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Response of chilli genotypes to yellow mite, *Polyphagotarsonemus latus* Banks population and biochemical basis of resistance

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Abstract
Host plant resistance to yellow mite was studied by quantifying phenols, sugars, protein, proline and enzymes such as peroxidise and phenylalanine lyase in chilli varieties. Damage by yellow mite, *Polyphagotarsonemus latus* (Banks) and resistance in chilli germplasms had higher levels of total sugars and protein contents to encourage the mite infestation in susceptible chilli entries, while chlorophyll contents in leaves did not show any relationship with mite infestation levels. Consequent to mite infestation, the levels of phenols, proline, peroxidase and PAL were found enhanced (16.80 to 22.80 mg/g; 4.42 to 6.54 µ moles/g tissue; 825 to 1362 units/g of tissue; 3.20 to 4.67x10^3µmoles/min/ml), might be due to induced resistance or hypersensitive reaction, particularly in resistant entries namely, Aparna, S 49, BVC 47, BVC 53 and *Capsicum frutescence* compared to susceptible entries which can be correlated to level of resistance to yellow mite.

Keywords: *Polyphagotarsonemus latus, biochemicals, resistance, chilli entries*

Introduction
Many insect and non-insect pests occur on chilli, out of which yellow mite *Polyphagotarsonemus latus* (Banks) is most destructive (Butani, 1976) causing nearly 25 percent loss in yield (Ahmed *et al*., 1987) [1]. The yield loss due to this pest may be more than 90 percent (Borah, 1987) [5] and at times complete devastation of the crop might occur. *P. latus*, a member of the family Tarsonemidae commonly known as yellow mite, broad mite *etc*. is an important mite pest of chilli with wide host range including many cultivated crops like potato, sweet pepper, tomato, egg plant, beans, melons, celery, pakchoi (Chinese white cabbage), cotton, pears, guava, passion fruit and flower crops like chrysanthemum, dahlia *etc* (Gibson and Valencia, 1978) [7].

Host plant resistance, as seen in the field by Painter (1951) [16] has been categorised into three mechanisms: non preference, antibiosis and tolerance. In most of the cases non preference and antibiosis types of resistance mechanisms are in most of the resistant varieties. The association between plant biochemicals and host plant resistance was well documented by several authors. Gibson and Valencia (1978) [7] studied the resistance in potato species, *Solanum polyadenium*, *S. tarjense* and *S. berthaultii*, which had foliar hairs with a sticky tip and type B glandular hairs to confer resistance to damage by *P. latus*. These hairs restricted the mite population by trapping them when were blown on to the plants. The hair exudates were toxic or repellent as in the case of tomato plants of *Lycopersicon* spp. Rani (2001) [17] reported that the potato variety TPS1/67 which recorded the lowest number of mites (22.33/compound leaf) at peak infestation period at Bangalore was attributed to higher leaf content of phenolic compounds (catechin 14mg/g), whereas the variety TPS 2/67 with more number of mites (168.50/compound leaf) was associated with lower content of phenolic compounds (6 mg/g).

Nawalagatti *et al*. (1999) [13] studied the biochemical resistance to murda complex in chilli varieties Byadgi, Sankeshwar, G3 & Jwala, Lines and hybrids. The resistant variety like Jwala had high total chlorophyll content, higher phenols and lower sugars. It was observed that the total phenols decreased after mite infestation in all the unprotected varieties. Percent reduction in total phenol increased with the age of the crop, indicating that the plants are more resistant at early stages than at the later stages. Ni *et al*. (2001) [14] studied the oxidative responses of resistant and susceptible cereal leaves to symptomatic and nonsymptomatic cereal aphid feeding.

The Russian wheat aphid, Diuraphis noxia feeding probably resulted in oxidative stress in plants. Moderate increase in peroxidase activity in resistant Halt variety of wheat compared with the susceptible Arapahoe wheat might contributed to its resistance, whereas nine folds increased peroxidase activity possibly contributed to susceptibility in barleys. The aphid feeding caused significant increase in total protein content and peroxidase activity in resistant plant.

