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GENETIC STUDIES ON THE INHERITANCE AND BIOCHEMICAL COMPONENTS OF LEAF WEBBER RESISTANCE IN SESAME (*Sesamum indicum* L.)

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ABSTRACT

The present investigation was carried out in the campus farm, Department of Agriculture, Kalasalingam Academy of Research and Education, Krishnan koil, Tamil Nadu-626126, India. The inheritance of resistance to Leaf webber in sesame was investigated through crosses between a resistant variety, TMV 3 and two susceptible genotypes, Theni local and Tenkasi local. The F_2 populations of the two crosses (Theni local $\times$ TMV 3 and Tenkasi local $\times$ TMV 3), along with their respective parents, were evaluated for Leaf webber resistance under natural field conditions. Infector rows of the highly susceptible variety GT-1 were used to ensure uniform disease pressure. Resistance screening was performed on individual plants using the standardized Leaf webber scoring system developed by Alice and Nadarajan. The segregation pattern observed in the F_2 generation of both crosses fit a 3:1 ratio (susceptible:resistant), as confirmed by the chi-square test for goodness of fit. This inheritance pattern indicates that resistance to Leaf webber in sesame is governed by a single recessive gene. The results provide valuable insights for breeding programs aimed at developing Leaf webber-resistant sesame cultivars through simple Mendelian selection.

Key words : Inheritance, Leaf webber, Pest resistance and Genetics.

Introduction

The sesame leaf webber, or *Antigastra catalaunalis* (Lepidoptera: Crambidae), is a significant and unique pest of sesame that can cause a 72% reduction in productivity. The low yield of sesame damage caused by insect pests can be attributed to a number of fundamental causes. Leaf webbers are one of the 67 insect pests that harm sesame crops and their damage is most noticeable during the start of flowers and the creation of capsules. Sesame local variations are gathered from various geographical areas (Boopathi *et al.*, 2023 and Omprakash *et al.*, 2024).

Criteria like leaf damage, webbing, larval mortality, and antibiosis are used to assess resistance. To find cultivars with notable resistance to the parasite, data was gathered. In local sesame cultivars, leaf webber resistance is a complicated, multigenic characteristic. Several

quantitative trait loci (QTLs) linked to resistance have been found using segregation and linkage analysis (Panday *et al.*, 2021 and Praveen *et al.*, 2024). The inheritance of leaf webber resistance has been explained by the additive-dominance model and the epistatic model. Breeding implications include genomic selection, marker-assisted selection, and selection for resistance utilising phenotypic and genotypic markers. To create cultivars with long-lasting resistance to leaf webber, future research avenues include genomic selection, fine mapping of QTLs, and pyramiding resistance genes (Karuppaiah *et al.*, 2013; Matina *et al.*, 2016; Manikandan *et al.*, 2022).

Materials and Methods

In the summer of 2024, the current study was carried out at the Department of Agriculture's Agriculture Farm in Krishnankovil, KSAH, KARE. Tamil Nadu. During

the summer, when insect vectors were most prevalent, 50 genotypes of sesame were tested for resistance to leaf webber disease using infector rows of extremely sensitive variety. The experiment's randomised complete block design included three replications.

The highly susceptible variety GT-1 was grown as border rows surrounding the experimental plots and as an infector row following every two rows of the genotype in order to provide a high pressure of leaf webber in the field. The agronomic guidelines unique to each crop were adhered to. Insecticides were not used to the field during the agricultural season to maintain a high enough population of whiteflies to promote the spread of viruses.

The crossing program's parents were selected from this experiment based on their high yield, genetic diversity studies, and field-tested insect resistance. Given its shown resistance to leaf webber and higher yield, the genotype TMV 3 was selected as the resistant parent for crossing. The two Leaf webber susceptible genotypes, Tenkasi local and Theni local, were selected as susceptible parents for the crossover program. Theni local is a local variety of the plant with lengthy pods and robust seeds that yield a lot. However, it is difficult to grow in Tamil Nadu because it is extremely vulnerable to the leaf webber. In the field, a local variety known as Tenkasi local shows a moderate amount of leaf webber susceptibility. The current study was carried out to improve these varieties and gain a better understanding of the genetics of resistance to leaf webber.

