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MOLECULAR IDENTIFICATION, HOST RANGE AND DISTRIBUTION OF *PHENACOCCUS SOLENOPSIS* TINSLEY (HEMIPTERA: PSEUDOCOCCIDAE) ON ORNAMENTAL PLANTS IN BAGHDAD GOVERNORATE, IRAQ

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Abstract

The solenopsis mealybug *Phenacoccus solenopsis* Tinsley (SMB) (Hemiptera: Pseudococcidae), appeared as a major invasive insect pest of many crops in Asia at the commencement of the 21st century. Species recognition is becoming more extensive - range in diagnostics and ecological studies, mainly with regard to insects for which morphological recognition is difficult or time - consuming. We used PCR and DNA nucleotide detection sequence technologies for species characterization. PCR results showed that total nucleotide length was 720 bp. Alignment of above sequence with NCBI database revealed that samples of mealybug adults showed 99 % similarity with SMB. Results in case of plants infestation by SMB according to location, revealed that Tagi and Greaat locations were the highest in infestation than others while Baghdad Park was the least, infestation percentage was highest in *Osteospermum* sp. and least in *Carissa macrocarpa*. Infestation intensity was highest in *Osteospermum* sp. and *Adhatoda vasica* and least in *C. macrocarpa*. It revealed 21 ornamental plant species belonging to 15 families as SMB hosts with various levels of infestations. The infestation categorized in grades 1- 4 based on the severity of infestation, .revealed three plant species namely, *Duranta erecta, . Adhatoda vasica and Hibiscus Rosa-sinensis* to be the preferred hosts (grade 4). The 18 others were grouped in grade 1 - 3 with low to moderate infestation.

Key words : Molecular identification, Host range, *Phenacoccus solenopsis* Tinsley, ornamental plants.

Introduction

SMB appeared .recently and reached the status of serious pest on an extensive range of host plants. .It is an exotic mealybug, .It was initially reported on ornamentals and fruit yields in New Mexico (Ben - Dov *et al.,* 2009) and then spread in different regions of the world, lately, as a polyphagous herbivore, SMB can feed on a multiplicity of plants in newly invaded regions (Fand and Suroshe 2015), therefore, it was noted in many countries outside the North American mainland, including Hawaii, South America, the Caribbean Islands, Central America, Africa, Asia, and Oceania (Hodgson *et al.,* 2008; Charleston and Murray 2010) and Iraq (Abdul – Rassoul *et al.,* 2015) Wang *et al.,* (2010) revealed that maximum occurrence of this pest was detected on China rose, .*Hibiscus chinensis* followed by okra, *Abelmoschus esculentus*. It was recorded on 154 plant species containing field crops, vegetables, ornamental, weeds, bushes and trees most of these belong to the families Malvaceae, Solanaceae, Asteraceae, Euphorbiaceae, Amarantheceae and Cucurbitaceae (Arif *et al.,* 2009).

SMB produces honey dew causing sooty mould growth, .which deters photosynthesis (Arif *et al.,* 2012). At high infestation rate, the infested plants become undersized, weak and produce only a few fruits or vegetable growth. The leaves looked distorted, became yellow and finally drop off causing severe damage to the crop (Culik and Gullan, 2005) .

Characterization of insect pests is considered an initial

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step in their lives and ecology study, injury evaluation and then its control. The most known means of mealybugs identification, based on morphological traits, morphological recognition of mealybug species is usually time-consuming, requires a high degree of taxonomic expertise and usually only mature females can be identified . . . . . (Saccaggi *et al.,* 2007). Along the latter decades, there has been an international trend in biological studies to use molecular methods for diagnosis analysis, among these approaches PCR, it is a reliable technique to identify these insect species. The use of molecular diagnostic approaches has been increasing in biological studies because of its high sensitivity, reliability and exactness for the detection and identification of DNA (Mendoza *et al.,* 2006; Barcenas *et al.,* 2005).

In the present study, a survey to detect the host range and distribution of SMB on ornamental plants in Baghdad governorate and molecular identification of SMB using mitochondrial COI gene (primers COI F and COI R) .infesting ornamental plants was carried out.

Materials and Methods

Molecular Identification

DNA extraction, amplification, sequencing and analysis

Adults of SMB were collected (during the survey to detect hosts), DNA was extracted to identify species and draw phylogenetic relationships among species, a set of primers (28S F and R) (Ashfaq *et al.,* 2010) were used for polymerase chain reaction (PCR) amplification of rDNA (Table 1). PCR amplifications using the primers (28S F and 28S R) was performed, then samples which electrophoresis results appeared in it DNA fragments amplification were sent to south Korean company (Microgene) to detect its sequencing.

Host Range and Distribution of SMB

Field surveys were carried out from 1 September to 1 December 2019 as this is the period with the highest abundance of mealybugs in ornamental plants - growing areas in Iraq. We surveyed in different locations in Baghdad governorate, these locations were Baghdad park, Greaat, Tagi, Zauraa and Rasheed. Surveys were conducted every 15 days and the plants were sampled at different stages, vegetative, flowering and fruiting stage. specimens of insects were sent to molecular identification, then morphological identification of pest was done using hand lens, and utilizing identification keys (Zim and Cottam, 1987). Plants sampled based on literature indicate their suitability to be SMB host plants, furthermore, .there is a previous knowledge of other plants were infested .by SMB based on work expertise. The ornamental plants were also collected and preserved as herbarium to confirm their botanical identity by the assistance of plant taxonomist. During each survey, the Plant species on which SMB adults or nymphs were found were defined as host plants of this insect.

