

**STUDIES ON GENETIC DIVERSITY OF
WHITEFLY, *Bemisia tabaci* (Genn.) (HEMIPTERA:
ALEYRODIDAE) AND MOLECULAR ANALYSIS
FOR ITS RESISTANT TRAITS IN TOMATO**

SACHIN U. S.



**DEPARTMENT OF ENTOMOLOGY
COLLEGE OF HORTICULTURE, BAGALKOT
UNIVERSITY OF HORTICULTURAL SCIENCES,
BAGALKOT- 587 104, KARNATAKA, INDIA**

AUGUST, 2019

**STUDIES ON GENETIC DIVERSITY OF
WHITEFLY, *Bemisia tabaci* (Genn.) (HEMIPTERA:
ALEYRODIDAE) AND MOLECULAR ANALYSIS
FOR ITS RESISTANT TRAITS IN TOMATO**

*Thesis submitted to the
University of Horticultural Sciences, Bagalkot
in partial fulfillment of the requirements for
the Degree of*

DOCTOR OF PHILOSOPHY

in

Entomology

By
SACHIN, U. S.
ID No. UHS15PGD126

**DEPARTMENT OF ENTOMOLOGY
COLLEGE OF HORTICULTURE, BAGALKOT**

AUGUST, 2019

UNIVERSITY OF HORTICULTURAL SCIENCES, BAGALKOT
COLLEGE OF HORTICULTURE, BAGALKOT
DEPARTMENT OF ENTOMOLOGY

CERTIFICATE

This is to certify that the thesis entitled “**STUDIES ON GENETIC DIVERSITY OF WHITEFLY, *Bemisia tabaci* (Genn.) (HEMIPTERA: ALEYRODIDAE) AND MOLECULAR ANALYSIS FOR ITS RESISTANT TRAITS IN TOMATO**” submitted by **Mr. SACHIN, U. S., UHS15PGD126** for the degree of **DOCTOR OF PHILOSOPHY in ENTOMOLOGY** to the University of Horticultural Sciences, Bagalkot, is a record of bonafied research work done by him during the period of his study at University of Horticultural Sciences, Bagalkot under my guidance and supervision and the thesis has not previously been formed the basis of the award of any other degree, diploma, associateship, fellowship or similar titles.

BAGALKOT
AUGUST, 2019

(VENKATESHALU)
Major Advisor

Approved by:

Chairman: _____
(VENKATESHALU)

Members: 1. _____
(Y. K. KOTIKAL)

2. _____
(B. FAKRUDIN)

3. _____
(R. K. MESTA)

4. _____
(H. P. HADIMANI)

5. _____
(S. RAGHAVENDRA)

ACKNOWLEDGEMENT

The completion of this thesis was made possible by the valuable assistance I received from many people. It is with pleasure that I acknowledge the efforts of the many people who have contributed to the development of this thesis.

*I have no words to express my deep sense of gratitude and indebtedness to **Dr. VENKATESHALU**, Professor and Head, Department of Entomology, COH, Bagalkot and the esteemed chairman of my advisory committee for his patience, immense knowledge, constructive comments, valuable and useful suggestions and support throughout the phases of analyzing data and writing of this thesis. Amidst of his busy schedule, he found much of his time and pain of commendable guidance throughout the research work. I am highly grateful to him for critically going through the manuscript and for his valuable suggestions for the improvement of the thesis. It was a great pleasure and privilege for me to have him as my guide.*

*I deem it a great pleasure to place on record my deep sense of gratitude and profound thanks to **DR. B. FAKRUDIN**, Professor and Head, Department of Biotechnology and Crop Improvement, COH, Bengaluru and Co-Chairmen of my Advisory committee, who acted as for his candid suggestions, wholehearted help and learned counsel during the course of study. Amidst of his busy schedule, he found much of his time and pain of commendable guidance throughout the research work. It was indeed a great pleasure to work under his meticulous guidance.*

*It gives me enormous gratification to express my intense and heartfull thanks to the members of my advisory committee **DR. Y. K. KOTIKAL**, Professor and Director of Extension, UHS, Bagalkot, **Dr. RAGHAVENDRA K MESTA**, Professor and Head, Department of Plant Pathology, COH, Bagalkot, **Mr. H. P. HADIMANI**, Assistant Professor, Department of Vegetable Science, COH, Bagalkot and **Dr. S. RAGHAVENDRA**, Assistant Professor, Department of Plant Biochemistry, COH Bagalkot for being on my committee and for immense help, valuable suggestion, constant encouragement during my research and guidance over the years.*

*I sincerely extend my profound thanks gratitude from my inner core heart to **Dr. JAYASHREE UGALAT**, Assistant Professor, Department of Plant Biochemistry, COH Bengaluru, for her immense help, valuable suggestion, constant encouragement during my research.*

*I wish to extend my heartfelt thanks to **Dr. K. S. SHANKARAPPA** and **Dr. J. JAYAPPA**, Assistant Professors, COH, Bengaluru and **Dr. SARVAMANGALA***

CHOLIN Assistant Professor, COH, Bagalkot for sharing research material, valuable suggestions and support for analyzing data.

*I express my heartfelt love and affection to my beloved parents **Mr. Sanjeeva Poojary, Mrs. Yashodha and Mrs. Lakshmi**, my uncle **Dr. Lakshman**, aunty **Damayanthi**, grandmother **Narsi Poojarthi**, lovely sister **Sowmya**, brothers **Nithi, Madhu, Shivakumar** and all other family members for their affection, words of encouragement, boundless love, unflagging inspiration, interest and selfless sacrifice. I owe all my success to them.*

*I am also thankful to my beloved seniors, **Sanjeev Sir, Poornima sis, Manju sir, Omkar sir, Anil Hake sir** and juniors, **Anil, Manju, Abhi, Sachin, Sudi, Chatri, Sachin, J, Deva, Muddu, Chethu, Sunil, Nagesh, Pramodh, Vinod, Utpal, Pradi, Sharan, Malli, Rashmi, Apoorva, Chaitra** and others who's timely support and co-operation helped throughout the study.*

*I express my heartfelt love and affection from the inner core of heart to my lovely **PETALS of MORNING GLORIES** especially to **Santosh, Sumuk, Darshan, Ravi, Abhi, Santhosh, Ambi, Guru, Manoj, Sundaresh, Beeresh** and lovely **FB BUDS-Gaurav sir, Sandeep sir, Nandini mam, Asif, Shreedhar, Nayana, Mamatha and Mahesh** ² for their constant encouragement, moral and financial support during critical days, love and affection has inspired me to hold tight to my position no matter how complicated it gets.*

*It is my pleasure to extend my sincere thanks to Lab assistants, **Mr. R. Nadaf, Mr. Yamanappa** and **Mrs. Pushpa, Mrs. Mamatha**, who helped me a lot during my research work. I am thankful to **Mr. Arjun** (Arjun Computers) for his co-operation in the preparation of thesis.*

*I gratefully acknowledge **UHS, Bagalkot** for giving me an opportunity to accomplish my doctoral studies at Bagalkot.*

I thank the eternal love of the great Almighty for gracing the peaceful atmosphere during the course of my study.

Last but not the least I thank all those who helped me directly or indirectly during period of my stay in both COH, Bagalkot and Bengaluru campus. In case of any omission or deletion does not mean lack of gratitude.

Bagalkot
August 2019

(Sachin, U. S)

Affectionately Dedicated to
My Beloved Mother Smt. Yashodha
and Morning Glories



CONTENTS

Chapter No.	Chapter Particulars	Page No.
	CERTIFICATE	iii
	ACKNOWLEDGEMENT	iv
	LIST OF ABBREVIATIONS	ix
	LIST OF TABLES	xi
	LIST OF FIGURES	xiv
	LIST OF PLATES	xvi
	LIST OF APPENDICES	xvii
1.	INTRODUCTION	1-5
2.	REVIEW OF LITERATURE	6-45
	2.1 Whitefly, <i>Bemisia tabaci</i> , Origin and Taxonomy	6
	2.2 Understanding the morphological traits plasticity among the populations of whiteflies	12
	2.3 Understanding the genomic flux and population genetic structure of <i>Bemisia tabaci</i>	15
	2.4 Frequency of mono and bipartite particle among <i>B. tabaci</i> populations	30
	2.5 Variations for traits related to whitefly resistance in tomato	33
	2.6 Association analysis of component traits of whitefly resistance in tomato	42
3.	MATERIAL AND METHODS	46-77
	3.1 Plasticity of morphological traits' among the populations of whiteflies prevailing in tomato ecosystems of Karnataka	46
	3.2 Genomic flux and population genetic structure of whitefly populations in tomato ecosystems of Karnataka	50
	3.3 To determine the frequency of mono and bipartite particle in populations of whitefly	58
	3.4 Variation for traits related to whitefly resistance in tomato association mapping panel (TAMP)	62
	3.5 Association analysis of component traits of whitefly resistance in tomato	77

Contd.....

Chapter No.	Chapter Particulars	Page No.
4.	EXPERIMENTAL RESULTS	78-136
	4.1 Plasticity of morphological traits' among whitefly populations in tomato ecosystems of Karnataka	78
	4.2 Genomic flux and population genetic structure of whitefly populations of tomato ecosystems of Karnataka	93
	4.3 Frequency of mono and bipartite virus particle in <i>B. tabaci</i> populations across tomato growing ecosystems of Karnataka	105
	4.4 Variation for traits related to whitefly resistance in tomato association mapping panel (TAMP)	111
	4.5 Association analysis of component traits of whitefly resistance in tomato	133
5.	DISCUSSION	137-168
	5.1 Plasticity for morphological traits among the populations of whiteflies prevailing in tomato ecosystems of Karnataka	137
	5.2 Genomic flux and population genetic structure of whitefly populations of tomato ecosystems of Karnataka	142
	5.3 Frequency distribution of mono and bipartite particle in populations of whitefly	149
	5.4 Assessing the variations for traits related to whitefly resistance in tomato association mapping panel (TAMP)	152
	5.5 Association analysis of component traits of whitefly resistance in tomato	166
6.	SUMMARY AND CONCLUSIONS	169-172
	REFERENCE	173-215
	APPENDICES	216-245

LIST OF SYMBOLS AND ABBREVIATIONS

Symbols	Abbreviations
%	Per cent
@	At
°C	Degree Celsius
<i>i.e.</i>	That is
µl	Microlitre
pm	Picometer
mm	Millimeter
cm	Centimeter
g	Gram
<i>viz.</i>	As follows
SSR	Simple Sequence Repeats
<i>RNase</i>	Ribonuclease
PCV	Phenotypic Coefficient of Variability
GCV	Genotypic Coefficient of Variability
GA	Genetic Advance
GAM	Genetic Advance as per cent mean
rpm	Revolutions Per Minute
UHS	University of Horticultural Sciences
h^2	Heritability in broad sense
nm	Nanometer
bp	Base pair
EtBr	Ethidium Bromide
<i>et al</i>	Et alii (and others)
S. Em±	Standard Error of Mean
CD	Critical difference
CV	Coefficient of variability
ha	Hectare
MT	Metric tones

Contd.....

Symbols	Abbreviations
DAT	Days after transplanting
EMS	Ethyl Methane Sulphonate
DNA	Deoxyribo Nucleic Acid
T ₁₀ E ₁	Tris EDTA
RAPD	Random Amplified Polymorphic DNA
µg	Microgram
UV	Ultra Violet
EC	Exotic Cultivars
min	Minute
DNTP	Deoxy Nucleotide Tri Phosphate
TAE	Tris Acetate EDTA
EDTA	Ethylene Diamine Tetra Acetic acid
PCR	Polymerase Chain Reaction
ml	Millilitre
l	Litre
CTAB	Cetyl Trimethyl Ammonium Bromide
Fig.	Figure

LIST OF TABLES

Table No.	Title	Page No.
1.	Details of locations selected for collection of <i>Bemisia tabaci</i> samples across agroclimatic zones of Karnataka	47
2.	Whitefly population used for the genetic diversity study	51
3.	Whitefly population used to determine frequency of mono and bipartite virus particles	59
4.	List of tomato accessions constituting minicore collections used for field evaluation	64
5.	Morphometrics of <i>Bemisia tabaci</i> puparia on tomato from different agro climatic zones of Karnataka	79
6.	Morphometrics of <i>Bemisia tabaci</i> males on tomato from different agro climatic zones of Karnataka	82
7.	Morphometrics of <i>Bemisia tabaci</i> females on tomato from different agro climatic zones of Karnataka	85
8.	Morphometrics of <i>Bemisia tabaci</i> adults (both male and female) based on 30 quantitative characters	89
9.	Morphometrics of <i>Bemisia tabaci</i> adults (both male and female) and puparia based on 42 quantitative characters	92
10.	Locus -wise information on the number of different alleles (Na), number of effective alleles (Ne), Shannon's Information Index (I), Observed Heterozygosity (Ho), Expected Heterozygosity (He), the number of migrants (Nm), Fixation Index (F) & F-statistics across populations of <i>Bemisia tabaci</i> in Karnataka	95
11.	Population-wise information on the number of different alleles (Na), number of effective alleles (Ne), Shannon's Information Index (I), Observed Heterozygosity (Ho), Expected Heterozygosity (He), Fixation Index (F) & percentage polymorphism (% P) observed across 17 microsatellite loci in <i>Bemisia tabaci</i>	97
12.	Pair-wise F_{ST} value for population of <i>Bemisia tabaci</i> across the sampling regions of Karnataka	99
13.	Pair-wise genetic distance of population for <i>Bemisia tabaci</i> across the sampling regions of Karnataka	100
14.	Summary of Analysis of Molecular Variance (AMOVA) and mean F-coefficients calculated over 11 populations of <i>Bemisia tabaci</i>	102
15.	Distribution of whitefly individuals distributed across different quadrant based on their genetic distance matrix	104

Contd.....

Table No.	Title	Page No.
16.	Tomato leaf curl virus (ToLCV) disease incidence across the sampling regions of Karnataka	106
17.	PCR amplification status of monopartite and bipartite virus particles in populations of <i>Bemisia tabaci</i> across the sampling regions of Karnataka	108
18.	Distribution frequency of virus particles among the <i>Bemisia tabaci</i> population	109
19.	Analysis of variance (ANOVA) for whitefly nymph population in minicore accessions field evaluated during <i>rabi</i> and summer seasons 2016-17 at COH, Bengaluru	112
20.	Analysis of variance (ANOVA) for biochemical and biophysical traits in minicore accessions field evaluated during summer 2016-17 at COH, Bengaluru	113
21.	Descriptive statistics of whitefly populations in 260 tomato minicore accessions	115
22.	Descriptive statistics of biochemical and biophysical component traits in 260 tomato minicore accessions	115
23.	Genetic variability parameters of biochemical and biophysical component traits in 260 tomato minicore accessions	117
24.	Effect of trichome type on <i>Bemisia tabaci</i> population in tomato accessions during <i>rabi</i> and summer season 2016-17 at COH, Bengaluru	119
25.	Influence of glandular and non glandular trichomes on whitefly population	121
26.	Correlation co-efficient for component traits and whitefly population in minicore accessions field evaluated during summer season, 2016-17 at COH, Bengaluru	122
27.	Locus -wise information on the number of different alleles (Na), number of effective alleles (Ne), Shannon's Information Index (I), Observed Heterozygosity (Ho), Expected Heterozygosity (He), the number of migrants (Nm), Fixation Index (F) & F-statistics across tomato minicore accessions.	125
28.	Population-wise information on the number of different alleles (Na), number of effective alleles (Ne), Shannon's Information Index (I), Observed Heterozygosity (Ho), Expected Heterozygosity (He), Fixation Index (F) & percentage polymorphism (% P) observed across 40 microsatellite loci	128

Contd.....

Table No.	Title	Page No.
29.	Pair-wise F_{ST} value for population of tomato minicore accessions	130
30.	Pair-wise genetic distance of population for tomato minicore accessions	130
31.	Summary of Analysis of Molecular Variance (AMOVA) and mean F-coefficients calculated over 260 tomato accessions	131
32.	List of minicore accessions distributed across different quadrant based on their genetic distance matrix	134
33.	Markers associated with biophysical and biochemical traits and their position on chromosomes	136

LIST OF FIGURES

Figure No.	Title	Between Pages
1.	Locations selected for collection of <i>Bemisia tabaci</i> samples around Karnataka	47-48
2.	Cluster analysis for <i>Bemisia tabaci</i> adults (both male and female) from different agro climatic zones of Karnataka based on 30 quantitative characters	88-89
3.	Scree plot analysis of the principal components for <i>Bemisia tabaci</i> adults (both male and female) based on 30 quantitative characters	90-91
4.	Score plot of principal components for <i>Bemisia tabaci</i> adults (both male and female) from different agro climatic zones of Karnataka based on 30 quantitative characters	90-91
5.	Cluster analysis for <i>Bemisia tabaci</i> adults (both male and female) and puparia from different agro climatic zones of Karnataka based on 42 quantitative characters	91-92
6.	Scree plot analysis of the principal components for <i>Bemisia tabaci</i> adults (both male and female) and puparia based on 42 quantitative characters	92-93
7.	Score plot of principal components for <i>Bemisia tabaci</i> adults (both male and female) and puparia from different agro climatic zones of Karnataka based on 42 quantitative characters	92-93
8.	Neighbour Joining (NJ) tree constructed using MEGA 7 based on pair-wise genetic distance across <i>Bemisia tabaci</i> populations	102-103
9.	Neighbour joining (NJ) tree constructed using MEGA 7 based on pair-wise genetic distance across <i>Bemisia tabaci</i> individuals	102-103
10.	Principle coordinates analysis (PCA) using pair-wise genetic distance matrix of eleven <i>Bemisia tabaci</i> populations sampled across Karnataka	103-104
11.	Principle coordinates analysis (PCA) using pair-wise genetic distance matrix of 140 <i>Bemisia tabaci</i> populations sampled across Karnataka	103-104
12.	Ln P (D) values presented as a function of the number of clusters.	105-106

Contd.....

Figure No.	Title	Between Pages
13.	Population genetic structure of 140 individuals of <i>Bemisia tabaci</i> at K=14 sampled across Karnataka	105-106
14.	Distribution frequency of monopartite and bipartite virus particles in Karnataka	109-110
15.	Neighbour Joining (NJ) tree constructed using MEGA 7 based on pair-wise genetic distance across tomato sub populations	132-133
16.	Neighbour joining (NJ) tree constructed using MEGA 7 based on pair-wise genetic distance across 260 tomato minicore accessions	132-133
17.	Principle coordinates analysis (PCA) using pair-wise genetic distance matrix of five tomato populations	132-133
18.	Principle coordinates analysis (PCA) using pair-wise genetic distance matrix of 260 tomato minicore accessions	133-134
19.	Ln P (D) values presented as a function of the number of clusters	135-136
20.	Population genetic structure of 260 tomato minicore accessions at K=7	135-136
21.	Position of trait-wise associated markers on different linkage groups	136-137
22.	Morphometrics of <i>Bemisia tabaci</i> puparia on tomato from different agro climatic zones of Karnataka	138-139
23.	Morphometrics of <i>Bemisia tabaci</i> males on tomato from different agro climatic zones of Karnataka	138-139
24.	Morphometrics of <i>Bemisia tabaci</i> females on tomato from different agro climatic zones of Karnataka	138-139
25.	Mean per cent disease incidence (PDI) for ToLCVD incidence across the sampling regions of Karnataka	150-15
26.	Overall frequency of virus particles among the <i>Bemisia tabaci</i> population	152-153
27.	Genetic variability of biochemical and biophysical component traits in 260 tomato minicore accessions	154-155
28.	Effect of trichome type on <i>Bemisia tabaci</i> population in tomato accessions field evaluated during <i>rabi</i> and summer season 2016-17 at COH, Bengaluru	158-159

LIST OF PLATES

Plate No.	Title	Between Pages
1.	Morphology of the <i>Bemisia tabaci</i> puparia	49-50
2.	Morphometric characters of the <i>Bemisia tabaci</i> puparia	49-50
3.	Nymphal population recorded significantly higher (a. Dharwad) and lower (b. Bagalkot) values for the morphological traits studied	49-50
4.	Morphology of the <i>Bemisia tabaci</i> adults	49-50
5.	Morphometric characters of <i>Bemisia tabaci</i> adults	49-50
6.	<i>Bemisia tabaci</i> female and male populations recorded significantly higher and lower values for the morphological traits studied	49-50
7.	Field overview of minicore accessions, a. <i>Rabi</i> season and b. Summer season 2016-17 at COH Bengaluru	65-66
8.	<i>Bemisia tabaci</i> adult and nymph population on abaxial surface of tomato leaves	65-66
9.	Tomato plants showing ToLCV symptoms	66-67
10a.	Different types of trichomes observed on tomato accessions	67-68
10b.	Different types of glandular and non glandular trichomes	67-68
11.	Allele size variation for SSR markers a) FbBEM31 b) FbBEM31 in 140 <i>B. tabaci</i> individuals collected from different geographical areas	93-94
12.	PCR amplification patterns in a) Monopartite and b) Bipartite virus particle by the specific DNA markers in <i>B. tabaci</i> adults	108-109
13.	Allelic variation for the SSR markers across 260 tomato TAMP accessions a) marker T0800 b) Marker P6-25	124-125

LIST OF APPENDICES

Appendix No.	Title	Page No.
I.	Details of locations selected for collection of <i>Bemisia tabaci</i> samples across agroclimatic zones of Karnataka and abbreviations used	216
II.	Details of various morphological characters recorded from <i>Bemisia tabaci</i> puparia and abbreviations used	217
III.	Details of various morphological characters recorded from <i>Bemisia tabaci</i> males and abbreviations used	218
IV.	Details of various morphological characters recorded from <i>Bemisia tabaci</i> females and abbreviations used	219
V.	List of microsatellite primer pairs of <i>Bemisia tabaci</i>	220
VI.	Meteorological data recorded during 2016 and 2017 covering the period of experimentation from agrometeorology unit University of Agricultural Sciences, GKVK, Bengaluru	221
VII.	List of stock solutions used in study	222
VIII.	List of primer pairs used in the genotyping the tomato association mapping panel	223
IX.	Mean values of different traits of tomato association mapping panel used in the study	225
X.	<i>Bemisia tabaci</i> population (nymphs/ 3 leaves) at different days interval and per cent disease incidence in the tomato association mapping panel field evaluated during summer 2016-17 at COH, Bengaluru	230
XI.	Categorization of tomato association mapping panel for reaction individual accessions to the ToLCV incidence at 60 DAT under field conditions during summer 2016-17 at COH, Bengaluru	235
XII.	Different types of trichomes identified in 260 tomato accessions and their effect on whitefly population analysed during field evaluation (Rabi and summer seasons of 2016-17)	235
XIII.	Effect of trichome type on <i>B. tabaci</i> population in tomato accessions during <i>rabi</i> and summer season 2016-17 at COH, Bengaluru	241
XIV.	Tomato association mapping panel arranged in different groups for diversity analysis	245

1. INTRODUCTION

Solanaceous crops are important group of vegetables consumed all over the world and grown in tropical and subtropical regions. Tomato (*Solanum lycopersicum* L.) is a warm-season crop originated in South America and at present one of the most popular and profitable crops among the commercial growers all over the world including India. Tomato being one of the most important protective food crops of India is a tender herbaceous perennial plant, but is cultivated as annual. It is rich source of vitamin A and C, potassium, minerals and fibres and consumed as vegetable in many ways like culinary purpose and also in the preparation of sauce, soup, puree, ketchup, salad, pickle, *etc.*

Globally, India ranks second in tomato production after China. In India, tomato has large area coverage in comparison to other vegetables with an area of 8.08 lakh ha. and production of 196.97 lakh MT (Anon., 2018). The leading tomato growing states in the country are Madhya Pradesh, Odisha, Karnataka, West Bengal, Andhra Pradesh and Telangana. In Karnataka, tomato is grown mainly in Kolar, Haveri, Belagavi, Chikkaballapura, Bengaluru Rural, Mandya, Tumkur, Davanagere, Mysuru, Chamarajanagara, Chikkamagluru, Bagalakote, Chitradurga, Vijayapura, Bellary, Koppal and Kalaburgi districts with the average area and production of 4.21 thousand ha. and 142.71 MT, respectively (Anon., 2018).

Among the biotic factors, insect pests are prime importance as they account for higher economic losses to the growers by both directly as crop pests and indirectly as vectors of viral diseases. Among the pests, whitefly, *Bemisia tabaci* (Gennadius) (Srivastava and Butani, 2009) and green house whitefly, *Trialeurodes vaporariorum* (Westwood) (Zaini, 2005) are reported as major whitefly species. Among these, *B. tabaci*, a sap feeder, reported to be infesting more than 900 host plants (Hsieh *et al.*, 2006; McKenzie *et al.*, 2012; Chaubey and Andrew, 2015) and has attained a major pest status globally (Brown, 2010). This polyphagous pest causes damage in different ways *i.e.* direct feeding on sap from the plants causing chlorotic spots on leaves and fruits, plant debilitation, excreting honeydew and development of sooty moulds (Anon., 2015; Chaubey and Andrew, 2015). However, the greatest economic threat is from the transmission of plant viruses, primarily begomoviruses. One of the most

damaging of these is the Tomato Leaf Curl Virus (ToYLCV) thus, accounting for 20 to 100 per cent loss during the vegetative stage of the crop (Muniyappa, 1980; Guo *et al.*, 2013).

Whiteflies are classified under the family Aleyrodidae, which comprises of more than 1500 species. They have an incomplete metamorphosis (Hemimetabolism) consisting of six developmental stages-egg, I instar referred as “crawler”, II instar and III instar nymph and IV instar as “pupae” and adult (Walker *et al.*, 2010). The egg stage of all whiteflies has a stalk at their larger end, called the ‘pedicel’ (Quaintance and Baker, 1914) which serves as an attachment for the egg. All whitefly nymphal stages are oval in shape and dorsoventrally flattened. The first nymphal instar is called as ‘crawler’, because it is highly mobile and probes the leaf surface for a suitable location to insert its stylets into the phloem sieve elements. The lateral margins of the crawlers have many setae that are absent in later instars. These are thought to be mechanosensory in nature enabling the crawler to sense leaf hairs (Walker *et al.*, 2010). Once the crawler locates a suitable feeding site, it begins feeding and moults into the subsequent instar, being attached at the same point (Gill, 1990). The insect goes through three additional nymphal instars (second-fourth). The fourth instar is also referred to as the ‘pupal’ stage (López-Avila, 1986). This stage has red eyes and yellow body pigment (Gill, 1990).

The wings of *B. tabaci* are covered with white powdery wax that is secreted soon after the adult eclosed from the last nymphal instar (Gill, 1990). The wings are held ‘roof-like’ over the abdomen, which gives them a long, narrow appearance on the leaf. Adults typically are found on the lower leaf surfaces of tomato. There is a sexual dimorphism in *B. tabaci*. Females are larger than the males and have a rounded abdomen while, the male abdomen is more pointed and with claspers. The generation time is dependent on temperature and the host plant (Tsai and Wang, 1996; Kakimoto *et al.*, 2007; Manzano and Van Lenteren, 2009). In tomato, the mean generation time of *B. tabaci* ranges from 24 to 32 days (Islam and Shunxiang, 2007).

