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Biochemical Characters of Selected Sesame Genotypes in Relation to Phyllody Disease Caused by Phytoplasma

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

An experiment was conducted at Department of Entomology, Sri Venkateswara Agricultural College, Tirupati during two consecutive seasons *i.e*., *rabi* 2019-20 and *rabi* 2020-21 to estimate the biochemical parameters such as phenols, proteins, amino acids, reducing sugars and chlorophyll in selected sesame genotypes showing field resistance to phyllody incidence. The experimental results revealed that proteins, total amino acids and total reducing sugars were found to be higher

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in susceptible genotypes (YLM 66 and Gowri) when compared to resistant genotypes (IC 203871 and EC 377002-2), whereas, phenols and total chlorophyll content were found to be higher in resistant genotypes than susceptible genotypes during *rabi,* 2019-20 and 2020-21. The correlation studies from both the seasons revealed a significant positive correlation between proteins (0.956 and 0.908 during 2019-20 and 2020-21, respectively), amino acids(0.967 and 0.924 during 2019-20 and 2020-21, respectively), reducing sugars (0.969 and 0.931 during 2019-20 and 2020-21, respectively)and per cent phyllody incidence and a significant negative correlation between chlorophyll content (-0.763 and -0.881 during 2019-20 and 2020-21, respectively), total phenols (-0.919 and -0.967 during 2019-20 and 2020-21, respectively)and per cent phyllody incidence. The genotypes exhibiting resistance to phyllody incidence complementing the biochemical characters can be used in further breeding programmes for development of resistant sesame varieties against phyllody disease.

Keywords: Sesame phyllody; phenols; proteins; amino acids; reducing sugars.

1. INTRODUCTION

Sesame (*Sesamum indicum* L.) popularly known as gingelly is an important ancient oilseed crop belonging to the family Pedaliaceae and probably the first oilseed crop used by human civilization. World production of sesame is nearly six million tones, with Sudan, Myanmar and India as the largest producers. India holds first place in world with nearly an area of 19.47 lakh ha and production of 8.66 lakh tones and productivity of 413 kg ha^{-1} (Evangilin *et al.*, 2020). In Andhra Pradesh, it is cultivated in an area of 0.39 lakh ha with an annual production of 0.14 lakh tones and an average yield of 343 kg ha^{-1} (AP Agricultural Statistics, 2019-20). The forecasted area, production and productivity of sesame in AP was estimated to be 51.66 thousand ha, 17.64 thousand tonnes and 323.43 kg ha^{-1}, respectively for the year 2020-21 (Evangilin *et al.,* 2020). Pests and diseases areone of the major constraints in causing considerable decline in yield in terms of both quality and quantity. The pest attack causes a heavy seed yield loss of about 25 to 90% (Ahuja and Kalyan, 2002, Gogi *et al.*, 2010).

Phyllody is one among the various biotic stresses causing considerable yield loss in sesame. Phyllody caused by *Phytoplasma* causes floral transformation, abnormal proliferation of shoots, stunted growth and reduced yield with poor seed quality. Host plant resistance is one of the important components needed to be employed in combating the yield losses caused due to insect pests. Induced resistance can be observed in plants due to temperature variations, soil chemicals, photoperiod induce production of plant secondary metabolites, which in turn affect the plant nutritional quality. The defensive strategies employed by the plants against insect attack may involve synthesis of many of biologically active compounds (Mithofer and Boland, 2012). Plants generally show greater variation in biochemical traits which play a major role in influencing the preference and non-preference behavior of insects. Upon attack by insects, plants presumed to generate signals that trigger differential expression of proteins, free amino acids and phenolic compounds. Host plants containing antibiosis mechanisms of resistance such asflavanoids, phenols *etc*. may result in reduction of survival rate of feeding insects, prolonged development time and also reduction in size of insects (Gogoi *et al.*, 2010). Hence, such defensive mechanisms conferring resistance to the plants against insect attack can be widely utilized in pest management and breeding programmes. Considering the prospective, the present investigation was carried out to know the biochemical basis of resistance in sesame genotypes showing field resistance against phyllody incidence.

