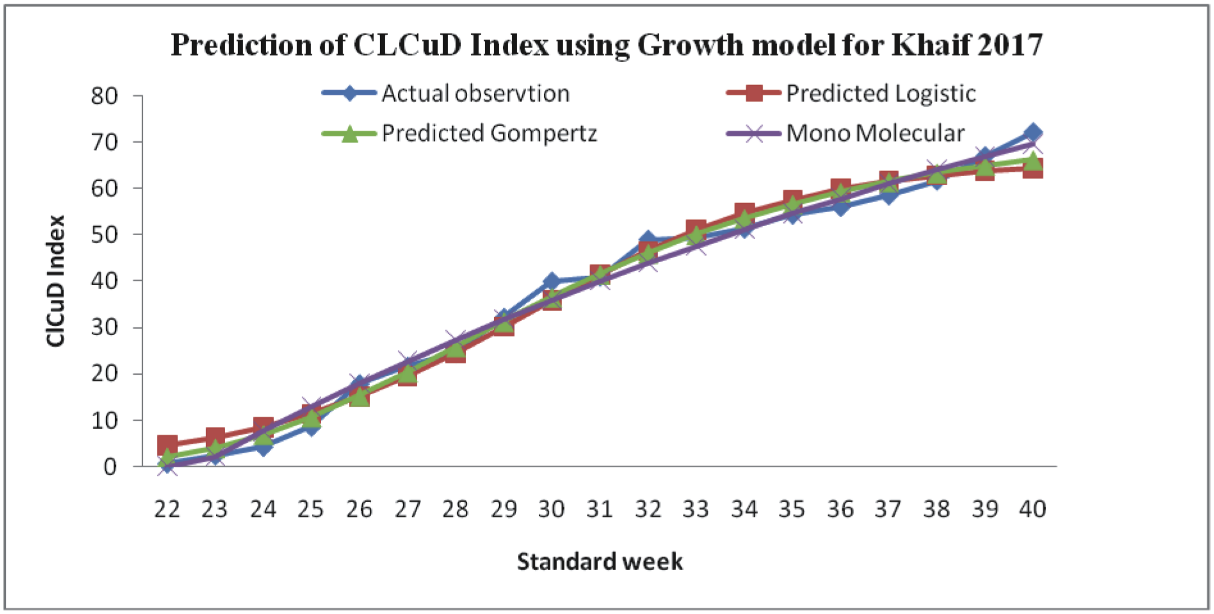

Fig 4. Prediction of ClCuD index using growth models for kharif 2017

Table 5. Parameter estimation of growth model for cotton leaf curl disease incidence (%) *kharif*, 2016

Model	a	b	c	R^2	MSE
Logistic	**1.520**	**0.00**	**100.00**	**0.995**	**11.455**
Gompertz Model	1.212	0.00	100.00	0.990	22.01
Monomolecular	0.165	0.00	117.148	0.858	300.86

Table 6. Parameter estimation of growth model for cotton leaf curl disease incidence (%) *kharif*, 2017

Model	a	b	c	R^2	MSE
Logistic	**0.947**	**4.55**	**99.79**	**0.998**	**3.04**
Gompertz Model	0.642	0.63	100.00	0.993	8.27
Monomolecular	0.272	0.00	100.0	0.949	61.77

Similarly, it was revealed from Table 5 and 6 that the Logistic model was found to be the best fitted model for the cotton leaf curl disease intensity for the year 2016 and 2017 with lowest mean square error (MSE) 11.45 and 3.04 and high coefficient of determination 0.995 and 0.998, respectively. The predicted value was calculated on the basis of the above model and shown in the Table 7 and 8. The predicted value was also shown graphically in the Fig. 7 and 8.