Whitefly occurring on tomato is known to be responsible for low productivity, and contributes to the yield loss both directly as crop pest and indirectly as vector of viral diseases. *Bemisia tabaci* originated in the tropics and subtropics and rapidly spread as a consequence of the international trade in flowers and vegetable crops.

Because of its wide host range, rapid proliferation, and superior ability to transmit virus, it has become one of the most important pests in field crops worldwide. *Bemisia tabaci* is a complex of numerous genetically distinct populations, previously recognized as cryptic species and now referred to as biotypes.

Bemisia tabaci is consisting of 24 morphologically indistinguishable species in 11 well-defined groups. These were later concluded as belonging to 36 putative species based on their differences in genetic structure, host plant preferences, bacterial symbionts (Liu *et al.*, 2012; Tay *et al.*, 2012; Boykin, 2013; Wang *et al.*, 2013; Ashfaq *et al.*, 2014; Boykin and De Barro, 2014) and interbreeding capabilities (Xu *et al.*, 2010). As of now, four major biotypes of *B. tabaci* are recognized viz., jatropha biotype, new world whitefly (new world) previously known as biotype-A, Middle East Asia Minor 1 whitefly (MEAM1), previously known as biotype-B or *B. argentifolii* Bellows and Perring (Dinsdale *et al.*, 2010; Boykin, 2013), the Mediterranean (MED) whitefly, previously known as biotype-Q and now known to be the original *B. tabaci*. Among them, two most widely distributed, polyphagous and invasive biotypes are B and Q biotypes (Brown, 2007).

Bemisia tabaci is known to transmit more than 110 plant viruses (Malumphy *et al.*, 2009; Chaubey and Andrew, 2015) belonging to genera, *Geminivirus*, *Closterovirus*, *Nepovirus*, *Carlavirus*, *Potyvirus* and a rod-shaped DNA virus (Baig *et al.*, 2015). It has been recorded as the only known vector of ToLCV and efficiently transmitted during the adult stage. It has short acquisition access period of 15 to 20 minutes and latent period of 8 to 24 hrs. In this plant-virus and vector system, females are more efficient than males in transmitting the virus.

ToLCV is a single-stranded DNA (ssDNA) plant virus, belong to genus *Begomovirus*, family Geminiviridae and is originated in Middle East. It is transmitted by *B. tabaci* in a persistent, circulative and nonpropagative manner. The geminiviruses are by far agriculturally most important, causing yield losses to crops between 20 and 100 per cent (Brown and Bird, 1992). *Geminiviruses* cause a range of symptoms which include yellow mosaics, yellow veining, leaf curling, stunting and vein thickening in tomato plants. There are two types of virus particles reported *i.e.* monopartite and bipartite. Monopartite genome with single segment *i.e.* DNA-A and more than 133 begomovirus species are having monopartite genomes (Scholthof *et al.*,

2011). Bipartite virus particles are having genome with two segments (referred to as DNA-A and DNA-B) that are packaged into separate particles (Brown *et al.*, 2012). Many begomoviruses do have a bipartite genome. Both segments are generally required for successful symptomatic infection in a host cell but DNA-B is dependent for its replication upon DNA-A, which can in some begomoviruses apparently cause normal infections on its own. Phylogenetic analysis is based on the A component while, B component may be exchanged between species and may result in new species (Green and Kalloo, 1994).

Bemisia tabaci is a species complex and its genetic groups or putative species are being discriminated through molecular studies using RAPD-PCR (Delatte *et al.*, 2005; Boukhatem *et al.*, 2007), AFLP (Abdullahi *et al.*, 2003) and analysis of mitochondrial cytochrome oxidase I (*mtCO1*), 16S and ribosomal ITS1 (Dinsdale *et al.*, 2010). These studies have revealed the occurrence of biotypes/ genotypes/ genetic groups/ putative species in the various geographic regions in which it is distributed, generally showing greater relatedness (Berry *et al.*, 2004). The taxonomic identification of *B. tabaci* is based on the morphology of puparia (Martin, 1987). But some studies have shown that, this has lot of phenotypic variation within the species (Gill and Brown, 2010). These phenotypic variations are largely determined by the host leaf morphology (Neal and Bentz, 1999) and other factors. Such phenotypic plasticity has led to confusion in recognition of its populations/ genetic groups/ putative species through established molecular or other studies. This has also led to redescriptions and synonymization (De Barro *et al.*, 2011).

The morphologically indistinguishable or indistinct populations have been designated as biotypes/ genetic groups/ putative species. Their distinction was always being established through characteristics other than morphological (Claridge *et al.*, 1997). Many studies which propose new genetic groups/ putative species and distinction of these in the *B. tabaci* species complex had been largely through non morphological definitions.

In the past decade, genome wide association mapping has emerged as a tool for studying the genetics of natural variation and economically important traits in plants (Atwell, 2010). It is rapidly becoming an important method to explore the genetic architecture of complex traits in plants and offers unique opportunities for

studying resistance to insect herbivores. Most studies, however, use a targeted approach that will easily miss important components of insect resistance. Genome-wide association mapping provides a comprehensive approach to explore the whole array of plant defense mechanisms in the context of the herbivore paradigm. As association mapping involves the screening of large number of plant lines, specific and accurate high throughput phenotyping (HTP) methods are needed (Kloth *et al.*, 2012).

In India, though some amount of work has been done in respect of tomato yellow leaf curl virus transmitting whitefly in tomato, the information on predominant whitefly species involved in transmission, its morphological traits plasticity, genomic flux, genetic structure, frequency of mono and bipartite virus particles, association analysis of resistant component traits in tomato to whitefly needs to be studied. Hence, considering the above points, research work on phylogenetic analysis of virus transmitting whitefly in tomato, its morphological and reproductive traits plasticity, genomic flux, genetic structure, frequency of mono and bipartite particle, association analysis of component traits for whitefly resistance was planned with the following objectives.

1. To understand the morphological traits plasticity among the populations of whiteflies prevailing in tomato ecosystem of Karnataka
2. To understand the genomic flux and population genetic structure of whitefly populations in tomato ecosystems of Karnataka
3. To determine the frequency of mono and bipartite particles across whitefly population.
4. To assess the variation for traits related to whitefly resistance in tomato association mapping panel (TAMP).
5. Association analysis of component traits of whitefly resistance in tomato.

2. REVIEW OF LITERATURE

The literature pertaining to morphological traits plasticity, genomic flux and population genetic structure, occurrence of different virus particle frequency among whitefly populations and also screening of tomato accessions at field and molecular screening for assessing whitefly resistance traits are reviewed here under.

2.1 Whitefly, *Bemisia tabaci*

Whitefly, *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) has been recorded from all the tropical and sub tropical areas of the world, as well as many temperate regions. It is considered as economically most important pest attacking over 600 plant species. The *B. tabaci* was first collected and described as *Aleyrodes tabaci* from tobacco, *Nicotiana* spp. from Greece in 1889. It was subsequently renamed as *B. tabaci* by Russell in 1957.

In India, *B. tabaci* was first recorded in 1905 (Misra and Lambda, 1929). The centre of origin of *B. tabaci* was suggested to be the Indian subcontinent because of the presence of large number of natural enemies against it (Lacey *et al.*, 1993; Fishpool and Burban, 1994). In India, *B. tabaci* reported as a pest of cotton, sweet potato, cassava, tobacco, tomato, eggplant, chilli, okra, sunflower and many more crop and weed plants (Muniyappa, 1980).

B. tabaci adults are small, white, active flying winged insects commonly seen on the abaxial (lower) surface of leaves of their host plants. They are more active during warmer periods of the day and rather inactive in the cooler hours. Adult male and female usually copulate on the under surface of leaves and has an arrhenotokous mode of reproduction; unmated females produce males and mated females produce both males and females (Gerling *et al.*, 1986). Elongate ovoid eggs are laid by females on abaxial leaf surfaces that were attached by a slender pedicel embedded into mesophyll tissue immediately beneath the epidermis (Avidov, 1956). Freshly laid eggs were oval and pale yellow, turning brownish-yellow within 24 h and dark brown shortly before hatching (Bhardwaj and Kushwaha, 1984; Fishpool and Burban, 1994). The number of eggs laid per female was highly variable depending on population, host and other environmental conditions (Gerling *et al.*, 1986). They have generation

time of upto 5 weeks. The first instar nymph or 'crawler' is elliptical in shape and can only move a short distance (a few mm) to locate a suitable feeding site (Pollard, 1955). Second, third, and fourth instar nymphs are sessile, shield-shaped, and similar in appearance, differing only in size. During the late fourth instar nymphal stage, red eyes and white wing buds become apparent beneath the translucent integument and the nymph swells becoming more convex and yellow in colour which is referred as pseudo pupa or pupa (Mound and Halsey, 1978; Lopez-Avilla, 1986; Byrne and Bellows, 1991).

The sex ratio is generally 2:1 (females: males) and more females develop when males are abundant. The generation time is dependent on temperature and the host plant (Tsai and Wang, 1996; Manzano and Van-Lenteren, 2009). On tomato, the mean generation time of *B. tabaci* ranges from 24 to 32 days (Islam and Shunxiang, 2007; Kakimoto *et al.*, 2007).

In *Bemisia tabaci*, Group Mediterranean-Middle East-Asia Minor I (former B-biotype) is one of the most devastating. It has a worldwide distribution, but mainly occupies tropical and subtropical habitats, although it also causes damage in more northern zones. *Bemisia tabaci* is not one species, but a cryptic species complex in which their members exhibit a considerable amount of genetic variation. However, they are morphologically indistinguishable from each other (De-Barro *et al.*, 2011). Recent research based on molecular data of the mitochondrial cytochrome oxidase I (mtCOI) gene and mating compatibility experiments suggest that the *B. tabaci* complex consists of at least 36 cryptic species (Dinsdale *et al.*, 2010, De Barro, 2012; Tay *et al.*, 2012, Firdaus *et al.*, 2013).

2.1.1 Origin and Taxonomy

The morphological plasticity, therefore, meant that it was difficult to use conventional taxonomy to identify populations of *B. tabaci*. The discovery of morphologically indistinguishable populations of *B. tabaci* showed clearly that the different biological traits with respect to host range and host plant adaptation marked the first recognition of the existence of distinct populations, commonly referred to as "strains" or "biotypes" (Diehl and Bush, 1984).

The taxonomic status of populations within *B. tabaci* group is complex and has been the focus of research and scientific debate for many years. Earlier whitefly taxonomists used morphological characters to separate various species (Quaintance and Baker, 1914). Consequently, the more distinctive morphological features of the late fourth instar nymphs (pupae) were exploited, making the fourth instar the preferred stage for diagnostics (Mound and Halsey, 1978; Lopez-Avilla, 1986).

The considerable variation in pupal morphology resulted in the description of a number of African species of *Bemisia*. Much of this variation was later shown by Mound (1963) to be host-induced and not genetic. Offspring developed distinct morphological features dependent on the surface characters of the host plant they were reared upon, seasonal changes in pupal morphology have also been noted for single populations of *B. tabaci* on particular hosts (Mohanty and Basu, 1986).

The genus *Bemisia* contains 37 species and the evolutionary affiliations of the *Bemisia* taxa within the family Aleyrodidae suggest that *B. tabaci* may have originated in tropical Africa and was introduced quite recently into the Neotropics and southern North America. Some evidence also suggests that *B. tabaci* may be native to India or Pakistan, where the greatest diversity of the species' parasitoids has been found, a criterion that has been considered a good indication of a genus epicentre (Brown *et al.*, 1995).

First reports of a newly evolved biotype of *B. tabaci*, the B biotype, appeared in the mid-1980s (Brown *et al.*, 1995) and renewed interest in the morphometrics of *B. tabaci*. Marked biological differences were evident between the two, with the 'B' strain having more rapid development rate (Cohen *et al.*, 1992), wider host range, greater insecticide resistance and greater capacity to transmit viruses than 'A' strain (Bedford *et al.*, 1992). An initial examination of morphological characters did not allow A to be distinguished from B, but then additional characters were discovered, such as absence of the fourth anterior margin setal pair, width of the thoracic tracheal folds, and width of wax extrusions from the folds, that enabled 'B' to be separated from 'A'. However, when *B. tabaci* from all parts of the world were included, morphological characters previously used to separate 'A' from 'B' showed considerable within-and between-group variability and failed to distinguish the groups (De-Barro *et al.*, 2011).

2.1.2 Biotype

The introduction of a novel *B. tabaci* strain designated as the B-biotype in the US during early 1990s has resulted in almost complete replacement of the indigenous A-biotype (Costa and Brown, 1991; Cohen *et al.*, 1992; Liu *et al.*, 1992; Brown *et al.*, 1995). This finding was noted as the most important evidence of the existence of a species complex in *B. tabaci*. The B-biotype was described as a new species, *Bemisia argentifolii* Bellows and Perring (Perring *et al.*, 1993; Bellows *et al.*, 1994), based on its inability to mate and reproduce with other whitefly biotypes and the distinctive biological, esterase and PCR banding patterns (Costa and Brown, 1991; Bedford *et al.*, 1994; Brown *et al.*, 1992; Costa *et al.*, 1993; Gawel and Bartlet, 1993; Byrne *et al.*, 1995). The B-biotype has more fecundity and has an extremely broad host-plant range, which has facilitated the transmission of new viruses from weed hosts to crop plants and *vice versa*. Bedford *et al.* (1994) defined 10 biotypes on the basis of esterase banding patterns viz., A, B, D, E, G, H, J, K, L, and M. The species complex has been found to differ in host range (Zang *et al.*, 2006 and Xu *et al.*, 2011), insecticide resistance, behaviour, virus transmission (Liu *et al.*, 2007; Crowder *et al.*, 2010; Li *et al.*, 2010; Luo *et al.*, 2010; Wang *et al.*, 2010).

B. tabaci is considered as a cryptic species complex or sibling species group comprises of a large number of genetically variable populations, some of which were referred to as biotypes or haplotypes (Brown, 2010 and Gill and Brown, 2010). While morphologically indistinguishable members of this species complex differ on a molecular level and exhibit full or incomplete reproductive isolation due to reproductive incompatibility (Oliveira *et al.*, 2001; De-Barro *et al.*, 2011).

Hu *et al.* (2011) summarized available genetic and behavioural data on reproductive incompatibilities derived from genetic studies and observations on mating behaviour. They identified 28 biotypes for *B. tabaci* based on the phylogenetic analysis of mitochondrial cytochrome oxidase I (*mtCOI*, a highly conserved gene). The biotypes may differ in virus transmission, efficiency, development rate, host utilization, fecundity, dispersal ability, infestation symptoms, insecticide resistance and endosymbiont populations.

Two of the best-known biotypes, B and Q are the globally most widespread and invasive of the biotypes, while others are generally confined to specific geographical locations. These two biotypes have been responsible for the whiteflies rising profile as a pest in the past two decades (Brown *et al.*, 1995; Liu *et al.*, 2007 and De-Barro *et al.*, 2011).

2.1.3 Whiteflies as Agricultural Pests

The silverleaf or sweetpotato whitefly (*B. tabaci* Genn, syn *B. argentifolii* Bellows and Perring) belongs to the family Aleyrodidae of the order Hemiptera. Economically it is one of the most important pests in tomato and pepper (Brown *et al.* 1995; Morales, 2007). It causes direct damage through feeding on plant phloem sap and indirect damage through virus transmission and sooty mold growth. Whitefly related damage reduces crop quality and quantity (Morales, 2007).

B. tabaci was mainly known as a pest of field crops in tropical and sub-tropical countries on cassava (*Manihot esculenta*), cotton (*Gossypium*), sweet potatoes (*Ipomoea batatas*), tobacco (*Nicotiana*) and tomatoes (*Lycopersicon esculentum*). However, *B. tabaci* had a composite range of around 300 plant species within 63 families (Mound and Halsey, 1978) and some estimates show host range of around 600 species (Li *et al.*, 2011). With the evolution of the highly polyphagous B biotype, *B. tabaci* has now become a pest of glasshouse crops in many parts of the world, especially on capsicum, courgettes (*Cucurbita pepo*), cucumbers (*Cucumis sativus*), hibiscus, gerbera, gloxinia, lettuces (*Lactuca sativa*), poinsettia (*Euphorbia pulcherrima*) and tomatoes (*Lycopersicon esculentum*).

2.1.4 Whitefly and tomato

Being a phloem-feeding insect, *B. tabaci* carefully maneuvers its stylet through the epicuticular layer, epidermis and sponge tissue to reach the phloem (Freeman *et al.*, 2001). The stylet is wrapped with a gel-like substance that is suggested to reduce plant defense responses. A heavy whitefly infestation can cause a reduction of plant vigour and yield, early wilting, leaf chlorosis and defoliation. Whitefly infestations may also result in leaf silvering of tomato, squash and cotton (Freeman *et al.*, 2001; Kaloshian and Walling, 2005).

Bemisia tabaci affects tomato and other crops directly through phloem sap feeding, which results in leaf spotting, plant weakening, irregular ripening of fruits and honeydew secretion on which sooty mold can grow. *Bemisia tabaci* is also responsible for several physiological disorders such as increased stomata resistance, and a reduced transpiration, photosynthesis and chlorophyll content in leaves (Muigai *et al.*, 2002; Fancelli *et al.*, 2003 and Inbar and Gerling, 2008). It also affects tomatoes indirectly as a vector of a large number of viruses (Begomovirus, Crinivirus, Closterovirus and Ipomovirus) both in persistent and in semi-persistent circulative manner (Brown and Bird, 1992 and Valverde *et al.*, 2004).

2.1.5 Viruses transmitted by *B. tabaci*

B. tabaci is a vector of 111 viruses, recognised as species in the genera *Begomovirus* (*Geminiviridae*), *Crinivirus* (*Closteroviridae*) and *Carlavirus* or *Ipomovirus* (*Potyviridae*).

Of these transferred viruses, over 90 per cent are Begomoviruses such as Tomato yellow leaf curl virus (TYLCV), Tomato chlorotic mottle virus (ToCMoV), Tomato crumple mottle virus (TCMV), Tomato curly stunt virus (ToCSV), Tomato golden mosaic virus (TGMV), Tomato golden mottle virus (ToGMoV), Tomato mottle virus (ToMoV), Tomato yellow leaf curl Sardinia virus (TYLCSV), Pepper yellow leaf curl virus (PYLCV), Chino del tomate virus (CdTV) and Pepper huasteco virus (PHV) (Morales and Jones, 2004; Tahiri *et al.*, 2006; Hidayat and Rahmayani, 2007).

Begomoviruses are the most numerous of the *B. tabaci*-transmitted viruses and cause crop yield losses of 20 to 100 per cent (Brown and Bird, 1992; Varma and Malathi, 2003).

Among the different virus diseases infecting tomato crop, ToLCV is one of the most important diseases in India. The natural occurrence of TLCV was observed on tomato in India by Pruthi and Samuel (1939). Subsequently ToLCV disease in tomato was reported in many parts of India (Vasudeva and Samraj, 1948; Srivastava *et al.*, 1975 and Muniyappa and Veeresh, 1984).

Sastry and Singh (1973) found that, ToLCV infected plants produced very few fruits when infected, within 20 days after planting and resulted in 92.3 per cent yield loss. Plants infected at 35 and 50 days after transplanting resulted in 74 and 22.9 per cent yield loss, respectively. An average of 39 per cent losses in tomato yield due to tomato leaf curl virus was reported from Somalia, annually (Castellani *et al.*, 1981).

2.2 Plasticity of morphological traits among the populations of whiteflies

Bellows *et al.* (2015) studied intraspecific and interspecific mating behaviour, analysis of allozymic frequencies, PCR analysis of genomic DNA and morphological evaluation. The description of the new species was done based on morphological and allozymic characters of *B. tabaci* strain B. The species is distinguished from *B. tabaci* in the fourth nymphal instar by the absence of a dorsal seta, the width of the thoracic tracheal folds, the width of the wax extrusions from the tracheal folds, and, in the adult, by migration distances of allozymes for three enzyme systems.

Rosell *et al.* (1997) compared the morphological characters of *Bemisia* spp. from 17 populations across the world. The characters of the 4th instar nymph *viz.*, its anterior submarginal setae, anterior and posterior wax fringes, dorsal setae, posterior submarginal setae, caudal setae, and tracheal folds. Anterior submarginal setae 4 (ASMS 4) were generally, but not always, absent in *B. argentifolii* and B biotype populations and in most non-A/non-B biotypes (E, K, L, P, and Q). However, ASMS 4 were found in A biotypes, in the N biotype and in *B. hancocki*. Dorsal setal pair 4 was absent in most populations and the lengths of dorsal setal pairs 1, 2, 3, 5, and 6 varied on individuals from several populations. Anterior wax fringes were highly variable in length and width in all populations. With the exception of the Nepal (P biotype) population, posterior wax fringes extended beyond the borders of the caudal setae in all individuals examined. Phylogenetic analysis did not resolve most-parsimonious trees.

Guershon and Gerling (2001) studied the influence of environmental trigger for the development of the setose phenotype of *B. tabaci* nymphs. Quantification tests revealed manifestation of phenotypic plasticity in whitefly and showed positive correlation between trichome density on tomentose leaves and the percentage of setose nymphs. Artificial simulation of leaf tomentosity provided sufficient stimulation to

induce the setose nymph phenotype. The crawler was found to be the only sensitive stage for this induction. Further, polymorphism of the nymphal phenotype was correlated with additional biological features of both nymph and adult. Results indicated that, setose nymphs were smaller and developed faster and adults emerging from such nymphs were smaller and had shorter lifespan.

The morphological study of three biotypes revealed that, the anterior and posterior wax fringes of the B, Q, and Cv biotypes significantly differed from each other. Based on this morphological characteristic, the three biotypes can be easily distinguished in greenhouses and fields (Qiu *et al.*, 2009).

Morphometric analyses of populations of *B. tabaci* collected from leucaena were compared with cotton populations (Thomas *et al.*, 2011). The results revealed significant differences in the length of egg, second, third and fourth instars. Out of 62 measurements of the puparia analysed, 70 per cent of those of the head, 44 per cent of thorax and 51 per cent of abdomen showed significant differences between cotton and leucaena populations. Mapping of the host association of samples onto principal component ordination showed their significant separation according to host plants, with the first three principal components accounting for 66 per cent of the total variation.

Morphometry of six biotypes (B, Q, Cv, ZHJ-1, ZHJ-2 and ZHJ-3) of *B. tabaci* were studied by Jing *et al.* (2013). Nymphal characters such as 4th instar body size (pupal case), vasiform orifice, operculum, lingula, length and thickness of anterior and posterior wax margins, width of thoracic tracheal combs and adult characters of both sexes *viz.*, body size, compound eyes, antennal segments, vasiform orifice, hind tarsi and genitals were recorded. The results indicated that, differences of some morphometrics were significant among the six biotypes of *B. tabaci viz.*, pupal sizes of the exotic biotypes (B and Q) were significantly larger than the indigenous biotypes in the following order as B>Q>ZHJ-1>Cv>ZHJ-3>ZHJ-2 and for both male and female adults, sizes of all characters investigated in the invading biotypes (B and Q), especially B, were much larger than those of the indigenous ones.

Chaubey and Andrew (2015) revealed that, out of the 62 characters evaluated for morphometrics of whitefly, *B. tabaci*, 30 characters showed significant variation ($P < 0.05$) reinforcing the complexity of species. Principal component analyses (PCA) revealed six principal components (PC) accounting for 73.6 per cent of total variation and further in canonical discriminant analyses (CDA) overlapped clustering was observed in all the six populations. Overall, 91.11 per cent of the classifications were correctly attributable by CDA and confirmed the distinctiveness of populations. For this distinction, maximum contributions were from the measurements of length of operculum, breadth of vasiform orifice, distance of transverse moulting suture, breadth of operculum, length of antennae, lingula and puparia. The morphometrics revealed distinct variations which could be explored for morphological delineation of genetic groups/ putative species of *B. tabaci* supplementing their molecular variations.

Baig *et al.* (2015) studied the biology and morphology of life stages of three species of whiteflies collected from different hosts. The duration with morphometrics and illustrations for each developmental stage are also provided. Males developed more quickly than and were outnumbered by females of the three species by a ratio of 3.5:1, 4:1 and 3:1, respectively. Nymphal developmental period was positively correlated with length and width and negatively correlated with length:width ratio. Considerable sexual variation was revealed by adult morphometrics.

The species complex of *B. tabaci* consists of 36 morphologically indistinguishable putative species (Chaubey *et al.*, 2015). They evaluated the morphometric variations of developmental stages, puparia and adults in three putative species of *B. tabaci* occurring in India. The results showed that, fourth instar and adult of Asia-II1 was comparatively larger than Asia-I and Asia-II7. The positioning of sensorial cone on antennal segment 7 is much apart and away from the sensorium in Asia-II1 while these are comparatively adjacent in Asia-I and Asia-II7 for both the sexes. The multivariate statistical analyses, principal components and canonical discriminant analysis (CDA) revealed that, 31 measurements in puparia, 23 of male and 22 of female show significant variations and separate clustering was obtained for Asia-I, Asia-II1, and Asia-II7. Overall 91 and 99 per cent of the classifications were correctly attributed by CDA for puparia and adults, respectively which confirmed the distinction of these groups.

Harish *et al.* (2016) evaluated the presence of different genetic groups, using morphometric variations among whitefly populations with fourteen different pupal characters and nine different adult characters from all agro-ecological zones of Kerala. There were no significant variations in most of the characters studied, between these agro-ecological zones. The principal component analysis revealed the presence of more variations in populations collected from Sulthan Bathery compared to others.

2.3 Genomic flux and population genetic structure of *Bemisia tabaci*

De-Barro (2000) demonstrated using microsatellites that, *B. tabaci* from the Asia Pacific region split into six genetic populations with little or no gene flow between them. These genetic populations bore only superficial similarity to the mitochondrial and ribosomal defined races. Further, four of the six further split into two subpopulations, which again showed little evidence of gene flow between them. While the patterns reflected a strong geographic structure, physical barriers alone could not explain all the observed structure. The lack of gene flow between genetic populations and some subpopulations further suggested that the barriers were either sufficiently impermeable to immigration or that reproductive isolation and competitive interactions were sufficiently strong to prevent gene flow.

Gocmen and Devran (2002) used amplified fragment length polymorphism (AFLP) technique to access eight populations of *B. tabaci* collected from cotton, protected vegetables (tomato, cucumber and eggplant) and peppermint in various locations in the province of Antalya, Turkey. Eleven AFLP primer pairs detected a total of 547 AFLP fragments in these populations and 389 of these showed polymorphism. Cluster analyses of AFLP data clearly separated these populations into two groups with a genetic variability between 42 per cent and 81 per cent. The results indicated that, *B. tabaci* may have biotypes based on adaptation to certain host plant species in Turkey.

Lima *et al.* (2002a) showed genetic diversity of *B. tabaci* populations in Brazil by RAPD markers. A total of 72 markers were generated by five RAPD primers and used in the analysis. All primers produced RAPD patterns that clearly distinguished the *Bemisia* biotypes and the two other whitefly species. Results also showed that

populations of the B biotype have considerable genetic variability. Cluster analysis demonstrated that, Brazilian biotype B individuals are scattered independently in the localities where samples were collected. The study showed that the B biotype is predominant over the A biotype.