2. MATERIALS AND METHODS

The sesame genotypes identified as resistant/susceptible under field screening experiment during *kharif*, 2019-20 and 2020-21 were assessed in the present investigation to know the biochemical basis of preference of leafhoppers to different genotypes. The experiment was taken up during the maximum vegetative period of the crop in two consecutive years *viz.*, 2019-20 and 2020-21. The fresh and healthy leaf samples at flowering stage were collected and brought to the laboratory of Department of Entomology for conductance of biochemical analysis. Standard protocols were followed for the estimation of phenols, proteins, reducing sugars, amino acids and chlorophyll content.

(i) Estimation of Phenols: The phenol content in the leaves of selected sesame varieties were estimated as per the method presented by Malick and Singh (1980). Phenols react with phosphomolybdic acid in Folin-ciocalteau reagent in alkaline medium and produce a blue coloured complex (Molybdenum blue) in alkaline medium.

From each leaf sample 0.5 g of leaf material was weighed and ground in a pestle and mortar, to which 10 times volume of 80 per cent ethanol was added. The homogenate was centrifuged at 10,000 rpm for 20 min. The supernatant was collected and residue was re-extracted with five times the volume of 80 per cent ethanol, centrifuged and the supernatants were pooled and evaporated to dryness. The dry residue was dissolved in 5 ml of distilled water and different aliquots of 0.2 to 2.0 ml were pipetted to test tubes, and the volume in each tube was made to 3 ml by adding distilled water. To this mixture, 0.5 ml of Folin-ciocalteau reagent was added. After 3 min, 1 ml of 20.0 per cent sodium carbonate solution was added to each tube. The material was mixed thoroughly and tubes were placed in boiling water exactly for 1 min. The tubes were cooled and the absorbance was measured at 650 nm against a reagent blank in Shimadzu UV Spectrophotometer. The standard curve was prepared by using different concentrations of catechol.

(ii) Estimation of Proteins: Estimation of protein content in the leaves of selected sesame genotypes was done as per the method developed by Lowry *et al.* (1951). The blue colour developed by the reduction of the Phosphomolybdic-Phosphotungstic components in the Folin-Ciocalteau reagent by the amino acids Tyrosine and Tryptophan present in the protein plus the colour developed by the Biuret reaction of the protein with the Alkaline cupric tartarate were measured inthe Lowry's method.

A sample of 0.5 g was weighed and ground in pestle and mortar with 5 ml of 10 per cent trichloro acetic acid (TCA). The ground material was washed with 5 ml of cold TCA and kept in ice for 15 min. The material was centrifuged at 3500 rpm for 15 min. The supernatant was discarded and the precipitate was dissolved in 4 ml of 2 N NaOH. It was allowed to stand for overnight. Then the solution was centrifuged and supernatant was collected and finally the aliquot was made upto 10 ml. From this aliquot, 0.1 ml of sample extract was pipetted out, to which 5 ml of reagent-C was added. The contents were mixed well and allowed to stand for 10 min. To this mixture, 0.5 ml of reagent-D was added, mixed well and incubated for 30 min at room temperature in dark. The colour intensity was read at 660 nm in Shimadzu UV Spectrophotometer.

(iii) Estimation of reducing sugars: Estimation of reducing sugars in the leaf samples of selected sesame genotypes was done as per the method given by Miller (1972). Reducing sugars have the property to reduce many of the reagents. One such reagent is 3,5-dinitrosalicylic acid (DNS). 3,5-DNS in alkaline solution is reduced to 3 amino 5 nitro salicylic acid and develops orange color.