Zhen *et al*. (2006) [21] observed changes in the levels of capsaicin, flavonoid, free phenolics and enzyme activity during the development of chilli fruit. The capsaicin content increased and reached maximum at 50 days after flowering, but decreased later. Maximum level of phenols and flavonoids was observed during early stage of the crop, further decreased with fruit ripening. The enzyme activity increased rapidly during 29-36 days after flowering. Saeidi and Mallik (2006) [19] studied the nature of resistance in *Lycopersicon* species to two spotted spider mite. Tomato cultivars/accessions were grouped into five categories based on the overall performance in leaf dip/thumb tack bioassay, as highly resistant, resistant, susceptible, highly susceptible and tolerant. Based on biochemical results the maximum content of phenolic compounds was observed in *L. pimpinellifolium* (19.24ppm) followed by *L. esculentum* (NDTVR 73) (14.89ppm) and the lowest concentration in *L. pennellii* accession (3.33ppm).

Though the occurrence of yellow mite as well as its damage on chilli crop is often reported throughout the cropping season, host plant resistance as an important component of integrated pest management suits well in the management of the yellow mite *P. latus* as well. To reduce the unwarranted pesticide load in the environment and also in the process of developing an economically feasible management strategy following study was conducted to screen the chilli lines/cultivars for resistance to yellow mite and identification of probable resistance mechanisms.

Material and Methods

Biochemical and enzymatic changes due to feeding of herbivores often result in physiological, morphological and chemical changes in the form of accumulation of the compounds having defensive properties (usharani and jyothsna, 2010) [20]. The study of biochemical changes resulting from insect herbivory is essential to coordinate the potential interaction of phytochemicals responsible for plant resistance. Some of the important biochemicals in host plant where their concentration increase or decrease as a defense mechanism against herbivore are phenols, sugars, proteins, peroxidise and phenylalanine lyase. The chilli genotypes were selected based on the genotype reaction against yellow mite population during the screening studies at green house and field conditions. Initially these seedlings were raised in a nursery and later 4 weeks old seedlings were planted in the main field. On either side of each entry a single row of susceptible chilli variety *Byadgi kaddi* was planted as an infector row to ensure natural mite infestation. Parameters considered for evaluation of chilli genotypes against yellow mite, *P. latus* were

Population density of yellow mite: The mite population density was recorded from five plants selected randomly from each plot/row and from each plant, one shoot tip with at least six fully opened young leaves were sampled and counts were made for the number of eggs and active stages of the mite under a stereobinocular microscope. Such observations for mite populations were recorded at fortnightly interval starting from 15 days after planting. The mite population was expressed as the number per six leaves. Data on mite population from 5 to 6 observations were pooled to compute the mean mite population.

At each interval the total number of plants and the number of mite infested plants in each entry were recorded at each interval and percent incidence (percentage of plants infested by yellow mite) in each entry was computed.

Scoring for the mite damage

Chilli plants showing the symptom of yellow mite damage *i.e.* downward curling of leaf margin were scored individually on 0 - 4 scale (Niles, 1980) [15] at fortnightly intervals, and pooled to compute the overall mean scoring for each entry (Table 1).

Table 1: Damage scale for screening chilli genotypes

Damage score	Leaf damage due to yellow mite
0	No Symptom of leaf curling due to mites
1	1-25 percent of leaves in a plant with downward leaf curling damage due to mites
2	26-50 percent of leaves in a plant with downward leaf curling damage due to mites
3	51-75 percent of leaves in a plant with downward leaf curling damage due to mites (malformation of growing tips, stunted growth etc.)
4	>75 percent of leaves in a plant with downward leaf curling damage due to mites (complete malformation of shoot tips, severe stunting etc.)

Observations for mite population and damage score were recorded and all these genotypes were studied for different biochemical constituents to understand the basis of biochemical resistance, if any, against the yellow mite. Mite infested (with visible symptoms of damage) plants were analyzed separately for different biochemical constituents. The leaves for biochemical analysis were collected from the plants in experiment and subjected to different biochemical analysis like chlorophyll, total sugar, total protein, total phenol, proline, total peroxidise and phenylalanine ammonia lyase (PAL) activity following the methods of Sadasivam and Manickham (1991) [18] with minor modifications.