Infestation percentage

During the survey times, number of individuals for every plant species was selected dependent on the total number of the plant in location of study (some plants may be found in few numbers and other plants in many numbers), 30 samples were randomly selected per survey date for each plant species and sampling was repeated 6 – 8 .times during study period, then examined for their SMB infestation, the data on infest. percentage was calculated as :

Infest. percentage =

$$\frac{\text{Number of infested plants}}{\text{Total number of examined plants}}\times 100$$

Infestation intensity

Infest. intensity was calculated for number of SMB - infested leaves and twigs as :

Infest. intensity for leaves .=

$$\frac{\text{Number of infested leaves}}{\text{Total number of leaves}}\times 100$$

Infest. intensity for twigs =

$$\frac{\text{Number of infested twigs}}{\text{Total number of twigs}}\times 100$$

Infestation level

Whole plants of the species under observation during sampling were examined and followed for occurrence and infestation level (grade) as described below :

The observation of host plant detailed as 0 - 4 grades (Nagrare et. al. 2009), where 0 - no infestation, 1 - scattered appearance of mealybug on plant, 2 -

Table 1: The specific primer 28S of gene used for DNA amplification and sequencing of SMB.

Primer	Sequence	Tm (ºC)	GC (%)	Product size
Forward	5'- GAG AGT TMA ASA GTACGT GAAAC- 3'	52.3	44	720 base pair
Reverse	5'- TCG GAR GGAACC AGC TAC TA - 3’	56	42	

appearance of mealybug on one branch, 3 - infestation on more than 2 branch or half portion of plant and 4 - severe infestation on whole plant.

Statistical analysis

Nucleotide sequence was analyzed using Mega X computer programs (Kumar *et al.,* 2018) and SDT (Muhire *et al.,* 2014). Statistical analysis of survey data obtained for infestation percentage and intensity was done using genstat program via complete randomized blocks design.

Results and Discussion

Molecular identification

The DNA of mealybug specimens that collected during survey have been matched to that of *Phenacoccus solenopsis* Tinsley from genbank (China populations [GenBank accession number KJ461274.1 and KY211350.1] and Brazil population (GenBank accession number MH248357.1) sequence with 99 % similarity (Fig. 1) (Table 2). The sequence was compared with sequences in the genbank using Mega x program, based on the results of the blast in the systems, these species were *P. peruvianus* (MN647620.1) with 44 % similarity and *P. madeirensis* (MH432262.1) with 38 % similarity (Fig. 1).

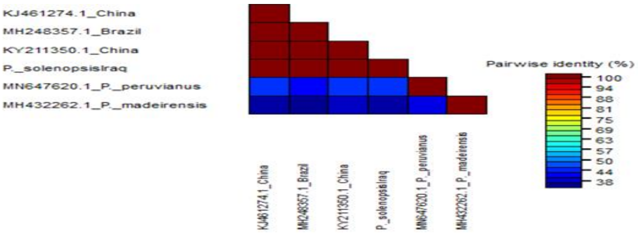

Fig. 1: Similarity between SMB and other *Phenacoccus* species populations from Iraq, China and Brazil.

The amplified PCR products using the set primers 28S from the rDNA .gene were 720 bp as expected and M represent the standard laddered DNA with 100 bp (Fig. 2) .The nucleotide alignment obtained of SMB population from Baghdad was registered to the NCBI Genbank under the accession number (SUB7061690 MH1 MT123784).

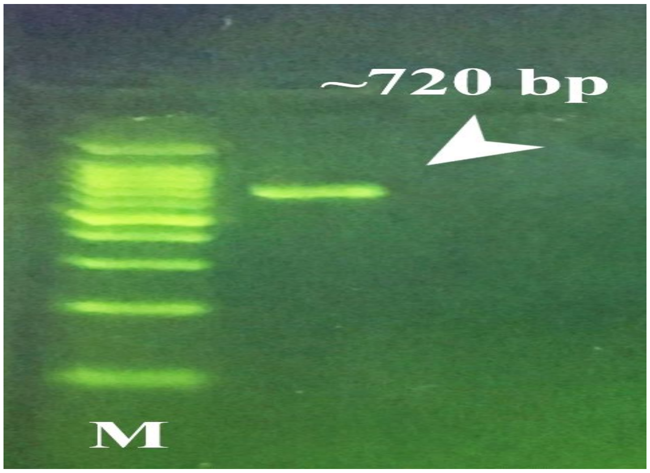

Fig. 2: Separation of PCR products during electrophoresis in agarose gels using 28S (F and R) primers.

According to the sequence alignments obtained from the Genbank, a phylogenetic tree was constructed. According to the neighbor - joining phylogenetic tree, there were three clades, first clade was SMB populations from china, Brazil and Iraq, second clade was *P. madeirensis* population and .third clade was *P. peruvianus* population. The specimens from Baghdad are placed in the same subgroup as those from China and Brazil (Fig. 3).