About 100 mg of the sample and sugars were extracted with hot 80% alcohol twice (5 ml each time). The collected supernatant was evaporated on water bath followed by the addition of 10 ml of water to dissolve the sugars. 0.5 to 3 ml of the extract was pipetted out in test tubes and equalized the volume to 3 ml with water in all the test tubes. 3 ml of Dinitro Salicylic acid reagent was added and the contents were placed in a boiling water bath for 5 minutes. When the contents of the tubes were still warm, 1ml of 40% Rochelle salt solution was added and then Cooled. The intensity of dark red colour was read at 510 nm. A series of standards using glucose (0 to 500 µg) were run simultaneously.

(iv) Estimation of free amino acids: The extraction and estimation of free amino acids from leaves of selected sesame genotypes was done according to Moore and Stein (1948). Ninhydrin, a powerful oxidizing agent, decarboxylates the alpha-amino acids and yields an intensely coloured bluish purple product.

About 0.5 g of plant material was made into small bits and immediately plunged into a container having 80 per cent ethanol. It was refluxed for 30 minutes over a boiling water bath for complete extraction of alcohol soluble compounds. The boiled material was ground in a mortar using additional volume of 80 per cent ethanol and centrifuged. The supernatant was collected and made up to known volume and used for the estimation of total amino acids. To 1.0 ml of sample, 1.0 ml of ninhydrin reagent was added and then aluminum foils were placed on each of the test tube to avoid evaporation. The contents of the tubes were kept in boiling water bath for 20 minutes and 5.0 ml of diluent (equal volumes of water and n-propanol) solution was added after incubation. Blank was maintained with distilled water. The tubes were cooled under running tap water and the contents were mixed thoroughly such that stable purple colour was observed. The absorbance of the colour was read at 570 nm in a spectrophotometer against reagent blank.

(v) Chlorophyll content: Chlorophyll content was measured with chlorophyll meter of Minolta (model SPAD 502). SPAD chlorophyll meter readings (SCMR) were recorded on 3rd leaf from top of each representative plant, between 8.00 AM to 11.00 AM. Five plants were randomly selected and the average data on chlorophyll content was recorded as SCMR units.

3. RESULTS AND DISCUSSION

(i) First season – *rabi*, 2019-20: The results pertaining to biochemical components studied during 2019-20 were presented in Table 1. The total phenol content estimated in selected sesame genotypes during *rabi*, 2019-20 varied from 1084.77 to 3238.08 µg g^{-1} of leaf with a mean value of 2113.31 µg g^{-1} of leaf. The highest phenol content was noticed in resistant genotypes, which recorded less incidence of phyllody disease. The susceptible genotypes Gowri (1084.77 µg g^{-1} of leaf) and YLM 66 (844.18 µg g^{-1} of leaf) recorded lowest amount of total phenols when compared to resistant genotypes identified namely IC 203871 (2882.31 µg g^{-1} of leaf) and EC 377002-2 (3238.08 µg g^{-1} of leaf). All the genotypes were found statistically significant with respect to phenol content. The descending order of phenol content in the categories studied was resistant (IC 203871, EC 377002-2) > moderately resistant (YLM 141, IC 204132) > moderately susceptible (IC 205470, IC 567285) > highly susceptible genotypes (Gowri and YLM 66).

Estimation of protein content in selected sesame genotypes during *rabi,* 2019-20 revealed that the quantity of proteins was in the array of 106.23 to 260.13 µg g^{-1} of leaf with an average protein content of 177.06 µg g^{-1} per leaf. Greater amounts of proteins were observed in highly susceptible genotypes namely Gowri (260.13 µg g^{-1} of leaf) and YLM 66 (215.47 µg g^{-1} of leaf).

The lower levels of protein content were found in identified resistant genotypes, IC 203871 (106.23 µg g^{-1} of leaf) and EC 377002-2 (132.33 µg g^{-1} of leaf). The decreasing order of protein content was highly susceptible genotypes (Gowri and YLM 66) > moderately susceptible (IC 205470, IC 567285) > moderately resistant (YLM 141, IC 204132) > resistant (IC 203871, EC 377002-2). The results proved that the genotypes show statistical differences with regard to protein content in conferring resistance to phyllody disease. However, the moderately resistant genotype IC 204132 was found statistically at par with resistant genotype, EC 377002-2.