Preparation of oven dried sample: The freshly collected plant samples were dried at 600C to a constant weight in a hot-air oven. The samples were then powdered using a waring blender and the leaf powder was stored in sealed polyethylene covers at room temperature.

Preparation of acetone powder: The plant samples were homogenized with pre-chilled acetone using a pestle and mortar. The resulting slurry was filtered immediately under suction using Whatman No.1 filter paper and washed with chilled acetone to remove chlorophyll and other pigments (Mahadevan and Sridhar, 1982) [11].

Biochemical Analysis

Estimation of chlorophyll

To quantify the chlorophyll loss due to mite feeding, the leaf chlorophyll content before and after mite infestation was estimated separately and compared. For chlorophyll estimation leaf samples were collected separately from each variety, before and after mite infestation (before flowering). One gram of leaf sample was taken and incubated over night in 20ml mixture of DMSO (Dimethyl sulphoxide) and acetone (80%) at 1:1 ratio. The supernatant extract (0.5ml) was diluted with 9.5ml DMSO and acetone mixture. Absorbance was recorded using Spectrophotometer (TranUV) at 645 and 663nm wave lengths and using these absorbance values total chlorophyll content was estimated (Arnon, 1949) as below.

Total Chlorophyll: [20.8 (A645) +8.02(A663) X V/W] X100

[V-volume of dilution by solvent in ml, and W-weight of leaves in grams, A663 and A645 -Absorbance values at 663 and 645nm, respectively].

Estimation of total sugar content

Reagents

1. Phenol reagent: 5g of redistilled phenol was dissolved in water and volume made 100ml.
2. Standard glucose solution: Glucose stock solution was prepared containing 15 mg glucose/10 ml in water. The solution was diluted 1:10 to obtain 150 µg glucose/ml working standard solution.

Sample extraction: 100mg of oven-dried leaf powder was used for extraction in 10 ml of 80% warm ethanol for one hour on a magnetic stirrer at room temperature. The extract was then centrifuged at 6000 rpm for 15 minutes. The supernatant was evaporated to dryness on a water bath and the residue was dissolved in 5 ml of distilled water. This alcohol free extract was used for the estimation of total soluble sugars (Dubois *et al*., 1956) [6].

Estimation: 0.1 ml of sample aliquot was diluted to 1ml with water. 1ml of 5% phenol reagent and 5ml of 98% H2SO4 were added and incubated for 10 minutes and then placed in a water bath at 300C for 20 minutes. The absorbance was read at 490nm against the reagent blank in a Colorimeter (TransUV). A standard curve was constructed using standard glucose in the range of 15-150 µg. The total sugar estimated was expressed as mg per gram of oven-dried sample.

Estimation of total protein content

Reagents

1. **Solution A:** 20g of anhydrous sodium carbonate (Na2 CO3 2H2O) and 4g of sodium hydroxide dissolved in 1000 ml of distilled water.
2. **Solution B:** 1ml of 1.35% sodium potassium tartarate and 0.1 ml of 5.5% CuSO4.5H2O solutions mixed together.
3. **Solution C:** 50ml of solution A mixed with 1 ml of solution B just before use.
4. **Folin-Ciocalteau reagent (FCR):** The commercial FCR diluted in the ratio of 1:1 before use.
5. **Standard bovine serum albumin (BSA) solution:** A stock BSA solution was prepared containing 2mg BSA/ml in water. This solution was diluted 1:10 to obtain 200µg BSA/ml of working standard solution.

Sample extraction: 100mg of oven-dried sample powder was used for extraction in 10ml of 0.1M sodium phosphate buffer, pH 7.0 for 1 hour on a magnetic stirrer at room temperature. The extract was centrifuged at 10,000 rpm for 20 minutes and the supernatant was used for the estimation of total soluble protein content (Lowry *et al*., 1951) [10].

Estimation: A known volume of sample aliquot was made to 1ml with distilled water. To this, 5ml of solution C was added, and mixed well. After 10 minutes, 0.5ml of FCR was added and mixed immediately. The blue colour complex developed was read at 660 nm after 30 minutes against a reagent blank in a Colorimeter (Trans UV).

A standard curve was constructed using BSA solution as a standard in the range of 20-200µg. The total protein content estimated was expressed as mg per gram of oven-dried sample.

