

EFFECT OF DIFFERENT SOYBEAN VARIETIES ON BIONOMICS OF *TETRANYCHUS URTICAE* (ACARI: TETRANYCHIDAE)

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ABSTRACT: Population density and spatial distribution pattern of *Tetranychus urticae* Koch on seven soybean varieties including: Williams, Tellar, Zane, Sahar, Dpx, L₁₇, Sari and one genotype, Ks3494, were determined in Tehran region, during 2007. The mean population density of the *T. urticae* per leaf on L₁₇ variety (14.15) was significantly more than other varieties and the genotype of soybean. The lower density of the mite population was observed on Zane and Ks3494 (6.1 and 4.65 mite per leaf, respectively). Spatial distribution pattern of *T. urticae* was determined on these varieties of soybean using Index of dispersion, Regression models (Taylor and Iwao), Morisita's coefficient and Lloyd's mean crowding. The index of dispersion, Morisita's index and Lloyd's mean crowding indicated an aggregated pattern for spatial distribution of this mite in all soybean varieties and the genotype. The spatial distribution pattern of this pest using Taylor's power law and Iwao's patchiness in most cases was aggregated and in few cases random. It could be concluded that different varieties of soybean can affect bionomics of *T. urticae*. Spatial distribution parameter can be used to improve the sampling program and exact estimating the population density of this pest.

KEY WORDS: Two-spotted spider mite, *Tetranychus urticae*, Population density, Spatial distribution, Soybean, sampling program.

The two-spotted spider mite, *Tetranychus urticae* Koch, is an extremely polyphagous species and a serious pest of a wide range of economically important crops including soybean in many parts of the world (Granham, 1985; Rott and Ponsoby, 2000; Fikru and Leon, 2003; Ragkou *et al.*, 2004; Khanjani and Haddad Irani-Nejad, 2006). This mite infests the underside of leaves, where profuse webbing may be present. *T. urticae* feeds using a piercing-sucking process that damages plant cells and tissue. This behavior leads to the appearance of characteristic yellow chlorotic spots on leaves. Because the chloroplasts in leaves are gradually destroyed as the population of feeding mites increases, photosynthesis declines, stomata close, and transpiration decreases, leading to reduced production (Martinez-Ferrer *et al.*, 2006).

Estimating the population density of arthropods is the cornerstone of basic research on agricultural ecosystems and the principal tool for building and implementing pest management programs (Kogan and Herzog, 1980). At this estimating plan, the reliable sampling program and suitable techniques should be selected (Pedigo and Buntin, 1994; Southwood and Henderson, 2000). A sampling program can be used in binomial sampling (Binns and Bostanian, 1990), assessing crop loss (Haughes, 1996), ecological investigations (Faleiro *et al.*, 2002), studying

the population dynamics (Jarosik *et al.*, 2003) and detecting pest levels that justify control measures (Arnaldo and Torres, 2005).

The most common methods used to describe the patterns of dispersion of arthropod populations have been summarized by Southwood and Henderson (2000). Several estimates based on the dispersion coefficient, k , of the negative binomial distribution and on the relationship between variance and mean are used as indices of aggregation (Krebs, 1999; Southwood and Henderson, 2000). Sampling plans based on these indices optimize the sampling effort and sampling precision (Kuno, 1991). Sequential sampling plans are used to more efficiently identification of mean pest populations at or above the economic threshold. These plans have reduced the time required for sampling up to 50%, in relation to conventional sampling plans (Patrick *et al.*, 2003). Although the objectives of sampling of a finite population can differ, the development of a sampling procedure requires the knowledge about the spatial distribution of populations (Liu *et al.*, 2002).

There are several studies that described the spatial distribution and population density of *T. urticae*. Aggregated spatial distribution of *T. urticae* was reported in different crops such as carambola (Shih and Wang, 1996), strawberry (Greco *et al.*, 1999), bean (Ahmadi *et al.*, 2005), clementine (Martinez-Ferrer *et al.*, 2006), rose (So, 1991), apple (Slone and Croft, 1998) and peanut (Margolies *et al.*, 1984).

