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Model Selection in Describing Disease Progress Curve of Fusarium Wilt (*Fusarium oxysporum F.SP. Sesami*) Disease in Sesame Varieties

Assefa Abadi Kebede[1*] and Weres Negash Golla[1]

[1]Crop Research Core Process, Humera Agricultural Research Centre, Tigray Agricultural Research Institute, P.O.Box 62, Humera, Ethiopia.

Authors' contributions

This work was carried out in collaboration between both authors. Author AAK designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors WNG managed the analyses of the study and managed the literature searches. Both authors read and approved the final manuscript.

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ABSTRACT

An epidemic of disease is the progress of the disease in time and space. The objectives of the present study are to understand and compare the four nonlinear models for disease progress curves of five sesame varieties. The regression parameters estimation, standard error, R-square, Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC) were estimated. The lowest values of standard error and the highest values of R-square were calculated from the monomolecular model. Also, the result showed that; the disease progress curve better fitted within the monomolecular model for each varieties with the smallest AIC and BIC values. This model is appropriate for modelling epidemics where there is a monocycle within a growing season. The Monomolecular model allows the estimation of the disease progression rate and an area under the disease progress curve was carried out to know the level of reaction to the disease. The lowest rate of fusarium wilt disease was recorded from Hirhir followed by Setit-2. However, the highest value was recorded from Setit-3 followed by Setit-1. A highest value of area under disease progress curve (AUDPC) was calculated from Setit-3. However, the lowest was calculated from Hirhir. Varieties with low disease incidence could be useful in breeding programs aimed at developing varieties with higher resistance to Fusarium wilt disease.

**Corresponding author: Email: asse2008ec@gmail.com;*

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1. INTRODUCTION

Sesame (*Sesamum indicum L.);* belongs to the family Pedaliaceae [1], it is well known for its high-quality oil seed [2]. Sesame is an important source of food worldwide. Nutritionally, it is important as sources of 48-60% oil, 18-23.5% protein and 13.5% carbohydrate [3]. It is extensively cultivated in the tropics and temperate zone of the world [4]. Despite its importance, sesame is affected by soil born disease like, *Fusarium* wilt which is caused by the pathogen *Fusarium oxysporum f. sp. sesami* is one of the most important that infects sesame at all growth stages starting from seedling to maturity, causes sudden death of plants and causing heavy economic losses depending on the severity of infection [5,6]. The pathogen caused vascular wilt and sesame fields infected with *Fusarium* wilt disease exhibits conspicuous patches of dead plants [5]. The fungus produces resting spores called Chlamydospores that are resistant to unfavourable environmental conditions and it can survive on infected crop debris in the soil for about three to six years, with infection reoccurring from seeds or soil [7,8].

In Ethiopia there are a large number of sesame germplasms available. Evaluation of some of the germplasms is important to screen out resistant genotypes against *Fusarium* wilt disease. Disease progress curve and rate over time are the parameters used in determining the resistant level of the sesame genotypes against the disease and plant epidemiologist widely used these parameters to understand an epidemic process. The disease progress is used to correlate the interaction of pathogen, host, and environment in disease development [9]. The dynamic process of plant disease increase in time needs critical analyses for comparison of disease progress curves. Although the plotting of the disease increase in a plant population is expected to give a typically sigmoid curve, such assumption becomes inappropriate in any biological system due to the wide interactions among the broad spectrum of host resistance, pathogen virulence, and the environmental variations.

The disease progress curve is quantified using statistical models to explain how the disease progress over time and most of the plant disease dramatically change after a certain time. Models are commonly used to describe temporal disease epidemics [10]. Development pattern of disease progress curve is well-fitted with nonlinear models [11,12] and these models are commonly used to describe temporal disease epidemics [10]. All models may not fit well to specific disease or a specific model may not fit to all plant disease but, one model may fit better than the other to a particular disease depending on the nature of the disease progress curves. The best fitted model for fusarium wilt disease can be used to estimate the area under the disease progress curve (AUDPC) and disease progress rate for determining the sesame cultivars reaction to the sesame *Fusarium* wilt disease. However, no effort has been reported so far regarding the use of disease progress curve to select the best fitted model for *Fusarium* wilt disease in sesame. Hence, the present study was conducted to identify the goodness of fit of the nonlinear models (exponential, monomolecular, logistic and Gompertz models) to the sesame *Fusarium* wilt (*Fusarium oxysporum f. sp. sesami*) disease.