CONCLUSION

It was revealed that Gompertz model performed better amongst the studied models in the experiment for the disease index whereas logistic models performed better for the disease incidence for the year 2016 and 2017. It is recommended that there is appearance of disease in the 24th week therefore management of disease should be taken at the 23rd week of

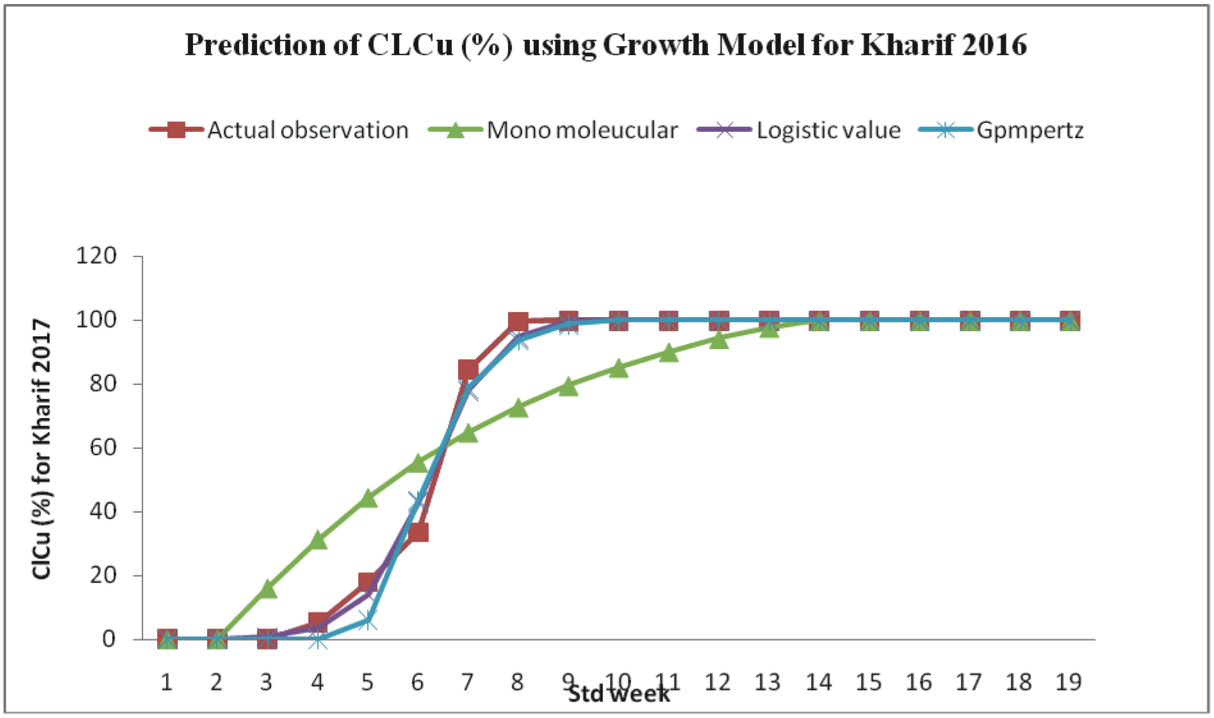

Fig 5. Prediction of ClCu(%)using growth models for *kharif* 2016

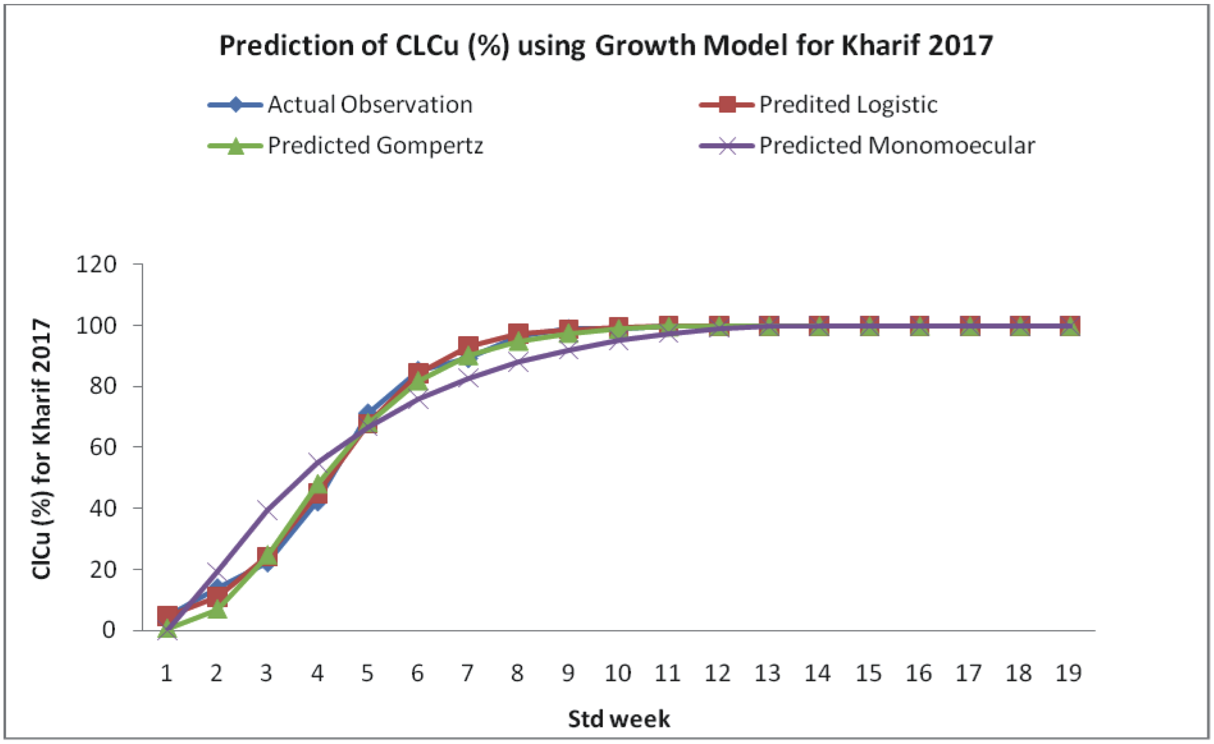

Fig. 6. Prediction of ClCu(%)using growth models for *kharif* 2017

Table 7. Forecasting of cotton CLCuD (%) for *kharif*, 2016 by using the different growth model

Standard week	Actual	Logistic Model	Gompert model	Mono Molecular Model
22	**0**	0	0.04	0
23	**0**	0	0.17	0
24	**0**	16.02	0.78	0
25	**5.33**	31.4	3.46	0.01
26	**18**	44.44	14.1	6.04
27	**33.6**	55.5	42.98	43.65
28	**84.6**	64.88	77.89	78.62
29	**99.66**	72.83	94.72	93.67
30	**100**	79.57	99.42	98.68
31	**100**	85.28	100	100