Lima *et al.* (2002b) estimated the genetic diversity, genetic relationships of *B. tabaci* populations of 109 female individuals of 12 populations in Brazil and compared to the A biotype from Arizona (USA) and B biotype from California (USA) and Paraguay. *Trialeurodes vaporariorum* Westwood and *Aleurodicus cocois* L. samples were also included. A total of 72 markers were generated by five RAPD primers and used in the analysis. All primers produced RAPD patterns that clearly distinguished the *Bemisia* biotypes and the two other whitefly species. Results also showed considerable genetic variability among B- biotype population. Cluster analysis demonstrated that, Brazilian biotype B individuals are scattered independently in the localities where samples were collected. Analysis of Molecular Variance (AMOVA) showed that, most of the total genetic variation is found within populations (56.70%), but a significant portion of the variation is found between crops (22.73%). The study showed that widespread distribution of biotype in sampled areas, infesting several host plants and predominated over the A biotype.

De-Barro *et al.* (2003) screened 33 populations of *B. tabaci* using fifteen microsatellite loci (335 alleles with 6- 44 alleles per locus). The microsatellites amplified best in individuals from genetic groups representing the Mediterranean, Middle East, Asia (three groups) and Australasia or Oceania and amplified less well with populations from sub-Saharan Africa and New World.

Lisha *et al.* (2003) for the first time reported the presence of biotypes of *B. tabaci* in India. Host plant performance, esterase and virus transmission tests revealed cassava-strain and sweetpotato-strain populations of *B. tabaci* biotypes in India. Individuals from the sweetpotato-reared population did not breed on cassava, *Manihot esculenta* Crantz, and the cassava-strain-reared individuals failed to develop on sweetpotato, *Ipomoea batatas* (L.) Lam.

The genetic structure of field populations of begomoviruses and their whitefly vector, *B. tabaci* in Pakistan was analyzed by Simón *et al.* (2003). Begomoviruses and

B. tabaci populations were sampled from different crops and weeds in different locations in Punjab and Sindh provinces, in areas where cotton leaf curl disease (CLCuD) occurs or does not occur. Analysis of the capsid protein (CP) open reading frame grouped isolates into three geographical clusters, corresponding to isolates collected in Punjab, Sindh, or both provinces. RAPD analyses of the *B. tabaci* population showed high intrapopulation diversity at both local and regional scales. Sequence analysis of *mt COI* gene showed that the *B. tabaci* population was structured into at least three genetic lineages corresponding to the previously described Indian, Southeast Asian, and Mediterranean-African clades. The Indian clade was present only in Punjab, the Mediterranean-African only in Sindh, and the Southeast Asian in both provinces. *Bemisia tabaci* haplotypes of the Indian clade were found only in Punjab, where CLCuD occurs.

Lima and Lara (2004) used RAPD-PCR to survey the B biotype and other biotypes of *B. tabaci* from 57 different localities and on 27 distinct crops and weeds in Brazil. RAPD analyses using two selected ten primers reliably identified the BR biotype and the B biotype of *B. tabaci* and also differentiated other whitefly species. The presence of the B biotype was confirmed in 20 Brazilian states. The BR and B biotypes of *B. tabaci* were found to coexist in the whitefly populations of three different localities viz., Jaboticabal SP, Rondonópolis and Cuiabá, MT and Goiânia, GO.

Dalmon *et al.* (2005) studied the genetic structure of *B. tabaci* in glasshouses in southern France. Seven microsatellite loci were scored in 22 populations sampled from various regions. Two genetic groups were distinguished using a Bayesian clustering method and were assigned to the biotypes B and Q using the gene sequence of *CO1*. A single sample site was notable for a decrease in expected heterozygosity and the mean number of alleles over the years. Lack of spatial genetic structure among biotype Q population was indicative of a recent colonization event combined with large dispersal at all spatial scales. They concluded that, the evolution of genetic diversity in glasshouses in France is part of the worldwide invasion of biotype Q.

De-Barro *et al.* (2005) conducted an experiment to study the genetic structure of whitefly by using 15 microsatellite loci and demonstrated that, the indigenous Asia-Pacific genotypes split into six genetic populations with little or no gene flow

between them. These bear only superficial similarity to the mitochondrial and ribosomal defined races. Moreover, four of the six can be further split into two subpopulations that again show little evidence gene flow between them. Differential host-plant utilization explained the substructure. Lack of gene flow between genetic populations and some subpopulations further suggested impermeability barriers to immigration or reproductive isolation and competitive interactions were sufficiently strong to prevent gene flow. Study indicated the presence of ten morphologically indistinguishable species indigenous to the Asia-Pacific region.

Delatte *et al.* (2005) distinguished two genetic types of *B. tabaci* using RAPD-PCR and Cytochrome Oxidase I (COI) gene sequence comparison. One type was assigned to B biotype and other was genetically dissimilar to the population named Ms after the Mascarenes Archipelago. Both B and Ms Population of *B. tabaci* induced silverleaf symptoms on *Cucurbita* spp, and were able to acquire and transmit TyLCV. So, Ms genetics type has been considered as a new biotype of *B. tabaci*.

Khasdan *et al.* (2005) studied genetic diversity and distribution of B and Q-biotypes. Sequence characterized amplified regions (SCAR) and cleaved amplified polymorphic sequences (CAPS) techniques, single RAPD fragments of B and Q biotypes, respectively, were used. Analysis of field samples collected in Israel for several years, indicated increase in the percentage of the Q biotype in field populations as time progresses. This may be attributed to the resistance of the Q biotype to neonicotinoids and pyriproxyfen and the susceptibility of the B biotype to these insecticides.

Delatte *et al.* (2006) investigated the temporal and spatial distribution, host-plant range and genetic structure of invasive biotype (B) and resident biotype (Ms). Results showed that, clustering methods separate two groups of individuals that can be identified as the B and Ms biotypes. The B biotype has invaded all regions of the island and showed no signs of genetic founder effect relative to the Ms biotype. The B and Ms biotypes coexist in sympatry throughout most of their geographical ranges, although they tend to segregate into different host plants. Asymmetrical and locus-specific introgression occurs between the two biotypes when they are in syntopy.

Phylogenetic analyses based on *mt COI* gene sequences of 21 *B. tabaci* populations from Bangladesh grouped into two independent clusters (Maruthi *et al.*, 2007). Some sequences from different countries, viz., Bangladesh, China, India, Nepal, Pakistan and Thailand were almost identical while others collected from plants within the same field diverged by 15 per cent, indicating high diversity even at the local level. None of the *B. tabaci* from Bangladesh grouped with the reference B- and Q-biotype sequences.

Hsieh *et al.* (2006) studied distribution and biotypes of *B. tabaci* in eastern Asia using *mt COI* gene sequence to distinguish biotypes. Phylogenetic analyses indicated three biotypes in eastern Asia viz., B, Nauru and An. Phylogenetic trees revealed that, the invasion of the B biotype in Taiwan was recent and multiple invasions may have occurred due to human trade activities. The B biotype is the most widely distributed biotype in Taiwan. Invasions by the Nauru and An biotypes in Taiwan may have included both natural movements and human trade activities. Otherwise, distributions of the Nauru and An biotypes overlap in Asia, and it is presumed that, they are closely related. The result supports that the Nauru biotype is of Asian origin, and the An biotype may be of Asian or Australian origin. In addition, the tree topology supported *B. tabaci* being differentiated into three major clades: the New World, Asia/Australia, and Mediterranean/Asia Minor/African groups.

Simon *et al.* (2007) observed variation at six microsatellite loci among a subset of nine *B. tabaci* populations. These loci showed considerable polymorphism in the Q and B biotypes populations although the presence of null alleles. The Iberian Q, Canarian-Q and Egyptian-B populations exhibit heterozygosity as a result of bottleneck events. Low genetic differentiation between the Israeli, Iberian Peninsula and Italian populations suggest that, these populations share a common gene pool. The genetic distances between the Canarian-Q population and the geographically close population from Morocco indicate spatial isolation and a limited gene flow and the microsatellite data for the B populations indicate that, the whiteflies from Egypt and Israel have a close phylogenetic relationship, but the source of these biotype B invasions into the Mediterranean area remains unknown.

The molecular characterization of *B. tabaci* populations collected from nine sites in southern Tunisia using the Bem-23 microsatellite marker showed the presence

of biotype B in seven of the eight geothermal sites and exhibited 220 bp bands that are typical. However, in the remaining geothermal sites, the *B. tabaci* population was a mixture of biotype B and Q and exhibited 410 bp bands (Bel-Kadhi *et al.*, 2008).

Gauthier *et al.* (2008) studied three PCR multiplex sets comprising three, five and four loci, optimized and characterized across 133 *B. tabaci* females from Israel. Results showed that, there were three to 24 alleles per locus and the observed heterozygosity was from 0.084 to 0.420. Deviation from Hardy-Weinberg equilibrium was detected at four loci associated with significant heterozygote deficiencies due to null alleles and presence of subpopulations and also 12 loci carried independent information.

McKenzie *et al.* (2009) determined the biotype status of *B. tabaci* samples by polymerase chain reaction (PCR) amplification and sequencing of a 700-800 bp *mt COI* gene fragment, PCR amplification and size determination of two unique microsatellite markers and esterase zymogram analysis. Eighteen per cent of all collections were found to be the Q biotype that came from greenhouse grown ornamental and herbs located in six countries. Sequence comparison of the *mt COI* gene identified three separate haplotypes within Florida that were defined as Q₁, Q₂ and Q₃.

Perumal and Marimuthu (2009) studied the influence of host plants on the *B. tabaci* population differences at molecular level using Random Amplified Polymorphic DNA (RAPD) markers. The total number of bands obtained from each primer ranged from 11 to 35 with an average of 23.60 bands per primer. Srivilliputhur population showed the highest similarity index (0.826) and lowest (0.111) was recorded by Namakkal population. Three major clusters were formed from UPGMA dendrogram, which was constructed based on Jaccard's similarity. The first cluster included population collected from okra and cotton, while second cluster comprised of population from eggplant and cauliflower and the third cluster included population from eggplant. It could be deduced that population from cotton and okra had 50% similarity, while 60-70 per cent similarity was observed for population from eggplant and cauliflower.

The RAPD-PCR analysis and DNA sequences of the COI gene of three biotypes viz., B and Q and Cv biotypes revealed the differences between these biotypes using the H16 primer. The B biotype has three bright DNA bands between 250 and 600 bp, Q biotype has only one bright band at 300 bp, while the Cv biotype has no band between 250 and 500 bp. Both the Cv and Q biotypes have two bright bands at 750 and 1000 bp while the B biotype has only one band at 1000 bp. Based on the COI gene, the genetic identity between B and Cv, B and Q, and Q and CV was 85.8 per cent, 94.7 per cent and 86.0 per cent, respectively. The MP tree indicated that the phylogenetic relationship between the B and Q biotypes is much closer than that between the B and Cv or the Q and Cv biotypes (Qiu *et al.*, 2009).

Delatte *et al.* (2011) analysed the genetic structure, geographical range and putative origin of *B. tabaci* species, in SWIO islands of the region and mainland Africa. Only B and Ms populations were detected across the islands. The exotic B was found only on the islands of Réunion and Mauritius, where as the Ms is found on all the SWIO islands. Very high isolation by distance was found for the Ms populations between islands of the SWIO, suggesting a long period of presence in this region. Ms populations from mainland Africa had a higher COI diversity than the Ms of the SWIO islands. This diversity is correlated with size and geological ages of the SWIO islands. The population genetic data obtained are in accordance with an origin of Ms in Africa, followed by its expansion and evolution across the SWIO islands prior to human arrival, confirming the status of Ms as indigenous in the SWIO islands.

Hu *et al.* (2011) used molecular markers to identify cryptic species. The evolutionary relationships between the different Asian *B. tabaci* were reconstructed using Bayesian methods. In the past the exotic invader Middle East-Asia Minor 1 was predominant across China, another newer invader Mediterranean is now the dominant species in the Yangtze River Valley and eastern coastal areas, and Middle East-Asia Minor 1 is now predominant only in the south and south eastern coastal areas. Based on *mt COI* four new cryptic species have been identified and in total 13 indigenous and two invasive species were recorded from China. Diversity was highest in the southern and southeastern provinces and declined to north and west. Only the two invasive species were found in the northern part of the country where they occur primarily in protected cropping. Indigenous species were mainly found in remote mountainous areas and were mostly absent from extensive agricultural areas.

Hsieh *et al.* (2011) investigated the genetic structure of multiple *B. tabaci* Q-biotype populations using *mt COI* gene and 12 microsatellite loci. The presence of only a few *COI* haplotypes and a low number of nucleotide differences suggested high genetic similarity among these populations. Microsatellite analyses also revealed low genetic differentiation and frequent gene flow among greenhouses. The molecular evidence supported the occurrence of a recent genetic bottleneck in the *B. tabaci* Q biotype. Phylogenetic analyses of microsatellites support Q biotype migration among greenhouses, which was likely facilitated by the frequent movement of host plants between greenhouses.

Valle *et al.* (2011) quantified genetic variability between and within populations of *B. tabaci* in Brazil by collecting three individuals from three host plant viz., soybean, pumpkin and tomato. The *COI* region of the *mt DNA* gene was partially amplified with the CI-J-2195 and L2-N-3014 pair of primers and the reaction products were sequenced. Based on distance based algorithm analyses, it was found that, all haplotypes belong to biotype B. Genetic structure analyses did not show the influence of host plant on population structuring.

Pairwise comparisons with *mt COI* consensus sequences of *Bemisia tabaci* adults showed that, the majority of the samples had <3.5 per cent sequence divergence from groups termed Asia I, Asia II-5, Asia II-7, and Asia II-8. The biotype-B from India clustered into the Middle East-Asia Minor 1 group. A new group of *B. tabaci* from coimbatore, collected on pumpkin, was most closely related to the Asia I group (6.2% sequence divergence from the consensus Asia I sequence) (Chowda-Reddy *et al.*, 2012).

Fontes *et al.* (2012) studied the genetic diversity of eight *Bemisia tabaci* populations from different cropping areas in Brazil and a cabbage population from Florida (USA) through a eight microsatellite analysis. The number of alleles varied between two and 13 and the average value of *FST* was 0.13. The population occurring in beans was genetically different. The American population presented a large diversity and small differentiation compared to the Brazilian populations, especially from the Southeast, supporting the hypothesis that the B biotype was probably introduced into Brazil by the trade of plant material between the USA and the State of São Paulo. The genetic diversity found within and among the populations is

geographically structured and the insects from the central region of Brazil had superior genetic divergence when compared to other Brazilian locations.

The genetic diversity and biotype status of the *B. tabaci* in Pakistan was assessed by Hameed *et al.* (2012) with RAPD-PCR using 10 primers. Based on Nei and Li's similarity coefficients, populations were grouped into 3 main clusters and clearly distinguished the non B biotype from the B biotype. The level of similarity among populations of same biotypes was high whereas between populations of non B and B biotypes appeared to be less closely related. This analysis showed that, non B biotype is prevalent in both provinces, however B biotype is restricted to few locations.

McKenzie *et al.* (2012) conducted survey of *B. tabaci* biotypes in North American states from different host plants to monitor the introduction and distribution of the Q biotype. The biotype status of *B. tabaci* samples was determined by PCR amplification and sequencing of a *mt COI* gene fragment and characterization of two biotype discriminating nuclear microsatellite markers or esterase zymogram analysis. The New World biotype was detected on field-grown tomatoes in Mexico (two) and in commercial greenhouses in Texas (three). Biotype Q was detected in 23 states in the US, Canada, Bermuda, and Mexico. Forty five per cent of all collections were found to contain biotype Q in samples from ornamentals, herbs and a single collection from tomato transplants located in protected commercial horticultural greenhouses, but there were no Q detections in outdoor agriculture. Ten of the 15 collections (67%) from Canada and a single collection from Bermuda contained biotype Q, representing the first reports of biotype Q for both countries.

The genetic variability of *B. tabaci*, in cassava growing areas of Kenya, Tanzania and Uganda was investigated by Mugerwa *et al.* (2012). Two distinct species were observed like sub-Saharan Africa 1 (SSA1), comprising of two sub-clades (I and II) and a South West Indian Ocean Islands (SWIO) species. Among the SSA1, sub-clade I sequences shared a similarity of 97.8- 99.7 per cent with the published Uganda 1 genotype and is diverged by 0.3- 2.2 per cent. A pairwise comparison of SSA1 sub-clade II sequences revealed a similarity of 97.2-99.5 per cent with reference to southern Africa genotypes and diverged by 0.5-2.8 per cent. The SSA1 sub-clade I whiteflies were widely distributed in East Africa (EA). In

comparison, SSA1 sub-clade II whiteflies were detected for the first time in the EA region and occurred predominantly in the coast regions of Kenya, southern and coast Tanzania. The SWIO species had a sequence similarity of 97.2- 97.7 per cent with the published Reunion sequence and diverged by 2.3-2.8 per cent. The SWIO whiteflies occurred in coast Kenya only.

Li *et al.* (2012) analyzed the composition, distribution and genetic diversity of mitochondrial haplotypes of *B. tabaci*. Result revealed that, five haplotypes were present in the Q1 subclade based on 773-bp *mt COI* fragment analysis. The diversity of haplotypes indicated that, the Q populations were derived from multiple invasion sources originating from the western Mediterranean region. Among the haplotypes, Q1H1 was dominant, followed by Q1H2. The whitefly populations were generally characterized by low levels of genetic diversity based on the 773-bp *mt COI* fragment.

Valle *et al.* (2012) studied genetic variability and population structure of whiteflies by developing thirteen polymorphic microsatellite markers and characterized 20 individuals from a natural population of soybean field. The number of alleles per locus ranged from one to two and the expected heterozygosity ranged from 0.000 to 0.505. The low polymorphism found in these molecular markers is probably associated with homology of genes expressed in these markers.

Xiao-jun *et al.* (2012) studied diversity and genetic differentiation of 19 populations of *B. tabaci* using cDNA AFLP. Prior to 2007, MEAM1 was a dominant species in many provinces in China. By 2007, MED was dominant in 11 provinces. MED and MEAM1 have broad host range and indigenous species have much narrower host ranges. All Asia II 3 samples were found on cotton except one on aubergine. China 3 has more host plants than Asia II 3. Twelve samples of China 3 were collected from sweet potato, Japanese hop, squash and cotton. A total of 677 reproducible bands amplified with 5 AFLP primer combinations were obtained. Unweighted pair-group method analysis indicated MED as the lowest degree of similarity than the other species.

Bouktila *et al.* (2013) used RAPD-PCR to assess the genetic diversity of 120 *B. tabaci* using 150 polymorphic markers. The genetic structure was analyzed, based on the molecular variance (AMOVA), genetic distances (F_{st}) and multidimensional

scaling (MDS). AMOVA revealed that, diversity between geographical domains (North vs. South) and between individuals within populations were the most determining factors in the partitioning of the total genetic diversity (50.19% and 44.85%, respectively). In addition, F_{st} and MDS indicated that, the populations of *B. tabaci* were structured according to their geographical origin.

Dickey *et al.* (2013) studied the genetic structure of MEAM1 and MED *B. tabaci* populations. 987 MEAM1 whiteflies and 340 MED whiteflies were genotyped at six and seven microsatellite loci, respectively. The results showed MED population exhibiting more genetic differentiation than MEAM1 and nuclear microsatellite markers exhibit a high degree of concordance with mitochondrial markers recovering a major east-west phylogeographic break within MED. The results suggested that MED was introduced into the United States on at least three occasions and rapidly spread throughout the United States..

New genetic variant of *B. tabaci* Asia-II-7 (Cv biotype) was reported for the first time in Pakistan (Shah *et al.*, 2013). Phylogenetic tree constructed showing all the sequences grouped into two genetic clades Asia-II-7 and Asia-II-1 (K, P, PCG-1, PK1, SY and ZHJ2 biotype). Report suggested ready adaptability of Asia-II-7 genetic variant adapts readily to ornamental plants as compared to vegetables.

Valle *et al.* (2013) examined the population variability of *B. tabaci* inhabiting six agricultural crops grown in five regions of Brazil and one region of the USA viz., BRrep whitefly population on cabbage, ILsoj on soybean, BJabo on pumpkin, CPsoj on soybean, UBman on cassava and PEmel on melon. Thirteen polymorphic loci with 50 alleles were observed, with an average of 2.37 alleles per population. Among the different populations UBman and PEmel *B. tabaci* populations were the most differentiated, which was attributed to insect adaptation to the host plant and the use of insecticides. A 33.87 per cent inter population variation was observed, indicating that microsatellites used to measure differentiation among *B. tabaci* populations were efficient and it also showed that, Middle East Asia minor 1 population of *B. tabaci* was found in six populations.

Chu *et al.* (2014) reported *B. tabaci* Q populations in agricultural fields derive from multiple secondary introductions. In addition, the common use of greenhouses

during the winter in certain locations in northern China helped to increase the genetic diversity and the genetic structure of the pest.

Diaz *et al.* (2014) investigated the genetic structure of *B. tabaci* in eight sampling locations from two infested regions (coastal and inland) using nine microsatellite markers and the *mt COI* gene. The mitochondrial analysis indicated that, only the invasive species of the *B. tabaci* complex Middle East-Asia Minor 1 (MEAM 1) known previously as biotype B) was present. The micro satellite data pointed to genetic differences among the regions and no isolation by distance within regions.

Ellango *et al.* (2014) analysed the genetic diversity of *B. tabaci* collected on various host plants. The diversity analysis was performed using two markers such as mitochondrial COI gene and the ribosomal ITS. The phylogenetic trees were constructed separately for two dataset using Neighbor-Joining method. The result confirmed presence of four putative species of *B. tabaci* such as Asia I, Asia II 1, Asia II 5 and Asia II 8 in India. The Asia I genetic group found most widely distributed and shows relative polyphagous nature.

Hadjistylli *et al.* (2014) isolated nine microsatellites from *B. tabaci* biotype B and examined polymorphism across 60 individuals of two populations. Observed and expected heterozygosities ranged from 0.033 to 0.967 and 0.033 to 0.854, respectively. There was no significant deviation from Hardy-Weinberg equilibrium and no significant linkage disequilibrium between loci. One locus showed evidence for null alleles.

Prasanna *et al.* (2014) investigated the whitefly species complex in soybean in major soybean growing states of India. The *mt COI* based phylogenetic relationships established using Bayesian methods indicated the existence of three cryptic species namely Asia I, Asia II 1, and Asia II 7. Of these, Asia II 1 was found to be predominant with wide spread distribution across the regions from cool temperate zones to hot and humid tropical plains. On the contrary, cryptic species, Asia II 7 showed localized distribution. The Asia II 1 exhibited the highest haplotype diversity and Asia I showed high level of nucleotide diversity. There was a significantly high genetic differentiation among these three cryptic species.

Bemisia tabaci is an important pest and affects a broad range of agricultural crops, vegetables and ornamental crops having many biotypes. Whitefly has been described with evidence that, *B. tabaci* should be considered a cryptic complex species of 11 well- defined high-level groups containing at least 24 morphologically indistinguishable species and this finding was based on the mitochondrial cytochrome oxidize I (*mtCO I*) sequence (Tomar *et al.*, 2014).

Tomar *et al.* (2014) analyzed *mtCO I* sequence of *B. tabaci* from population samples collected from different host plants-potato, brinjal and ladys finger from Meerut district, Uttar Pradesh, India. The results revealed that, amplification of *mtCO I* gene fragment using the primers (C1-J-2195 and L2-N-3014) produced *B. tabaci* specific ~800bp band in all the samples of whitefly. Further sequencing, homology search by Blast and comparison against the consensus sequences of Dinsdale revealed that, these samples belong to group Asia II 1 which includes K, P, ZHJ2, PCG-1, SY and PKI, respectively.

Wang *et al.* (2014) identified 358, 433 and 322 new polynucleotide microsatellites separately from the transcriptome sequences of three cryptic species of the *B. tabaci* complex and also validated cross species transfer ability of 57 microsatellites experimentally. The results highlighted that, these markers are conserved and have high inter-taxon transferability. Thirteen markers were employed to assess the genetic relationships among six cryptic species of the *B. tabaci* complex. The inferred phylogeny was consistent with that of *mitochondrial COI* sequences, indicating that microsatellites have the potential to distinguish species of the *B. tabaci* complex. These markers can be used to analyze the population genetics and evolutionary patterns of the *B. tabaci* complex.

Charaabi *et al.* (2015) studied the genetic identity of 146 whitefly populations by PCR-RFLP analysis of the COI gene and revealed that only MEAM1 and MED species have been found in Tunisia. Among them, MEAM1 species was dominant in 96 populations (100.0%), MED was dominant in 34 populations (100.0%) and the 16 remaining were mixed populations. Species differentiation between localities was not significant, however, strong differences was observed according to host plants type. Thus, the MEAM1 species was resulted largely predominant on vegetable crops (86.7%), whereas MED was consistently found on ornamental plants (97.3%).

Diaz *et al.* (2015) examined the genetic structure of *B. tabaci* in eight sampling locations from two infested regions (coastal, inland) using nine microsatellite markers and the mitochondrial COI gene. The mitochondrial analysis indicated that, only the invasive species of the *B. tabaci* complex Middle East-Asia Minor 1 (biotype B) was present. The microsatellite data pointed to genetic differences among the regions and no isolation by distance within regions. The coastal region in the Caribbean appears to have been the initial point of invasion, while the inland region in the Southwest showed genetic variation among populations most likely reflecting founder events and on going changes associated with climatic and topographical heterogeneity.

Ellango *et al.* (2015) sequenced 850bp of the mitochondrial COI (*mt COI*) gene from *B. tabaci* populations surveyed across India. BLAST analysis of the *mt COI* sequences from the *mtCOI* dataset showed the presence of one invasive group, MEAM1 and eight other groups of *B. tabaci* in India. *mtCOI* sequence analyses showed the presence of AsiaI, Asia I -India, Asia II-1, Asia II-5, Asia II-7, Asia II-8 and Asia II-11 genetic groups. Also found China-3 in a field in Birbhum district, West Bengal, India,

Roopa *et al.* (2015) analyzed mitochondrial cytochrome oxidase I sequences from 71 samples of *B. tabaci* to determine the prevalence of genetic groups on various host plants in India. Results revealed that, the prevalence of the 4 previously existing genetic groups Asia-I, Asia-II-7, Asia-II-8 and Middle East Asia Minor-1 (MEAM-1) and of a new group called Middle East Asia Minor-K, which is genetically close (92.6%) to MEAM-1.

Population structure of *B. tabaci* was explored in a global context using nuclear data from variable microsatellite markers (Hadjistylli *et al.*, 2016) by examining worldwide collections representing most of the available diversity, including known monophagous, polyphagous, invasive and indigenous haplotypes. Well-characterized biotypes and other related geographic lineages discovered represented highly differentiated genetic clusters with little or no evidence of gene flow. The invasive B and Q biotypes exhibited moderate to high levels of genetic diversity, suggesting they stemmed from large founding populations that have

maintained ancestral variation, despite homogenizing effects due to human-mediated gene flow.