Despite the economic importance of this pest on soybean, little research has focused on development of an efficient sampling program, the determination of population density and the spatial distribution coefficients of this mite. To improve the management of *T. urticae* on soybean, a sampling plan to estimate population levels is needed. This plan is crucial to further develop and implement integrated pest management (IPM) strategies on this crop. As a first step toward this objective, this study examined the population density and spatial distribution of *T. urticae* on different varieties and a genotype of soybean. The results of this research can be used to optimize monitoring methods for establishing IPM strategies against this pest.

MATERIALS AND METHODS

Experimental protocol

The experiments were carried out in a research field of Tarbiat Modares University in the suburbs of Tehran, Iran, from August to October 2007. Seven soybean varieties including: Willams, Tellar, Zane, Sahar, Dpx, L₁₇, Sari and a genotype, Ks3494, were planted in a randomized complete block design. A field of 638.4 m² was divided into five blocks of 100.8 m and each block consisted of eight plots of 4.2×3 m. There were not any other mite host-plants surrounding the plots.

Sampling program

A sampling technique is a method by which information is collected from a single sample unit. Although the sample unit and sampling technique are a distinct attribute of a sampling program, both are intimately related, since the sampling technique often dictates the type of the sampling unit (Pedigo and Buntin, 1994). Different life stages of *T. urticae* usually colonize on the under-surface of leaves thus one leaf of the soybean was selected as a sampling unit. Leaves were selected randomly and different life stages of mite (immatures and adults) were counted using stereomicroscope in the laboratory, to get an unbiased estimate of the population mean.

A basic tenet of all samplings is random collection, so that the sampling units have an equal chance of being sampled. On this basis, sampling of leaves and the movement among plants were performed randomly. All counts were performed in mid-morning. The sampling was conducted twice a week from 8th August to 14th October 2007.

In order to determine sample size, primary sampling was taken in the equal number of different soybean varieties and the genotype on 8th August 2007. Relative variation (*RV*) is used to compare the efficiency of various sampling methods (Hillhouse and Pitre, 1974). The *RV* of the sampling data was calculated as follows:

$$RV = (SE/m) 100$$

where *SE* is the standard error of the mean and *m* is the mean of primary sampling data. The reliable sample size was determined using the following equation:

$$N = (ts/dm)^2$$

where *N* = sample size, *t* = *t*-student, *s* = standard deviation, *d* = desired fixed proportion of the mean and *m* = the mean of primary data (Pedigo and Buntin, 1994).

Population density

Population density of *T. urticae* was determined in plots of different soybean varieties from 8th August to 10th October in 2007. The mean density of total life stages (immatures and adults) of *T. urticae* were statically analyzed using analysis of variance (ANOVA) and compared among soybean varieties within each sampling data and overall dates.

Spatial distribution pattern

The spatial distribution of *T. urticae* determined by five methods: Index of dispersion, Taylor's power law, Iwao's patchiness regression, Morisita's coefficient of dispersion and Lloyd's mean crowding.

Index of dispersion

Dispersion of a population can be classified by calculating the variance to mean ratio: $S^2/m = 1$ random, <1 regular and >1 aggregated. Departure from a random distribution can be tested by calculating the index of dispersion (I_D), where n is the number of samples:

$$I_D = (n-1) S^2/m$$

I_D is approximately distributed as χ^2 with $n-1$ degree of freedom. Values of I_D which fall outside a confidence interval bounded with $n-1$ degree of freedom and selected probability levels of 0.95 and 0.05, for instance, would indicate a significant departure from a random distribution. This index can be tested by Z value as follows:

$$Z = \frac{\sqrt{2I_D} - \sqrt{(2\nu - 1)}}{\sqrt{2\nu - 1}}$$

$$\nu = n - 1$$

If $1.96 \geq Z \geq -1.96$ the spatial distribution would be random but if $Z < -1.96$ or $Z > 1.96$ it would be uniform and aggregated, respectively (Pedigo and Buntin, 1994).