The total reducing sugars were in the horizon of 101.53 to 817.93 µg g^{-1} of leaf with an average value of 448.05 µg g^{-1} of leaf. There exists statistically significant difference of total reducing sugars in selected sesame resistant and susceptible genotypes. The highest amounts of total reducing sugars were found in highly susceptible genotypes like YLM 66 (714.13 µg g^{-1} of leaf) and Gowri (817.93 µg g^{-1} of leaf). The higher levels were observed in resistant genotypes IC 203871 (101.53 µg g^{-1} of leaf) and EC 377002-2 (125.10 µg g^{-1} of leaf). The genotypes were found statistically significant over one another in the context of reducing sugars. The decreasing order of reducing sugars was observed as highly susceptible genotypes (Gowri and YLM 66) > moderately susceptible (IC 205470, IC 567285) > moderately resistant (YLM 141, IC 204132) > resistant (IC 203871, EC 377002-2).

Amino acid content during *rabi*, 2019-20 was in the range of 48.50 to 141.23 µg g^{-1} of leaf with a mean value of 93.98 µg g^{-1} of leaf. Resistant genotypes such asIC 203871 (57.17 µg g^{-1} of leaf) and EC 377002-2 (48.50 µg g^{-1} of leaf) recorded lowest amount of total amino acids content as compared to highly susceptible genotypes Gowri (141.23 µg g^{-1} of leaf) and YLM 66 (132.87 µg g^{-1} of leaf). The genotypes were found statistically significant with regard to amino acid content during the present study.The descending order of amino acid content was observed as highly susceptible genotypes (Gowri, YLM 66) > moderately susceptible (IC 567285, IC 205470) > moderately resistant (IC 204132, YLM 141) > resistant (IC 203871, EC 377002-2).

Chlorophyll content in selected genotypes was in the range of 32.09 to 42.35 SCMR units with an average value of 38.12 SCMR units. The resistant genotypes recorded higher values of chlorophyll content when compared to highly susceptible genotypes during *rabi*, 2019-20. The genotypes show statistical differences with regard to chlorophyll content, but the resistant genotypes IC 203871 and EC 377002-2 were found on par with each other. The moderately resistant genotype, YLM 141 and moderately susceptible genotype, IC 567285 were found statistically at par with each other.

Pearson's correlation coefficient was calculated between biochemical characters in selected sesame genotypes with mean leafhopper population and per cent phyllody incidence(Table 3).The correlation studies during *rabi*, 2019-20 revealed that total amino acids (0.786), proteins (0.850) and total reducing sugars (0.842) exhibited a significant positive correlation with mean leafhopper population, while total phenols (-0.803) and chlorophyll content (-0.908) showed significant negative association with leafhopper incidence. Similar trend in correlation was observed with biochemical characters of resistance in sesame plants and phyllody incidence. Significant positive correlation was observed with proteins (0.908), total amino acids (0.924), total reducing sugars (0.931) and phyllody incidence, while, total phenols (-0.967) and total chlorophyll content (-0.881) had a significant negative association with per cent phyllody incidence.

(ii) Second season – *rabi*, 2020-21: The findings regarding biochemical parameters during second season 2020-21 were given in Table 2. Assessment of total phenols in selected genotypes during *rabi*, 2020-21 indicated that the mean value of total phenol content was 2176.48 µg g^{-1} of leaf. Greater amounts of phenols were observed in resistant genotypes namely, IC 203871 and EC 377002-2 with 3461.13 and 3143.45µg g^{-1} of leaf, respectively and lowest phenol content in highly susceptible genotypes, Gowri (1166.44 µg g^{-1} of leaf) and YLM 66 (929.17 µg g^{-1} of leaf). Phenol content estimated during the present study was found statistically significantin different genotypes. The descending order of phenol content in the categories studied was resistant (IC 203871, EC 377002-2) > moderately resistant (IC 204132, YLM 141) > moderately susceptible (IC 205470, IC 567285) > highly susceptible genotypes (Gowri and YLM 66). However, the moderately resistant genotypes IC 204132 and YLM 141 were found statistically at par with each other.