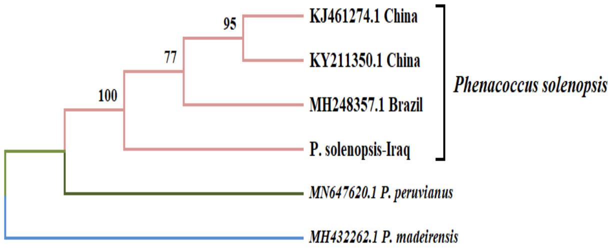

Fig. 3: Phylogenetic tree from Genbank sequences of SMB populations.

The sequence homology was highest with the species (SMB) *P. solenopsis* recorded in china (KJ461274.1 and KY211350.1) and Brazil (MH248357.1) .from the genus *Phenacoccus* with 99% similarity. With the species *P. peruvianus* (MN647620.1) reduced the nucleotide similarity (44%) was observed between our .specimens and the closest match and reduced more with the species, *P. madeirensis* (MH432262.1) with similarity 38 %. Based on the significant homology of the barcoding region of 28S from our specimens with that of SMB, we are inclined to recognize the findings by (Abdul-Rassoul et.

Table 2 : DNA amplification of SMB in primer 28S (F/R) using PCR.

No. of sample	Type of substitution	Location	Nucleotide	Sequence ID	Score	Identities	Source
1	Transvertion	1062	C>A	ID: KJ461274.1	1317	99%	*Phenacoccus solenopsis* 28S ribosomal RNA gene
	Transvertion	1063	C>T				

al. 2015) that the mealybug species damaging ornamental, fruit and vegetable plants in Baghdad .was SMB. Results revealed that the nucleotide sequence for SMB population from Baghdad (Iraq) was as below :

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TTAACCATACGTGAAACCGTTCGGGGGTAAACGGACAGAGCCCGTGAA
TCCGGGCGGCAGAATTCAGAGACGATGGCGGCAACGTTGTCGGTTCGA
TATTTCTGTCGCCGGCACGGACGTCGCGACCCGTTTGGTGTCGGTCTCA
GGAGACGCGTTTCACGTTCGTCGACGCGTCGTCTGCCTCGGTAGGCGCG
CGTTGCGAGTACGCGTTCGTGTTCCGGCCGACTCGCCAGACGGTAGGTT
AATGGTGGCCGCGGCGGTCGTTCGCTTCGCGGCGATCAGCGCCGTCCG
CGGTGCCGGTTTGCGACGAATCTTCGGGCCTCTTTCCGACCCGTCTTGA
AACACGGACCAAGGAGTCTAACGTGCGCGCGAGTCGCGGGGTGTCGAG
CGGCGGTCGTGTTTCGGCACGACCGTCGTTCGTTACGACGCGAAACCCG
TACCGTTCATTCGGAAGGCGCAATGAAAGTGAAATGGGGAAGATGGCG
TTACCGAGTTCACGTTTCGCGACTCGATCGCGACCGGTCGCCCGCATTC
CCAGGGCGTCCCAACGGCTCGGCGGCGTTGCGGATCGTCGTTCCTTCGG
GAACGGCGGTCGGGCGTCGTCGGTCCGGGGCGCACCTACAGCGTGCAC
GTTGGTACCCGAAAGATGGTGAACTATGCCCGGCCAGGATGAAGTCAG
GGGAAACCCTGATGGAGGTCCGCAGCGATTCTGACGTGCAAATCGATC
GTCTGAGCTGGGTATA
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In our study on the molecular characterization of SMB, reconstructed the phylogenetic relations of 3 *Phenacoccus* species based on nucleotide sequence, we determined that the phylogenetic tree was divided into three major clades and that *P. madeirensis* was placed in the third lineage, *P. peruvianus* in the second linage and SMB (from Iraq, Brazil and China) in the first lineage. Our study registered with Genbank the first rDNA region sequence of SMB population from Baghdad in Iraq . Data recorded in Genbank can be used as a reference for further studies.

Infestation percentage of SMB on ornamental plants according to location

Results in (Fig. 4) showed that Al-Tagi location was with high infest. By SMB on ornamental plants, infest. Percentage was 73.3 %, while lowest infest. Was in Baghdad park location which didn't exceed 25.8 %, other locations graded in their infest., it were 63.2, 40.33 and 32.23% in each of Greaat, Al-zauraa and Al-Rasheed respectively.

Regarding the infest. percentage according to location, its revealed that ornamental plants infestation with SMB in north locations (Tagi and Greaat) were more than in other locations, this may due to its geographical location near agricultural fields heavily planted by different plants such as vegetable, fruit, field and as well as ornamental plants.