Taylor's power law and Iwao's patchiness regression

Taylor found a function between mean and variance as:

$$S^2 = am^b$$

where S^2 is the variance; m is the sample mean; a is a scaling factor related to sample size and b measures the species aggregation. If $b = 1$, <1 and >1 , the distribution is random, regular and aggregated, respectively (Taylor, 1961).

By using a log transformation, we can estimate the coefficients with linear regression as:

$$\text{Log}(S^2) = \text{Log}(a) + b\text{Log}(m)$$

where a and b are the parameters of the model, which were estimated by linearizing the equation by a log-log transformation (Martinez-Ferrer *et al.*, 2006).

Iwao's patchiness regression method was used to quantify the relationship between mean crowding index (m^*) and mean (m) using the following equation:

$$m^* = \alpha + \beta m$$

where α indicates the tendency to crowding (positive) or repulsion (negative) and β reflects the distribution of population on space and is interpreted in the same manner as b of Taylor's power law (Iwao and Kuno, 1968). Student t -test can be used to determine if the colonies are dispersed randomly.

$$\text{Test } b = 1 \quad t = (b - 1) / S_b \quad \text{and} \quad \text{Test } \beta = 1 \quad t = (\beta - 1) / S_\beta$$

where S_b and S_β are the standard error of the slope for the mean crowding regression. Calculated values are compared with tabulated t -values with $n-2$ degrees of freedom. If the calculated $t (t_c) < t$ -table (t_t), the null hypothesis ($b = 1$) would be accepted and spatial distribution would be random. If $t_c > t_t$, the null hypothesis would be rejected and if $b > 1$ and < 1 , the spatial distribution would be aggregated and uniform, respectively.

Morisita's coefficient of dispersion I_δ

Morisita (1962) reported a hypothesis for testing the uneven distribution coefficient of I_δ and is calculated by the following equation:

$$I_\delta = \frac{n \sum x_i (x_i - 1)}{N(N - 1)}$$

where n = the number of sample unites, x_i = the number of individuals in each sample unit and N = total number of individuals in n samples.

To determine if the sampled population significantly differs from random, the following large sample test of significance can be used:

$$Z = \frac{(I_\delta - 1)}{\left(\frac{2}{nm^2}\right)^{\frac{1}{2}}}$$

If $1.96 \geq z \geq -1.96$ the spatial distribution would be random but if $z < -1.96$, $z > 1.96$ it would be regular and aggregated, respectively (Pedigo and Buntin, 1994).

Lloyd's mean crowding x^*

Mean crowding (x^*) was proposed by Lloyd to indicate the possible effect of mutual interference or competition among individuals. Theoretically mean crowding is the mean number of other individuals per individual in the same quadrat:

$$x^* = m + \frac{S^2}{m} - 1$$

As an index, mean crowding is highly dependent upon both the degree of clumping and population density. To remove the effect of changes in density, Lloyd introduced the index of patchiness, expressed as the ratio of mean crowding to the mean. As with the variance-to-mean ratio, the index of patchiness is dependent upon quadrat size $x^* / m = 1$ random < 1 regular and > 1 aggregated (Lloyd, 1967).

Sample size model

Taylor's a and b coefficients, taken from Taylor's power law describe the relationship between variance and mean ($S^2 = am^b$) for individuals distributed in a natural population. The mean and variance of sampled mites were determined for each weekly sampling date. Taylor's a and b coefficient were calculated by log-log linear transformation of the mean-variance data, where b is the slop of the transformed data and a equals the antilog of transformed intercept. An equation for estimating pest sample size was developed by Karandinos (1976). Ruesink (1980), Wilson and Room (1982) incorporated Taylor's power law into Karandinos' equation to form the sample size model used in this study (Cullen et al., 2000):

$$N = t_{\alpha/2}^2 d^{-2} am^{b-2}$$

The model contains both variable and constant factors. The variable factors are:

N = Sample size, $t_{\alpha/2}$ = Standard normal variance for a two-tailed interval, m = Mean density of mites in each sampling unit, d = the range of accuracy and a, b = Taylor's coefficients.