The results during *rabi*, 2020-21 proved the presence of higher values of protein contents in highly susceptible genotypes (YLM 66 with 250.03 µg g^{-1} of leaf and Gowri with 194.94 µg g^{-1} of leaf) when compared to moderately susceptible, moderately resistant and resistant genotypes. The genotypes with lower protein content showed resistant reaction to phyllody incidence. Similar trend in decreasing order of protein content was observed during *rabi*, 2020-21 *i.e*., highly susceptible genotypes (Gowri, YLM 66) > moderately susceptible (IC 205470, IC 567285) > moderately resistant (YLM 141, IC 204132) > resistant (EC 377002-2, IC 203871).

Resistant genotypes namely IC 203871 (184.20 µg g^{-1} of leaf) and EC 377002-2 (157.07 µg g^{-1} of leaf) recorded lower levels of reducing sugars as against highly susceptible genotypes like YLM 66 (916.87 µg g^{-1} of leaf) and Gowri (1101.47 µg g^{-1} of leaf) with a mean reducing sugar content of 552.27 µg g^{-1} of leaf. The decreasing order of reducing sugars was observed as highly susceptible genotypes (Gowri, YLM 66) > moderately susceptible (IC 205470, IC 567285) > moderately resistant (IC 204132, YLM 141) > resistant (IC 203871, EC 377002-2). The genotypes were found statistically significant and the resistant genotypes IC 203871 and EC 377002-2 were found statistically at par with each other.

The experimental results on amino acid content in selected genotypes during *rabi*, 2020-21 showed the presence of higher amount of amino acids in highly susceptible genotypes like YLM 66 (153.27 µg g^{-1} of leaf) and Gowri (167.37 µg g^{-1} of leaf) when compared to moderately susceptible, moderately resistant and resistant genotypes. The decreasing order of amino acid content was observed to be highly susceptible genotypes (Gowri, YLM 66) > moderately susceptible (IC 567285, IC 205470) > moderately resistant (IC 204132, YLM 141) > resistant (IC 203871, EC 377002-2). There was a significant difference statistically between the genotypes studied. However, the resistant genotypes IC 203871 and EC 377002-2 were found statistically at par with each other.

Mean chlorophyll content was observed to be 38.45 SCMR units during *rabi*, 2020-21. Chlorophyll content ranged from 29.15 to 45.97 SCMR units. The highly susceptible genotypes like YLM 66 (35.26) and Gowri (29.15) recorded lower readings of chlorophyll content compared to resistant genotypes namely IC 203871 (45.97) and EC 377002-2 (43.32). The genotypes exhibit statistically significant difference with respect to chlorophyll content. However, the moderately resistant genotype (IC 204132), moderately susceptible genotype (IC 205470) and resistant genotype (EC 377002-2) were statistically at par with each other.

Table 1. Biochemical characters of selected sesame genotypes during *rabi*, 2019-20

Genotype	Proteins ($\mu g\ g^{-1}$ of leaf)	Phenols ($\mu g\ g^{-1}$ of leaf)	Total amino acids ($\mu g\ g^{-1}$ of leaf)	Total reducing sugars ($\mu g\ g^{-1}$ of leaf)	Chlorophyll content (SCMR units)
IC 203871	106.23^{g}	2882.31^{b}	57.17^{g}	101.53^{h}	42.35^{a}
EC 377002-2	132.33^{f}	3238.08^{a}	48.50^{h}	125.10^{g}	41.65^{a}
YLM 66	215.47^{b}	844.18^{h}	132.87^{b}	714.13^{b}	34.62^{e}
YLM 141	156.58^{e}	2682.05^{c}	75.93^{e}	363.63^{e}	36.69^{d}
IC 205470	208.23^{c}	1942.73^{e}	109.60^{d}	609.90^{c}	39.51^{c}
IC 567285	201.80^{d}	1718.41^{f}	123.67^{c}	512.93^{d}	37.31^{d}
IC 204132	135.73^{f}	2513.97^{d}	62.83^{f}	339.27^{f}	40.72^{b}
Gowri	260.13^{a}	1084.77^{g}	141.23^{a}	817.93^{a}	32.09^{f}
Overall Mean	177.06	2113.31	93.98	448.05	38.12
F-test	Sig.	Sig.	Sig.	Sig.	Sig.
SEm±	2.114	45.880	1.763	3.697	0.258
CD (P=0.05)	6.411	139.161	5.346	11.213	0.783
C.V (%)	2.067	3.760	3.249	1.429	1.173