2. MATERIALS AND METHODS

Description of the study area: The experiment was conducted naturally at areas of a highly wilt prone soil condition by the virulent pathogen during the 2018 main cropping season in western Tigray, Ethiopia. The location is sited at 14° 00' 85'' North latitude and 36° 34' 52'' East longitudes. The research site is characterized by hot to warm temperatures and high evaporation. The elevation of the station in which the experiment was conducted is about 646 meters above sea level. The maximum temperature is 42°C in March-Mayday and the minimum varies from 22.2°C in July to 17.5°C in August. The South westerly monsoon winds bring rainfall to the areas during the summer mainly from June to September.

Experimental materials and treatments: Seeds of sesame cultivars were obtained from Humera Agricultural Research Centre, which were maintained from a crop grown in the previous year. A total of five varieties currently commonly grown in the area were used as experimental material. Four released sesame verities (Setit-1, Setit-2, Setit-3, and Humera-1) and one local variety were used as treatments (Hirhir).

Experimental design and management: The experiment was laid out in a randomized complete block design (RCBD) with three replications. Each treatment was randomly

assigned into a plot area of 14.4 m^2 (3 m row length and 4.8 m width), which consisted of 12 rows of sesame. The spacing between blocks and plots were 2 m and 1 m, respectively. The spacing between plants and rows was 10 cm and 40 cm, respectively. The seed was sown on July 4, 2018 at May-kadra on three time's ploughed plots of land. Each experimental plot were received the same rate of NPS (100 kg/ha) and Urea (50 kg/ha) fertilizers. All NPS and half of the Urea (N) fertilizer were applied during planting and the rest split of Urea was applied 45 days after planting (DAP). Recommended agricultural practices were applied at the proper time as per the local practice of sesame growing.

Disease measurement:

Disease incidence: Disease incidence was recorded by counting the infected plant compared to an initial stand count as proposed by [13]. Infected plants were characterized by yellowing, stunted growth, brown and black sign on the stem, others were wilted, died, and fall on the ground. Disease incidence is the mean percentage of infected plants showing a typical symptom of sesame *Fusarium* wilt disease in the field compared to the total plant units investigated. The percentage of diseases incidence was calculated as follows using the following formula;

> Diseases incidence (DI %) = [(number of wilt infected plants/ Total number of assessed plants) X 100]

Disease incidence was recorded by counting the infected plant compared to initial stand count and the reaction of sesame cultivars against *Fusarium* wilt disease were categorized according to the criteria provided by [13] 1-10%: Resistance, 11-20%: Moderately resistance, 21-30%: Moderately susceptible, 30-50%: Susceptible and 50-100% Highly susceptible).

Disease progress data: *Fusarium* wilt disease incidence at the experimental sites were assessed and noted from the time of disease appearance after planting until the crop attains its physiological maturity. Incidences of disease were assessed five times from the middle rows in each plot at fourteen days interval from the time of disease appearance or twenty-five (25) days after planting until the crop attains its physiological maturity.

Fitting disease progress curves using nonlinear models: There are several nonlinear models that are used to describe the plant disease progress/development such as exponential model, monomolecular model, logistic model, and Gompertz model [14] as described in Table 1.