TVM 3, a resistant variety, was used as a pollen parent, while Theni local and Tenkasi local, two susceptible parents, and were used as female parents. In order to facilitate coordinated flowering throughout the crossover procedure, parents were seeded in batches at seven-day intervals. The parents (Tenkasi local $\times$ TMV 3 and Theni local $\times$ AVT-8) were crossed in an effort to combine resistant and vulnerable features. Morning pollination was followed by evening emasculation throughout the crossover program.

The two crosses' three parents and F₂ plants were all examined in the field for yellow mosaic disease science. The F₂ generation was bred from the molecularly confirmed F₁ plants. Using infector rows of susceptible variety GT-1, the two crossings' F₂ populations were then analysed alongside the parents in the same area, which is a disease hotspot. The field screening for TMV3 resistance took place during the summer.

The plants were separated by 30 cm $\times$ 10 cm. After every two rows of F₂ plants, two rows of the TMV3 sensitive variety GT-1 were cultivated as an infector row

to boost the quantity of virus inoculums in the field. During the trial, no insecticide spraying was done to maintain the insect vector population in the field.

We continually monitored the plants for whitefly activity and any indications of the Leaf Webber disease. Leaf webber resistance was assessed when disease signs were present in 90% of the infector rows. Each individual F₂ plant in each cross was evaluated for disease reactivity to Leaf webber using the standard 1–9 disease grading system by Alice and Nadarajan¹. Table 1 displays the findings. Leaf webber ratings, which varied from 0 to 4, were used to classify plants into resistant and vulnerable groups. The chi-square test was employed to evaluate how well the observed segregation fit the Mendelian segregation ratio for Leaf webber reactivity in the F₂ populations of both crosses.

Biochemical studies

To determine the biochemical basis of resistance in sesame to leaf webber, biochemical components were studied in the unprotected crop. Total proteins, total sugars and total phenols content were estimated in the leaf samples at 35 days after sowing. The procedures used for estimation of different biochemical components are as follows.

Estimation of total protein

The per cent total protein was estimated as per the procedure described by Jackson (1965).

Percentage of total protein in the given sample = % N $\times$ 6.25

Estimation of phenol

- Half a gram of the leaf sample was taken and ground with pestle and mortar in 10 times volume of 80 per cent ethanol.
- The homogenate was centrifuged at 10,000 rpm for 20 minutes, and the supernatant was saved. Reextracted the residue with 5 times the volume of 80 per cent ethanol centrifuged and pooled the supernatants.
- Evaporated the supernatant to dryness.
- Dissolved the residue in known (5 ml) volume of distilled water.
- Pipetted different aliquots (0.2 to 2 ml) into test tubes.
- Made the volume in each tube to 3ml with water.
- 0.5 ml of Folin-ciocalteu reagent was added.
- After 3 minutes, 2 ml of Na₂CO₃ solution was added to each tube.

- The contents were mixed thoroughly, the tubes were placed in boiling water exactly for one minute, cooled and the absorbance was measured at 650 nm against a reagent blank.
- The standard curve was prepared using different concentrations of catechol, the concentration of phenols was found in the test samples and expressed as μg phenols/ one gram material.

Estimation of reducing sugars

- One hundred milligrams of leaf sample was taken and the sugar was extracted with hot 80 per cent ethanol twice (5 ml each time).
- The supernatant was collected and evaporated by keeping it on a water bath at 80°C.
- Ten millilitres of water was added to dissolve the sugar.
- Then, 0.5 to 3 ml of the extract was pipetted out in test tubes and the volume made up to 3 ml with water in all tubes.
- 3 ml of 3,5-Dinitrosalicylic acid (DNS) reagent was added.
- The contents were heated in a boiling water bath for 5 min.
- When the contents of the tubes were still warm, 1 ml of 40 per cent Rochelle salt solution was added.
- Samples were cooled and the intensity of dark red colour was read at 510 nm.
- A series of standards were run using glucose (0 to 500 μg) and the graph was plotted.
- The amount of total sugars present in the sample was then calculated using the standard graph.