RESULT

Sampling program

One leaf of the soybean varieties was selected as a sampling unit, due to the activity of *T. urticae*. The results from primary sampling showed that the reliable sample size of leaves with maximum variation of 20% was 50, 80, 60, 45, 65, 70, 50 and 60 for Williams, Tellar, Zane, Sahar, Dpx, Ks3494, L₁₇ and Sari, respectively. The relative variation (RV) of the primary sampling data was about 12%, 15%, 13%, 11%, 13%, 14%, 12% and 13% for above-mentioned varieties, respectively, which was very appropriate for a sampling program (Table 1).

Population density

The population density estimated as the mean number of overall life stages of *T. urticae* (immatures and adults) per leaf on seven soybean varieties and a genotype is shown in Table 2. The results indicated that there was a significant difference ($P < 0.01$) between population density of *T. urticae* on different varieties of soybean in overall dates. The highest population density of overall life stages of *T. urticae* per leaf was observed on L₁₇ variety (14.15) during sampling dates, which was significantly different from other soybean varieties. During sampling dates, the lowest population density of the mite was observed on Ks3494 genotype and

Zane variety (4.65 and 6.10 overall life stages per leaf, respectively) that was significantly different from other soybean varieties.

Spatial distribution

The results of the variance to mean ratio (S^2/m), coefficient of dispersion (I_D) and Z test are presented in Table 3. The results of sampling showed that the spatial distribution in all soybean varieties and the genotype was aggregated.

In Taylor's model, the regression between $\log S^2$ and $\log m$ was significant for all soybean varieties ($P < 0.01$) and the genotype ($P < 0.05$). Taylor's slope was varied from 1.25 to 1.92 and it was significantly greater than one on all soybean varieties, whereas it was less than one on Ks3494 genotype (Table 4). The calculated $t(t_c)$ was greater than t -table (t_i) for all varieties, indicating an aggregated spatial distribution of *T. urticae*, but Ks3494 genotype had a t_c less than t_i , indicating a random spatial distribution of *T. urticae*.

Iwao's model showed that there was a significant relationship between the mean crowding and the density of *T. urticae* (Table 4). Iwao's slope was varied from 1.47 to 2.11. During sampling periods, all soybean varieties had an aggregated (slope > 1) spatial distribution of *T. urticae*, but Ks3494 genotype had a random pattern with t_c less than t_i .

Morisita's index (I_δ') and Lloyd's mean crowding revealed an aggregated pattern for *T. urticae* on all varieties and the genotype of soybean (Table 5 and 6). Calculated Z was significantly greater than 1.96 in 100% sampling dates. The values of m^*/m was significantly more than one.

Re-calculated sample size using Taylor's coefficient (a and b) on Williams, Tellar, Zane, Sahar, Dpx, L₁₇, Sari varieties and Ks3494 genotype was 12.99, 49, 20.62, 18.38, 29.27, 16.3, 27.73, and 58.62, respectively. These values of sample size can help to improve sampling program of *T. urticae*.

DISCUSSION

Several methods are available for the sampling of spider mites in row crops such as individual plant unit observation, imprint, machine brushing on to a plate, beat cloth, paper, or funnel techniques. The most precise method is direct counting of all life stages of mite on plant leaflets using a stereomicroscope (Kogan and Herzog, 1980). Regarding the life site of *T. urticae*, plant leaves were selected as sampling unit and sampling was conducted for *T. urticae* using stereomicroscope. Roy *et al.* (2005) used the stereomicroscope to count the number of spider mites on raspberry leaves. The population density of *T. urticae* was determined on carambola leaves using stereomicroscope (Shih and Wang, 1996).

In developing sampling programs for either research or management purposes, one must determine two characteristic features of any population, its density and dispersion.