Hasan *et al.* (2016) used RAPD markers for diversity analysis of *B. tabaci* biotypes in Jordan. Whiteflies were collected from cultivated plants, wild plants and weeds. RAPD analysis identified B-Biotypes as well as cluster analysis demonstrated that, biotype B individual which are scattered independently in the localities according to the host plant and coexists with cultivated plants. While an intermediate whitefly population BA having biotype A distinguish band only with ORP-04 according to Jaccard's similarity. They have higher genetic distance with B Biotypes as well as percentage of biotypes A, B and BA samples.

Mandali *et al.* (2016) characterized whiteflies from different districts of Andhra Pradesh, through RAPD-PCR technique and the results revealed the presence of the 750 bp amplification specific to B biotype of whitefly in Shamshabad and Moinabad of Rangareddy district, Patancheru of Medak district and Madanapalli of Chittoor district with similar banding pattern to whiteflies (B biotype) collected from Kolar district of Karnataka. There is every possibility that this biotype may spread to other parts of the state and may cause substantial losses to vegetable production.

Abdelkrim *et al.* (2017) studied the patterns of biodiversity, biotype status, genetic structure and migration routes of *B. tabaci* populations collected from various agricultural areas using nuclear microsatellite loci. An analysis of landscape resistance to *B. tabaci* genetic flow was thus applied to take into account habitat suitability, genetic relatedness and functional connectivity of habitats within a varied landscape matrix. The occurrence of three geographically delineated genetic groups with high levels of genetic differentiation within each of them also studied. Potential migration corridors were established providing significant advances toward the understanding of genetic features and the dynamic dispersal of whitefly.

Janssen *et al.* (2017) investigated the transmission of Tomato leaf curl new Delhi virus (ToLCNDV) by collecting 35 populations from different crops in different regions of southern Spain. Comparison of partial *mt COI* sequences from the collected whiteflies revealed the existence of seven different haplotypes belonging to the Mediterranean-Q1 (MED- Q1) cryptic species. ToLCNDV was detected in 15

populations collected from tomato, zucchini, and melon crops and from five different localities. The results suggested involvement of MED-Q1 for the spread of ToLCNDV in Spain.

2.4 Frequency of mono and bipartite particle among *B. tabaci* populations.

In India, tomato leaf curl disease (ToLCD) was first reported by Vasudeva and Samraj in 1948 from northern India, later by Varma in 1959 from central India and Govindu in 1964 from southern India. ToLCD is one of the most important viral diseases, belonging to begomoviruses. Leaf curl disease of tomato in India is associated with 14 species of begomovirus out of which 8 is having only DNA-A (monopartite) genome and three are having both DNA-A and DNA-B (bipartite) genome (Varma and Malathi, 2003).

The genus Begomovirus belong to family Geminiviridae which have circular ssDNA as their genome. The distinguish characteristic of this family is that the genome is encapsidated in geminate particle of 18-20 nm. (Fauquet *et al*, 2008; Varsani *et al.*, 2014).

2.4.1 Vector-Host interaction

Gotz *et al.* (2012) conducted studies using *B. tabaci* microarrays to specifically describe the responses of the transcriptomes of whole insects and dissected midguts following TYLCV acquisition and retention. Microarray, real-time PCR, and Western blot analyses indicated that *B. tabaci* heat shock protein 70 (HSP70) specifically responded to the presence of the monopartite TYLCV and the bipartite *Squash leaf curl virus*. Immunocapture PCR, protein co-immuno precipitation, and virus overlay protein binding assays showed *in vitro* interaction between TYLCV and HSP70. Fluorescence *in situ* hybridization and immuno localization showed co-localization of TYLCV and the bipartite *Watermelon chlorotic stunt virus* virions and HSP70 within midgut epithelial cells. Finally, membrane feeding of whiteflies with anti-HSP70 antibodies and TYLCV virions showed an increase in TYLCV transmission, suggesting an inhibitory role for HSP70 in virus transmission, a role that might be related to protection against begomoviruses while translocating in the whitefly.

2.4.2 Virus-Vector-Host interaction

Zeidan and Czosnek (1991) studied acquisition of TyLCV by individual whiteflies in relation to the length of the access period, the virus concentration in and the developmental stage of plant tissues. The frequency of TYLCV detection increased with the length of the access period; DNA was detected in 15 per cent of whiteflies tested after a period of access to infected tissue of 30 min, regardless of its high or a low virus content and in all insects tested after an eight hour period of access to all the plants. Those insects which had access to the youngest leaves have a high virus content, acquired detectable TYLCV DNA within two hours.

Ghanim *et al.* (1998) reported the detection of TyLCV DNA in *B. tabaci* by PCR and Southern blot hybridization in progeny of single viruliferous whiteflies developed on eggplant or on cotton. TYLCV DNA was present in the progeny of insects that had acquired the virus through the egg. The adult progeny of the viruliferous insects and their own progeny were able to infect tomato test plants, producing typical disease symptoms. Ovaries and maturing eggs of viruliferous insects contained viral DNA. So, whitefly may serve as a reservoir of the virus between growing seasons.

Chowda-Reddy *et al.* (2012) tested virus transmission efficiency of *B. tabaci* of an indigenous Asia I and the exotic biotype-B population from South India using Tomato leaf curl Bangalore virus (ToLCBV) and results showed that, biotype-B having more efficient transmission characteristics.

Gemini viruses are transmitted by the *B. tabaci* in a circulative manner. Some begomoviruses have been shown to be transovarially transmitted to adult progeny. Monopartite as well as bipartite begomoviruses can also be transmitted during mating (Czosnek, 2008; Ghanim and Czosnek, 2015; Czosnek *et al.*, 2017).

Das *et al.* (2017) reported a strong vector and pathogen relationship in Tomato Leaf Curl Virus (ToLCV), and *B. tabaci* because of a chaperone GroEL protein that binds the virus particles and protects them from degradation in gut and hemolymph.

Shi *et al.* (2018) reported that, ToCV acquisition, accumulation and transmission of ToLCV was significantly higher by MED than MEAM1. In addition, ToCV persisted for more than 4 days in MED but only 2 days in MEAM1.

2.4.4 Genome organization

2.4.4.1 Bipartite begomovirus

Kumar *et al.* (2008) reported a distinct bipartite Begomoviruses associated with tomato plants showing yellowing, curling and crumpling of the leaves from sub-temperate region in India. They used rolling circle amplification (RCA) using 0-29 DNA polymerase to amplify the DNA-A and DNA-B genome. The genome organization of their isolate was typical of an old world bipartite Begomovirus and DNA-A showed <89 per cent sequence identity with known Begomoviruses. They named it as Tomato leaf curl Palampur virus (ToLCPV).

2.4.4.2 Monopartite begomovirus

Muniyappa *et al.* (2000) reported that, ToLCV isolates from Australia and Taiwan have a single genomic component (designated DNA-A), those from Northern India have two components (DNA-A and DNA-B) and from Southern India (Bangalore), have a DNA-A-like monopartite genome. The phylogenetic analysis showed that, ToLCV isolates from Bangalore constitute a group of viruses separated from those of Northern India. ToLCV-Ban4 was detected in tomato and in its whitefly vector *B. tabaci* by one or by a combination of ELISA, Southern blot hybridization and PCR.

The monopartite begomoviruses are associated with smaller DNA components of about 1.3 kb in size, known as satellite DNAs. Depending on the genome organization and the symptom they produced with helper virus the satellite DNA is classified as alphasatellites and betasatellites (Briddon *et al.*, 2003).

Pandey *et al.* (2010) described the genetic diversity of two isolates of monopartite Tomato leaf curl virus infecting tomato in two extreme regions (North and South) of Indian subcontinent. According to them the ToLCVCTM and ToLCV-K3/K5 viruses were found to be monopartite, as neither DNA-B component nor betasatellite associated with Begomovirus species. The complete nucleotide sequence of DNA-A genome of CTM exhibited highest sequence homology (88%) to Croton yellow vein mosaic virus (AJ507777) and isolate K3/K5 (88.5%) to Tomato leaf curl Pakistan virus. This was less than the threshold value for demarcation of species in the

genus Begomovirus. K3/K5 and CTM are considered to be novel isolates of Tomato leaf curl virus.

Majority of the begomoviruses have monopartite genome, where the DNA-A is capable of inducing disease e.g., tomato yellow leaf curl virus (TYLCV) (Scholthof *et al.*, 2011). The genome organization of monopartite begomovirus is similar to the DNA-A of bipartite begomovirus, they differ having unique ORFs. The monopartite begomovirus have at least six ORFs that encode proteins, AV1 and AV2 (CP) in the sense direction where as AC1 (Rep), AC2, AC3 and AC4 in complimentary direction. The AV2, AC1, AC2 and AC3 are functionally analogous to the corresponding genes in bipartite begomoviruses (Bisaro, 1996; Navot *et al.*, 1991; Kheyr-pour *et al.*, 1991).

Nucleotide sequence analysis of DNA-A showed that, it shared highest 97.6 per cent identity with Tomato leaf curl New Delhi virus-India and lowest 87.9 per cent identity with Tomato leaf curl New Delhi virus, while DNA-B showed highest 94.1 per cent identity with ToLCNDV-IN and lowest 76.2 per cent identity with ToLCNDV-India. Thus, it appears that this begomovirus is a variant of ubiquitous ToLCNDV and hence, the name ToLCNDV-India for this variant (Pratap *et al.*, 2011).

2.5 Variations for traits related to whitefly resistance in tomato

Muigai *et al.* (2003) evaluated 32 accessions of wild tomato (*Lycopersicon* spp.) germplasm for resistance to the whitefly *Bemisia argentifolii* Bellows in a greenhouse choice bioassay. Density data were recorded for the adaxial and abaxial leaf surfaces for all life stages of *B. argentifolii* and types I, IV, V and VI trichomes. Individual plant selections (33 from 22 wild tomato accessions) with high resistance were subsequently tested in the field to verify the resistance found in the greenhouse screening. Resistance was defined by the density of all life stages of the whitefly observed on the eight leaflets sampled at nodes 5 and 7. Only type IV trichome density had a consistent and significant negative correlation with whitefly density. The highest whitefly resistance was observed in *Lycopersicon pennellii* accessions LA 716, LA 1340 and LA 2560. The most resistant *L. hirsutum* f. *typicum* accessions were LA 1777 and LA 1353.

Maruthi *et al.* (2005) reported four tomato cultivars (TLB111, TLB130, TLB133, and TLB182) as resistant/tolerant to South Indian ToLCV. were screened against the Bangladesh ToLCVs in 2003-04. They found that, disease incidence remained low (6 to 45%) in the resistant cultivars compared with local cultivars (68 to 100%).

Azizi *et al.* (2008) evaluated 134 accessions of *Solanum lycopersicum* L. and six accessions of *Solanum peruvianum* L. to assess the resistance to an Iranian isolate of TYLCV. Plants were inoculated using *B. tabaci* and the reaction of plants was evaluated based on either disease symptoms or viral DNA amplification. All accessions of *S. lycopersicum* had demonstrated various degrees of disease symptoms. However, all six accessions of *S. peruvianum* were resistant and remained symptomless. Phenotypic evaluation was confirmed by amplification of a 670bp TYLCV DNA fragment in all tested accessions of *S. lycopersicum*. Based on both phenotypic and molecular evaluations it was reported that, no accession provided complete resistance to TYLCV, whereas nine accessions were tolerant. The high level of resistance noted in whitefly inoculated accessions of *S. peruvianum* was not observed in graft inoculated plants of these accessions. The TYLCV DNA fragment was detected five weeks post-inoculation when plants were inoculated by grafting.

Rajasri and Vijayalakshmi (2011) artificially screened the tomato genotypes using viruliferous whiteflies under glass house conditions. Among the examined materials, one wild accession, EC- 251672 recorded highly resistant reaction without any symptoms. This is the first report of the immune reaction of wild accession against ToLCV in India. Ten genotypes comprising of nine hybrids viz., Akash-918, NS-539, NS- 515, Siri-9005, STH-803, STH-807, To-1827, US-1196, US-2175 and variety, Vybhav showed resistant reaction to ToLCV under artificial screening in the glass house. Hence, these resistant sources can be used in the development of future molecular breeding programmes against ToLCV in tomato.

Segbefia *et al.* (2015) conducted the study to evaluate the susceptibility of tomato genotypes to TYLCV under field conditions. Ten tomato genotypes were planted in the field and left to natural infestation by whitefly vectors. Triple antibody sandwich enzyme-linked immunosorbent assay (TAS-ELISA) detected TYLCV in five out of ten genotypes, while polymerase chain reaction using six primers (virus-

specific and degenerate) detected the virus in eight out of ten genotypes. The polymerase chain reaction (PCR) technique detected the virus in three samples that tested negative to TAS-ELISA, implying its enhanced sensitivity

Zeshan *et al.* (2016) screened 27 tomato varieties/ lines for the source of resistance against tomato leaf curl virus disease (TLCVD) in field trial. The observations of TLCVD incidence were recorded on weekly basis. Varieties/lines were evaluated on the basis of symptomology. Further grafting and whitefly mediated inoculation techniques were adopted to confirm the virus. Out of twenty seven varieties/lines, three were highly susceptible, six were susceptible, four were moderately susceptible, six were moderately resistant and eight cultivars were resistant. No variety/line was highly resistant or immune against TLCVD.

2.5.1 Trichome type and density as a source for whitefly resistance in tomato

Channarayappa *et al.* (1992) screened more than 1200 cultivars, breeding lines, and wild species of tomato. Morphological analysis by light and scanning electron microscopy revealed distributions of different types of trichomes on leaf surfaces. Among them, *L. hirsutum* proved to be the least affected by the leaf curl virus because it did not support whitefly infestation to any extent. However, *L. hirsutum* differed from other species by the presence of glandular trichomes designated type VIc. Whiteflies became entrapped in the exudate of type VIc trichome glands before they could transmit the virus.

In contrast to glandular trichomes, non-glandular trichomes, especially type V, are not involved in pest resistance. Whiteflies prefer hairy leaf (Toscano *et al.*, 2002). Non-glandular trichomes also provide a more suitable microclimate for oviposition and protects the eggs and larvae from their enemies.

Trichomes have been considered as the most important pest resistance factor. Seven types of trichomes are known in tomato of which type I, IV, VI and VII are glandular trichomes, and type II, III and V are non-glandular trichomes (Gurr and McGrath 2001; Simmons and Gurr, 2005).

In tomato, trichomes and their exudates play a crucial role in insect resistance. Trichomes are hair-like epidermal protuberances showing large variation among

tomato species. Based on the absence or presence of a glandular head, tomato trichomes can be divided into non-glandular and glandular. Non-glandular and glandular trichomes are further classified based on the number of basal cells, the length and number of cell in the stalk, on the presence/absence of glandular head and the number of cells on the glandular head (Luckwill, 1943; Channarayappa *et al.*, 1992; Peralta *et al.*, 2008).

Whiteflies prefer hairy leaves but the presence and density of type IV and VI trichomes has a negative effect on whitefly adult survival and oviposition rate on tomato (Channarayappa *et al.*, 1992; Toscano *et al.*, 2002). Exudates of these trichomes played a major role in whitefly resistance, which might act as repellants and/or natural pesticides (Fancelli *et al.*, 2005; Bleeker *et al.*, 2009).

Maluf *et al.* (2007) evaluated the feasibility of selection for higher glandular trichome densities, as an indirect criterion of selection for increasing repellence to spider mites *Tetranychus urticae*, in tomato populations. Trichome counts were made both on the adaxial and abaxial leaf surfaces and trichomes were classified into glandular types IV and VI, other glandular types (types I+VII), and non glandular types. Spider mite repellence biotests indicated that, higher densities of glandular trichomes (especially type VI) decreased the distances walked by the mites onto the tomato leaf surface. Selection of plants with higher densities of glandular trichomes can be an efficient criterion to obtain tomato genotypes with higher resistance (repellence) to spider mites.

An association between insect resistance and the presence and density of glandular trichomes was reported by Sajjanar and Balikai (2009). The primary components of exudates from glandular trichomes viz., the acylsugars and 2-tridecanone secreted by type IV trichomes of *L. pennellii* and type VI trichomes of *L. hirsutum*, respectively mediate the insect resistance. The development of tomato cultivars with the ability to synthesize sugar esters and increased 2-tridecanone content substantially increase the level of insect resistance in cultivated tomato.

Aerial tissues of cultivated tomato (*S. lycopersicum*) are populated by several morphologically distinct trichome types, the most abundant of which is the type VI glandular trichome that produces various specialized metabolites (Kang *et al.*, 2010).

Rodríguez-López *et al.* (2011) developed a breeding line, ABL 14-8 by introgressing type IV leaf glandular trichomes and secretion of acyl sucroses from the wild tomato, *S. pimpinellifolium* accession TO937 into the genetic background of the whitefly and virus susceptible tomato cultivar Moneymaker. Results indicated that, presence of type IV glandular trichomes and the production of acylsucrose deterred the landing and settling of *B. tabaci* on ABL 14-8. Electrical penetration graph studies indicated that, *B. tabaci* adults spent more time in nonprobing activities and showed a reduced ability to start probing. This behaviour resulted in a reduced ability to reach the phloem. The superficial type of resistance observed in ABL 14-8 against *B. tabaci* probing significantly reduced primary and secondary spread of TYLCV.

In tomato, higher density of the non-glandular trichomes, type V were correlated with increasing survival and oviposition rates of *B. tabaci* (Heinz and Zalom, 1995; Firdaus *et al.*, 2012; Firdaus *et al.*, 2013). Glandular trichomes, also function as place of synthesis, storage and secretion of secondary metabolites whose principal function can be related to mediate the herbivore-plant chemical interaction (Schillmiller *et al.*, 2008; Glas *et al.*, 2012).

Neiva *et al.* (2013) conducted a study to compare the degree of resistance to the silverleaf whitefly of tomato plant lines with higher densities of glandular trichomes. The results showed that, all lines selected based on high trichome density exhibited fewer nymphs than the susceptible controls, indicating that selection for more glandular trichomes was generally effective in promoting increased resistance to the silverleaf whitefly.

Glandular trichomes (type I, IV and VI) of different wild relatives of tomato (*S. pennellii*, *S. habrochaites*, *S. pimpinellifolium* and *S. galapagense*) were shown to be associated with an increase in resistance against insect herbivores (Antonious *et al.*, 2005; Baldin *et al.*, 2005; Firdaus *et al.*, 2012; Lucatti *et al.*, 2014).

Eleven wild tomato accessions resistant to *Bemisia tabaci* were evaluated for resistance to the two-spotted spider mite (*T. urticae*) at AVRDC by Rakha *et al.* (2016) based on egg numbers using the leaf disc and Tanglefoot no-choice bioassays and damage scores in choice bioassays. Highest resistance based on choice and no-choice bioassays was identified in AVRDC *S. galapagense* accessions VI057400,

VI045262, VI037869 and VI037239 and *S. cheesmaniae* accession VI037240, all of which were new sources of *T. urticae* resistance. In addition, *S. pimpinellifolium* accession VI030462 exhibited resistance only in the no-choice bioassay based on egg numbers. Resistance to *T. urticae* based on the number of eggs from the no-choice bioassays was positively correlated with density of type IV glandular trichomes and negatively correlated with densities of type V trichomes. All resistant accessions accumulated high levels of total acylsugars, which were positively associated with type IV trichomes.

Rakha *et al.* (2017) conducted studies to characterize 255 accessions of *Solanum galapagense* L., *Solanum cheesmaniae* L. and *Solanum pimpinellifolium* L. for trichome types and to evaluate selected accessions with high densities of glandular trichomes for resistance to whitefly. The highest whitefly resistance was detected in *S. galapagense* accessions VI063177 and VI037239 based on choice and no-choice bioassays. High levels of whitefly resistance was found in *S. cheesmaniae* accession VI037240 based on the choice bioassay and in *S. pimpinellifolium* accession VI030462 based on the no-choice bioassay. Whitefly resistance in VI037240 and VI030462 is note worthy because these species are closely related to cultivated tomato and introgression of whitefly resistance should be relatively straightforward. High densities of type IV trichomes and low densities of type V trichomes were associated with reduced numbers of whitefly adults, nymphs, puparium and eggs in the choice bioassay and with high adult whitefly mortality in the no-choice bioassay.

2.5.2 Secondary metabolites (Biochemicals) and plant defence

Duffey and Stout (1996) reported that, in tomato, phenolics and oxidative enzymes act together to affect insects during ingestion, digestion and metabolism. The tannin activity showed a significant negative correlation with the leaf damage, but were less effective than peroxidase; while flavonoid activity, although showed negative association to damage, there was no significant correlation to damage (Mwila *et al.*, 2017). The tannin may decrease damage as they are bitter polyphenols that deter insect infestation (War *et al.*, 2012). They also reduce the nutritive availability by nonspecific protein precipitation and chelating of metal ions (Hagg *et al.*, 2013).

Perveen *et al.* (2001) investigated the role of phenolics in plant defense using cotton varieties to study their total phenols at various growth stages, change in phenolics as a result of insect exposure and their effect on growth and survival of cotton boll worm larva. More resistant variety Ravi showed 1.00 to 1.20 mg more phenolics than susceptible varieties at all growth stages. A direct correlation was observed between insect attack and phenol production. Bollworm diet incorporated with tannic acid and phenolic mixture at 0.1 per cent concentration showed phagodeterreny, 61 to 96 per cent weight retardation, 44 to 50 per cent mortality in first week of experiment and 94 to 100 per cent mortality in second week of experiment. Phenols showed 5.05 per cent pupation delay, while no pupation in tannic acid treatment. Methanolic extract of variety Ravi showed more effect on bollworm larvae than susceptible variety, S-12.

Phenolics of high molecular weight such as tannins usually present in the leaves, is toxic (oxidation) to *Orgyia leucostigma* L. (Lepidoptera) (Barbehenn *et al.*, 2008)

Jindal and Dhaliwal (2009) observed no significant effect of phenols and tannins in *G. hirsutum* and *G. arboreum* on population of whitefly, however the epicuticular waxes were found to have positive effect on whitefly population

The insecticidal properties of plant toxins are diverse. They may act as repellents or feeding deterrents or induce direct toxicity leading to symptoms ranging from the inhibition of larvae or insect growth to death. Elucidation of the plastic nature of such defence responses, modulated both by phytophagous (and pathogens) attacks and abiotic factors including nutrient availability (Sampedro *et al.*, 2011), light (Roberts and Paul, 2006) and drought (Gutbrodt *et al.*, 2011). Some of these compounds are always synthesised in the plant (constitutive resistance) while others are produced only after initial damage (Baldwin, 1999). Induced defences rely on mobile metabolites with a relatively low molecular weight produced at a low cost only in the event of insect attack (Baldwin, 1998; Heil and Baldwin, 2002).

Al-Shareef (2011) investigated the effect of the sweet potato whitefly, *B. tabaci*, infestation on the mean content of plant pigments (chlorophyll a, chlorophyll b and carotene), as well as the percentage of moisture content in the leaves of three

different plant varieties (cantaloupe, cucumber and zucchini) in a greenhouse. Results indicated that, infestation with *B. tabaci* reduced mean content of each plant pigments (chlorophyll a, chlorophyll b and carotene) in all plant varieties. Feeding of the whitefly decreased total percentage of moisture content in all plant varieties as well.

Plants have evolved a whole arsenal of defence strategies against herbivores, including the synthesis of a tremendous variety of chemical compounds. Chemical defence products may range from low molecular weight compounds called secondary metabolites, to peptides and proteins that are active against insects (Ibanez *et al.*, 2012).

Taggar *et al.* (2012) found a negative correlation between tannins and flavonols with *B. tabaci* plant population, indicating that increase in the activity of these biochemicals could contribute to the bioprotection of host plants against whiteflies by deterring the feeding and/or produce toxins that reduce the plant digestibility, which leads to nutrient deficiency in insects with drastic effects on their growth and development (Chen *et al.*, 2009). The expression of several defense metabolites is induced within minutes after damage and hours in undamaged leaves, as a systemic response (Hagg *et al.*, 2013). In particular, peroxidase has been reported as a defense enzyme, which increases in various plants due to *B. tabaci* attack (Binu and Paliniswami, 2006) and specific accumulation at the site of the attack (Kerchev *et al.*, 2012).

Elsy and Farnham (1994) reported that red color of the leaf is an important feature of whitefly resistance in cotton. They observed less whitefly infestation in red leafed varieties of *Brassica oleracea*. Red foliage may serve as a true defensive cue, as it reliably indicates the plant's low quality (Maskato *et al.*, 2014).

Petro and Redak (2000) showed that some light green leaf poinsettia varieties are more susceptible to *B. tabaci* than those with dark green leaves (Petro *et al.*, 2002). Whiteflies are generally attracted to yellow or yellow-green (Berlinger, 1980; Mound, 1962; Hasanuzzaman *et al.*, 2016).

Usman *et al.* (2015) reported that, biochemical contents of the tomato such as non-reducing sugar and phenols present in higher quantities were found negatively correlated with fruit worm *H. armigera* infestation (Selvanarayanan and

Narayanasamy, 2006). Further, phenol content was higher in resistant accession and it exerted a significant negative correlation with larval feeding. According to Selvanarayanan and Narayanasamy (2006) high phenol content could contribute to the development of resistant variety. Annadurai *et al.* (1995) also reported that, high concentration of phenols and other secondary metabolites led to resistance against *H. armigera*. Similarly Banerjee and Kallo (1989) also found that, tomato varieties with high phenol content were resistant to *Heliothis*.

Phenolics serve a dual function of both repelling (Dar, 2012 and Dar *et al.*, 2014) and attracting different organisms in the plants surroundings, while as sugars do reverse of it. They act as protective agents, inhibitors, natural animal toxicants and pesticides against invading herbivores, nematodes, phytophagous insects, and fungal and bacterial pathogens (Lattanzio *et al.*, 2006 and Dar *et al.*, 2017)

Divya *et al.* (2017) reported that, the aphid infestation increased the total phenols, condensed tannin and enzymatic activities in cotton genotypes. The enhanced activities of enzymes and phenolic compounds may contribute bioprotection of cotton plants against aphid infestation.

Golan *et al.* (2017) conducted study to compare the changes in the content of free amino acids, phenolic compounds and the activity of PAL and TAL caused by two piercing sucking arthropods viz., the grape mealybug (*Pseudococcus maritimus* Ehrh.) and the two-spotted spider mite (*Tetranychus urticae* Koch) in the leaves of orchid and strawberry, respectively. The results showed that, the amino acid content and the ratio of amino acids to phenolic compounds increased in both plant species infested by the mealybug and the mite. The pest feeding affected accumulation of the phenolic compounds, since the induction of the PAL activity in mealybug-infested orchid leaves during the first 5 h of the experiment preceded. The increased activity of TAL was accompanied by elevated levels of phenolic compounds in the leaves of strawberry infested by mites.

Mwila *et al.* (2017) conducted a study to evaluate changes in peroxidase, tannin and flavonoid activity in cassava genotypes attacked by *B. tabaci*. There were significant differences among genotypes for leaf damage ($P < 0.01$) of three to six months plants. All genotypes showed significant ($P < 0.05$) differences for peroxidase

activity, with CS1-144 having a high activity rate three months after planting. The lowest activity was observed in UG 120170, a susceptible genotype. A significant ($P < 0.01$) negative correlation ($r = -0.84$) was observed between peroxidase activity and cassava leaf damage scores, as well as between tannin and damage ($r = -0.57$), indicating that peroxidase and tannin play a part in cassava resistance to *B. tabaci*.