Sig. – Significant at 5 per cent level of significance; Values followed by same letter in each column are not significantly different

Table 2. Biochemical characters of selected sesame genotypes during *rabi*, 2020-21

Genotype	Proteins ($\mu g\ g^{-1}$ of leaf)	Phenols ($\mu g\ g^{-1}$ of leaf)	Total amino acids ($\mu g\ g^{-1}$ of leaf)	Total reducing sugars ($\mu g\ g^{-1}$ of leaf)	Chlorophyll content (SCMR units)
IC 203871	117.67^{g}	3461.13^{a}	50.81^{h}	184.20^{g}	45.97^{a}
EC 377002-2	132.73^{f}	3143.45^{b}	58.84^{g}	157.07^{g}	43.32^{b}
YLM 66	250.03^{b}	929.17^{g}	153.27^{b}	916.87^{b}	35.26^{cd}
YLM 141	161.60^{e}	2474.50^{c}	75.06^{f}	288.13^{f}	34.32^{d}
IC 205470	225.53^{c}	2087.79^{d}	94.87^{d}	716.20^{c}	41.13^{b}
IC 567285	187.17^{d}	1539.16^{e}	118.52^{c}	616.66^{d}	36.78^{c}
IC 204132	138.37^{f}	2610.23^{c}	85.88^{e}	437.57^{e}	41.69^{b}
Gowri	346.40^{a}	1166.44^{f}	167.37^{a}	1101.47^{a}	29.15^{e}
Overall Mean	194.94	2176.48	100.58	552.27	38.45
F-test	Sig.	Sig.	Sig.	Sig.	Sig.
SEm±	4.702	48.287	2.063	10.015	0.734
CD (P=0.05)	14.262	146.464	6.258	30.376	2.225
C.V (%)	4.178	3.843	3.553	3.141	3.304

Sig. – Significant at 5 per cent level of significance; Values followed by same letter in each column are not significantly different

Table 3. Correlation between biochemical characters of sesame genotypes Vs mean leafhopper population and per cent phyllody incidence during *rabi*, 2019-20 and 2020-21

Parameter	2019-20		2020-21	
	r-value with mean leafhopper population	r-value with per cent phyllody incidence	r-value with mean leafhopper population	r-value with per cent phyllody incidence
Proteins	0.810*	0.956*	0.850*	0.908*
Total Phenols	-0.520 ^{NS}	-0.919*	-0.803*	-0.967*
Total Amino Acids	0.669 ^{NS}	0.967*	0.786*	0.924*
Chlorophyll	-0.818*	-0.763*	-0.908*	-0.881*
Total Reducing Sugars	0.641 ^{NS}	0.969*	0.842*	0.931*

** ----- Significant at 0.05 per cent level of significance; NS – Non Significant*

The correlation studies during *rabi*, 2020-21 with biochemical characters revealed that proteins (0.810), total amino acids (0.669) and total reducing sugars (0.641) were observed to show positive correlation with leafhopper population, however, the correlation was significant with proteins alone whereas, amino acids and reducing sugars showed a non-significant association (Table 3). Total phenols(-0.520) and chlorophyll content (-0.818) showed negative correlation with mean leafhopper population, however, the association was non-significant with phenols and significant with total chlorophyll content. In case of correlation studies with per cent phyllody incidence, biochemical characters like proteins (0.956), amino acids (0.967) and reducing sugars (0.969) exhibited a significant positive correlation, whereas, chlorophyll content (-0.763) and phenols (-0.919) resulted a significant negative correlation with per cent phyllody incidence.