Estimation of proline

Reagents

1. Acid ninhydrin: Warmed 1.25 g ninhydrin in 30 ml glacial acetic acid and 20 ml 6M phosphoric acid, with agitation until dissolved. Stored at 40C and used within 24h.
2. 3% Aqueous sulphosalicylic acid
3. Glacial acetic acid
4. Toluene
5. Standard proline solution: 5mg of proline was dissolved in 10 ml of water in a volumetric flask. 1 ml of this stock was diluted to 10ml for working standard solution. A series of volumes from 0.1 to 1ml of this working standard gave a concentration range of 5 µg to 50 µg. A standard curve was constructed using absorbance versus concentration.

Assay: 0.5g of plant material was homogenized in 10 ml of 3% aqueous sulphosalicylic acid and the homogenate was filtered through Whatman No. 2 filter paper. 2 ml of filtrate was taken in a test tube and 2 ml of glacial acetic acid and 2 ml acid ninhydrin were added and the content was heated over boiling water bath for 1h. The reaction was terminated by placing the tube in an ice bath. 4 ml toluene was added to the reaction mixture and stirred well for 20-30 sec. The toluene layer was separated and warmed to room temperature. The intensity of red colour was measured at 520 nm. Standard curve was drawn for pure proline in a similar way. The amount of proline in the test sample was determined from the standard curve and expressed on fresh-weight basis as µ moles per gram tissue.

Estimation of total phenol content

Reagents

1. **Folin-ciocalteau reagent (FCR):** Commercial grade reagent diluted to 1:1 with water.
2. **20% Sodium carbonate solution:** 20g of Na2 CO3 dissolved in water and volume made to 100ml.
3. **Acidified methanol:** 10 ml of HCl mixed with 90 ml of methanol.
4. **Standard catechol solution:** A stock catechol solution was prepared containing 0.025 mg catechol/ml in water. This solution diluted with distilled water to obtain 2.5µg catechol/ml for working standard solution.

Extraction: 100mg of oven-dried leaf powder was used for extraction in 10ml of 80% warm ethanol for 1 hour at room temperature. The extract was then centrifuged at 6000 rpm for 15 minutes. The supernatant was evaporated to dryness in a water bath and the residue was dissolved in 5ml of water. The alcohol free extract was used for the estimation of total phenols (Malick and Singh, 1980) [12].

Estimation: 0.1 ml sample aliquot was diluted to 3ml with distilled water and 0.5 ml of FCR was added and mixed. Exactly after 3 minutes, 2ml of 20% sodium carbonate solution was added and kept in a boiling water bath for one minute. After cooling under running tap water, the absorbance was read at 650nm, against the reagent blank in a Colorimeter (TransUV). A standard graph was constructed with catechol as standard in the range of 0.25-2.5 µg. The total phenol content determined was expressed as the mg per gram of oven-dried sample.

Enzyme assays

Total peroxidase activity

Reagents

1. **Hydrogen peroxide solution:** 0.14ml of 30% hydrogen peroxide was diluted to 100ml with 0.1M sodium phosphate buffer of pH 7.0 to get 12.3mM solution.
2. **Guaiacol solution (20mM):** 1ml of 1M guaiacol solution was diluted to 100ml to get 20mM. It was stored frozen until use.

Preparation of enzyme extract: 100mg acetone powder of plant sample was used for extraction with 10ml of ice-cold 0.1 M sodium phosphate buffer of pH 7.0 containing 0.1 percent polyvinylpyrrolidone in a pestle and mortar for 2-5 minutes. The slurry was centrifuged at 10,000 rpm for 20 minutes at 40C. The supernatant was used as enzyme source for the estimation of total peroxidase.

Assay: 3ml of 0.1 M sodium phosphate buffer of pH 7.0, 0.1ml of 20mM guaiacol solution and 0.1ml of 12.3mM hydrogen peroxide were taken in a cuvette. The reaction was initiated by adding 0.1ml of enzyme extract pre-incubated at 250C and the increase in absorbance was measured at 470nm at a time interval of 30 seconds upto 5 minutes in a Spectrophotometer (Trans UV). The activity of the enzyme was calculated from the linear part of the progress curve. One unit of peroxidase is defined as increase in absorbance of 0.01/minute under standard assay conditions and the activity was expressed as units/g acetone powder.