2.5.4 STRUCTURE

The software STRUCTURE allows the identification of genetically homogeneous groups using Bayesian algorithm. However, the ability of this algorithm to detect the true number of clusters (K) in a sample of individuals when patterns of dispersal among populations are not homogeneous has not been tested. The result showed that, in most cases the estimated 'log probability of data' does not provide a correct estimation of the number of clusters, K. However, using an ad hoc statistic ΔK based on the rate of change in the log probability of data between successive K values, the STRUCTURE accurately detects the uppermost hierarchical level of structure for the scenarios tested. As might be expected, the results are sensitive to the type of genetic marker used (AFLP vs. microsatellite), the number of loci scored, the number of populations sampled and the number of individuals typed in each sample (Evanno *et al.*, 2005; Porras-Hurtado *et al.*, 2013)

2.6 Association analysis of component traits of whitefly resistance in tomato

Association mapping is rapidly becoming an important method to explore the genetic architecture of complex traits in plants and offers unique opportunities for studying resistance to insect herbivores. Recent studies indicated a trade-off between resistance against generalist and specialist insects. Most studies, however, use a targeted approach that will easily miss important components of insect resistance. Genome-wide association mapping provides a comprehensive approach to explore the whole array of plant defence mechanisms in the context of the generalist-specialist paradigm (Kloth *et al.*, 2012).

Tomato is an excellent model crop for investigating the molecular basis of study using association mapping (Klee and Tieman, 2013). To date, few association mapping studies have focused on biochemical and biophysical in major crops (Kumar *et al.*, 2015). Association study (AS) is a useful tool to detect candidate loci

responsible for the natural variations in a targeted phenotype. This tool can identify significant associations between polymorphic molecular markers and targeted traits in a large natural population (Weigel, 2012; Matsuda *et al.*, 2015; Zhang *et al.*, 2015). Many factors can impact the results of association mapping, including type and size of mapping population, targeted traits, number of environments and years for phenotypic evaluations and the type and genome coverage of molecular markers (Ruggieri *et al.*, 2014).

Comeault *et al.* (2014) stated that, the genetic architecture of adaptive traits can reflect the evolutionary history of populations and also shape divergence among populations. They quantitatively describe the genetic architecture of traits that are subject to known intensities of differential selection between host plant species in *Timema cristinae* insects using phenotypic measurements of 10 traits and 211,004 single-nucleotide polymorphisms (SNPs) to conduct multilocus genome-wide association mapping and identified a modest number of SNPs that were associated with traits and explained a large proportion of trait variation. They discovered both major and minor effect loci using SNPs which varied in their strength of association with traits.

Ruggieri *et al.* (2014) conducted Genome Wide Association Studies (GWAS) to dissect complex quantitative traits and identify candidate genes affecting phenotype variation of polygenic traits with 96 cultivated tomato genotypes, ten quality traits and metabolites in red ripe fruits as phenotypic characters. The Mixed Linear Model associations between 20 SNP markers, identified that, they were significantly associated with seven out of ten traits considered. The analysis revealed two markers associated with phenolic compounds, three with ascorbic acid, β -carotene and trans-lycopene, six with titratable acidity and only one with pH and fresh weight. Moreover, 19 putative genes in linkage disequilibrium with markers were found.

Broekgaarden *et al.* (2015) studied the genetic architecture of defense against the phloem-feeding insect cabbage whitefly (*Aleyrodes proletella* L.) in *Arabidopsis thaliana* L. by determining survival and reproduction of whitefly females, on worldwide selected 360 natural accessions and subsequently performed Genome-wide association (GWA) mapping using 214,051 SNPs. Substantial variation for whitefly adult survival and oviposition rate was observed between the accessions and identified

39 candidate SNPs for either whitefly adult survival or oviposition rate, all with relatively small effects, underpinning the complex architecture of defence traits. Among the corresponding candidate genes, *i.e.* genes in linkage disequilibrium (LD) with candidate SNPs, none have previously been identified as a gene playing a role in the interaction between plants and phloem-feeding insects. Whitefly performance on knock-out mutants of a number of candidate genes was significantly affected, validating the potential of GWA mapping for novel gene discovery in plant-insect interactions.

Eggplant (*Solanum melongena* L.) association panel of 191 accessions was SNP genotyped and phenotyped for key breeding fruit and plant traits by Portis *et al.* (2015). A genome wide association (GWA) analysis using the mixed linear model, showed that, GWA analysis validated many of the known controlling loci and detected a large number of new marker/ trait associations. Exploiting established syntenic relationships between eggplant chromosomes and those of tomato and pepper recognized orthologous regions in ten egg plant chromosomes harbouring genes influencing breeders' traits.

Albert *et al.* (2016) phenotyped 141 highly diverse small fruit tomato accessions for 27 traits under two contrasting watering conditions. 6100 single nucleotide polymorphisms (SNPs), association mapping revealed 31, 41 and 44 quantitative trait loci (QTLs) under drought, control, and both conditions, respectively. Twenty-five additional QTLs were interactive between conditions, emphasizing the interest in accounting for QTLs by watering regime interactions in fruit quality improvement.

Zhao *et al.* (2016) used 174 tomato accessions composed of *S. lycopersicum* (123 accessions) and *S. lycopersicum* var *cerasiforme* (51 accessions) to detect significantly associated loci controlling the variation of main sugars and organic acids with 182 SSRs markers. Association mapping using mixed linear model (MLM) detected a total of 58 significantly associated loci ($P < 0.001$) for the 17 sugars and organic acids, including fructose, glucose, sucrose, citric acid and malic acid. These results not only co-localized with several reported QTLs, including fru9.1/PV, suc9.1/PV, ca2.1/HS, ca3.1/PV, ca4.1/PV, and ca8.1/PV, but also provided a list of candidate significantly associated loci to be functionally validated.

2.6.1 TASSEL

Association analyses that exploit the natural diversity of a genome to map at very high resolutions are becoming increasingly important. TASSEL (Trait Analysis by association, Evolution and Linkage) implements general linear model and mixed linear model approaches for controlling population and family structure. For result interpretation, the program allows for linkage disequilibrium statistics to be calculated and visualized graphically. Database browsing and data importation is facilitated by integrated middleware. Other features include analyzing insertions/deletions, calculating diversity statistics, integration of phenotypic and genotypic data, imputing missing data and calculating principal components (Bradbury *et al.*, 2007).

3. MATERIAL AND METHODS

The present study on “Genetic diversity of whitefly, *Bemisia tabaci* (Genn.) (Hemiptera: Aleyrodidae) populations and molecular analysis for its resistant traits in tomato” involved morphological traits plasticity, genomic flux and population genetic structure, occurrence of different virus particle frequency among whitefly populations collected from different districts of Karnataka and also screening of tomato minicore accessions at field and molecular screening for assessing whitefly resistance traits. The study was carried out at the College of Horticulture, Bagalakote and College of Horticulture, Bengaluru during 2016-17 and 2017-18. The details of material used and methods adopted are described in this chapter under the following headings;

3.1 Plasticity of morphological traits' among the populations of whiteflies prevailing in tomato ecosystems of Karnataka

3.1.1 Survey for whitefly collection

Based on the analytical data of crop area, survey was undertaken in major tomato growing regions of Karnataka to collect puparia and adults of whitefly, *B. tabaci* to understand the population morphological and molecular variation.

3.1.2 Sample collection areas

Survey was conducted in different geographical areas covering 11 districts distributed in seven agroclimatic zones of Karnataka. At least five populations (field) were collected from each district (Table 1 and Fig. 1).

3.1.3 Method of collection of samples

Tomato leaves containing sufficient number of puparia and adult whiteflies were collected in separate polythene bags of 30 × 40 cm size with proper labels. The samples were handled carefully and brought to the laboratory. The adults and puparia of whitefly were separated from the host plants with the help of camel hair brush and transferred to the different glass vials containing 70 per cent alcohol as preservative

Table 1. Details of locations selected for collection of *Bemisia tabaci* samples across agroclimatic zones of Karnataka.

Sl. No.	Agro climatic zones	District	Location/ Village	Latitude	Longitude
1	Central dry zone	Davanagere	Mayakonda	14 ⁰ 17' 22.2" N	76 ⁰ 4' 58.799"E
	Southern transition zone		Tholahunase	14 ⁰ 24' 37.44"N	75 ⁰ 56' 55.68"E
			Channapura	14 ⁰ 8' 53.88" N	75 ⁰ 57' 46.08"E
2	Northern transition zone	Haveri	Battikoppa	14 ⁰ 31' 26.04"N	75 ⁰ 30' 57.96"E
			Byadagi	14 ⁰ 40' 19.2" N	75 ⁰ 29' 8.879"E
			Motebennur	14 ⁰ 43' 2.64"N	75 ⁰ 28' 43.32"E
3	Northern transition zone	Dharwad	Narendra	15 ⁰ 30' 31.32" N	74 ⁰ 58' 36.84"E
			Garag	15 ⁰ 34' 31.08" N	74 ⁰ 55' 52.679"E
4	Northern dry zone	Belagavi	Mutaga	17 ⁰ 10' 16.68"N	77 ⁰ 0' 7.199"E
			Banakatti	16 ⁰ 9' 4.68" N	75 ⁰ 48' 31.68"E
5	Eastern dry zone	Chikkaballapura	Buragamakalahalli	13 ⁰ 23' 36.24"N	78 ⁰ 4' 41.519"E
			Gollahalli	13 ⁰ 40' 14.88"N	77 ⁰ 7' 8.039"E
6	Eastern dry zone	Kolar	Balageri	13 ⁰ 17' 58.56"N	78 ⁰ 5' 29.758"E
			Sugaturu	13 ⁰ 12 ' 35.28" N	78 ⁰ 5' 57.47"E
			Pathapalli	13 ⁰ 21' 38.16"N	78 ⁰ 9' 43.56"E
7	Eastern dry zone	Bengaluru rural	Kelaginanaikarahalli	13 ⁰ 22' 45.12 "N	77 ⁰ 30' 47.519"E
			Lakshmidevipura	13 ⁰ 21' 21.552"N	77 ⁰ 33' 28.945"E
			Tubagere	13 ⁰ 22' 25.519"N	77 ⁰ 34' 12.626"E
8	Northern dry zone	Bagalkot	Kaladagi	16 ⁰ 12' 25.719"N	75 ⁰ 29' 58.919"E
			Hiresansi	16 ⁰ 13' 41.16"N	75 ⁰ 31' 38.639"E
9	Southern dry zone	Chamarajanagar	Nanjedevanapura	11 ⁰ 55' 24.5"N	76 ⁰ 50' 48.004"E
			Kengaki	11 ⁰ 53' 29.413"N	76 ⁰ 46 ' 32.25"E
			Sattegala	12 ⁰ 14' 30.48" N	77 ⁰ 8' 48.839"E
10	Hilly zone	Chikkamagaluru	Allampura	13 ⁰ 21' 15.84"N	75 ⁰ 45' 29.519"E
			Chikkagowja	13 ⁰ 19' 20.316"N	75 ⁰ 46' 26.4"E
			Amble	13 ⁰ 16' 40.511"N	75 ⁰ 47' 54.157"E
11	Southern transition zone	Shivamogga	Alada halli	13 ⁰ 55' 53.76"N	75 ⁰ 34' 4.44"E
			Kunchenahalli	14 ⁰ 3' 16.28"N	75 ⁰ 33' 17.647"E

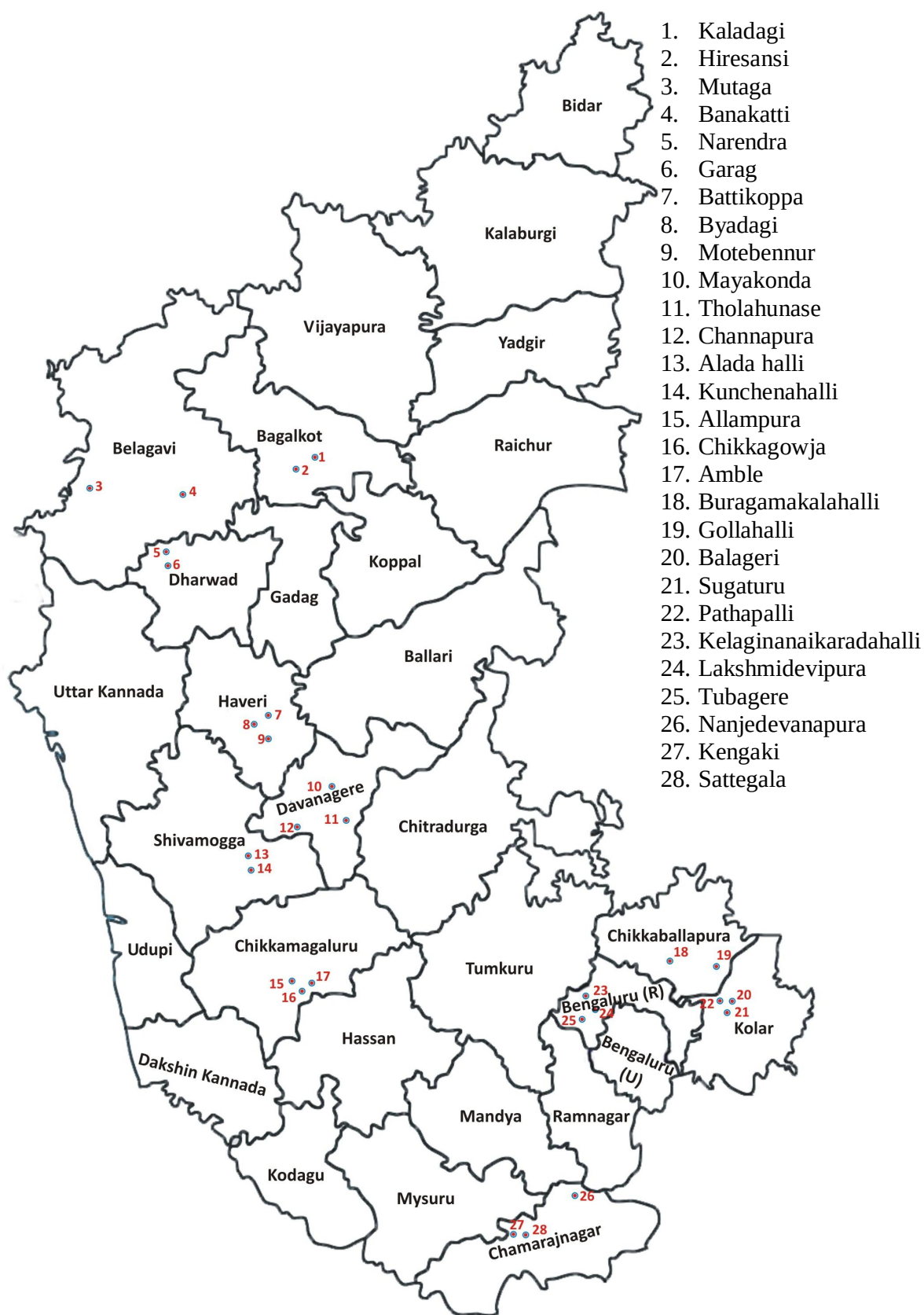


Fig 1. Locations selected for collection of *Bemisia tabaci* samples around Karnataka

and stored at -4°C for molecular studies. Sufficient number of puparia and adult whiteflies (ensuring more than 25 in number) of both female and male were separated visually based on presence of claspers at the tip of the abdomen in males. The samples were drawn at random from each population and used for morphological studies according to the methods of Simón *et al.* (2003) and Prathibha (2015).

3.1.4 Morphometric studies

A set of five puparia and adult whiteflies (both male and females) from each populations were prepared for morphometric studies.

3.1.4.1 Preparation of samples

3.1.4.1.1 Slide mounting of puparia (modified protocol of Hodges and Evans, 2005)

1. Specimens (puparia) were placed in 10 per cent potassium hydroxide (KOH) and allowed to remain in solution for 12 h.
2. Specimens were removed from KOH and placed in distilled water, allowed for 10-15 min.
3. Added three drops of acid fuchsin dye (stain) to distilled water. Allowed the specimens to soak in this for 15 min.
4. Specimens removed from stain and placed in 75 per cent ethyl alcohol (EtOH) and kept for 10-15 min (to de-stain all non-sclerotized areas).
5. Specimens removed from 75 per cent EtOH and placed in 95 per cent EtOH. Allowed for 10-15 min (to complete de-staining process).
6. Specimens removed from 95 per cent EtOH and mounted on a glass slide using D.P.X. mountant.
7. Dropped a cover slip on specimen and slides were labelled.
8. Slides were allowed for complete drying at room temperature.

3.1.4.1.2 Preparation of adult specimens

Adult female and male whiteflies were dipped in 10 per cent KOH for 5 min. to remove waxy substance on the body surface and later transferred to glass cavity block containing 70 per cent alcohol.

The morphological parameters from both nymphs and adult whiteflies were measured under trinocular stereo zoom HD microscope make MEIJI EMZ 13 TR with 6MP HDMI camera attachment in the laboratory and the photography was made under trinocular stereo zoom microscope Olympus SZX7 with cam (5 MP) attachment and Q-Imaging software in the laboratory.

3.1.4.2 Observations recorded

3.1.4.2.1 Morphological traits of puparia

Puparia characters such as, puparia length and breadth, distance of transverse moulting suture from anterior end, distance of vasiform orifice from anterior end, length and breadth of vasiform orifice, length and breadth of lingula, length of caudal furrow, length of caudal setae, distance between caudal setae were recorded (Plate 1, 2, 3) (Appendix II) following the standard methods (Chaubey and Andrew, 2015; Chaubey *et al.*, 2015; Harish *et al.*, 2016).

3.1.4.2.2 Morphological traits of adults

The adult characteristics viz., proboscis length, leg morphometry (femur, tibial and tarsal length of fore and hind legs), length of the antennae, wing size (length and width of fore wing and hind wing), fore wing vein length in both male and female and claspers length and length of last abdominal segment in male were measured (Plate 4, 5, 6) (Appendix III and IV) (Qiu *et al.*, 2009; Prathibha, 2015; Chaubey and Andrew, 2015; Chaubey *et al.*, 2015; Harish *et al.*, 2016)

3.1.4.3 Statistical analysis

3.1.4.3.1 Descriptive statistical analysis

Descriptive statistical parameters such as, mean, range (minimum and maximum), standard error, standard deviation and sample variance for individual characters were calculated by using SPSS 16.0 statistical package (SPSS, 2004).

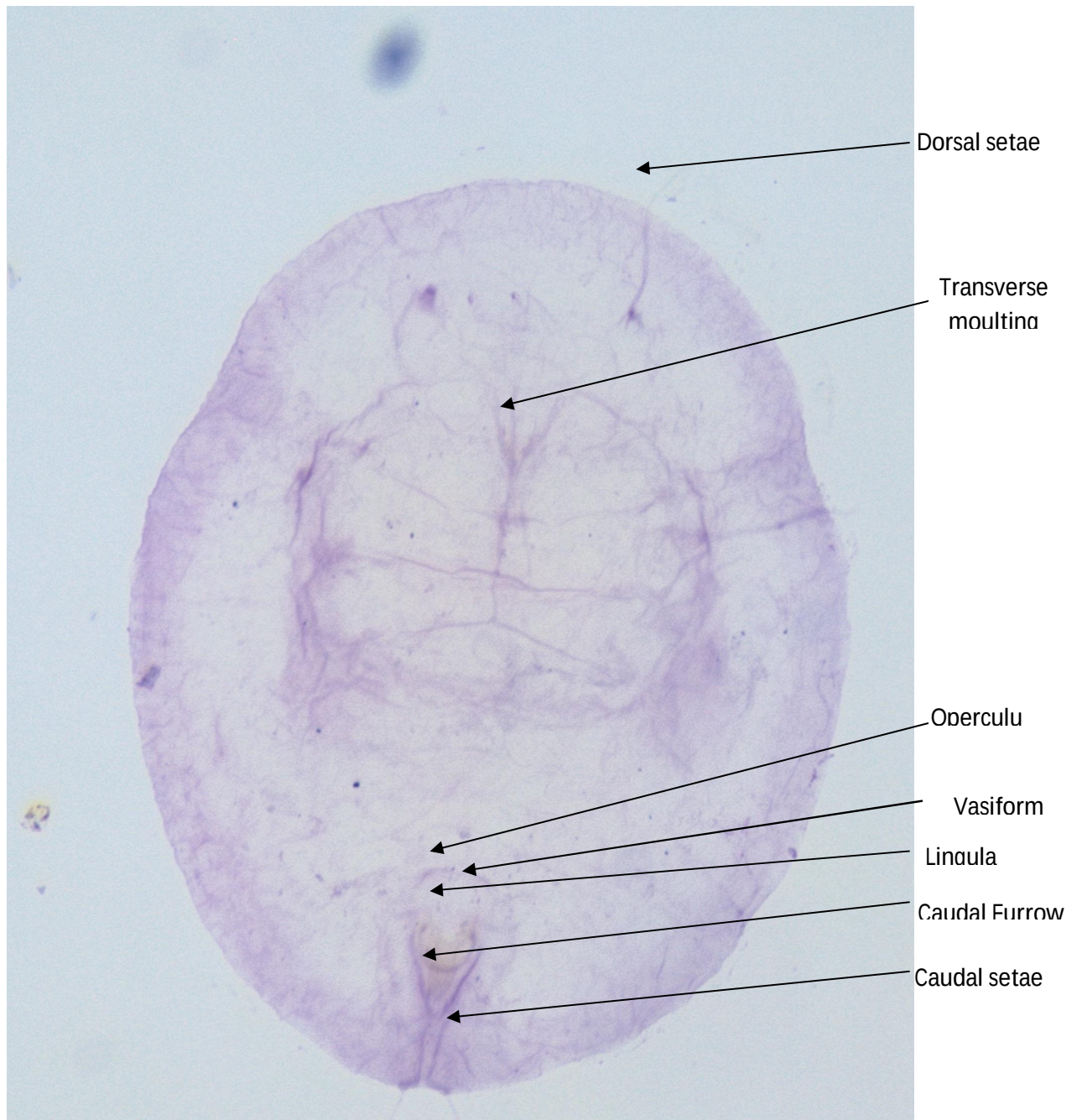
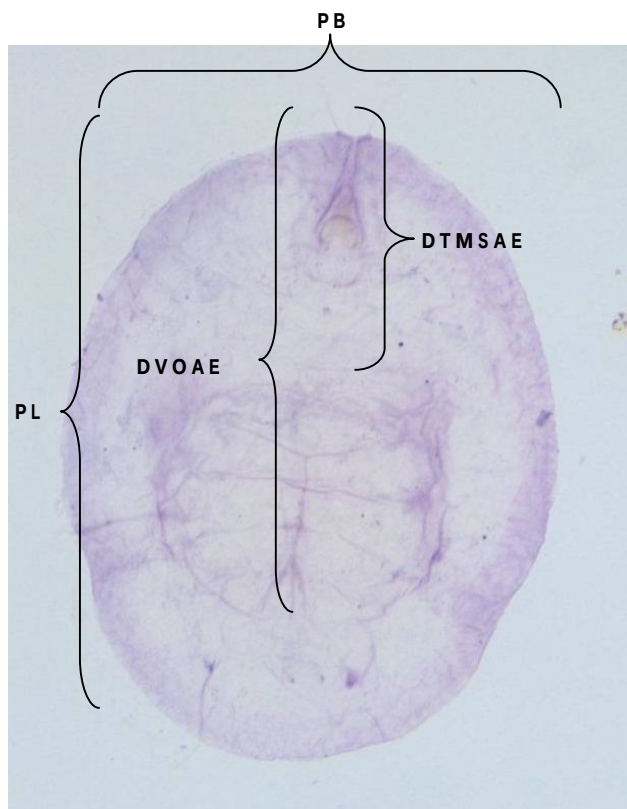
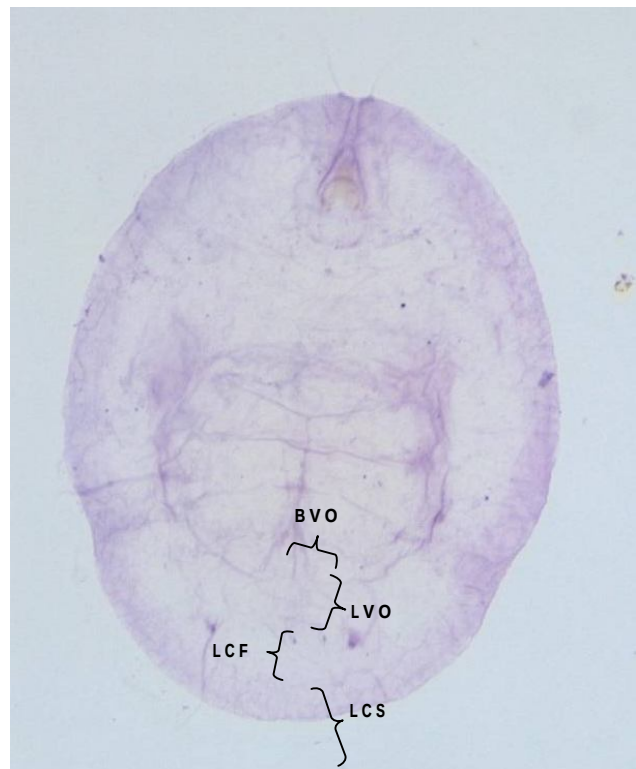


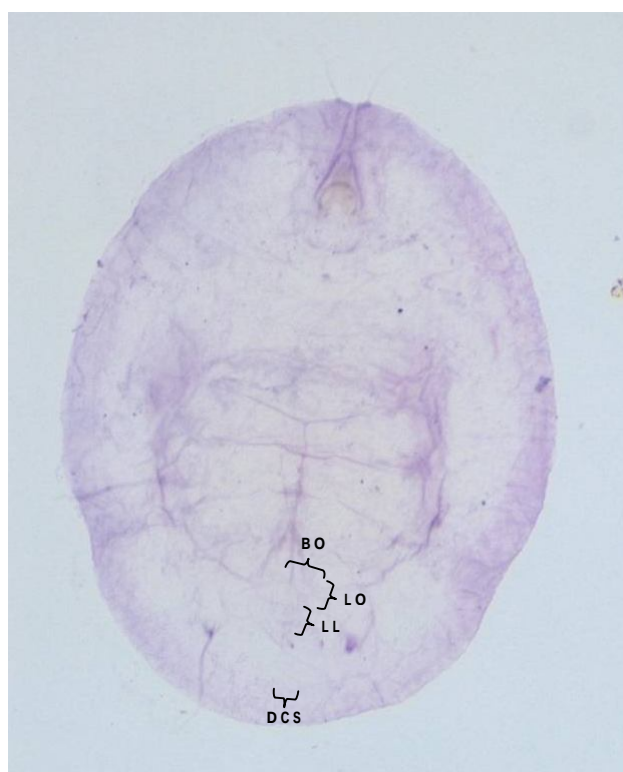
Plate 1. Morphology of the *Bemisia tabaci* puparia