In most sampling dates, the highest population density of the mite was significantly recorded on L₁₇ in comparison with the other soybean varieties and the genotype (Table 2), suggesting that the presence of dens trichomes, softness of leaf tissue and the large size of the leaves of this variety may be the most important factors for its suitability leading to increase the mite population density. The lowest population density of total life stages of the *T. urticae* was on Ks3494 genotype and Zane variety (Table 2). The absence of trichomes, waxy leaves, the small size of the leaves and short growing period of this variety and this genotype of soybean may be the most important reasons for unsuitability and decrease of the population density of the mite. Ahmadi *et al.* (2005) reported the same results with *T. urticae* on bean.

For an applied population biologist, knowledge of a population's aggregation is necessary to develop sequential, binomial or other sampling plans. A change in the aggregation of a species needs an alternation for the sampling plan to have an accurate population count (Slone and Croft, 1998).

The result from variance to mean ratio, Morisita's coefficient and Lloyd's mean crowding indicated that *T. urticae* had an aggregated distribution on all soybean varieties and the genotype (Table 3, 5 and 6), suggesting that the presence of an mite individual at one point lead to increase the probability of another individual being nearby, and habitat occupation probability have not been the same for all individuals. Aggregation distribution of *T. urticae*, is probably due to its high fecundity and its oviposition behavior in laying eggs as clumps. In addition, *T. urticae* females have limited mobility, once a female colonized on a new leaf and started producing offspring, aggregation increases. This behavior has been described for *T. urticae* on other crop systems (Kennedy and Smitley, 1985), and it implies that large samples are required to obtain density estimates at an acceptable level of precision. Aggregated spatial distribution of *T. urticae* in a carambola orchard was evaluated by Shih and Wang (1996). The high degree of patchiness created by the aggregative behavior of *T. urticae* minimizes the attack rate from the predators (Sabelis, 1981) and enhances the advantages of a complex life type, a fitness of survival and a reproductive strategy of this pest (Shin and Wang, 1996). Greco *et al.* (1999) demonstrated that spatial distribution of *T. urticae* on strawberry was aggregated. So (1991) estimated that spatial distribution of *T. urticae* on rose was non-random and follows a negative binomial distribution. Ahmadi *et al.* (2005) reported that spatial distribution pattern of *T. urticae* in bean, using index of dispersion, was aggregated. These results were similar to those found by Raworth (1986) on strawberries and Margolies *et al.* (1984) on peanut. Although some studies have used chi-square goodness of fit test to compare the observed and expected

frequency data under the negative binomial or poisson distributions, this statistical procedure is not usually recommended. Since Morisita's coefficient estimate spatial distribution of each date using the mean and variance of each sampling date separately, therefore it seems it would be more accurate than the index of dispersion.

Regression models of Taylor's power law and Iwao's patchiness were more accurate than the variance to mean ratio, since the mean and variance of each sampling date was used separately. Spatial distribution pattern of *T. urticae* using Taylor's power law and Iwao's patchiness were obtained random on Ks3494 genotype and were recorded aggregated on all soybean varieties (Table 4), suggesting that different plant varieties can affect spatial distribution of this mite. The random distribution pattern on Ks3494 genotype using Taylor's power law and Iwao's patchiness, suggesting that the different statistical methods have various results and accuracy in calculating spatial distribution of an organism. The random distribution pattern of Ks3494 genotype showed that the presence of an individual on a leaf is not affected by the presence of another individual, and all leaves had similar probabilities of being occupied by an individual. This can be due to the lower population density of *T. urticae* on this genotype. Ahmadi *et al.* (2005) reported that the spatial distribution pattern of *T. urticae* on four bean varieties, using variance to mean ratio, was aggregated but using Taylor's power law, on three varieties was aggregated, and on one variety was random. Martinez-Ferrer *et al.* (2006) determined the distribution pattern of *T. urticae* for different types of leaves and fruit of clementine's in Spain and noted that dispersion patterns generated by Taylor's power law demonstrated the occurrence of aggregated pattern ($b > 1.21$) on both leaves and fruit of clementine's. Shih and Wang (1996) observed that by using Taylor's power law and Iwao's patchiness regression analysis, spatial distribution of *T. urticae* in carambola orchard was aggregated. However, the data obtained for Sari variety and Ks3494 genotype had better fit with Taylor's power law ($r^2 = 87.6\%$ and 70.3% , respectively) in comparison with Iwao's model ($r^2 = 75.3\%$ and 54.6% , respectively).