Infestation percentage by SMB on ornamental plants according to host plant

The results in Fig. 5 referred that the plants *Osteospermum* sp, *Duranta plumieri* and *Lantana camara* were had the highest infestation by SMB than other plants, infest. Percentage were 100, 80 and 58.3 % .respectively. then followed by *Euphorbia trigona*, *Sansevieria trifasciata* and *Adhatoda vasica* as their infest. Percentage were 50, 50 and 46.5 % respectively. Infest. Percentage on *Carissa macrocarpa* was the lowest along other plants, it was only 1.85 %. while the plants *Rosa regosa*, *Alternanthera dentata*, *Leucophyllum frutescens*, *Duranta erecta*, *Portulaca grandiflora*, *Carthoranthus vinca* and *Vier agnus-castus* were with more infest. Than C. macrocarpa, its infest. Percentage were 4.44, 7.25, 8.33, 25, 26.4, 27.8 and 28.1 % respectively. while the plants *Ipomoea batatas*, *Agave sisclane*, *Dodonae angastifolia*, *Aphelandra squarrosa*, *H. rosa-sinensis* and *Tagetes patula* graded in infest. Percentage which were 20.8, 33.3, 34.2, 35, 37.26 and 40 % respectively.

Abbas *et al.,* (2010) reported the infest. percentage of SMB on *H. rosa-sinensis*, it reached to 96.4 %, L. *camara* 38 %, *Duranta repens* 35.3%, *P. greandiflora* 23.3 % and *E. .prostrate* 14.9 %. So they referred (Abbas *et al.,* 2010) that *Gossypium hirsutum* (Malvaceae) and *H. rosa-sinensis* were the top two favored host - plant

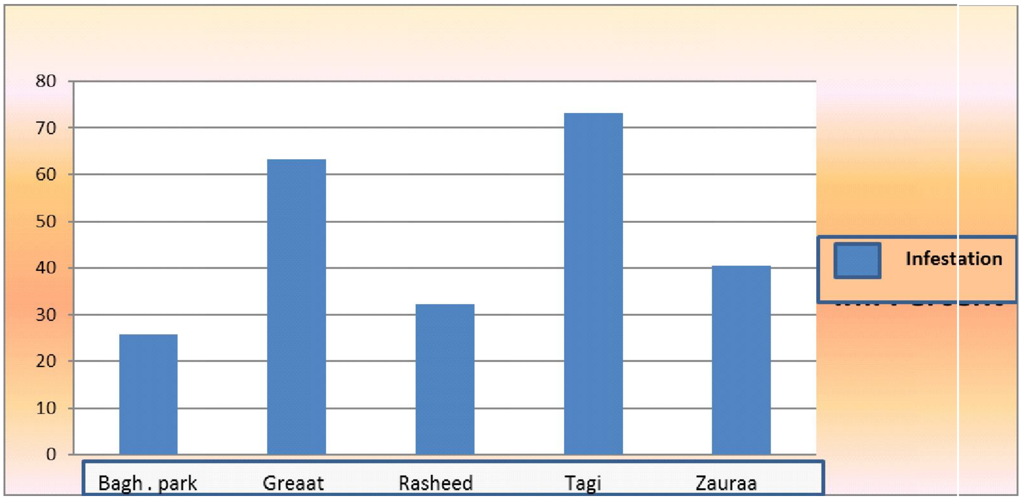

Fig. 4: Infestation percentage by SMB on ornamental plants according to location.