Model selection using information criteria: Described as the use of data to select one model from the list of competing models to find the best fitting model to the data [15,16]. To identify the best-fitted model, Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC) tests were used due to better performance than R-square as studied by [17], because R-squared shows only how close the data to the fitted regression line. Akaike Information Criterion (AIC) is one of the most common criterion information used to select the best-approximating model to the unknown true data [18] which is calculated by:

$$AIC = 2k - 2\ln(L)$$

With k = number of estimated parameters in the model and ln (L) = maximum log-likelihood of the estimated model and ln (L) was calculated as follows:

$$\ln(L) = 0.5*[-N(\ln(2N)+1-\ln(N)+\ln(\sum(X_1,X_2..X_n)^2]$$

The Bayesian Information Criterion (BIC) on the other hand, is derived within a Bayesian framework as an estimate of the Bayes factor for competing models [19] and is calculated as:

$$BIC = p\ln(n) - 2\ln(L)$$

With p = number of parameters, n = sample size and L = maximum likelihood of the estimated model.

Table 1. Summary of differential and integrated equations for growth curve models in plant disease epidemiology

Model	Disease progress rate equation	y Estimated parameters
Exponential	$dy/dt=r_E y$	y0 is the initial disease intensity. rE, rM, rL and rG are the rate parameter (constant).
Monomolecular	$dy/dt=r_M(1-y)$	
Logistic	$dy/dt=r_L y(1-y)$	
Gompertz	$dy/dt=rG\, y[Ln(1)-Ln(y)]$	

Estimating the area under the disease progress curve: AUDPC has been widely used in plant pathological research especially crop loss assessment and assessment of partial or quantitative resistance [20] which is calculated using the formula given by [14].

$$\textbf{AUDPC} = \sum_{i-1}^{n-1} 0.5(x_{i+1} + x_i)(t_{i+1} - t_i)$$

Xi - Is the incidence percentage of the disease at ith assessment,
ti - Is the time of the ith assessment in days from the first assessment date and
n - Is the total number of disease assessments [9] since incidence is expressed in percentage and time in days, AUDPC is expressed in %-days

Data analysis: Analysis of variance was done for disease parameters (incidence, disease progress rate and area under disease progress curve) using R-software (version 3.6.2.).

3. RESULTS AND DISCUSSION

Disease progress curve: *F. oxysporum* is an abundant and active saprophyte in the soil. It is a common soil born fungus. It survives in the soil debris as a mycelium and all spore types, but is most commonly recovered from the soil as chlamydospores. Sesame fusarium wilt (*Fusarium oxysporum f.sp. sesami*) is one of the most important vascular wilt diseases that cause sudden death of plants and causing heavy economic losses [5,6]. Several sesame cultivars widely grown in sesame cultivated areas do not possess high level of resistance to *Fusarium* wilt disease [5]. The amount of initial inoculum in the soil is the main important factor for sesame *Fusarium* wilt disease epidemics. Growing host resistance crops are the best management options of fusarium oxysporum disease [21,22].

Comparison between non-linear models: The fitted models were identified using the ANOVA test and confidence interval. F-value of the nonlinear Least-Squares Analysis of Variance, parameters estimation, asymptotic standard error and 95% confidence interval for parameters of five sesame varieties on the four models were given in (Table 2). The F-values in all the nonlinear models were significant at a 95% confidence level. This shows all models were fitted-well to the sesame fusarium wilt disease progress curve data.

Estimated parameter is significantly contributed to the fitted nonlinear models by validated that 95% confidence interval results showed that almost all of the estimated parameters are significantly contributed to the fitted nonlinear models at 5% significant level. Besides, the values of R-square and standard error were also revealed (Table 2). The highest value of R-square and the smallest value of standard error were calculated from the monomolecular model as compared to other models.

Observations on different disease progress curves of five tested sesame varieties throughout one season have been well reflected in the figure drawn on average disease progress curves as well as the corresponding linearized line (Fig. 1). The plot fitted nonlinear models to the disease incidence observations in each variety showed that the monomolecular model fitted well to the data compared to another three nonlinear models (Fig. 1). The monomolecular model was better fitted to the data as cross lines to the actual observations data (Fig. 1).