Phenylalanine ammonia lyase (PAL) activity

Reagents

1. **Substrate solution:** 165mg of L-phenylalanine was dissolved in 5ml of water. pH was adjusted to 9.0 with 0.1N KOH and the volume was made up to 10ml to obtain 100mM L-phenylalanine solution.
2. **Trans-cinnamic acid solution:** 29.64mg of trans-cinnamic acid was dissolved in 10ml of water. 100µl of this solution was diluted to 10ml to obtain 2µ moles trans-cinnamic acid/ml working standard solution.

Preparation of enzyme extract: 100 mg of acetone powder of plant sample was used for extraction with 10 ml of ice cold 25mM borax-HCl buffer of pH 9.0 containing 5 mM mercpatoethanol in a pestle and mortar for 2-5 minutes. The extract was centrifuged at 10,000 rpm for 20 minutes at 40C. The supernatant was used as the enzyme source for assay.

Assay: 0.5ml of 25mM borax-HCl buffer, pH 9.0, 0.6 ml of enzyme extract, 0.9 ml of water was pre-incubated at 370C for 5 minutes. The reaction was initiated by adding 1 ml of 0.1M L-phenylalanine substrate solution. The reaction was terminated after 40 minutes by adding 0.5ml of 1M TCA solution. A control was run in which the substrate solution was added after the TCA. The change in absorbance was read at 290 nm in a Spectrophotometer (Incline nanophotometer). The trans-cinnamic acid liberated in the reaction mixture was calculated from the standard graph constructed using trans-cinnamic acid with the range of 0.02 to 0.2 µ moles and expressed as µ moles of product (trans-cinnamic acid) formed /min/ml of enzyme extract.

Results & discussion

Genotypes screened represented to harbour mite population ranging from <5 mites (2 genotypes), 6-10 mites (3 genotypes), 11-50 mites (26 genotypes) and more than 50 mites (2 genotypes) per six leaves (Table 1).The percentage of mite infested plants ranged from 0 (S 49) to 94.44 percent (*Byadgi kaddi* & CMS 5 B). The mean damage score ranged from 0 (Aparna and S 49) to 3 (KNG 1). The total mite population including eggs and active stages ranged from 0.9 mites/6 leaves (Aparna) to 87.20 mites/6 leaves (*Byadgi kaddi).*

30 genotypes were grouped based on total mite population (eggs + active stages)/6 leaves as below. In most of the genotypes since there was no consistency in mite damage scoring data (probability due to recovery from the symptom) mean mite population was considered for assessing the reaction of different chilli genotypes for mite infestation. Thus 30 genotypes were categorized into 5 major reaction groups based on mean mite population (including eggs and active stages recorded from 5 fortnightly intervals between 15 and 75 days from planting). Two genotypes which harboured <5 mites/6 leaves namely, Aparna & S 49 were designated as highly resistant; 1 entry BVC 47 with 5 to 10 mites/6 leaves as resistant; 2 genotypes BVC 53 and *Capsicum frutescens* as moderately resistant with 11 to 20 mites/6 leaves; 3 genotypes namely CA 2, KDC 2 and CA 9 which recorded 21 to 30 mites/6 leaves as susceptible; remaining 22 genotypes including *Byadgi kaddi* (87.20 mites/6 leaves) were categorized as highly susceptible with >30 mites/6 leaves (Table 2).

Table 2: Category of chilli genotypes based on mean mite population

Highly resistant	<5 mites	2 genotypes (Aparna & S 49)
Resistant	5-10 mites	1 entry (BVC 47)
Moderately resistant	10-20 mites	2 genotypes (BVC 53, C. frutescens)
Susceptible	20-30 mites	3 genotypes (CA 2, KDC 2 and CA 9)
Highly susceptible	>30 mites	22 genotypes (PMR 21, KNG 2, KDC 1, G 4, PBC 631, LCA 273, PBC 142, CA 960, Phule jyothi, LCA 334, KNG 1, Vamsi, LCA 336, CA 10, Koira, AVNPC 131, CMS5B, ICPN 14, Pusa sadabahar and Punjab gucchedhar, Oothgod local, Byadgi kaddi)

Biochemical basis of resistance

Chlorophyll, total sugars and protein: Among the 30 chilli genotypes there was no much difference in chlorophyll content. Total sugars and proteins content was high in susceptible genotypes (like *Byadgi kaddi*, *Oothgod local*) which might supported mite infestation compared to the resistant genotypes (like Aparna, S 49, BVC47, BVC 53 and *Capsicum frutescens*) with lower levels of sugars and proteins (Table 3).