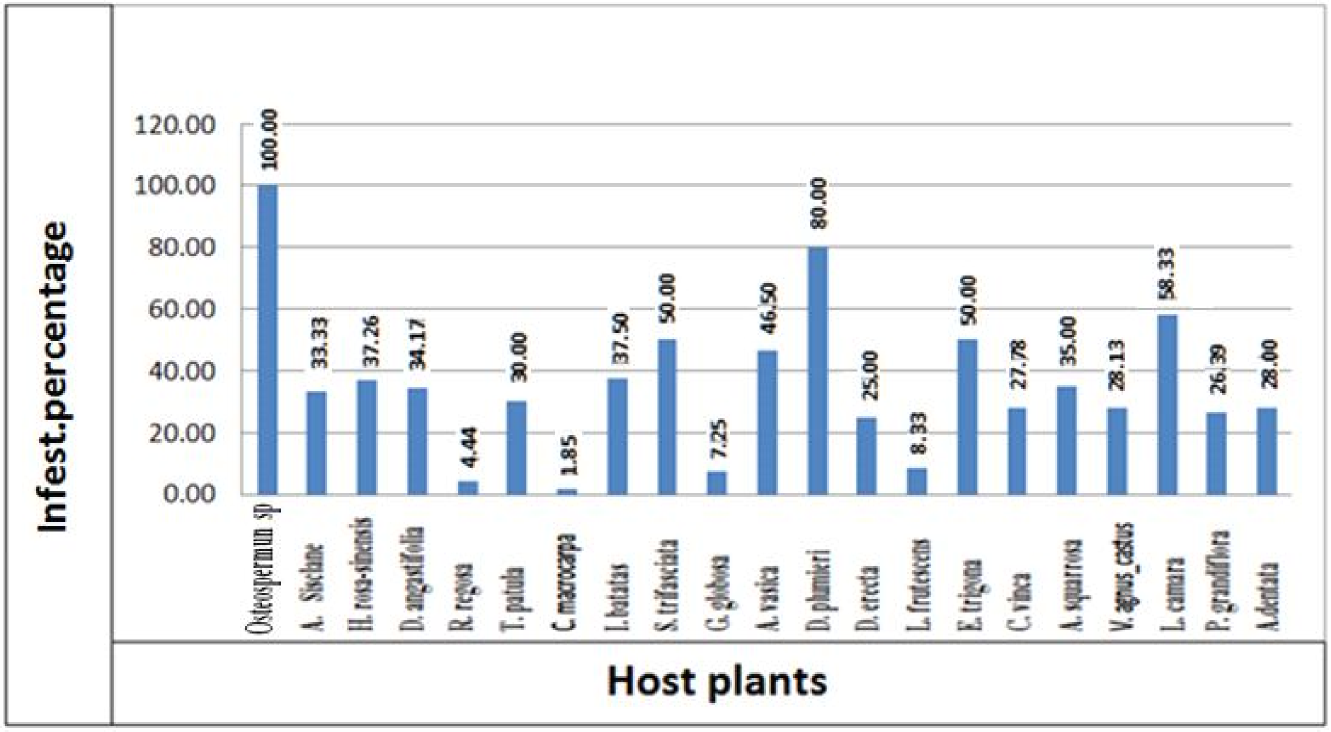

Fig. 5: Infestation percentage by SMB on ornamental plants according to host plant.

species, when assessed in the field by SMB infestation intensity and percentage on observed plants.

Infestation intensity

Infestation intensity on upper level of host plant

It is illustrated from the results in fig.6 that highest infest. Intensity by SMB on upper level of ornamental plants in this study was on each of *D. plumieri* and *A. sisclane* as it reached 55.5 and 33.33 % respectively. Followed by *H. rosa-sinensis*,*E. trigona*, L. *camara* and *D. angastifolia* as infest. Intensity reached in it, 22.57, 16.67, 13.24 and 2.79 % respectively. while there was no infest. in the plants *S. trifasciata*, *p. grandiflora*, *V. agnus-castus*, *C. vinca*, L. *frutescens*, *D. erecta*, *A. vasica*,*I. batatas*, *C. macrocarpa*, *A. squarrosa*, *Osteospermum* sp, *A. dentata*, *T. patula*, *R. regosa* and *Gomphrena globosa*.

Infestation intensity on middle leaf level .of host plant

In case of infest. intensity on the middle level of plant, results in Fig. 7 referred that there were higher infest. intensity on *D. plumieri* which reached 67.80 %, then followed by *Osteospermum* sp with infest. intensity reached 55.56 % while it reached 33.33 % on each of *A. sisclane* and *E. trigona*. Infest. intensity on L. *camara* and *H. rosa-sinensis* reached 19.34 and 17.18 % respectively. The lowest infest. intensity was recorded on each of *D. angastifolia* and *D. erecta*, and there were no infestation on other plants.

Infestation intensity on lower level .of host plant

Unlike the other plant levels, infest. intensity on lower plant level in fig. 8 was high on each of *A. vasica* and *O. spermum* which reached 100%, while it was near to its average on previous levels for *D. plumieri* as it reached 69.49 %. While infest. do not appeared on the upper and middle levels of plants, it appeared on lower level in it, such as Vi agnus-castus, *C. vinca*, *P. grandiflora*, L. *frutescens*, *S. trifasciata*, *I. batatas*, *A.squarrosa*, *A. dentate*, *T. patula*, *R. regosa* and *G. globosa.*

The difference in SMB preference for plants level may due to difference in plant nutrients in each level, Liu *et al.,* (2004) also mentioned that nutrients in plants play important role in the suitability of feeding insect pest, because of quantitative and qualitative nutritional requirement of insect pest for food. Nitrogen being a important element of chlorophyll and protein molecules helps in the construction of chloroplasts and accumulation of chlorophyll in them that make plant juicy (Daughtry, 2000; Amaliotis *et al.,* 2004).

Infestation intensity on total levels of host plant

In the comparison of infest. intensity on different plant levels, results in Fig. 9 showed that there was infest. on all of plant levels in each of *D. plumieri*, *A. sisclane, E. trigona*, *H. rosa-sinensis*, L. *camara* and *D. angastifolia*, the highest infest. intensity was on *D.*