A

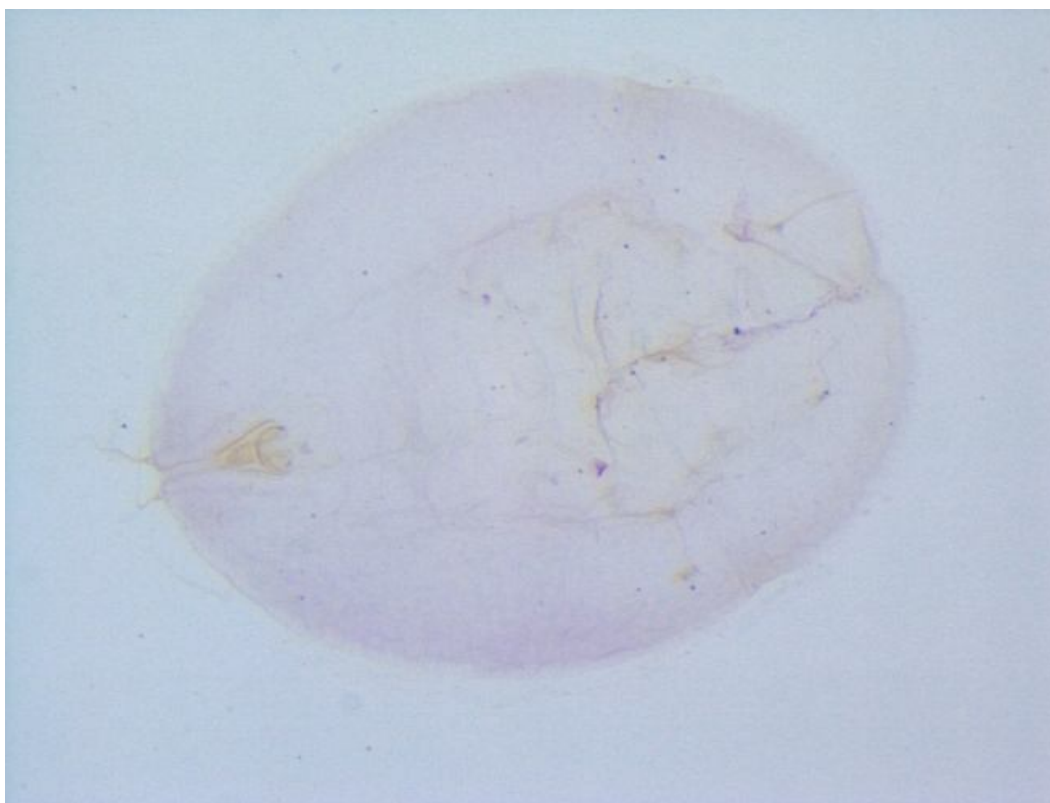


B

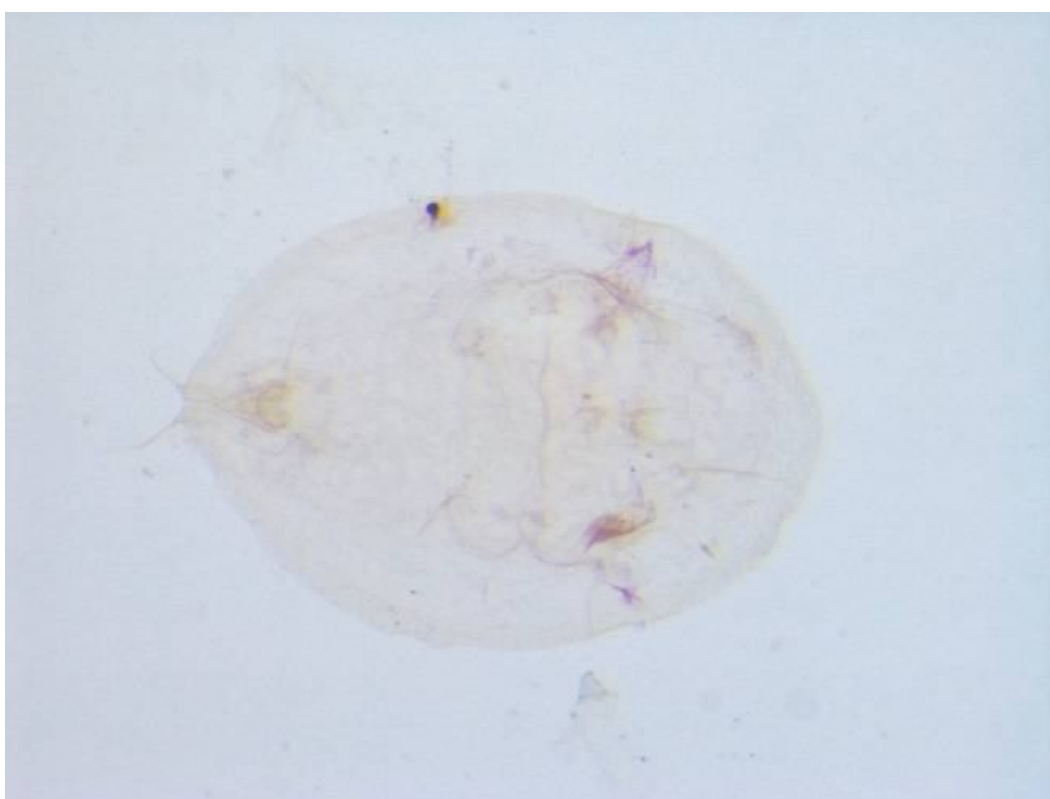


C

Plate 2. Morphometric characters of the *Bemisia tabaci* puparia

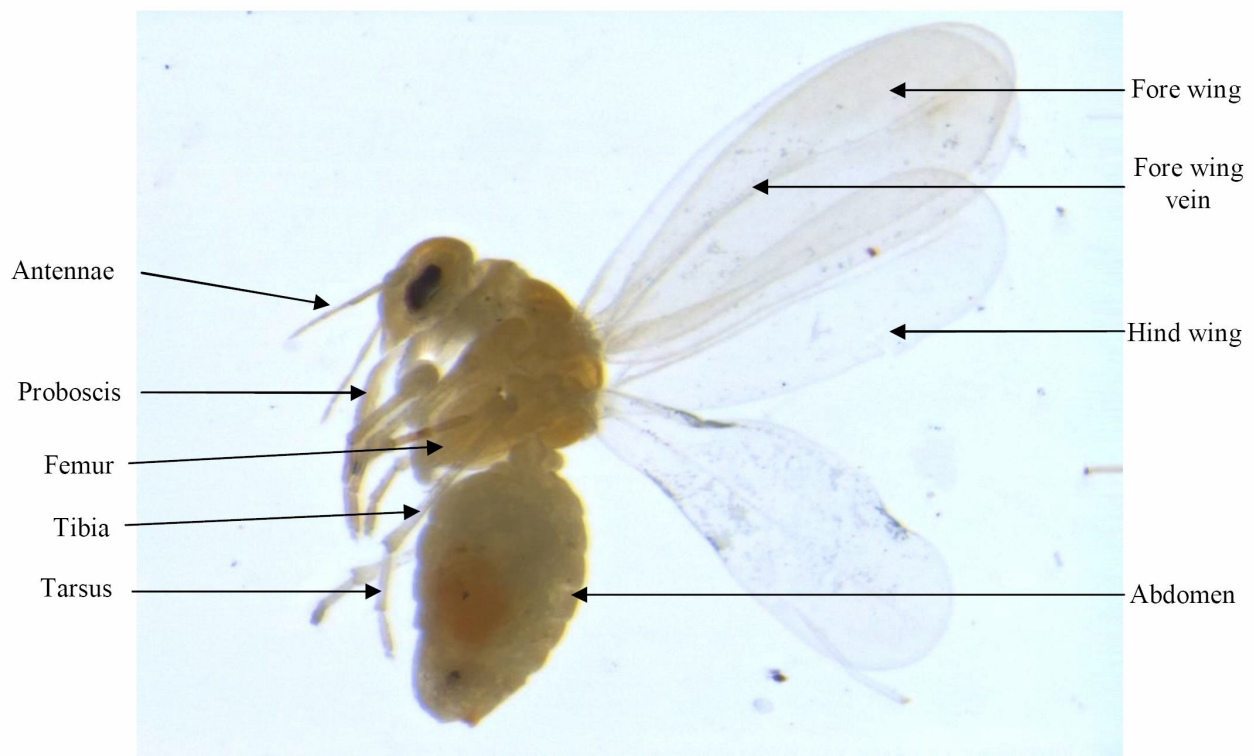


a. Dharwad

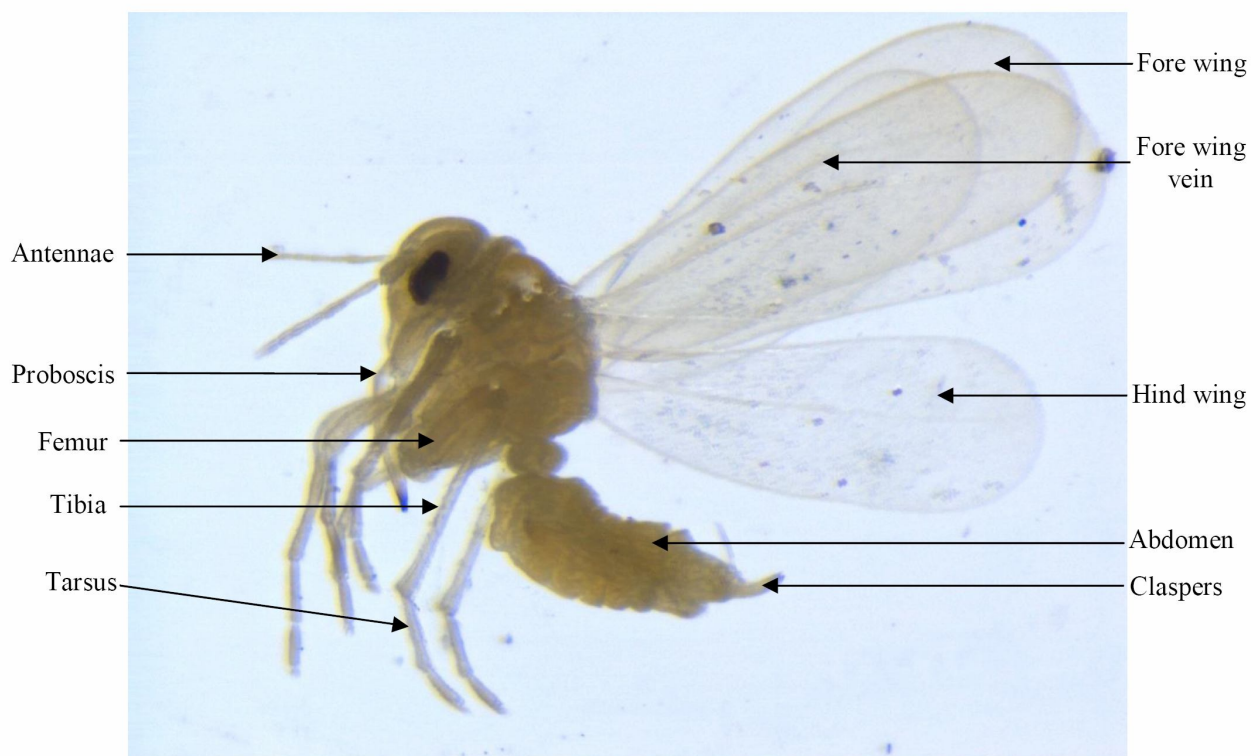


b. Bagalkot

Plate 3. Nymphal population recorded significantly higher (a. Dharwad) and lower (b. Bagalkot) values for the morphological traits studied.



Female



Male

Plate 4. Morphology of the *Bemisia tabaci* adults



Plate 5. Morphometric characters of *Bemisia tabaci* adults (A and B. Wing; C. Leg; D. Abdomen; E. Antennae; F. Proboscis; G. Claspers).



Female



Male

a. Chikkaballapura



Female



Male

b. Bengaluru rural

Plate 6. *Bemisia tabaci* female and male populations recorded significantly higher (a. Chikkaballapura) and lower (b. Bengaluru rural) values for the morphological traits studied.

3.1.4.3.2 Cluster and principal compound analysis

Cluster analysis and principal compound analysis was performed using software NTSYS-PC, Version 2.11w and Past 3.x software package for all quantitative features (Hammer *et al.*, 2001). The aim of the cluster analysis was to have some preliminary segregation of specimens and to generate hypothesis suggesting the existence of grouping of populations, using taxonomic units.

3.2 Genomic flux and population genetic structure of whitefly populations in tomato ecosystems of Karnataka

3.2.1 Sample preparation

Whitefly populations collected from different geographical areas and preserved in 70 per cent ethanol were used for present study (Table 2).

3.2.2 DNA extraction from adult whiteflies

Five female *B. tabaci* individuals were used for the total genomic DNA extraction. The method followed was given by Singh *et al.* (2012) with minor modifications. The purity of the DNA prepared and its suitability in ensuring repeatability of PCR amplification across the SSR loci were ensured.

3.2.2.1 De Barro and Driver method (De Barro and Driver, 1997)

3.2.2.1.1 Protocol

1. A single whitefly was transferred to a 1.5 ml microcentrifuge tube and 25 µl of extraction buffer (50 mM KCl, 10 mM Tris, pH 8.4, 0.45% Tween 20, 0.2% gelatin, 0.45% NP40, 500 µg/ml proteinase K) was added. The whitefly was ground thoroughly using a micropestle.
2. Homogenate was incubated at 65°C for 30 min in a hot water bath
3. After incubation, a small hole was made at the top of the microcentrifuge tube and kept for the pressure while boiling at 100°C for 10 min to inactivate the proteinase K.

Table 2. Whitefly population used for the genetic diversity study

Sl. No.	Districts	Sample location	Sample code	Sl. No.	Districts	Sample location	Sample code
1.	Davanagere	Mayakonda	DVN_M_1	7.	Bengaluru rural	Pathapalli	KLR_P_1
			DVN_M_2				KLR_P_2
			DVN_M_3				KLR_P_3
			DVN_M_4				KLR_P_4
			DVN_M_5				KLR_P_5
		Channapura	DVN_C_1			Kelaginanaikaradahalli	BR_K_1
			DVN_C_2				BR_K_2
			DVN_C_3				BR_K_3
			DVN_C_4				BR_K_4
			DVN_C_5				BR_K_5
		Tholahunase	DVN_T_1			Lakshmidhevapura	BR_L_1
			DVN_T_2				BR_L_2
			DVN_T_3				BR_L_3
			DVN_T_4				BR_L_4
			DVN_T_5				BR_L_5
2.	Haveri	Battikoppa	HR_Ba_1	8.	Bagalkot	Tubagere	BR_T_1
			HR_Ba_2				BR_T_2
			HR_Ba_3				BR_T_3
			HR_Ba_4				BR_T_4
			HR_Ba_5				BR_T_5
		Byadagi	HR_By_1			Kaladagi	BGK_K_1
			HR_By_2				BGK_K_2
			HR_By_3				BGK_K_3
			HR_By_4				BGK_K_4
			HR_By_5				BGK_K_5
		Motebennur	HR_Mo_1			Hiresamsi	BGK_H_1
			HR_Mo_2				BGK_H_2
			HR_Mo_3				BGK_H_3
			HR_Mo_4				BGK_H_4
			HR_Mo_5				BGK_H_5
3.	Dharwad	Narendra	DVD_N_1	9.	Chamarajanagar	Nanjedevanapura	CHA_N_1
			DVD_N_2				CHA_N_2
			DVD_N_3				CHA_N_3
			DVD_N_4				CHA_N_4
			DVD_N_5				CHA_N_5
		Garag	DVD_G_1			Kengaki	CHA_K_1
			DVD_G_2				CHA_K_2
			DVD_G_3				CHA_K_3
			DVD_G_4				CHA_K_4
			DVD_G_5				CHA_K_5

Sl. No.	Districts	Sample location	Sample code	Sl. No.	Districts	Sample location	Sample code
4.	Belagavi	Muttaga	BLV_M_1 BLV_M_2 BLV_M_3 BLV_M_4 BLV_M_5			Sattegala	CHA_S_1 CHA_S_2 CHA_S_3 CHA_S_4 CHA_S_5
		Benakatti	BLV_B_1 BLV_B_2 BLV_B_3 BLV_B_4 BLV_B_5	10.	Chikkamagaluru	Allampura	CM_AI_1 CM_AI_2 CM_AI_3 CM_AI_4 CM_AI_5
5.	Chikkaballapura	Buragamakalahalli	CBR_B_1 CBR_B_2 CBR_B_3 CBR_B_4 CBR_B_5			Chikkagouja	CM_C_1 CM_C_2 CM_C_3 CM_C_4 CM_C_5
		Gollahalli	CBR_G_1 CBR_G_2 CBR_G_3 CBR_G_4 CBR_G_5			Amble	CM_Am_1 CM_Am_2 CM_Am_3 CM_Am_4 CM_Am_5
6	Kolar	Balageri	KLR_B_1 KLR_B_2 KLR_B_3 KLR_B_4 KLR_B_5	11.	Shivamogga	Alada halli	SHI_A_1 SHI_A_2 SHI_A_3 SHI_A_4 SHI_A_5
		Sugaturu	KLR_S_1 KLR_S_2 KLR_S_3 KLR_S_4 KLR_S_5			Kunchenahalli	SHI_K_1 SHI_K_2 SHI_K_3 SHI_K_4 SHI_K_5

4. 25 µl 1x TE buffer was added to yield a final sample volume of 50 µl and samples were stored at -20°C.
5. Two µl of sample was used for the PCR analysis.

3.2.2.2 Singh *et al.* (2012) method

This method was used for DNA extraction from whiteflies with minor modifications and the modified protocol is as follows.

3.2.2.2.1 Protocol

1. Each adult whitefly was washed twice with sterile water.
2. Thereafter it was homogenized in 14 µl of lysis buffer (100 mM Tris-Cl pH 8.0, 100 mM EDTA pH 8.0, 100 mM NaCl and 1% SDS) and one per cent proteinase K.
3. The homogenate was incubated at 65°C for 20 min.
4. Further, 27 µl of pre chilled mixture of 5 M potassium acetate was added and incubated on ice for another 15 min before centrifuging at 10,000 rpm, 4°C for 15 min.
5. The supernatant was transferred to a fresh microcentrifuge tube to which 0.6 volume of isopropanol was added.
6. This was again centrifuged at 10,000 rpm, 4°C for 15 min.
7. The pellet, thus obtained was washed with 70 per cent ethanol.
8. The air dried pellet was dissolved in elution buffer (10 mM Tris-Cl, pH 8.0) before giving the RNase-A treatment.
9. After the RNase treatment the DNA samples were kept at -20 °C till its further use.

Both the above described methods were used for DNA extraction former method for half of the samples and later method for remaining samples and PCR analysis, however, among them, Singh *et al.* (2012) method was found easy and quick with good quantity of DNA.

3.2.3 Quantification of extracted genomic DNA

The ratio between the readings at 260 and 280 nm (OD 260/OD 280) was used as an estimate of purity of the DNA samples. Pure preparations of DNA had 260 nm/ 280 nm OD ratios ranging between 1.7 and 1.8 (Sambrook and Russel, 2001). Computed OD values were used to dilute the DNA samples to the working concentrations of 5ng/ μ l. The stock DNA solutions were diluted to 5 ng/ μ l of 100 ng/ μ l working solution for PCR. Then the amount of stock DNA solution to be taken for dilution was calculated using the following formula,

$$M_1V_1 = M_2V_2$$

$$(100 \text{ ng/ } \mu\text{l})V_1 = (5 \text{ ng/}\mu\text{l}) (100 \mu\text{l})$$

$$V_1 = (5 \text{ ng/}\mu\text{l}) (100 \mu\text{l}) / (100 \text{ ng/}\mu\text{l})$$

$$V_1 = 5 \mu\text{l}$$

Where, M_1 is the stock DNA concentration (for example, 100 ng/ μ l), V_1 is the volume of stock to be diluted, M_2 is the concentration of working solution (5 ng/ μ l) and V_2 is the volume of working solution to be prepared (for example, 100 μ l).

Then, the appropriate volume from the stock was transferred to 0.5 ml micro centrifuge tube and the volume was made to 100 μ l using distilled water. The DNA working solutions were stored at -20 $^{\circ}$ C till further use.

3.2.4 Screening of DNA markers

Total 17 SSR markers linked to whitefly, *Bemisia tabaci* were screened across the 140 individual samples (Appendix V).

3.2.4.1 The PCR reaction mixture and concentration of components

Component	Quantity (μ l/reaction)
Genomic DNA (100 ng/ μ l)	1.0
Forward primer (5 pM/ μ l)	0.5
Reverse primer (5 pM/ μ l)	0.5
Taq 2x master mix	3.0
Sterile water	5.0

PCR reactions were carried out using the Master Cycler gradient 5331 (Eppendorf version 2.30.31-09, Germany). The cycler was programmed as follows;

Step	Temperature	Duration	No.of cycles
Initial denaturation temperature	: 94.0 °C	: 3 min.	1
Denaturation	: 94.0 °C	: 1 min.	} 35
Primer annealing	: 50-56 °C	: 1.3 min.	
Primer extension	: 72.0 °C	: 1 min.	
Complete primer extension	: 72.0 °C	: 10 min	1
Store	: 4.0 °C	: up to removed	1

3.2.5 Agarose gel electrophoresis

Agarose was casted in 3 per cent gel in TAE buffer (1x). Slabs were casted in a horizontal gel frame (Hoefer HE99X 18 x 30 cm Amersham Bioscience Pvt. Ltd. USA); products were visualized by incorporating 1 μ l (10 mg/ml) ethidium bromide per 10 ml of gel solution and viewed in a gel documentation system (Syngene, Pvt. Ltd., USA). The procedure followed for gel electrophoresis as follows;

1. The perspex tray and comb were thoroughly cleaned with 70 per cent alcohol using tissue paper.

2. The ends of perspex tray were sealed with spacers/tape and comb was inserted.
3. Agarose gel (3 %) was prepared by adding 3 g agarose to 100 ml of TAE (1x) buffer (EDTA 0.5 M at pH 8).
4. The solution was boiled by putting the flask in microwave oven and allowed to cool to 60 °C.
5. Ethidium bromide (10 µl of conc. 10 mg/ml) was added to the gel and mixed gently.
6. The gel was poured into the tray and air bubbles were removed by using pipette. When the gel was completely set, tape was removed and the gel was placed into the electrophoresis tank.
7. Approximately 500 ml of TAE (1x) buffer was poured into the electrophoresis tank, sufficient to cover the gel to a depth of 5 mm.
8. Comb was removed carefully.
9. DNA samples *i.e.* PCR amplified products were loaded onto the wells and the power supply of about 80 V was provided to run the gel.
10. The power supply was switched off when loading dye was about 2.5 cm from positive end, and the gel was removed from the gel apparatus.
11. The gel was viewed and photographed by using gel documentation system (UVI Tech, England).
12. The occurrence of specific amplicons were linked to the presence of specific allele.

Data obtained by scoring the molecular marker profiles of the primers were subjected for cluster analyses. PCR amplification products of the samples were scored as presence of different allelic size. The similarity values were used for further analyses (Simon *et al.*, 2003).

3.2.6 Statistical analysis

3.2.6.1 Genetic diversity analysis

The level of polymorphism among the samples were assessed with the short listed 17 microsatellites. The microsatellite data was analysed for mean number of alleles (N_a), percentage of polymorphic loci (% P), mean unbiased estimates of observed (H_o) and expected (H_e) heterozygosity (Nei, 1987), number of effective alleles (N_e), number of effective migrants (N_m) and F-coefficients, population allele frequencies, genetic distance and pair wise population F_{ST} values were calculated using GenAlEx V 6.41 (Peakall and Smouse, 2006).

3.2.6.2 Analysis of Molecular Variance (AMOVA)

The microsatellite data was subjected to a hierarchical analysis of molecular variance (AMOVA) at individual, population and intrapopulation level using Arlequin Ver 3.5 (Excoffier *et al.*, 2005).

3.2.6.3 Principal coordinate analysis

The principal coordinate analysis using genetic distance was plotted using GenAlEx V 6.41 (Peakall and Smouse, 2006).

3.2.6.4 Phylogenetic analysis

The Neighbor Joining tree at population and individual levels were constructed using genetic distance matrix from GenAlEx with 1000 bootstrap values, carried out using MEGA 7.0.26 (Kumar *et al.*, 2015) software. Neighbor joining tree takes distance matrix as an input specifying the distance between each pair of taxa. The algorithm starts with a completely unresolved tree, whose topology corresponds to that of a star network and iterates over the following steps until the tree is completely resolved and all branch lengths are known.

3.2.6.5 Structure analysis

Population structure was examined using the Bayesian cluster algorithm STRUCTURE Ver 2.3.4 (Pritchard *et al.*, 2000). The data was computed in STRUCTURE algorithm for 10,000 iterations with a burn-in period of 1,000 steps

with 20 replicate runs for each value of K (1 to 15). The population was assumed to be admixture in the correlated allele frequency model. The number of true clusters (K) in the output data of the structure was estimated using Structure Harvester (Earl *et al.*, 2012), which identified the optimal K value based on posterior probability of the data for a given K (Evanno *et al.*, 2005).

3.3 To determine the frequency of mono and bipartite particle in populations of whitefly

3.3.1 Sample preparation

Whitefly populations collected from different geographical areas and preserved in 70 per cent ethanol were used for present studies. From each district selected five individuals were used for the study to determine the frequency of virus particles (Table 3).

3.3.2 DNA extraction from adult whiteflies

Randomly selected five individuals of *B. tabaci* were analyzed from each district. Total genomic viral DNA was extracted from individual adult female whitefly and extraction was done by following the modified method of Singh *et al.* (2012) and compared for ease of extraction, band clarity and reproducibility in SSR-PCR.

3.3.2.1 Singh *et al.* (2012) method

This method was used to extract viral DNA from adult whiteflies for PCR analysis with minor modifications as this method was found easy and quick. The modified protocol is as follows.

3.3.2.1.1 Protocol

DNA isolation protocols was followed as explained in 3.2.2.3.1

3.3.3 Quantification of extracted genomic DNA

The quantification of isolated DNA was done as mentioned in 3.2.3

Table 3. Whitefly population used to determine frequency of mono and bipartite virus particles

Sl. No.	Districts	Sample code	Sl. No.	Districts	Sample code
1	Davanagere	DVN_M_1 DVN_M_4 DVN_C_2 DVN_C_4 DVN_T_3	7	Bengaluru rural	KLR_P_1 KLR_P_5 BR_K_2 BR_K_5 BR_L_3
2	Haveri	HVR_Ba_4 HVR_Ba_5 HVR_By_1 HVR_By_5 HVR_Mo_4	8	Bagalkot	BR_T_1 BR_T_2 BGK_K_1 BGK_K_2 BGK_K_3
3	Dharwad	DWD_N_1 DWD_N_2 DWD_N_5 DWD_G_3 DWD_G_4	9	Chamarajanagar	BGK_H_3 BGK_H_4 CHA_N_4 CHA_N_5 CHA_K_1
4	Belagavi	BLV_M_1 BLV_M_2 BLV_M_3 BLV_B_3 BLV_B_4	10	Chikkamagaluru	CHA_K_5 CHA_S_1 CKM_A1_1 CKM_A1_5 CKM_C_4
5	Chikkaballapura	CKBR_B_1 CKBR_B_5 CKBR_G_3 CKBR_G_4 CKBR_G_5	11	Shivamogga	CKM_C_5 CKM_Am_2 SHI_A_2 SHI_A_3 SHI_A_4
6	Kolar	KLR_B_2 KLR_S_1 KLR_S_2			SHI_K_1 SHI_K_2

3.3.4 Screening of DNA markers linked to monopartite and bipartite virus particle

DNA markers linked to monopartite and bipartite ToLCV virus particle were screened across the whitefly collection.