In addition, the monomolecular model was best fitted for the disease progression from the rest of models when tested with the two tests (Akaike Information Criterion and the Bayesian Information Criterion) for each of the sesame varieties. The current result was similar with Chang, et al. [23] who reported that Gompertz models better fitted for cocoa black disease with the smallest AIC and BIC values. According to who Hughes, [24] justified that monomolecular model was appropriate for modelling epidemics where there is no secondary spread during a single cycle on the growing season.

Sesame *Fusarium* wilt disease is among monocyclic/simple interest disease. This pathogen was the cause primary infection because their life cycle requires at least one season to complete. The diseases have a maximum of one generation per growing season and possess a characteristic disease progress curve. The monocyclic disease is a simple interest disease that initial inoculum, rate and time have equal weight in their effect on incidence of disease [14,24]. A reduction in the initial inoculum or the rate of infection will result in a reduction in the level of disease by the same proportion at any time, throughout the epidemic. One can think of monocyclic epidemics as consisting of only primary infections.

Table 2. Estimation, asymptote standard error and 95% confidence interval of four nonlinear models fitted at five different sesame varieties on *Fusarium* wilt disease incidence

Models	Parameter estimation		SE_b	R^2	Confidence interval (95%)	
	a	b		(%)	Lower boundary	Upper boundary
Hirhir						
Monomolecular	0.002	0.084**	0.037	0.99	-0.028	0.197
Logistic	-5.825	-2.494*	0.448	0.92	-2.896	-2.091
Gompertz	-1.762	-0.938**	0.165	0.97	-1.147	-0.729
Exponential	-5.828	-2.578**	0.41	0.88	-2.898	-2.258
Humera-1						
Monomolecular	0.032	0.533**	0.121	0.99	0.42	0.646
Logistic	-3.448	-0.367**	0.297	0.91	-0.769	0.035
Gompertz	-1.243	0.117**	0.196	0.97	-0.091	0.326
Exponential	-3.481	-0.9**	0.176	0.85	-1.22	-0.58
Setit-1						
Monomolecular	0.058	0.621**	0.068	0.99	0.508	0.734
Logistic	-2.964	-0.152**	0.148	0.93	-0.554	0.25
Gompertz	-1.087	0.259**	0.103	0.97	0.05	0.468
Exponential	-3.022	-0.774**	0.08	0.89	-1.094	-0.453
Setit-2						
Monomolecular	0.008	0.268**	0.058	0.98	0.155	0.381
Logistic	-5.03	-1.195**	0.263	0.88	-1.598	-0.793
Gompertz	-1.607	-0.375**	0.136	0.95	-0.583	-0.166
Exponential	-5.038	-1.464**	0.205	0.86	-1.784	-1.144
Setit-3						
Monomolecular	0.049	0.882**	0.078	0.99	0.77	0.995
Logistic	-2.993	0.346**	0.134	0.91	-0.055	0.7492
Gompertz	-1.112	0.6269**	0.103	0.97	0.417	0.835
Exponential	-3.042	-0.536**	0.055	0.85	-0.856	-0.216

a: initial inoculum; b; Final inoculum; R2: R-square; Su_bstandard error of final inoculum

Table 3. *Fusarium* wilt disease progress curve fitted with four different nonlinear models on five sesame varieties

Verities	Model	ACI	BIC
Hirhir	Monomolecular	-78.9704	-75.4302
	Logistic	-5.339023	-8.879275
	Gompertz	-36.1559	-32.6156
	Exponential	-3.698045	-7.238296
Humera-1	Monomolecular	-41.7921	-38.2519
	Logistic	-1.08074	-2.459508
	Gompertz	-20.795	-17.2548
	Exponential	-7.53489	-3.99464
Setit-1	Monomolecular	-54.5555	-51.0153
	Logistic	-5.942076	-9.482327
	Gompertz	-17.0536	-13.5134
	Exponential	-3.644155	-7.184406
Setit-2	Monomolecular	-64.1013	-60.5611
	Logistic	-12.00554	-15.54579
	Gompertz	-29.9824	-26.4421
	Exponential	-10.80257	-14.34282
Setit-3	Monomolecular	-48.3658	-44.8255
	Logistic	-17.8574	-14.3172
	Gompertz	-35.6936	-32.1533
	Exponential	-28.6671	-25.1269