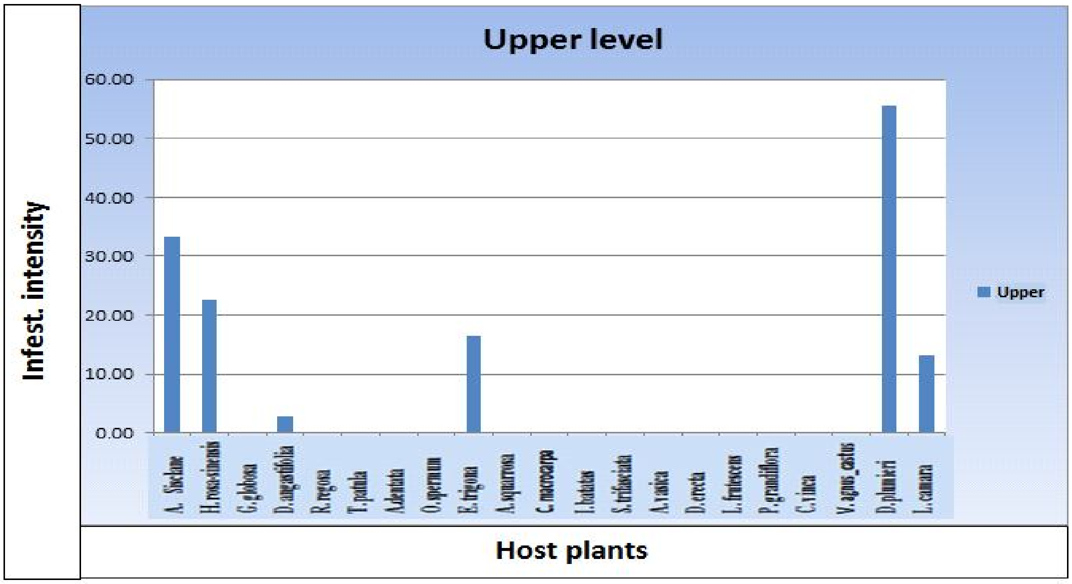

Fig. 6: Infestation intensity on upper level of host plant.

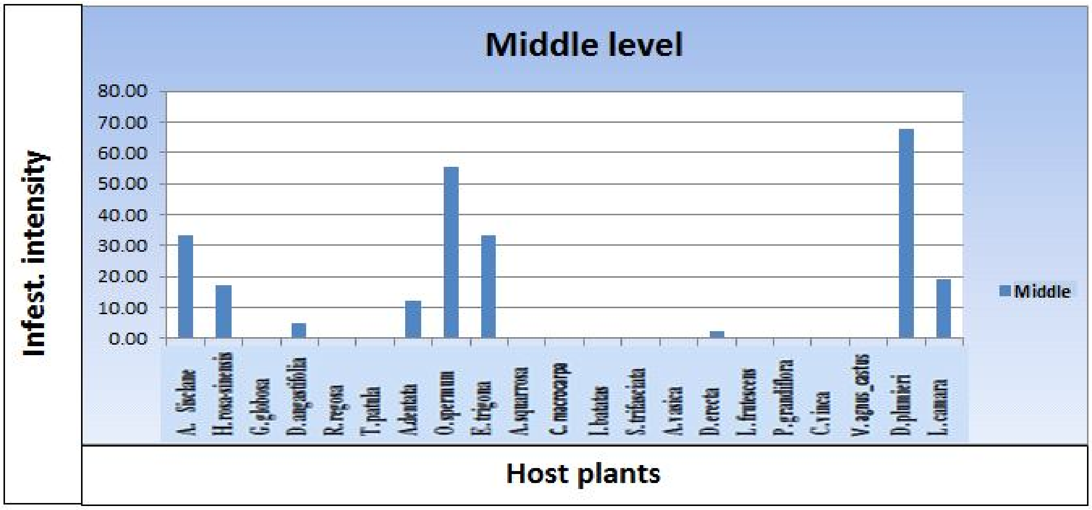

Fig. 7: Infestation intensity on middle leaf level of host plant.

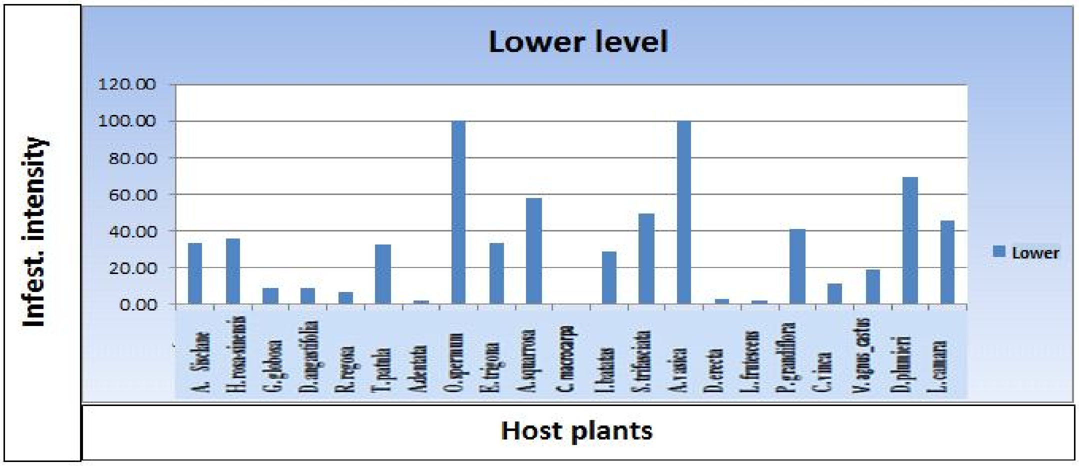

Fig. 8: Infestation intensity on lower level of host plant.

plumieri and the lowest was on *D. angastifolia*. While in the plants *Osteospermum* sp, *A. dentata*, *D. erecta*, infest. intensity was only on upper and middle levels, and it was only on upper level in each of *V. agnus-castus*, *C. vinca*, *P. grandiflora*, *L. frutescens*, *A. vasica*, *S. trifasciata*, *I. batatas*, *A. squarrosa*, *T. patula*, *R. regosa* and *G. globosa*. Results showed that there was no infest. on *C. macrocarpa*.