3.3.5 DNA markers linked to different monopartite and bipartite virus particle

Primer name	Sequence of the primer	Expected amplicon size
Monopartite (Pm)	F: GGCTAGGCTGTGTTGCACTT	270 bp
	R: GTCGACCCG CATTATCTAAA	
Bipartite (Pb)	F: TTGACGAGACCAATCGACG	477 bp
	R: CATCAAG ATCTGTAGAGAGC	

3.3.6 The general PCR reaction mixture and concentration of components

Component	Quantity (μ l/reaction)
Genomic DNA (100 ng/ μ l)	1.0
Forward primer (5 pM/ μ l)	0.5
Reverse primer (5 pM/ μ l)	0.5
Taq 2x master mix	3.0
Sterile water	5.0

PCR reaction was carried out using Master Cycler gradient 5331 (Eppendorf version 2.30.31-09, Germany). The cycler was programmed as follows;

Step	Temperature	Duration	No. of cycle
Initial denaturation temperature	: 94.0 °C	: 4 min.	1
Denaturation	: 94.0 °C	: 1 min.	38
Primer annealing			
Monopartite	: 54.0 °C	: 1 min.	
Bipartite	: 58.0 °C	: 1 min.	
Primer extension	: 72.0 °C	: 2 min.	
Complete primer extension	: 72.0 °C	: 20 min	1
Store	: 4.0 °C	: up to removed	1

3.3.7 Agarose gel electrophoresis

The protocol followed was similar to 3.2.5 except that the agarose was casted in 1.5 per cent gels in TAE buffer (1X) instead of 3 per cent gel. Agarose gel (1.5 %) was prepared by adding 1.5 g agarose to 100 ml of TAE (1×) buffer (EDTA 0.5 M at pH 8).

Finally, the alleles representing monopartite virus particle were amplified at 270bp whereas, the alleles representing bipartite virus particle were amplified at 477 bp. Data obtained was scored to check frequency of monopartite and bipartite virus particles.

3.3.8 Per cent leaf curl disease incidence

Disease incidence of ToLCV was recorded during the survey in each field from randomly selected 10 tomato plants by counting number of infested leaves out of total number of leaves per plant. Thus, the disease incidence percentage was calculated as under:

$$\text{Disease incidence (\%)} = \frac{\text{No. of infected leaves per plant}}{\text{Total no. of leaves per plant}} \times 100$$

3.3.8.1 Disease rating scale

The disease incidence was evaluated by modified Ssekyewa (2006) scale.

Grades	Disease incidence (%)	Infection category
0	All plants free of virus symptoms	HR
1	1-20	R
2	21-40	MR
3	41-60	MS
4	61-80	S
5	81-100	HS

HR= Highly resistant, R= Resistant, MR= Moderately Resistant, MS= Moderately Susceptible, S= Susceptible, HS= Highly susceptible.

Further, frequency of mono and bipartite virus in whitefly was correlated with per cent leaf curl disease incidence.

3.4 Variation for traits related to whitefly resistance in tomato association mapping panel (TAMP)

3.4.1 Details of field experiment location, weather and soil conditions

The experimental field was located at an altitude of 930 m above MSL 12° 58¹ North latitude and 77° 35¹ East-longitude in the Eastern Dry Zone (Zone-5) of College of Horticulture, Bengaluru campus, Karnataka during rabi and summer seasons of 2016-17. Soil of the experimental site was red sandy loam with a pH of 6.4. The details of monthly meteorological data for the crop growth period are presented in Appendix VI.

3.4.2 Experimental material

A set of 260 tomato germplasm accessions-‘mini-core’ collection constituted in collaboration with ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi

and UHS Bagalkot, were subjected to field evaluation which contains varieties and hybrids released from Indian public and private sectors, accessions collected from different Universities, from AVRDC Taiwan (EC and CLN series) and other countries. These accessions were grouped based on their place of collection for diversity and structure analysis. The tomato accessions constituting the mini-core used in the study are presented in Table 4.

3.4.3 Experimental design

Main field was prepared by ploughing and harrowing and brought to fine tilth. FYM at 25t per ha along with the basal dose of NPK was incorporated into the soil. Augmented Block Design was employed for phenotypic evaluation of 260 minicore accessions. Ridges of 3.5 meter length was prepared and spacing of 60 cm row to row and 45 cm plant to plant days old seedlings of all accessions were transplanted along with repeated whitefly resistant (Nandi and Sankranti) and susceptible (Pusa ruby) lines at each block and they are used as checks. Twelve plants from each accessions were planted. Crop was raised in a field by following all agronomic practices as per the package of practices of UHS, Bagalkot except for whitefly management. The overview of field experiment is presented in Plate 7.

3.4.4 Observations recorded

3.4.4.1 Observation on whitefly

Five plants of each tomato accessions were randomly selected and tagged three fully expanded compound leaves (top, middle and bottom) were selected randomly and collected in a polythene cover with proper labeling. The leaf samples were brought to the laboratory for further observations.

The leaf samples were observed for number of whitefly nymphal population under stereo zoom binocular microscope. The observations were taken at 30, 45 and 60 days after transplanting. *Bemisia tabaci* adult and nymph population present on abaxial surface of tomato leaves is presented in Plate 8.

Table 4. List of tomato accessions constituting minicore collections used for field evaluation.

SL. No	Accessions/ Germplasm	SL. No	Accessions/ Germplasm	SL. No	Accessions/ Germplasm
1	Ageta-32	41	DVRT-1	81	EC-538439
2	Angoorlata	42	DVRT-2	82	EC-538440
3	Arka Abha	43	E-4-3	83	EC-538441
4	Arka Alok	44	EC-2791	84	EC-538455
5	Arka Meghalli	45	EC-13904	85	EC-552141
6	Arka Vikas	46	EC-317-6-1	86	EC-560340
7	Avinash-2-2-1	47	EC-273966	87	EC-570028
8	Azad T-2	48	EC-381263	88	EC-605694
9	Azad T-5	49	EC-381554	89	EC-605695
10	B-4-1	50	EC-501574	90	EC-605696
11	B-7-2	51	EC-501575	91	EC-620362
12	Bhillai	52	EC-501576	92	EC-620366
13	BL-1208	53	EC-501577	93	EC-620370
14	BTH-9 M	54	EC-501580	94	EC-620373
15	C-1-4	55	EC-501582	95	EC-620374
16	C-3-2	56	EC-501583	96	EC-620375
17	C-4-1	57	EC-519730	97	EC-620383
18	C-8-1	58	EC-520046	98	EC-620386
19	C-9-2	59	EC-520059	99	EC-620398
20	C-10-2	60	EC-520061	100	EC-620401
21	C-11-1	61	EC-520071	101	EC-620403
22	C-11-2	62	EC-520074	102	EC-620406
23	C-11-3	63	EC-520075	103	EC-620409
24	C-20-1	64	EC -520078	104	EC-620410
25	C-20-2	65	EC -521039	105	EC-620411
26	C-26-1	66	EC -521056	106	EC-620413
27	CHRT-4	67	EC -521078	107	EC-620419
28	CH-155	68	EC -526139	108	EC-620421
29	Co-3	69	EC-528372	109	EC-620438
30	CLN-2026	70	EC-528374	110	EC-620444
31	CLN-2116	71	EC -529080	111	EC-620446
32	CLN-1621	72	EC -529083	112	EC-620455
33	CLN-2366	73	EC-538138	113	EC-620456
34	D-1-1	74	EC -538155	114	EC-620464
35	D-2-2-1	75	EC-538380	115	EC-620469
36	D-3-2	76	Ec-538404	116	EC-620470
37	D-5-1	77	EC-538405	117	EC-620474
38	DARL-66	78	EC-538408	118	EC-620476
39	Dhrubya	79	EC-538419	119	EC-620480
40	DT-10	80	EC-538423	120	EC-620486
121	EC-620500	161	H-88-78-5	201	NDT-1
122	EC-620502	162	Hawai	202	NDT-8
123	EC-620514	163	Hisar Anmol	203	NDT-4
124	EC-620519	164	Hisar Arun (Sel-7)	204	NDTVR-60

SL. No	Accessions/ Germplasm	SL. No	Accessions/ Germplasm	SL. No	Accessions/ Germplasm
125	EC -620530	165	Hisar Lalit	205	NDTVR-73
126	EC -620533	166	I-4-4	206	NF37SB-8
127	EC -620540	167	IC-373378	207	Palam Pink
128	EC -620556	168	IC-427766	208	Pant T-3
129	EC -620568	169	IC-447708	209	pant T-5
130	EC -620575	170	IC-469626	210	Parul
131	EC -620598	171	IIHR-01	211	Pb-Chhuhara
132	EC -625644	172	IIHR-2202	212	Pb.Upma
133	EC -625645	173	INDAM-2102	213	Persia Bed
134	EC -625651	174	INDAM-2103	214	PDT-3-1
135	EC -625652	175	INDAM-2103-1	215	PDVT-14
136	EC -625660	176	INDAM-2103-1-1	216	PKM-1
137	EC-6202041	177	INDAM-2103-4	217	PS-1
138	F-5020	178	INDAM-2103-6	218	Prestige
139	F-6022	179	INDAM-2103-6-1	219	Pusa Gaurav
140	F-6050-1	180	INDAM-2103-6-4	220	Pusa Ruby
141	F-6059	181	Jawahar-99	221	Pusa-120
142	F-7012	182	Kashi Hemant	222	Punjab Barkha Bahar-2
143	F-7025	183	Kashi Sharad	223	Pusa Hybrid-2
144	F-7028	184	Kashi Vishesh	224	Roma
145	F-6009	185	Kashi Amrit	225	Sanjeevani
146	FEB.-02	186	Kashi Anupam	226	Sankranti
147	FEB.-04	187	Kajla	227	Sel-18
148	FLA-7171	188	Kalyanpur Type-1	228	Sioux
149	FLA-7421	189	Kashmiriya	229	Solan Gola
150	Flora-dade	190	LA-3772	230	Solan Vajr
151	G-4-5	191	LA-3957	231	Sun-Cherry
152	G-5-4	192	LA-3997	232	Swarna Naveen
153	G-6-3	193	M-1-4	233	Swarna Vaibhav
154	GT-1	194	M-3-2	234	TLBR-6
155	GT-2	195	Mukthi	235	TLH-17
156	GT-3	196	Money Maker	236	TLH-27
157	H-24	197	Monte Favet	237	TLH-30
158	H-88-78-2	198	N-2-2	238	Tripura Local
159	H-88-78-3	199	N-2-3	239	Utkal Pragyan
160	H-88-78-4	200	Nandhi	240	Utkal Raja
241	VRT-32-1	247	97/384	253	Switzerland
242	VRT-101A	248	97/753	254	Utkal Urvashi
243	WIR-3957	249	97/754 (Kewalo)	255	WIR-13717
244	WIR-5032	250	15 SB	256	Pallavi
245	WIR-13706	251	Rio Grande	257	Punjab Keshri
246	WIR-13708	252	S.Lalima	258	V. Pragyan
259	DMT1	260	DMT3		



a. *Rabi* season

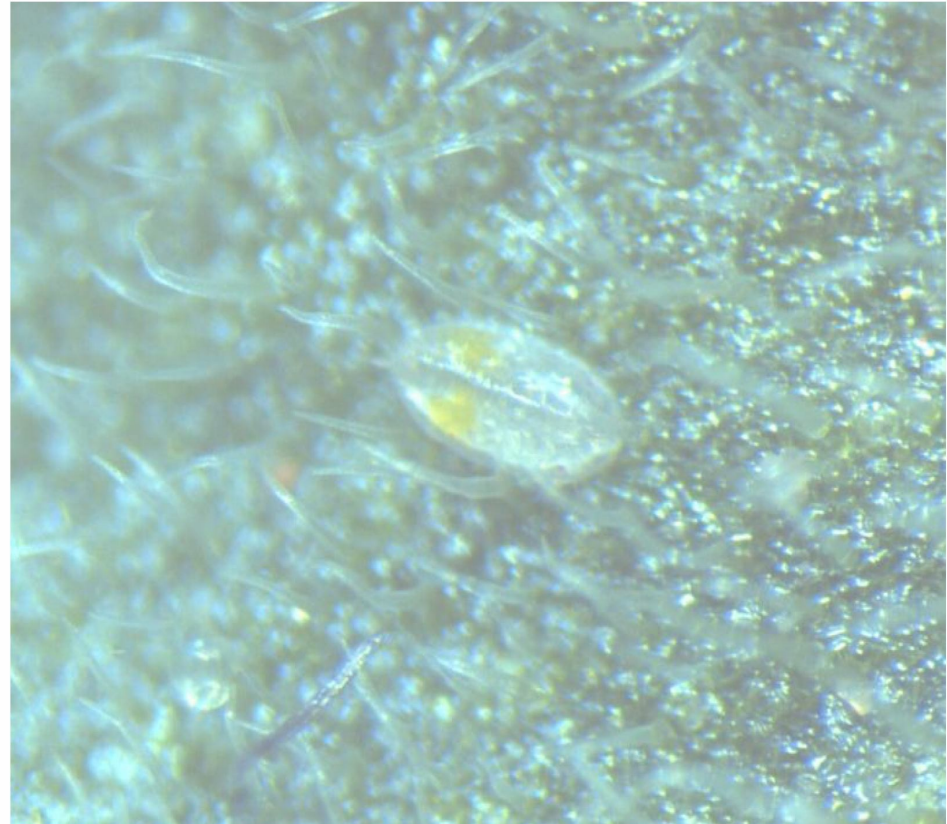


b. Summer season

Plate 7. Field overview of minicore accessions, a. *Rabi* season and b. Summer season 2016-17 at COH Bengaluru.



a. Adults



b. Nymph

Plate 8. *Bemisia tabaci* adult and nymph population on abaxial surface of tomato leaves

3.4.4.2 ToLCV disease scoring

Disease incidence scoring was done at 60 days after transplanting (Plate 9) by recording number of infected plants and total plants *i.e.* twelve plants and the disease incidence was calculated as follows.

$$\text{Disease Incidence (\%)} = \frac{\text{Number of plants infected}}{\text{Total number of plants observed}} \times 100$$

Scale for grading tomato accessions against ToLCV (Singh *et al.*, 2014)

Scale	Response category	Symbol	Disease infection (%)
01	Immune	I	0.00
02	Resistant	R	0.10-5.00
03	Moderately resistant	MR	5.10-10.00
04	Moderately susceptible	MS	10.10-25.00
05	Susceptible	S	25.10-50.00
06	Highly susceptible	HS	>50.10

3.4.4.3 Biophysical characters

3.4.4.3.1 Assessment of trichome density on leaf surfaces.

Trichome density was assessed from a pair of leaflets sampled from equivalent positions (the second pair of leaflets proximal to the terminal leaflet) of the upper, middle and lower leaves of each plant. One leaflet of each pair was used to obtain adaxial trichome counts and the corresponding opposite leaflet was used for counts on the abaxial surface. Leaf discs of 6 mm dia. were cut using cork borer from freshly harvested leaves and the disc was mounted on a microscopic stage and the trichomes were counted under a stereozoom microscope. The number of trichomes within the interveinal area near to the centre of each leaflet were counted. Leaf disc diameters were determined and the trichome densities were calculated as the number of trichomes per mm² (Channarayappa *et al.*, 1992).



Plate 9. Tomato plants showing ToLCV symptoms

3.4.4.3.2 Characterization of trichome types

The types of trichomes present were recorded separately for 260 accessions. The criteria for determining the type of trichome was followed as described by Luckwill (1943) and Channarayappa *et al.* (1992). The observations were made under a Trinicular stereo zoom microscope built with adapter to fix camera at a magnification of 40 X. Photographs of both adaxial and abaxial surfaces of fresh leaflets were taken (Plate 10a and 10b). Trichomes were classified into the following types.

Sl. No.	Trichome Type	Trichome characters
1	Type 1	Straight, long and small gland on tip of the trichome (glandular).
2	Type 2	Straight, medium long and sharp tip.
3	Type 3	Straight, long and sharp tip.
4	Type 4	Straight, short and small gland on tip (glandular)
5	Type 5	Straight or hooked, short and sharp tip
6	Type 6	Straight, medium long and big gland on tip (glandular)
7	Type 7	Straight, short and lobed gland on tip (glandular)
8	Type 8	Bent, short and hooked tip

3.4.4.4 Biochemical characters

Total chlorophyll, total phenols, tannins, terpenoides were estimated from top leaf samples collected at 45 days after transplanting (Muigai *et al.*, 2003; Azizi *et al.*, 2008).

3.4.4.4.1 Chlorophyll content (SPAD Value)

SPAD chlorophyll meter reading (SCMR) as an indication of chlorophyll status in the leaf was measured using portable SPAD meter. Fifth leaf from top of the plant was selected for recording SPAD reading. This leaf was inserted between the measuring head where receptor window will read the chlorophyll content. The reading



a) Trichome type I



b) Trichome type II



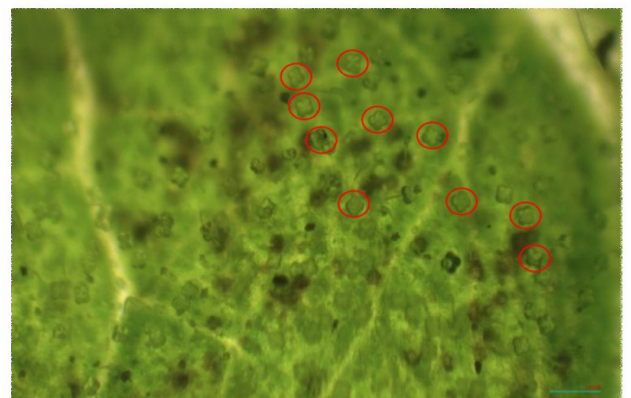
c) Trichome type III



d) Trichome type IV



e) Trichome type V



f) Trichome type VII

Plate 10a. Different types of trichomes observed on tomato accessions.

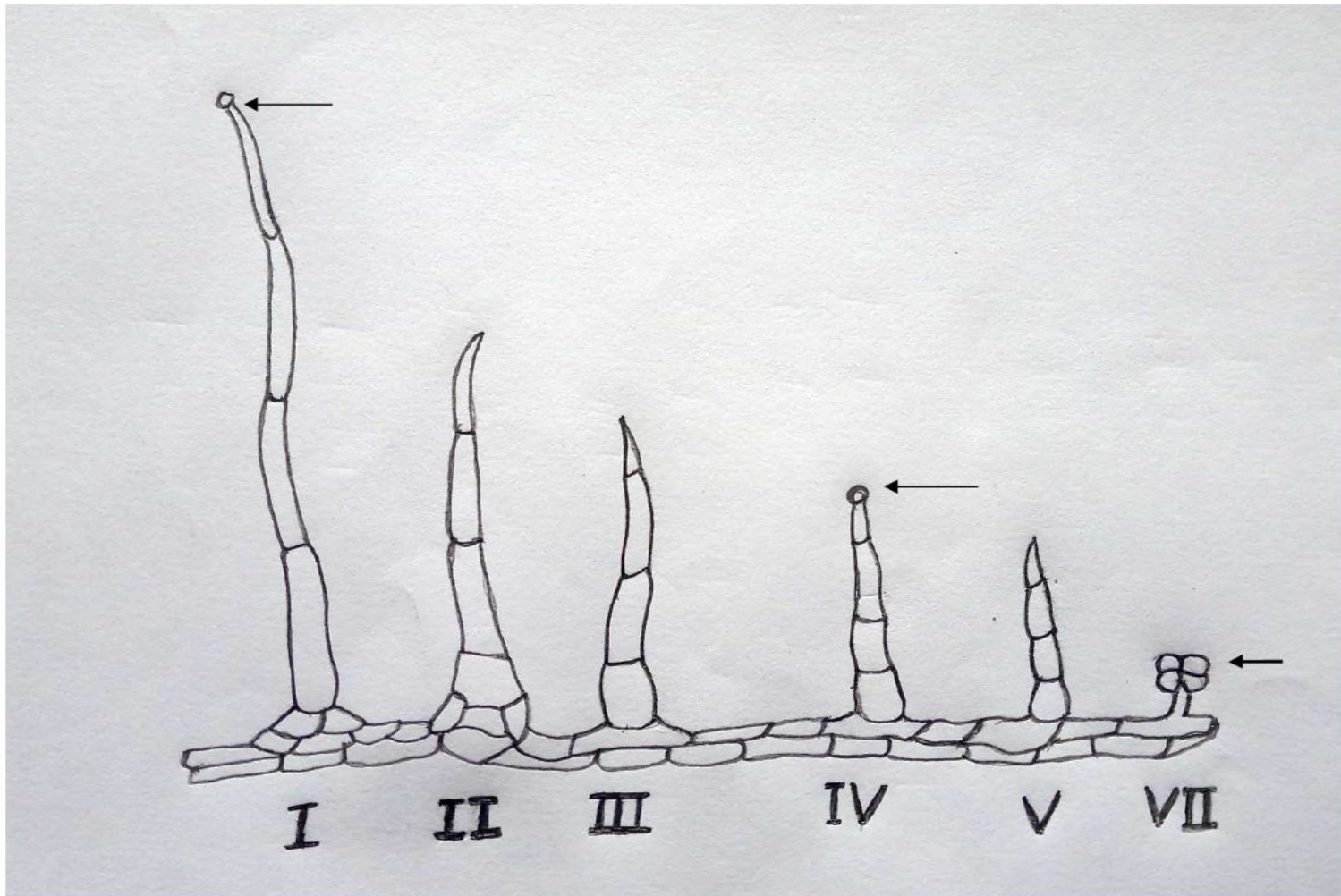


Plate 10b. Different types of glandular (Type I, IV and VII, indicated with arrow mark) and non glandular (Type II, III and V) trichomes.

will be seen on the display. The mean of SPAD value was taken out in end and presented as average SPAD value.

3.4.4.4.2 Phenol content

Total phenol estimation was done by following the Folin-Ciocalteu reagent method with slight modification.

Procedure

Exactly 1.0 g of the leaf sample was weighed and ground with a pestle and mortar in 10 ml of 80 per cent ethanol. The homogenate was centrifuged at 10000 rpm for 20 min. The supernatant was saved and residues were re- extracted with five times the volume of residue with 80 per cent ethanol, centrifuged and was dried.

Residue was dissolved in 5 ml of distilled water. Pipetted different aliquots (0.2 to 2ml) into test tubes and volume made to 3ml with water. 0.5 ml of Folin-Ciocalteu reagent was added. After 3min, 2ml of 20 per cent was added Na_2CO_3 to each tube and mixed thoroughly. The tubes were placed in a boiling water for one min, cooled and measured the absorbance at 650 nm using UV absorption spectrophotometer against a reagent blank. The standard curve was prepared using different concentrations of catechol. The concentration of phenols in the test sample was estimated from the standard curve and expressed as mg/ 100g material.

3.4.4.4.3 Tannins content

Tannin content was estimated by following the Folin-Denis reagent method with slight modification.

Procedure

Exactly 1.0 g of the powdered leaf sample was weighed and transferred to a 250ml conical flask. 75 ml distilled water was added and the flask was boiled for 30 min. Later, it was centrifuged at 2,000 rpm for 20 min and collected the supernatant in 100ml volumetric flask and made up the volume. 1ml of the sample extract was transferred to a 100ml volumetric flask containing 75 ml water. 5 ml of Folin-Dennis reagent, 10ml of sodium carbonate solutions were added and diluted to 100ml with water and shaken well.

The blank was prepared with water instead of the sample and the absorbance was read at 700 nm using UV absorption spectrophotometer after 30 min. Standard graph was prepared by using 0-100µg standard tannic acid. Tannin content was calculated as tannic acid equivalents from the standard graph and expressed as g/ 100g

3.4.4.4 Terpenoid content

Procedure

Exactly 0.1g of the powdered leaf sample was weighed and transferred to a 25 ml conical flask. 5 ml of methanol was added to it and shaken well. After 15 min. 2ml of the sample extract was transferred to a test tube and 2ml chloroform was added to the test tube and mixed well. 3ml of sulphuric acid was added to the test tube and mixed well. Reddish brown colour was formed which indicated the presence of terpenoids.

Absorbance was read at 538nm using UV absorption spectrophotometer, five minutes after adding sulphuric acid using methanol as a blank instead of the sample. Standard graph was plotted by using Linalool solution. From the standard curve, the concentration of terpinoid was expressed as mg/ 100g.

3.4.5 Screening of tomato accessions with DNA markers

The genomic DNA was extracted from leaf samples collected from 260 tomato mini-core collection. The reagents, stocks and solutions used for DNA isolation are presented in Appendix VII. The genomic DNA was prepared following the method given by Murray and Thompson (1980) with minor modifications as follows;

3.4.5.1 Genomic DNA isolation

1. Frozen tissue sample (2 g collected from individual) was ground into fine powder in liquid nitrogen, using autoclaved mortar and pestle.
2. Immediately ground tissue was transferred to 2.0 ml Eppendorf tube containing 900 µl of extraction buffer and 90 µl of 20 per cent sodium dodesyl sulphate (SDS). At this step the grounded tissue was not allowed to thaw.

3. The contents were mixed well and incubated at 65 °C for 10 min with intermittent shaking of the tubes for proper mixing of contents.
4. The contents were then cooled on ice for 10 min.
5. Potassium acetate (300 µl) was added and mixed thoroughly.
6. The contents were centrifuged for 20 min at 13000 rpm at 4°C.
7. About 600 µl of supernatant was transferred to fresh tube and remaining was discarded along with the tube.
8. About 600 µl of isopropanol-ammonium acetate mixture was added to supernatant to precipitate nucleic acids.
9. The contents were mixed thoroughly and centrifuged for 20 min at 13000 rpm to pellet the nucleic acids.
10. The supernatant was discarded and the pellet was washed with 70 per cent alcohol, tubes were inverted on blotting paper to dry the pellet (The supernatant should be carefully be drained to avoid damage/slippage at this step).
11. Pellet was dissolved in 200 µl of T₁₀E₁.
12. RNAase (5 µl) (10 mg/ml) was added to each tube. DNA was redissolved by tapping the pellet suspended in RNAase and incubated at room temperature (37 °C) for 30 min.
13. The DNA was precipitated by adding 1/10th volume of 3 M sodium acetate and 2.5 volume of absolute ethanol.
14. The contents were mixed gently and incubated at 4°C for 30 min.
15. The contents were centrifuged for 1 min at 3000 rpm.
16. Pellet was rinsed with 70 per cent ethanol twice and centrifuged at 3000 rpm for 1 min.
17. Supernatant was discarded and the tubes were put upside down on paper towel to get rid off excess ethanol (It is important, not to allow the DNA to over dry).

Pellet was dissolved in 100 µl of T₁₀E₁ buffer and stored in -20 °C for further use.