AIC: Akaike Information Criterion, BIC: Bayesian Information Criterion

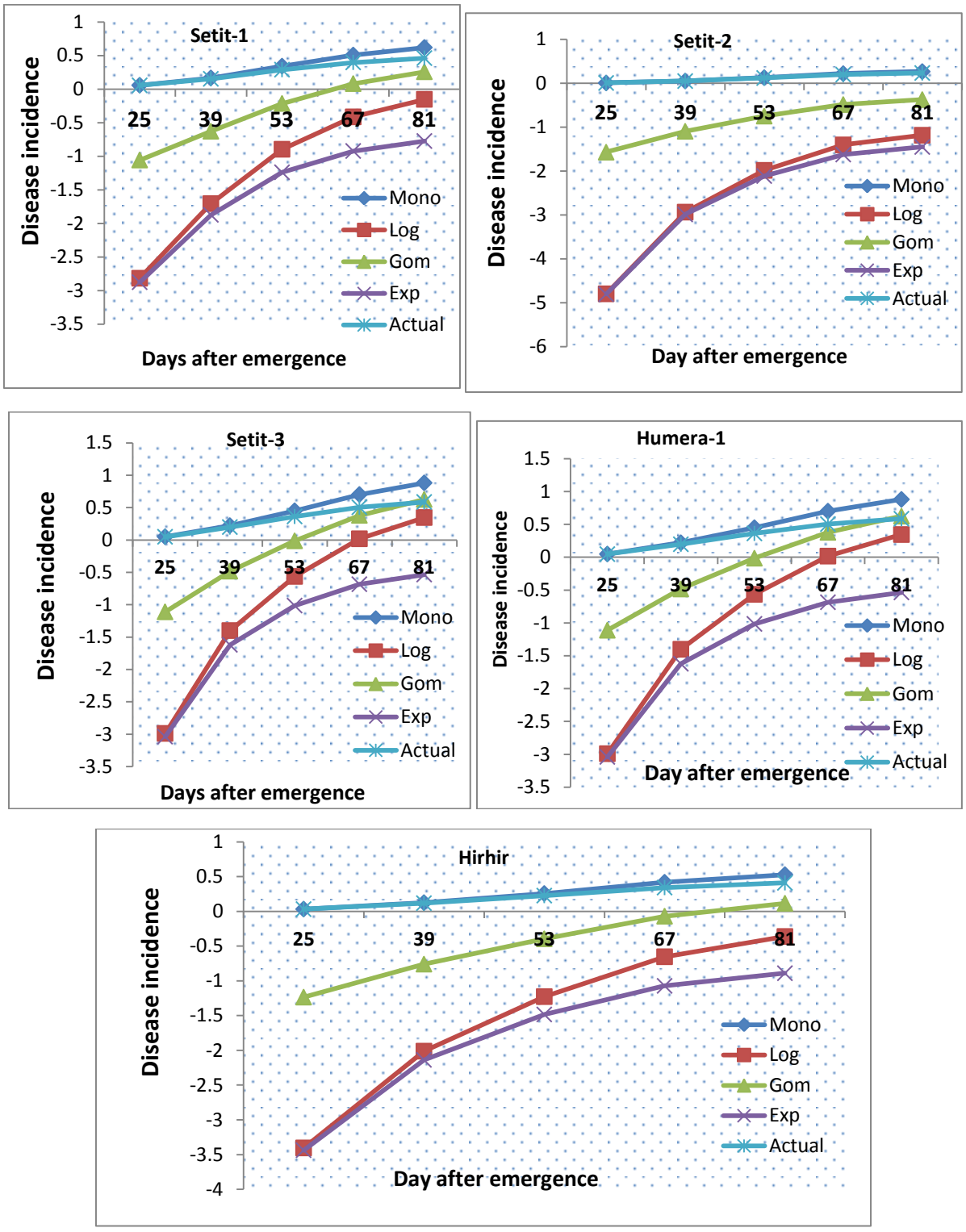

Fig. 1. Disease progress curve for the incidence of *Fusarium* wilt disease on different sesame varieties