The variation in SMB plant and plant level preference between different plants may due to imbalanced food nutrients for the proper growth and development of this pest. Nutritive requirement and fitness of insect pests depends upon the nutrient quality of host plant. The additive effects of biochemical elements especially dietary necessities influence the life parameters of herbivorous insect pest (GoncalvesAlvim *et al.,* 2004; Mierziak, *et al.,* 2014). These depict the impact of biochemical factors in antibiotic mechanism against sucking insects and support our finding against SMB which is also a sucking insect pest (Felkl *et al.,* 2005).

Infestation grade

Results in table 3 referred that a total of 21 ornamental plants species from 15 families,were identified as host plants of SMB. The families were Verbenaceae (3 species accounting for 14.28 % of the total), Acanthaceae, Amaranthaceae , Apocynaceae and Asteraceae (2 species, 9.52 % of .the total for each), Lamiaceae, Rosaceae, malvaceae, sapindaceae, Euphorbiaceae, Convolvolaceae, Solanaceae, Asparagaceae, Scrophulariaceae .and Portulacaceae (1 species, 4.76 % of the total for each).

The list that explained in table 3 revealed that *Adhatoda vasica*, *H. rosa-sinensis* and *D. erecta* were the best host plants of SMB because it infest. grade was 4, followed by *D. angastifolia* and L. *camara* which their infest. grade was 3. Most of plants were laddered in the grade 1 were : *A. sisclane*, *T. patula*, *Osteospermum* sp., *E. trigona*, *C. macrocarpa*, *S. trifasciata*, *D. plumieri*, *L. frutescens*, *P. greandiflora*, *C. vinca* and *V. agnus-castus* . Other plants were in the grade 2 : *G. globose, A. dentata*, *A. squarrosa I. batatas* and *R. rugosa.*

P. greandiflora infest. grade was 1 in our study, while Arif *et al.,* (2009) referred that it infest. grade was 3. The plants *D. erecta* and *H. rosa-sinensis* (grade 4), *L. camara* and .*D. angastifolia* (grade 3) seemed to be a good hosts for SMB, this result corresponds with what found Shahid *et al.,* (2017) who mentioned that *L. camara* and *H. rosa-sinensis* had high attractiveness and .less mortality to first instar of SMB, and they referred that Mortality of pest was negatively associated with nitrogen and but positively with potassium, phosphorus, sodium, reducing sugar and total sugar in plants. While, *P. greandiflora* .was less attractive to SMB in our study (grade 1) unlike what concluded Shahid *et al.,* (2017) that *P. oleracea* was attractiveness and fewer mortality to first instar nymph of this pest.

SMB infested *G. globosa* L. and it infest. grade was 2 as Vennila and Agarwal (2014) concluded that it served as SMB host at South zone in India during cotton off

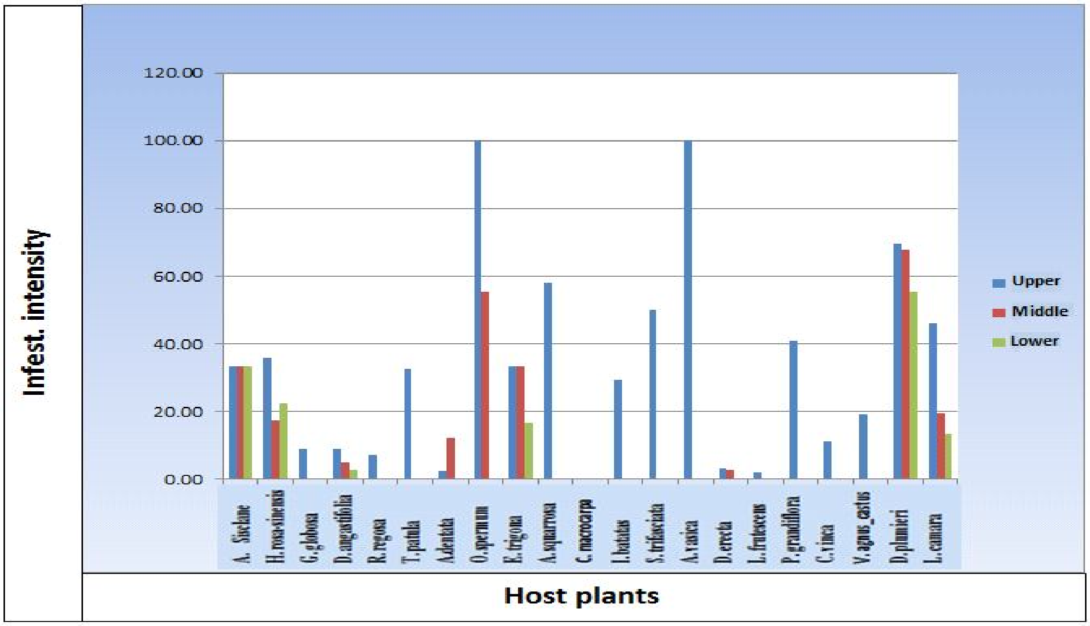

Fig. 9: Infestation intensity on total level of host plant.

Table 3: Infestation grade of SMB on ornamental plant hosts.