CONCLUSIONS

This research demonstrated that the different soybean varieties and genotypes had significant effects on the population density and spatial distribution patterns of *T. urticae*. During growing season, population density of the mite on different varieties and one genotype of soybean was significantly different. The highest population density of the pest was seen on L₁₇ and the lowest density was obtained on Ks3494 genotype and Zane variety. Other varieties of soybean had intermediate values. The coefficients obtained from spatial distribution models can be used in developing a sampling program and evaluating the efficiency of natural enemies for controlling of *T. urticae* on different varieties of soybean.

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Table 1. Estimated parameters by primary sampling of *T. urticae* on different soybean varieties and the genotype in 2007.

Var. and gen.	n	SE	SD	RV	m	d	N
Williams	50	1.056	7.44	12.11	8.72	0.20	50
Tellar	50	0.181	1.286	15.68	1.16	0.20	80
Zane	50	0.771	5.457	13.26	5.82	0.20	60
Sahar	50	0.149	1.059	11.70	1.28	0.20	45
Dpx	50	0.164	1.166	13.74	1.2	0.20	65
Ks3494	50	0.19	1.348	14.44	1.32	0.20	70
L ₁₇	50	2.168	15.33	12.17	17.82	0.20	50
Sari	50	0.55	3.95	13.18	4.24	0.20	60

Var and gen = Varieties and the genotype of soybean, n = Number of samples, SE = Standard error of the mean, SD = Standard deviation of the mean, RV = Relative variation, m = Mean of primary data, d = Desired fixed proportion of the mean and N = Sample size

Table 2. Mean (\pm SE) population density of overall life stages of *T. urticae* (per leaf) on different soybean varieties and the genotype in 2007.

Date	Wil.	Tel.	Zan.	Sah.	Dpx	Ks3.	L ₁₇	Sar.
10Aug.	7.98 \pm 0.96 b	1.98 \pm 0.32de	5.68 \pm 0.70bc	1.42 \pm 0.15e	2.32 \pm 0.42de	1.71 \pm 0.40e	16.82 \pm 1.92a	4.63 \pm 0.66cd
19Aug.	16.10 \pm 1.9 0b	7.99 \pm 0.90c	9.17 \pm 1.33c	5.71 \pm 1.00c	9.23 \pm 1.23c	4.90 \pm 0.66c	25.34 \pm 4.13a	8.45 \pm 1.36c
23Aug.	13.34 \pm 1.4 9b	10.96 \pm 1.48b c	11.17 \pm 1.64bc	6.93 \pm 1.40bc	11.95 \pm 1.53bc	5.83 \pm 0.68c	28.18 \pm 4.09a	11.77 \pm 1.81bc
27Aug.	10.00 \pm 1.1 5bc	12.73 \pm 1.33b c	9.50 \pm 1.36bc	7.49 \pm 1.36c	24.46 \pm 3.05a	6.59 \pm 1.04c	29.22 \pm 4.22a	15.63 \pm 1.89b
31Aug.	5.00 \pm 0.70 cd	11.65 \pm 1.59b	4.23 \pm 0.75d	9.80 \pm 1.61bc	17.29 \pm 1.973a	4.40 \pm 0.53d	17.04 \pm 1.97a	12.90 \pm 1.60ab
4 Sep.	4.42 \pm 0.65 d	10.68 \pm 1.10b c	3.38 \pm 0.43d	10.37 \pm 1.41bc	15.69 \pm 1.52a	6.95 \pm 1.23cd	13.66 \pm 1.94ab	13.60 \pm 1.39ab
8 Sep.	2.36 \pm 0.36 c	8.27 \pm 1.021b	2.60 \pm 0.45c	7.82 \pm 1.35b	9.10 \pm 1.21ab	2.14 \pm 0.47c	6.64 \pm 1.37b	12.36 \pm 1.78a
12 Sep.	3.66 \pm 0.65 cd	8.05 \pm 1.07bc d	3.03 \pm 0.55d	11.87 \pm 1.59b	18.09 \pm 2.33a	—	8.24 \pm 1.38bc	11.62 \pm 1.49b
16 Sep.	1.96 \pm 0.42 c	6.95 \pm 0.88b	—	12.62 \pm 1.87a	11.13 \pm 1.39ab	—	8.32 \pm 1.27b	10.68 \pm 1.18ab
20 Sep.	.92 \pm 0.22c	5.87 \pm 0.85b	—	11.28 \pm 1.77a	8.41 \pm 1.04ab	—	6.28 \pm 1.22b	9.40 \pm 1.47ab
24 Sep.	—	5.12 \pm 0.59ab	—	4.35 \pm 0.83b	6.21 \pm 0.69ab	—	5.78 \pm 1.04ab	7.50 \pm 1.016a
28 Sep.	—	6.22 \pm 0.83b	—	5.82 \pm 1.16b	5.35 \pm 0.793b	—	4.22 \pm 0.85b	10.56 \pm 0.85a
2 Oct.	—	6.95 \pm 1.0b	—	5.60 \pm 1.10b	17.74 \pm 3.09a	—	—	11.57 \pm 1.75ab
6 Oct.	—	5.32 \pm 0.83b	—	6.71 \pm 1.49b	—	—	—	12.07 \pm 1.94a
10 Oct.	—	—	—	2.42 \pm 0.62a	—	—	—	2.16 \pm 0.47a
Overalls dates	6.57 \pm 0.38 de	7.85 \pm 0.29d	6.10 \pm 0.38ef	6.97 \pm 0.34de	12.08 \pm 0.52b	4.65 \pm 0.30f	14.15 \pm 0.78a	10.33 \pm 0.40c