Proline: Among the genotypes proline profile and the yellow mite infestation, there was significantly higher and rapid accumulation of proline after mite infestation in all the susceptible genotypes. The proline content ranged from 1.9 to 3.25 µmoles/g in resistant and 2.25 to 4.2 µmoles/g in susceptible genotypes (Table 3).

Phenols: genotypes studied for total phenol showed mite infested plants had significantly higher quantity of phenol (16.80 to 22.80 mg/g) in all the genotypes which were resistant or highly resistant to mite attack and these genotypes also recorded lower number of mites. In susceptible genotypes (with 10 to 18.50 mg/g phenols) this trend was not so evident. Thus in resistant genotypes increase in the levels of total phenol observed with mite infestation, might have been induced to enhance the synthesis of phenolic precursors and their further oxidation into toxic quinones which prevented the further buildup of mite population as a hypersensitive reaction or induced resistance (Table 3).

Enzyme activity: The peroxidase level in different genotypes showed a range of 825 to 1362 units/g of tissue after infestation particularly in resistant genotypes (5 genotypes). In other genotypes improvement in enzyme activity did not exceed 68.80 percent ranging from 322.70 to 698 units/g of tissue in susceptible entry. Thus the activity of peroxidase in relation to mite infestation clearly indicated its negative impact on the further buildup of mites. While, phenylalanine ammonia lyase activity showed its level from 2.22 to 4.67 x 10^{-3} µmoles /min/ml in different genotypes with higer activity in resistant genotypes damaged plants compared to susceptible genotypes (Table 3).

Table 3: Biochemical constituents and mite population in different genotypes of chilli