Results and Discussion

Theni local $\times$ TMV 3 and Tenkasi local $\times$ TMV 3 crosses were screened for field resistance against yellow mosaic disease in order to determine the inheritance pattern of leaf webber resistance in green gramme. The results are shown in Tables 2 and 3. The Chi-square test results are shown in Table 4, which validated the Mendelian F_2 segregation ratio's goodness of fit in these populations. The leaf webber resistance gene is recessive, as evidenced by the fact that all of the F_1 plants in both crosses were susceptible to the disease. Similar findings were published by Ubor *et al.* (2015), Hika *et al.* (2015), Teklu *et al.* (2022).

The Tenkasi local $\times$ TMV 3 cross produced 272 plants in its F_2 generation, of which 204 were sensitive and 68

Table 1 : Grading method for evaluation of sesame genotypes against leaf webber.

Cumulative score	Grade	Degree of resistant
0-1	1	Highly resistant
1-2	3	Resistant
2-3	5	Moderately resistant
3-5	7	Susceptive
5-9	9	Highly susceptible

Table 2 : The leaf webber reaction of F_2 Population of the cross, Theni local $\times$ TMV3.

Leaf webber reaction	No. of plants		Classification
Highly Susceptible	58	207	Susceptible
Susceptible	96		
Moderately susceptible	53		
Moderately resistant	10	61	Resistant
Resistant	51		

Table 3 : The Leaf webber reaction of F_2 Population of the cross, Tenkasi local $\times$ TMV3.

Leaf webber reaction	No. of plants		Classification
Highly susceptible	40	148	Susceptible
Susceptible	74		
Moderately susceptible	34		
Moderately resistant	16	52	Resistant
Resistant	36		

were resistant. Of the 192 F_2 plants generated by the Theni local $\times$ TMV 3 cross, 48 were resistant to leaf webber and 144 were sensitive. The results were published by Karuppaiah *et al.* (2013), Matina *et al.* (2016), Manikandan *et al.* (2022). Using these observed values for leaf webber resistance, the Chi-square test was used to evaluate the good-ness of match for the Mendelian segregating ratio of 3:1 (susceptible: resistance). The computed values were not significant at one degree of freedom in both crossings at the 5% and 1% levels of significance (Patidar *et al.*, 2020; Khuimphukhio *et al.*, 2020; Teklu *et al.*, 2021).

This suggests that the observed F_2 segregation ratios do not significantly deviate from the 3:1 Mendelian monogenic cross ratios. This implies that the resistance to leaf webber in both crossings is controlled by a monogenic recessive gene. Several researchers have also documented the green gram's monogenic recessive inheritance for leaf webber resistance. Similar findings were reported by El-Bramawy *et al.* (2006), Divya *et al.* (2018), Mudhalvan *et al.* (2024).

Table 4 : Mean values of biochemical components in selected F_2 segregants among two different crosses relative to leaf webber infestation.

Jassid injury grade	Total sugars (mg/g)	Total phenols (mg/g)	Total proteins (%)
Cross I			
1	2.240	3.410	10.270
2	2.440	2.890	12.260
3	3.590	2.450	15.860
4	3.930	1.910	17.30
Mean	3.050	2.670	13.920
SE$\pm$	0.420	0.320	1.610
Cross II			
1	2.030	3.420	12.060
2	2.910	2.910	13.020
3	2.940	2.250	13.800
4	3.80	1.630	17.430
Mean	2.920	2.550	14.080
SE$\pm$	0.360	0.390	1.170
Check-1	3.240	0.370	23.530
Check-2	2.810	2.650	13.240

Cross I – Thenkasi local $\times$ TVM 3Cross II – Theni local $\times$ TVM 3

The most crucial stage in creating leaf webber-resistant genotypes is screening them for resistance. Patidar *et al.* (2020), Khumiphukhieo *et al.* (2020), Teklu *et al.* (2021) are among the numerous writers who have previously documented screening sesame for leaf webber resistance in natural field conditions. Although, several researchers employed various disease grading measures, Alice and Nadarajan (2007) suggested a 1–9 scale and grouping for the current investigation (Table 1). The Tenkasi local $\times$ TMV 3 cross produced 272 plants in its F_2 generation, of which 204 were sensitive and 68 were resistant. 48 plants in the Theni local $\times$ TMV 3 hybrid

showed resistance to leaf webber, whilst 192 F_2 plants showed vulnerability. The results were published by Singh *et al.* (2007), Ubor *et al.* (2015), Hika *et al.* (2015), Teklu *et al.* (2022), Rao *et al.* (2012) and Mudhalvan *et al.* (2024).