* The means followed by different letters in the same row are significantly different ($p < 0.01$, LSD)

* Dashes in the columns indicate the end of sampling

Wil. = Williams, Tel. = Tellar, Zan. = Zane, Sah. = Sahar, Ks3. = Ks3494, Sar. = Sari

Table 3. Spatial distribution parameters (variance to mean ratio) of *T. urticae* on different soybean varieties and the genotype during 2007.

Var. and gen.	S^2/m	I_D	Z
Williams	10.99	5487.48	73.165
Tellar	12.259	13717.657	118.34
Zane	11.512	5514.31	74.082
Sahar	12.196	8769.117	94.523
Dpx	19.43	15455.486	134.742
Ks3494	9.711	4748.873	66.2
L ₁₇	26.215	15702.986	142.62
Sari	13.963	12552.93	116.04

Var. and Gen. = Varieties and the genotype of soybean

Table 4. Spatial distribution of *T. urticae* on different soybean varieties and its genotype during 2007 using Taylor's power law and Iwao's patchiness regression analysis.

Var. and gen.	Taylor		Iwao										
	a	b	SE_b	r^2	P_{reg}	t_c	α	β	SE_β	r^2	P_{reg}	t_c	t_t
Wil.	0.437	1.44	0.07	97.4	0.00	6.10	1.71	1.47	0.05	98.6	0.00	8.10	2.30
Tel.	0.538	1.50	0.15	87	0.00	3.33	81.10	1.85	0.24	81.1	0.00	3.46	2.17
Zan.	0.326	1.74	0.18	92.5	0.00	4.11	0.47	2.11	0.18	94.9	0.00	6.03	2.44
Sah.	0.187	1.92	0.20	86.5	0.00	4.65	4.29	1.63	0.21	79.6	0.00	2.88	2.16
Dpx	0.307	1.74	0.14	92.3	0.00	5.28	-0.54	2.07	0.25	84.1	0.00	4.16	2.20
Ks3.	0.722	1.25	0.32	70.3	.011	0.78	2.34	2.08	0.72	54.6	0.03	1.48	2.57
L ₁₇	0.531	1.59	0.13	92.9	0.00	4.53	2.71	1.89	0.15	93.5	0.00	5.93	2.22
Sar.	0.563	1.51	0.15	87.6	0.00	3.40	4.15	1.69	0.255	75.3	0.00	2.70	2.16

Var. and Gen. = Varieties and the genotype of soybean, Wil. = Williams, Tel. = Tellar, Zan. = Zane, Sah. = Sahar, Ks3. = Ks3494, Sar. = Sari

Table 5. Parameters of Morisita's index and Z calculated of *T. urticae* on different soybean varieties and the genotype in 2007.