32	**100**	90.13	100	100
33	**100**	94.24	100	100
34	**100**	97.72	100	100
35	**100**	100	100	100
36	**100**	100	100	100
37	**100**	100	100	100
38	**100**	100	100	100
39	**100**	100	100	100

Table 8. Forecasting of cotton CLCuD (%) for *kharif*, 2017 by using the different growth model.

Standard week	Actual	Logistic Model	Gompertz model	Mono Molecular Model
22	**0**	4.55	0.63	-
23	**0**	10.95	6.99	19.18
24	**0**	24.07	24.71	39.59
25	**5.33**	44.95	48.05	55.14
26	**18**	67.75	68.19	67
27	**33.6**	84.33	81.99	76.03
28	**84.6**	93.17	90.34	82.92
29	**99.66**	97.12	95.07	88.16
30	**100**	98.74	97.66	92.16
31	**100**	99.38	99.06	95.21
32	**100**	99.63	99.8	97.53
33	**100**	99.73	100.00	99.3
34	**100**	99.77	100.00	100.00
35	**100**	99.78	100.00	100.00
36	**100**	99.79	100.00	100.00
37	**100**	99.79	100.00	100.00
38	**100**	99.79	100.00	100.00
39	**100**	99.79	100.00	100.00
40	**100**	99.79	100.00	100.00

2016-2017 and 2017-2018.

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