Mono: Monomolecular; Log: logistic; Gom: Gompertz; Exp: Exponential

Disease progress rate of sesame *Fusarium* wilt disease: Monomolecular model was well-fitted for the disease progress of each sesame cultivar and hence, disease progress rate was obtained by regressing the wilt incidence overtime after data was fitted to the

Table 4. Disease progress rate of *Fusarium* wilt disease on sesame varieties

Varieties	Disease progress rate unit/day			
	25-39 DAE	40-53 DAE	54 – 67 DAE	68-81 DAE
Set-1	0.00698	0.009779	0.007757	0.004573
Set-2	0.003023	0.00505	0.005464	0.002656
Set-3	0.010758	0.011846	0.01018	0.00582
Humera-1	0.006148	0.007799	0.008285	0.004888
Hirhir	0.000354	0.002151	0.002138	0.000897

DAE: Date after emergence

Table 5. AUDPC of *Fusarium* wilts disease on sesame varieties

Varieties	AUDPC (%-day)	Incidence (%)	Varietal reaction
Set-1	1146.46	46.2148	S
Set-2	467.302	23.4409	MS
Set-3	1577.32	58.5593	HS
Humera-1	930.925	41.0474	S
Hirhir	140.569	8.0433	R

HS: Highly susceptible, MS: Moderately susceptible, R: Resistance, S: susceptible

monomolecular model. The highest disease progress rate was calculated from the variety Setit-3 at all dates of assessment followed by Setit-1. However, the lowest disease progress rate was calculated from Hirhir followed by Setit-2 (Table 4). The disease progress rate is an important epidemiological parameter to evaluate the efficacy of wilt management options. The present finding is in line with Yimer, et al. [25] who reported that disease progression in a screening of resistances chickpea genotype to *Fusarium* wilt disease, while using disease progress rate for evaluation of genotypes.

Area under disease progress curve (AUDPC): The highest AUDPC value was recorded from variety Setit-3 (1577.32%-day). However, the lowest value was recorded from the local cultivar Hirhir (140.569%-day) (Table 5). This result indicated that the lowest disease epidemic was calculated from Hirhir cultivar. This might be due to the fact the variety posse a resistance gene (R) to *Fusarium* wilt disease. Because, once *Fusarium* wilt is established in the area, the use of resistant varieties is the most effective means to manage this disease. Besides, Gordon, [26]; El-Shazly, et al. [27]; Kavak and Boydak, [28] indicated that planting resistant varieties, using clean seeds, cleaning of infected crop residue and removing infected plant tissue to prevent overwintering of the disease, could help to reduce the prevalence of the disease. In addition, Ploetz, [21,22] reported that the use of resistant cultivars as the main effective measure to manage diseases caused by *Fusarium oxysporum*. Immunity or total resistance is often unobtainable and many varieties differ on resistance level, allowing the plant to grow despite some disease development.

4. CONCLUSION

Modelling is used to know about the behaviour of a disease in a population. In this study, the monomolecular model was well fitted to the disease progress curve of sesame *Fusarium* wilt disease for the sesame varieties due to the lowest value of standard error, Akaike Information Criterion (AIC) and the Bayesian Information Criterion (BIC) values as well as highest values of R-squared values scored than other models. Using the well fitted model; disease progress rate and area under disease progress curve were calculated and compared for the sesame varieties against *Fusarium* wilt disease. The lowest rate of sesame *Fusarium* wilt disease and AUDPC values were computed from the local variety Hirhir while the highest disease progress rate and AUDPC values were obtained from variety Setit-3. Cultivars with low disease incidence could be useful in breeding programs aimed at developing varieties with higher resistance to *Fusarium* wilt disease. Finally, monomolecular model is appropriate and well fitted for sesame fusarium wilt (*Fusarium oxysporum f. sp. sesami*) disease than the other models.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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