Host plant	Family	Infest. Degree
Duranta erecta	Verbenaceae	4
Lantana camara	Verbenaceae	3
Duranta plumieri	Verbenaceae	1
Tagetes patula	Asteraceae	1
Osteospermum sp	Asteraceae	1
Gomphrena globosa	Amaranthaceae	2
Alternantha dentata	Amaranthaceae	2
Carissa macrocarpa	Apocynaceae	1
Carthoranthus vinca	Apocynaceae	1
Adhatoda vasica	Acanthaceae	4
Aphelandra squarrosa	Acanthaceae	2
Ipomea batatas	convolvolaceae	2
Agave sisclane	Solanaceae	1
Sansevieria trifasciata	Asparagaceae	1
Leucophyllum frutescens	Scrophulariaceae	1
Portulaca greandiflora	Portulaceae	1
Vitex agnus - castus	Lamiceae	1
Hibiscus rosa-sinensis	Malvaceae	4
Dodonaea angastifolia	Sapindaceae	3
Rosa rugosa	Rosaceae	2
Euphorbia trigona	Euphorbiaceae	1

seasons and they mentioned that twelve of the 24 documented ornamental

hosts for SMB belonged to three families, *viz.,* Asteraceae, Malvaceae and Euphorbiaceae. Aheer *et al.,* (2009) and Abbas *et al.,* (2010) also have reported shoe flower (*H. rosa - sinensis*) as the greatest preferred ornamental plant species by SMB in Pakistan and Kedar and Saini (2015) referred that *Hibiscus rosa sinensis* and *Lantana camara,* were prominent hosts supporting the pest during off season, while the infest. grade for *T. patula* was 3, for *Portulaca oleracea* L. (4) and *L. camara* L. (3).

From results in table 3, it revealed that two host plants for SMB are from the family Asteraceae and one from Solanaceae, this correspond with the results of Shahid *et al.,* 2017 who referred that *Helianthis annuus* and *Parthenium hysterophorus* (Asteraceae) and *Solamum melongena*, *Capsicum frutescens* and *Withania somnifera* (Solanaceae) had high attractiveness and less mortality to SMB first instar. Unlike, they referred that *Achyranthes aspera* and *Digera arvensis* (Amaranthaceae) had fewer attractiveness and high mortality to SMB first instar while we reported those two hosts from this family with moderate infestation (infest. grade was 2). Other families such as Asparagaceae, Scrophulariaceae, Lamiaceae, .Portulaceae and Euphorbiaceae, everyone had one plant infested weakly by SMB (infest. grade 1), therefore, it considered as least preferred host plants for SMB,this result may due to that these families include plants do not have enough quantity and good quality of SMB nutrition requirements. Among the plant families, Verbenaceae had the highest number of host plants for SMB. The high host preference for *H. rosa-sinensis* (Verbenaceae) by SMB might be due to the presence of latex (Fahn, 1988). Arif *et al.,* (2009) documented 154 host - plant species infested by SMB, 45 species of it were ornamental plants, belonging to a total of 53 plant families.

The infestation on ornamental plants confined on only these 21 plants, this may due to that other plants repelled SMB first instar or induced high mortality, this correspond with result of Shahid *et al.,* 2017 who mentioned that from the biochemical results it was reported that among phosphorus, nitrogen, potassium, sodium, total soluble sugar, reducing sugar components, the nitrogen contents played significant role toward attractiveness of SMB and they concluded that great variation in the life cycle of SMB was observed among tested plant species. It was clear that dropping in attractiveness of SMB was also due to increased reducing sugar contents that function as olfactory and gustatory stimuli and imbalanced nutrition for insect pest (Hu *et al.,* 2010). Studies reported that potassium contents had negative effect on the attractiveness of mealybug, the reason was due to physiological action of the plants and increase in defense system of plant species against pest (Du *et al.,* 2004; Liu *et al.,* 2004). Sucking insects are commonly attracted toward juicy plants that are enriched with chlorophyll (Amaliotis *et al.,* 2004; Tucker, 2004).

In our study, *I.batatas* .and *E. trigona* was low infested by SMB while Muniappan *et al.,* (2008) listed *Euphorbia* sp. and *I. batatas* .as being suitable hosts of *phenacoccus marginatus* and Caraphin News (2001) listed *Jatropha* sp and *.Acalypha* sp. (Euphorbiaceae) as being best hosts of *P. marginatus. G. globosa* and *A. dentata* (Amaranthaceae) were low infested by SMB (infest. grade was 2), this corresponds with results of Prishanthini and Vinobaba (2009) who revealed that *Alternanthera sessilis* L. was low infested by SMB (infest. grade was 2), and mentioned that, *Hibiscus rosa-sinensis* L infest. grade was 4 and L. *camara* L. was infested and it infest. grade was 3. Vijay and Suresh (2013) revealed that *T. erecta*, *Euphorbia multipida, H. rosa-sinensis*, *L. camara* and *D. repens* were a host plants for SMB and it infest. grades were 4, 2, 4, 3, and 4 respectively. Harde *et al.,* (2018) referred to that

L.camara, *P. grandiflora*, *Amaranthus paniculata* (Amaranthaceae) *and H. rosa sinensis* were infested by SMB and the infestation grade were 3, 2, 2 and 4 respectively.

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