Sl. No.	Genotypes	Population (Total Mean number/6 leaves)	Mean Damage score	Percentage of plants infested by mites	Total Chlorophyll (mg/g)	Total Sugars (mg/g)	Protein (mg/g)	Proline (µ moles /g tissue)	Total phenols (mg/g)	Peroxidase (units/g of tissue)	Phenylalanine ammonia lyase (x 10^{-3} µmoles /min/ml)
1	Aparna	0.90	0.00	5.56	3.78	26.50	14.05	4.89	21.60	883.00	4.34
2	S 49	1.10	0.00	0.00	3.85	28.50	14.38	6.18	22.80	960.00	4.67
3	BVC 47	6.80	0.40	11.11	3.54	29.00	13.26	4.42	18.00	900.00	3.20
4	BVC 53	16.50	0.80	61.11	3.36	25.00	14.43	6.54	21.45	825.00	3.90
5	*Capsicum frutescens*	18.00	1.60	19.44	3.51	28.00	15.93	5.36	16.80	1362.00	3.40
6	CA 2	27.50	1.00	83.33	3.35	30.50	15.37	5.67	15.00	612.00	2.90
7	KDC 2	27.50	1.20	72.22	3.19	27.00	14.47	4.15	13.80	367.50	2.97
8	CA 9	28.70	1.20	69.44	3.33	21.60	14.50	3.78	13.00	520.00	3.40
9	PMR 21	30.30	1.20	77.78	3.23	33.50	16.93	4.82	12.50	675.50	3.40
10	KNG 2	30.50	1.40	88.89	3.32	30.94	17.18	5.42	12.34	678.00	3.08
11	KDC 1	30.60	1.40	88.89	3.59	31.75	16.36	5.71	13.00	486.50	3.28
12	G 4	30.90	1.60	63.89	3.39	30.64	15.37	6.12	15.40	512.34	3.40
13	PBC 631	31.00	1.80	69.44	3.84	31.42	16.12	4.64	10.00	674.00	3.10
14	CMS 1B	31.30	2.40	91.67	3.23	32.12	15.86	6.00	16.75	487.50	2.98
15	LCA 273	31.40	1.60	66.67	3.26	34.64	17.32	5.71	18.50	575.00	3.12
16	PBC 142	32.90	2.40	58.33	3.08	32.29	16.34	6.32	16.48	578.50	3.63
17	CA 960	33.10	1.80	75.00	3.49	32.46	15.45	6.06	14.80	587.00	3.47
18	*Phule jyothi*	34.60	1.80	63.89	3.37	31.45	16.88	7.27	14.76	537.50	3.40
19	LCA 334	34.70	1.40	91.67	3.54	32.89	17.28	5.44	14.32	322.60	2.94
20	KNG1	35.20	3.00	77.78	3.36	33.18	18.32	5.61	14.54	498.00	3.45
21	Vamsi	35.50	2.00	61.11	3.16	35.67	18.86	8.48	17.42	767.00	3.24
22	LCA 336	35.80	2.20	88.89	3.11	34.89	17.68	8.52	14.78	468.00	3.00
23	CA10	36.90	2.20	86.11	3.64	32.58	17.36	7.09	12.54	338.00	3.50
24	Koira	37.50	1.40	80.56	3.25	35.86	17.14	5.67	13.54	678.00	3.02
25	AVNPC 131	38.00	1.40	86.11	3.29	39.16	17.48	8.01	14.60	687.00	2.67
26	ICPN 14	38.20	2.00	88.89	3.40	42.00	16.36	4.98	13.24	678.00	3.24
27	*Pusa sadabahar*	40.30	2.80	38.89	3.80	44.34	18.25	7.09	12.80	428.00	2.78
28	*Punjab gucchedhar*	46.10	1.90	91.67	3.23	48.87	18.42	4.34	15.80	698.00	3.40
29	*Oothgod local*	59.60	2.40	91.67	3.56	53.35	18.68	7.87	14.96	514.28	3.08
30	*Bydagi kaddi*	87.20	2.90	94.44	3.45	58.50	19.52	8.96	15.78	654.00	2.22
F test		*	*	-	*	*	*	*	*	*	*
SEM±		9.76	0.13	-	0.08	0.26	0.11	0.10	0.10	2.55	0.10
CD at P=0.05		21.27	0.28	-	0.24	0.82	0.34	0.33	0.33	8.16	0.33

Table 4: Relationship between yellow mite and biochemical constituents in chilli

Biochemical constituents	Total chlorophyll	Total sugars	Proteins	Proline	Total phenols	Peroxidase activity	PAL activity
'r' value	-0.17^{NS}	0.81**	0.78**	0.18^{NS}	-0.11^{NS}	-0.11^{NS}	-0.35*
R^2 value	-	0.656	0.624	-	-	-	0.126

NS-Non significant, *Significant ; ** Highly significant

Relationship between yellow mite population and biochemical constituents in 30 chilli cultivars. Only total sugars and total protein content in leaves showed positive significant relationship with mite population, while the relationship between mite population and phenylalanine ammonia lyase was negative and significant. Thus total sugars and proteins content in leaves of chilli varieties encouraged mite population, while phenylalanine ammonia lyase content adversely influenced the buildup of yellow mites. Chlorophyll, proline, phenols, and peroxidise content in leaves were not observed to influence yellow mite infestation significantly (Table 4).

Differences in the levels of biochemical constituents in chilli entries were attributed to the corresponding mite infestation levels. The chlorophyll content decreased after mite infestation in susceptible entries compared to the resistant ones, while in susceptible entries higher total sugars and protein content encouraged the mite infestation. After mite infestation, the levels of phenols, proline, peroxidase and PAL were high (16.80 – 22.80 mg/g; 4.42 – 6.54 µ moles/g tissue; 825 - 1362 units/g of tissue; 3.20 – 4.67x10^3 µmoles /min/ml) in resistant entries compared to susceptible entries (18.50 mg/g in LCA 273; 8.96 µ moles/g tissue in *Byadgi kaddi*; 767 units/g of tissue in Vamsi; 3.63x10^3 µmoles/min/ml in PBC 142) (Table 3). This is attributed to the phenomenon of induced resistance/hypersensitive reaction particularly with resistant entries.

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