Correlation of biochemical components responsible for leaf webber resistance in sesame

The reducing sugars were positively and significantly correlated with leaf webber injury grade and leaf webber population in F_2 generation of all the four crosses. This is in accordance with the reports of Karuppaiah *et al.* (2013), Matina *et al.* (2016) and Manikandan *et al.* (2022). The phenols content was negatively correlated with leaf webber injury grade and jassids population. Similar results were obtained by Ubor *et al.* (2015), Hika *et al.* (2015) and Teklu *et al.* (2022).

The crude protein was positively correlated with leaf webber injury grade and leaf webber population in all the four crosses except with leaf webber population in Cross II. Similar kind of association was observed by Singh *et al.* (2007), Ubor *et al.* (2015), Hika *et al.* (2015), Teklu *et al.* (2022), Rao *et al.* (2012) and Mudhalvan *et al.* (2024). Crude protein was negatively associated with phenol and gossypol contents in all the four crosses.

The total protein content was negatively significantly correlated with injury grade and jassids population in all the four crosses except with leaf webber population in Crosses I and II. Similar kind of association was reported by the Teklu *et al.* (2022), Rao *et al.* (2012) and Mudhalvan *et al.* (2024) (Table 4).

Inheritance pattern of Leaf Webber resistance in sesame

Parents selected for the present study differed significantly for Leaf Webber infection. The compact parent Tenkasi local and Theni local had good yield with susceptible type. The parent TVM 3 were resistant to Leaf Webber, but had low yield. All the selected parents were true breeding for the Leaf Webber reaction.

Table 5 : Segregation pattern for reaction to leaf webber in F_2 generation of the four crosses.

Cross	Number	Reaction to leaf webber			Ratio	Chi-square value	P
	F ₂						
Cross I		Resistant	Susceptible	Total	3:1	0.645	0.75-0.5
	Observed	182.00	68.00	250			
	Expected	187.50	62.50				
Cross II		Resistant	Susceptible	Total	3:1	1.541	0.5-0.25
	Observed	179.00	71.00	250			
	Expected	187.50	62.50				

When the highly jassid resistant parent TVM 3 was crossed with the compact parent Tenkasi local (Tenkasi local $\times$ TVM 3) the frequency distribution in the F_2 population indicated a clear grouping into two distinct classes having a good fit for the 3:1, resistant to susceptible, segregating ratio.

In the cross between the compact parent Theni local and the jassid resistant parent TVM 3 (Theni local $\times$ TVM 3), the frequency distribution in the F_2 population was again separate into groups as resistant and susceptible types in the 3: 1 segregation ratio.

In both the above crosses the 3:1 ratio suggested dominant genes with epistatic gene action responsible for the expression of resistant-to- leaf webber phenotype in sesame. Similar results were reported by Hika *et al.* (2015), Teklu *et al.* (2022), Rao *et al.* (2012) and Mudhalvan *et al.* (2024).

In both these crosses, a single gene difference between the parents existed indicating monogenic control of leaf webber resistance. These results were in conformity with the report of Singh *et al.* (2007), Ubor *et al.* (2015) and Hika *et al.* (2015) in sesame (Table 5).

Hence, from the present study, it can be said that leaf webber resistance in sesame is controlled by dominant gene action making it easier to produce leaf webber resistant genotypes in sesame by simple breeding strategies.

Conclusion

Sesamum is an excellent source of oil, proteins, minerals, and dietary fiber. Leaf webber is one of the most destructive pest in Sesamum. The most effective and cheapest method to manage this pest is the cultivation of Leaf webber-resistant Sesamum varieties. Understanding the nature of inheritance is essential for breeding resistant varieties. The present study was done to study the inheritance of Leaf webber resistance in Sesamum from the two crosses Tenkasi local $\times$ TMV 3 and Theni local $\times$ TMV 3. Using infector rows of the Leaf webber-susceptible variety, we screened the F_2 populations of both crosses for Leaf webber resistance in the field during the summer 2024. The F_2 population of both crosses segregated in a ratio of 3:1 (susceptible: resistant), indicating that a single recessive gene was involved in imparting resistance against Leaf webber in seasmum.

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