The present results revealed that plants resist pest attack by various morphological and biochemical mechanisms of resistance that exhibit repellent or toxic or anti-nutritional impact on the insect pests. The biochemical analyses from the present study drive support from the results of previous research findings by Showket*et al.* (2017) who reported an increased level of phenols in resistant genotypes with lowest per cent fruit infestation caused by *Leucinodes orbonalis* in brinjal. Total phenols had negative correlation with jassid infestation (Rizwan *et al.*, 2021). Phenols were one of the components of plant secondary metabolites produced in response to insect attack providing defense against many insects (War *et al.*, 2012).

The biochemical analyses conducted by Raju *et al.* (2020) revealed that the cotton genotypes with high phenol content exhibited resistance against leafhoppers by recording lower number of leafhopper population when compared to genotypes having less phenol content which were in close association with the present findings. The results from the total phenol content were in agreement with Jat and Pareck (2003) who reported a significant negative correlation between phenols and fruit infestation caused by *Luecinodes orbonalis* in brinjal but was in contradictory with Reddy (2019) who noticed higher amounts of phenols in susceptible genotypes than resistant genotypes owing that the defence responses in plants were induced rather than constituted.

Genotypes with high protein content were found susceptible to sucking pests (Rizwan *et al.*, 2021; Athar *et al.*, 2011 and Sonalkar, 2020). The genotypes with high protein and sugar content make the plants vulnerable to insect attack thereby causing more damage in susceptible ones. Results obtained in the present investigations *i.e*., positive correlation between reducing sugars with mean leafhopper population and per cent phyllody incidence were in close agreement with Bommesha *et al.* (2012) who observed significant positive correlation between total sugars and incidence of leafhoppers in pigeonpea. Challa *et al.* (2021) reported positive correlation between reducing sugars and per cent fruit infestation in brinjal. Singh *et al.* (1990) recorded that the genotypes containing lower contents of reducing sugars in leaves and flowers resulted least damage in sesame by leaf webber, *Antigastra catalaunalis* confirms the present study. However, the results were in contradiction with Nath *et al.* (2017) who reported that elevated levels of reducing sugars were observed in resistant genotypes when compared to susceptible genotypes. This could be due to the fact that sugars play a key role in metabolic pathways that trigger defence plants to produce higher quantities of secondary metabolites.

From the results, it was evident that the highly susceptible genotypes recorded lower chlorophyll content compared with that of resistant genotype recording lower phyllody incidence. This could be due to the fact that the phyllody disease inhibits biosynthesis of chlorophyll thus, affecting the photosynthetic activity (Pathak, 2011). The higher incidence of phyllody infection might cause considerable damage to the chloroplasts which resulted in reduction of total chlorophyll content (Shukla *et al.*,1988). Similar trend in decreased chlorophyll content was noticed by Liu *et al.* (2016) who reported that many pathogen infections in plants are closely related to reducing rate of photosynthesis and affect the chloroplast number, ultrastructure and chlorophyll metabolism. Deterioration of chloroplast structure, pigment composition and electron transport can be attributed to the damage in PSII mostly caused by infection stress.

4. CONCLUSION

The present findings depicted that the responses of host plants to insect attack were complex and may differ among different sesame genotypes. The resistant genotypes (IC 203871 and EC 377002-2) identified from the screening experiment recorded more quantity of phenols, less amount of proteins, amino acids and reducing sugars when compared to moderately resistant (YLM 141 and IC 204132), moderately susceptible (IC 567285 and IC 205470) and highly susceptible genotypes (Gowri and YLM 66). From the study, it can be inferred that the biochemical components might impart resistance in the plants to counter attack insect injury. Hence, the genotypes exhibiting resistance to insect injury complementing the biochemical characters can be used in further breeding programmes for development of resistant varieties.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declares that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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