Date	Wil.		Tel.		Zan.		Sah.		Dpx		Ks3.		L17		Sar.	
	I_s	Z	I_s	Z	I_s	Z	I_s	Z	I_s	Z	I_s	Z	I_s	Z	I_s	Z
10Aug.	6.44	766.19	2.62	182.02	1.76	181.75	0.803	-8.97	2.7	181.82	4.38	287	1.58	348.48	2	196.82
19Aug.	1.55	315.42	1.88	400	2.14	446.62	2.18	215.8	2.03	439.92	2.29	313.35	2.26	1046.4	2.43	502.9
23Aug.	1.54	256.13	2.36	850.6	2.2	568.68	2.67	368.2	1.97	534.96	1.79	229.12	2	998.3	2.57	748.2
27Aug.	1.56	199.29	1.78	1962.5	2.11	450.2	2.34	319.8	1.95	1073.6	2.57	512.11	1.99	1023	1.88	483.2
31Aug.	1.79	139.82	2.39	932	2.66	299	2.09	342.3	1.7	617.46	1.81	177.49	1.59	360.8	1.54	315.6
4 Sep.	1.87	138.25	0.175	-499	1.7	229.64	1.72	238.0	1.54	392.35	3.01	695.25	1.92	445.2	2.14	600.7
8 Sep.	1.75	63.19	2.08	518.5	2.45	160.05	2.2	299.9	2.02	430.34	4.02	320.34	2.9	462.9	1.89	439.7
12 Sep.	2.30	169.09	2.29	616.15	2.68	216.35	1.71	268.9	2.11	880.54	-	-	2.26	368.8	2.36	514.4
16 Sep.	2.82	127.01	2.14	457.2	-	-	1.89	359.4	1.9	465.33	-	-	2.04	306.8	2.34	536.3
20 Sep.	2.84	59.93	2.51	503	-	-	1.99	358.8	1.86	279.83	-	-	2.7	379	1.95	303.8
24 Sep.	-	-	1.88	260.58	-	-	2.39	193.4	1.69	197.38	-	-	1.34	94.62	2.31	632.4
28 Sep.	-	-	2.27	456.78	-	-	2.6	297.1	2.22	301.2	-	-	2.76	263.93	2.26	621.9
2 Oct.	-	-	2.67	671.2	-	-	2.54	274.5	2.89	1545.9	-	-	-	-	2.45	744.5
6 Oct.	-	-	2.78	541.81	-	-	3.04	435.7	-	-	-	-	-	-	3.4	129.17
10 Oct.	-	-	-	-	-	-	3.57	198.6	-	-	-	-	-	-	-	-

* Dashes in the columns indicate the end of sampling

Wil. = Williams, Tel. = Tellar, Zan. = Zane, Sah. = Sahar, Ks3. = Ks3494, Sar. = Sari

Table 6. Estimated parameters by Lloyd's mean crowding and Lloyd's mean crowding to mean for *T. urticae* on different varieties and the genotype of soybean in 2007.

	Wil.	Tel.	Zan.	Sah.	Dpx	Ks3.	L17	Sar.
m^*	16.56	19.1	16.61	18.16	30.48	13.35	39.36	2.78
m^*/m	2.52	2.43	2.72	2.6	2.52	2.87	23.29	2.25

Wil. = Williams, Tel. = Tellar, Zan. = Zane, Sah. = Sahar, Ks3. = Ks3494, Sar. = Sari