3.4.5.2 Purification and quantification of extracted genomic DNA

1. Equal volume (100 µl) of phenol: chloroform: isoamylalcohol (25:24:1) mixture was added to each tube and the contents were mixed by inverting in fume hood.
2. The contents were centrifuged at 2500 rpm for 10 min and supernatant was transferred to fresh tubes. Supernatant was removed with wide-bore tip (cut-off blue tip) to clean tube (supernatant should be clear).
3. Step 1 and 2 from above were repeated.
4. To the above supernatant, 10 µl of 3 M sodium acetate (1/10th volume of aqueous layer) and 2.5 volumes of chilled absolute ethanol was added, mixed gently and incubated at -20°C for 15-20 min.
5. The DNA was pooled in 1.5 ml eppendorf tubes using a glass hook, washed with 70 per cent alcohol and dried.
6. DNA was dissolved in 100 µl T₁₀E₁ buffer and kept at -20 °C for further use.
7. The ratio between the readings at 260 and 280 nm (OD 260/OD 280) was used as an estimate of the purity of the DNA samples. Pure preparations of DNA should have 260/ 280 nm OD ratio ranging between 1.7 and 1.8 (Sambrook and Russel, 2001). Computed OD values were used to dilute the DNA samples to the working concentrations of 5ng/µl. The stock DNA solutions were diluted to 5 ng/µl of 100 ng/µl working solution for PCR. Then the amount of stock DNA solution to be taken for dilution was calculated using the formula,

$$M_1V_1 = M_2V_2$$

$$(100 \text{ ng/}\mu\text{l})V_1 = (5 \text{ ng/}\mu\text{l}) (100 \mu\text{l})$$

$$V_1 = (5 \text{ ng/}\mu\text{l}) (100 \mu\text{l}) / (100 \text{ ng/}\mu\text{l})$$

$$V_1 = 5 \mu\text{l}$$

Where, M_1 is the stock DNA concentration (for example, 100 ng/ μ l), V_1 is the volume of stock to be diluted, M_2 is the concentration of working solution (5 ng/ μ l) and V_2 is the volume of working solution to be prepared (for example, 100 μ l).

Then, the appropriate volume from the stock was transferred to 0.5 ml micro centrifuge tube and the volume was made to 100 μ l using distilled water. The DNA working solutions were stored at -20 °C for further use.

3.4.5.3 Screening of DNA markers

Total 40 SSR markers linked to tomato, were screened across the 260 tomato mini-core accessions (Appendix VIII).

3.4.5.4 The general PCR reaction mixture and concentration of components

Component	Quantity (μ l/reaction)
Genomic DNA (100 ng/ μ l)	1.0
Forward primer (5 pM/ μ l)	0.5
Reverse primer (5 pM/ μ l)	0.5
Taq 2x master mix	3.0
Sterile water	5.0

PCR reaction was carried out using Master Cycler gradient 5331 (Eppendorf version 2.30.31-09, Germany). The cycler was programmed as follows;

Step	Temperature	Duration	No. of cycle
Initial denaturation temperature	: 94.0 °C	: 4 min.	1
Denaturation	: 94.0 °C	: 1 min.	35
Primer annealing	: 55-58 °C	: 1 min.	
Primer extension	: 72.0 °C	: 1 min.	
Complete primer extension	: 72.0 °C	: 10 min	1
Storage	: 4.0 °C	: up to removed	1

3.4.5.5 Agarose gel electrophoresis

The protocol was followed as explained in 3.2.5

3.4.6 Statistical analysis

3.4.6.1 Analysis of variance (ANOVA)

Augmented Block Design introduced by Federer and Raghav Rao (1975) was used for field evaluation of 260 genotypes with 3 checks distributed in 13 blocks. The quantitative data consisting of different biochemical, biophysical and whitefly population data were subjected to Analysis of Variance (ANOVA), where the source of variation was divided into Block (ignoring treatments), Genotypes + Checks (Eliminating blocks), Checks, Checks + Gen vs. Gen, Error, Blocks (eliminating check + Genotypes), Entries (Ignoring Blocks), Genotypes, Check vs Genotypes. The analysis of Variance (ANOVA) was carried out with the help of a software Windowstat (version 8.2). The structure of analysis of variance (ANOVA) in augmented design is presented below:

ANOVA

Source of variation	Degrees of freedom	Sum of Square	Mean Sum of Square	F-ratio
Blocks	r-1	BSS	BMS	BMS/ERMS
Entries (e)	e-1	eSS	Ems	eMS/ErMS
Checks (c)	c-1	cSS	cMS	cMS/ErMS
Genotypes (g)	n-1	gSS	gMS	gMS-ErMS
Check vs genotype	1	cgSS	cgMS	cgMS/ErMS
Error	(c-1) (r-1)	ErSS	ErMS	
Total	N-1	TSS		

Where,

r = Number of blocks

e = Total number of entries

c = Number of checks

n = Total number of genotypes

N = Total number of blocks

The significance was tested by referring the table given by Snecedor (1946).

3.4.6.2 Descriptive statistics

The per cent of different types of each qualitative trait was calculated for 260 tomato accessions. Descriptive statistical parameters such as mean, range, standard error, standard deviation and sample variance for selected quantitative traits were calculated using the software Windowstat[®] (version 8.2)

3.4.6.3 Components of variance

The genotypic and phenotypic components of variance were computed according to formulae given by Lush (1940) and Chaudhary and Prasad (1968) for the observed characters.

$$\text{Genotypic variance (Vg)} = \frac{\text{Tr.M.S.S-E.M.S.S.}}{r}$$

E.M.S.S- Error variance (Ve)

r- Number of replications or blocks

The phenotypic variance was calculated by the following formula

$$\text{Phenotypic variance (Vp)} = \text{Vg} + \text{Ve}$$

3.4.6.4 Genetic variability and heritability parameters

Quantitative data for all biochemical and biophysical traits were also subjected to genetic variability component analysis such as, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and to know the extent of heritability of these traits to next generation, the heritability components such as h^2 (heritability) in broad sense and the Genetic advance as per cent mean (GAM) were estimated for each trait with the help of Windowstat (version 8.2) software and interpreted the results based on the following categorization as suggested by Shivasubramanian and Menon (1973).

$$\text{Genotypic coefficient of variability (GCV)} = \frac{\sqrt{V_g}}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variability (PCV)} = \frac{\sqrt{V_p}}{\bar{X}} \times 100$$

Where,

V_g = Genotypic variance

V_p = Phenotypic variance

$\bar{X}$ = General mean of character

The PCV and GCV values are ranked as low (0-10%), moderate (10-20%) and high (> 20%) (Shivasubramanian and Menon, 1973).

3.4.6.4.1 Heritability

Broad sense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson *et al.*, 1956).

$$h^2 = \frac{V_g}{V_p} \times 100$$

Where,

V_g = Genotypic variance

V_p = Phenotypic variance

Heritability values were categorized as low (0-30%), moderate (30-60%) and high (> 60%) (Robinson *et al.*, 1949).

3.4.6.5 Genetic advance

Genetic advance (GA) was computed according to the formula given by Johnson *et al.* (1955).

$$\text{Genetic advance (GA)} = ih^2\sqrt{V_p}$$

Where,

i = Selection differential (2.06) at 5 per cent selection intensity

h^2 = Broad sense heritability

$\sqrt{V_p}$ = Phenotypic standard deviation

3.4.6.6 Genetic advance as per cent of mean (GAM)

Genetic advance as per cent of mean (GAM) expressed in percentage was computed by using the following formula;

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = Mean of the population.

Genetic advance as per cent of mean was classified as low (0-10%), moderate (10-20%) and high (> 20%) (Johnson *et al.*, 1955).

3.4.6.7 Correlation studies between biophysical and biochemical traits

Simple correlation coefficients were worked out for different biochemical and biophysical parameters against whitefly population and per cent disease incidence (Panse and Sukhatme, 1967). Significance of correlation was tested by comparing with critical 'r' value which was obtained by using formula given below;

$$r = \frac{\sqrt{t^2}}{t^2 + n - 2}$$

Where,

r = Critical coefficient value

t = Table value at 5 or 1 per cent

n = Number of observations used for analysis.

3.4.7 Molecular analysis

The statistical analysis for molecular traits of tomato accessions were done as mentioned in 3.2.6

3.5 Association analysis of component traits of whitefly resistance in ton

Association analysis was done by using phenotypic data of diverse tomato minicore accessions, genotypic data of 40 SSR markers and population structure data (by structure analysis) by using software TASSEL (Bradbury *et al.* 2007). The marker-trait association analysis was conducted using TASSEL 3.0 software following the mixed linear model (MLM) in order to reduce false positive associations. To reduce false positive associations or spurious associations, the K+Q model (kinship matrix and genetic structure) was used to detect associations between the selected traits and 40 SSR markers. The mixed linear model (MLM) which takes the population structure into consideration was used for the analysis. Probability of $P < 0.005$ as the value to detect associations. Further, $P < 0.001$ was also observed to ascertain the significant value to reduce false positive associations. The marker associated with the trait was considered highly significant when the marker p value was showing >0.001 . The amount of phenotypic variation explained by each marker was estimated by R^2 .

4. EXPERIMENTAL RESULTS

Results of the present study on “Genetic diversity of whitefly, *Bemisia tabaci* (Genn.) (Hemiptera: Aleyrodidae) populations and molecular analysis for its resistant traits in tomato (*Solanum lycopersicum* L.)” are presented in this chapter under different headings.

4.1 Plasticity of morphological traits' among whitefly populations in tomato ecosystems of Karnataka

The morphometric analysis of randomly selected 140 each male, female and puparia samples of whitefly were collected from different agroclimatic zones belonging to 11 districts of Karnataka. The different characters which were phenotyped with adults and puparia during the study are presented in the Tables 5 to 7 and Appendix II to IV. A set of 16 characters of males, 14 characters of females and 12 characters of puparia were measured under microscope in laboratory. The data obtained are analyzed by using relevant software and the findings are elaborated as under.

4.1.1 Morphometrics of *Bemisia tabaci* puparia from different locations

Among the 12 morphological characters analyzed, six characters were statistically non significant across populations. Remaining six characters were highly significant ($p \leq 0.001$) among different locations (Table 5).

Length of the puparia was significantly highest in Dharwad population (5.43 mm) followed by Bengaluru rural (5.31 mm), Shivamogga (5.25 mm) population and significantly lowest length was recorded from Bagalkot population (4.58 mm) which was statistically on par with Chamarajanagara population (4.65 mm) followed by Chikkamagaluru population (4.77 mm). Puparia breadth was significantly highest in Dharwad population (4.07 mm) which was statistically on par with the populations of Bengaluru rural (3.99 mm), Shivamogga (3.94 mm) and Chikkaballapura (3.89 mm). Significantly lowest breadth was recorded from Bagalkot population (3.42 mm) which was statistically on par with Chikkamagaluru population (3.46 mm) followed by Kolar (3.63 mm) populations.

Table 5. Morphometrics of *Bemisia tabaci* puparia on tomato from different agro climatic zones of Karnataka

Puparia Characters [#]	Measurements from different districts (mm) ^{##}											Mean± SE	C.D (0.05)	C.V (%)	Statistical significance
	DVN	HVR	DWD	BLV	CKBR	KLR	BR	BGK	CHA	CKM	SHI				
PL	4.90 (3.37-5.85)	4.96 (4.09-5.83)	5.43 (5.19-5.70)	5.08 (4.28-5.69)	5.18 (4.45-5.68)	4.92 (4.11-5.71)	5.31 (4.28-5.83)	4.58 (4.05-5.29)	4.65 (4.28-5.30)	4.77 (4.32-5.25)	5.25 (4.84-5.75)	5.00±0.04	0.11	1.78	< 0.001
PB	3.77 (3.12-4.53)	3.79 (2.79-4.65)	4.07 (3.72-4.49)	3.76 (2.64-4.25)	3.89 (2.98-4.40)	3.63 (3.00-4.35)	3.99 (2.88-4.35)	3.42 (2.90-4.15)	3.63 (2.87-5.46)	3.46 (2.56-4.13)	3.94 (3.31-4.49)	3.76±0.08	0.22	4.53	< 0.001
DVOAE	4.21 (3.66-4.87)	4.14 (3.50-4.89)	4.46 (4.28-4.69)	4.21 (3.51-4.79)	4.29 (3.66-4.68)	4.05 (3.44-4.66)	4.37 (3.55-4.87)	3.72 (3.01-4.38)	3.76 (3.16-4.79)	3.68 (2.21-4.87)	4.35 (3.98-4.73)	4.11±0.03	0.10	1.88	< 0.001
DTMSAE	2.12 (1.74-2.52)	2.14 (1.51-2.53)	2.43 (1.95-3.22)	2.19 (1.86-2.45)	2.24 (1.80-3.10)	2.07 (1.03-2.48)	2.21 (1.79-2.60)	1.87 (1.01-2.30)	1.95 (1.69-2.38)	2.29 (1.74-4.35)	2.22 (1.98-2.45)	2.16±0.03	0.08	2.96	< 0.001
LVO	0.51 (0.42-0.60)	0.50 (0.41-0.56)	0.56 (0.50-0.60)	0.52 (0.40-0.58)	0.52 (0.44-0.59)	0.47 (0.38-0.57)	0.52 (0.41-0.57)	0.48 (0.39-0.57)	0.46 (0.37-0.51)	0.50 (0.43-0.55)	0.53 (0.46-0.63)	0.51±0.03		13.64	NS
BVO	0.39 (0.34-0.42)	0.37 (0.32-0.43)	0.41 (0.38-0.43)	0.38 (0.32-0.42)	0.39 (0.33-0.43)	0.37 (0.31-0.42)	0.39 (0.32-0.43)	0.35 (0.32-0.39)	0.35 (0.31-0.40)	0.38 (0.31-0.42)	0.37 (0.31-0.40)	0.38±0.02		9.02	NS
LL	0.18 (0.13-0.23)	0.18 (0.14-0.22)	0.19 (0.16-0.23)	0.18 (0.13-0.27)	0.18 (0.11-0.22)	0.17 (0.14-0.23)	0.17 (0.11-0.22)	0.16 (0.11-0.20)	0.16 (0.11-0.21)	0.17 (0.11-0.21)	0.20 (0.16-0.24)	0.18±0.00	0.01	6.13	< 0.001
LO	0.23 (0.18-0.27)	0.23 (0.18-0.27)	0.24 (0.21-0.26)	0.23 (0.20-0.28)	0.22 (0.16-0.26)	0.22 (0.18-0.25)	0.24 (0.17-0.27)	0.21 (0.11-0.26)	0.21 (0.15-0.25)	0.22 (0.17-0.28)	0.23 (0.17-0.30)	0.23±0.01		10.40	NS
BO	0.31 (0.25-0.34)	0.31 (0.26-0.34)	0.32 (0.31-0.34)	0.30 (0.23-0.33)	0.31 (0.24-0.38)	0.28 (0.19-0.34)	0.31 (0.25-0.35)	0.28 (0.24-0.32)	0.28 (0.23-0.36)	0.29 (0.25-0.33)	0.31 (0.26-0.43)	0.30±0.02		12.82	NS
LCF	0.36 (0.25-0.46)	0.34 (0.21-0.42)	0.41 (0.38-0.45)	0.37 (0.30-0.45)	0.37 (0.32-0.43)	0.35 (0.26-0.46)	0.40 (0.32-0.46)	0.33 (0.24-0.42)	0.39 (0.30-0.46)	0.35 (0.27-0.41)	0.37 (0.28-0.44)	0.37±0.02	0.04	9.54	< 0.001
LCS	0.57 (0.40-0.74)	0.61 (0.47-0.69)	0.56 (0.45-0.72)	0.54 (0.42-0.63)	0.50 (0.43-0.63)	0.59 (0.48-0.79)	0.54 (0.42-0.70)	0.49 (0.36-0.68)	0.53 (0.44-0.66)	0.54 (0.43-0.67)	0.53 (0.42-0.67)	0.55±0.03		14.35	NS
DCS	0.28 (0.23-0.41)	0.26 (0.20-0.36)	0.26 (0.20-0.30)	0.25 (0.18-0.31)	0.26 (0.20-0.30)	0.25 (0.17-0.29)	0.25 (0.22-0.28)	0.24 (0.17-0.28)	0.24 (0.20-0.27)	0.24 (0.18-0.31)	0.27 (0.21-0.31)	0.25±0.01		12.72	NS

For expansion of the row abbreviations, refer Appendix I.
Figures in the parenthesis are range values

For column abbreviations, refer Appendix II
NS p > 0.001

Distance of vasiform orifice from anterior end (DVOAE) was recorded highest in Dharwad population (4.46 mm) which was statistically on par with Bengaluru rural (4.37 mm) followed by Shivamogga population (4.35 mm) and significantly lowest DVOAE was recorded from Chikkamagaluru population (3.68 mm) which was statistically on par with Bagalkot (3.72 mm) and Chamarajanagara population (3.76 mm).

Distance of transverse moulting suture from anterior end (DTMSAE) was significantly highest in Dharwad population (2.43 mm) followed by Chikkamagaluru and Chikkaballapura populations (2.29 mm), respectively. Significantly lowest DTMSAE was recorded from Bagalkot population (1.87 mm) which was statistically on par with Chamarajanagara (1.95 mm) followed by Kolar population (2.07 mm).

Length of lingula was significantly highest in Shivamogga population (0.20 mm) which was statistically on par with Dharwad population (0.19 mm), followed by Davanagere population (0.18 mm) and significantly lowest length was recorded from Chamarajanagara population (0.16 mm) which was statistically on par with Bagalkot, Bengaluru rural, Kolar and Chikkamagaluru populations.

Length of caudal furrow was significantly highest in Dharwad population (0.41 mm) which was statistically on par with Bengaluru rural (0.40 mm) and Chamarajanagara (0.39 mm) populations. Significantly lowest length was recorded from Bagalkot population (0.33 mm) which was statistically on par with Haveri (0.34 mm), Kolar (0.35 mm) and Chikkamagaluru (0.35 mm) populations.

Length of vasiform orifice ranged from 0.46 mm (Chamarajanagara) to 0.56 mm (Dharwad) with the mean value of 0.51 mm. The breadth of vasiform orifice was ranged from 0.35 mm (Chamarajanagara and Bagalkot) to 0.41 mm (Dharwad) with the mean of 0.38 mm. Length of operculum ranged between 0.21 mm (Bagalkot and Chamarajanagara) and 0.24 mm (Bengaluru rural and Dharwad) with the mean value of 0.23 mm. The breadth of operculum ranged between 0.28 mm (Kolar, Chamarajanagara and Bagalkot) to 0.32 mm (Dharwad) with the mean of 0.30 mm. Length of caudal setae ranged from 0.49 mm (Bagalkot) to 0.61 mm (Haveri) with the mean value of 0.55 mm. Distance between caudal setae ranged from 0.24 mm (Bagalkot, Chikkamagaluru and Chamarajanagara) to 0.28 mm (Davanagere) with the

mean of 0.25 mm. All these six characters were found non significant among the different populations.

4.1.2 Morphometrics of *B. tabaci* adult males from different locations

Among the 16 morphological characters analyzed, four characters showed statistically non significant result. Remaining 12 characters were highly significant ($p \leq 0.001$) across different locations (Table 6) and found to be very helpful in differentiating the populations of *B. tabaci* from different locations.

4.1.2.1 Wing morphometry

Fore wing length was significantly highest in Chikkaballapura population (5.94 mm) followed by Chikkamagaluru (5.75 mm) population and significantly lowest length was recorded from Belagavi population (5.31 mm) which was statistically on par with Dharwad (5.32 mm), Bengaluru rural (5.41 mm), Haveri (5.41 mm) and Kolar (5.44 mm) populations. Fore wing width was recorded significantly highest from Chikkamagaluru (2.37 mm) population which was statistically on par with the populations of Chikkaballapura (2.31 mm), Shivamogga (2.18 mm) and Chamarajanagara (2.10 mm). Significantly lowest width was recorded from Kolar (1.67 mm) population followed by Belagavi (1.79 mm), Dharwad (1.86 mm) and Haveri (1.88 mm) populations.

Fore wing vein length of (FWVL) was significantly highest in Chikkaballapura population (5.01 mm) followed by Chikkamagaluru (4.74 mm) and Shivamogga (4.70 mm) population and significantly lowest FWVL was recorded from Dharwad population (3.55 mm) followed by Bengaluru rural population (4.36 mm).

Hind wing length was significantly highest in Chikkaballapura population (5.23 mm) followed by Bagalkot (5.11 mm) and Belagavi (5.07 mm) populations. Significantly lowest length was recorded from Haveri population (4.72 mm) which was statistically on par with Shivamogga (4.72 mm), Bengaluru rural (4.75 mm), Dharwad (4.78 mm) and Kolar (54.81 mm) populations. Hind wing width was

Table 6. Morphometrics of *Bemisia tabaci* males on tomato from different agro climatic zones of Karnataka

Male Characters [#]	Measurements from different districts (mm) ^{##}											Mean± SE	C.D (0.05)	C.V (%)	Statistical significance
	DVN	HVR	DWD	BLV	CKBR	KLR	BR	BGK	CHA	CKM	SHI				
FWL	5.65 (5.21-6.06)	5.41 (4.93-5.90)	5.32 (4.88-5.75)	5.31 (4.95-5.77)	5.94 (5.35-6.70)	5.44 (4.64-5.87)	5.41 (4.72-5.93)	5.64 (5.24-6.08)	5.63 (5.11-6.07)	5.75 (5.34-6.32)	5.60 (5.32-6.00)	5.55±0.05	0.15	2.07	< 0.001
FWW	2.02 (1.75-2.50)	1.88 (1.43-2.32)	1.86 (1.65-2.08)	1.79 (1.63-1.97)	2.31 (2.13-2.62)	1.67 (1.43-1.83)	1.91 (1.65-2.26)	2.02 (1.81-2.35)	2.10 (1.66-2.38)	2.37 (1.98-2.63)	2.18 (1.95-2.62)	2.01±0.10	0.27	10.73	< 0.001
LFWV	4.50 (4.10-4.79)	4.42 (4.14-4.84)	3.55 (3.29-3.91)	4.07 (3.54-4.59)	5.01 (4.54-5.25)	4.05 (3.55-4.46)	4.03 (3.36-4.49)	4.51 (4.19-4.78)	4.59 (4.10-5.12)	4.74 (4.31-5.39)	4.70 (4.39-5.12)	4.38±0.07	0.19	3.34	< 0.001
LHW	4.98 (4.61-5.55)	4.72 (4.28-5.24)	4.78 (4.37-5.17)	5.07 (4.80-5.41)	5.23 (4.73-6.13)	4.81 (4.46-5.25)	4.75 (4.05-5.32)	5.11 (4.70-5.48)	4.93 (4.21-5.41)	5.04 (4.59-5.56)	4.72 (4.53-5.32)	4.92±0.04	0.10	1.64	< 0.001
WHW	1.74 (1.51-1.90)	1.70 (1.44-1.99)	1.68 (1.55-1.91)	1.76 (1.66-1.91)	1.97 (1.82-2.18)	1.56 (1.32-1.99)	1.61 (1.39-1.90)	1.97 (1.82-2.11)	1.95 (1.59-2.29)	1.93 (1.73-2.09)	2.04 (1.86-2.27)	1.81±0.08	0.24	10.21	< 0.001
LFFe	1.07 (0.85-1.21)	1.00 (0.82-1.16)	1.02 (0.91-1.16)	1.05 (0.89-1.18)	0.92 (0.71-1.19)	0.99 (0.82-1.16)	1.12 (1.02-1.27)	1.13 (0.94-1.23)	1.07 (0.86-1.26)	1.12 (1.02-1.24)	1.02 (0.90-1.13)	1.05±0.05		10.42	NS
LFTi	1.21 (1.02-1.40)	1.21 (1.05-1.34)	1.33 (1.20-1.50)	1.22 (1.03-1.44)	1.12 (0.92-1.43)	1.16 (0.91-1.39)	1.54 (1.42-1.66)	1.33 (1.13-1.56)	1.32 (1.15-1.46)	1.36 (1.26-1.51)	1.26 (1.03-1.41)	1.28±0.04	0.12	7.15	< 0.001
LFTa	0.97 (0.73-1.13)	0.92 (0.73-1.07)	0.95 (0.89-1.01)	0.94 (0.77-1.08)	0.86 (0.69-1.18)	0.90 (0.60-1.12)	0.98 (0.77-1.19)	1.07 (0.87-1.19)	0.92 (0.73-1.04)	0.93 (0.81-1.06)	0.89 (0.68-1.06)	0.94±0.05		10.92	NS
LHFe	1.22 (1.03-1.37)	1.15 (0.95-1.26)	1.18 (1.03-1.32)	1.12 (0.91-1.34)	1.09 (1.02-1.18)	1.10 (0.96-1.22)	1.26 (1.14-1.56)	1.17 (1.04-1.34)	1.15 (0.95-1.30)	1.14 (1.08-1.22)	1.28 (1.04-1.61)	1.17±0.04	0.12	8.07	< 0.001
LHTi	2.20 (1.94-2.44)	2.00 (1.81-2.19)	1.90 (1.80-1.98)	1.77 (1.54-2.05)	1.54 (1.12-2.50)	1.76 (1.23-2.09)	1.90 (1.45-2.45)	2.09 (1.92-2.40)	1.78 (1.21-2.32)	2.20 (2.07-2.37)	2.34 (1.94-2.64)	1.95±0.03	0.10	3.98	< 0.001
LHTa	1.08 (0.87-1.19)	1.00 (0.82-1.09)	0.99 (0.92-1.04)	0.93 (0.75-1.02)	0.99 (0.93-1.06)	0.99 (0.83-1.17)	0.96 (0.81-1.08)	1.02 (0.92-1.13)	1.00 (0.83-1.12)	1.03 (0.92-1.17)	1.20 (1.02-1.36)	1.02±0.05	0.14	11.17	< 0.001
LA	1.25 (0.96-1.43)	1.18 (1.10-1.32)	1.14 (1.05-1.27)	1.20 (1.11-1.27)	1.97 (1.86-2.11)	1.19 (1.08-1.29)	0.90 (0.74-1.11)	1.31 (1.22-1.41)	1.08 (0.95-1.21)	1.24 (1.13-1.42)	1.49 (1.43-1.55)	1.27±0.04	0.10	6.20	< 0.001
LP	1.63 (1.42-2.08)	1.70 (1.39-1.98)	1.91 (1.75-2.08)	1.82 (1.40-2.03)	1.88 (1.47-2.15)	1.27 (1.08-1.62)	1.44 (1.18-1.59)	2.32 (2.11-2.71)	1.41 (1.22-1.65)	1.61 (1.44-1.73)	1.62 (1.49-1.74)	1.69±0.04	0.11	5.12	< 0.001
LAB	2.33 (1.98-2.63)	2.24 (1.94-2.56)	2.51 (2.43-2.60)	2.73 (2.43-2.89)	2.85 (2.72-2.98)	1.95 (1.75-2.14)	2.17 (1.92-2.33)	2.77 (2.45-3.05)	2.22 (1.93-2.65)	2.16 (2.05-2.38)	2.52 (2.37-2.77)	2.40±0.05	0.15	4.81	< 0.001
LLAb	0.34 (0.31-0.36)	0.32 (0.30-0.34)	0.32 (0.31-0.34)	0.33 (0.30-0.35)	0.34 (0.31-0.37)	0.30 (0.27-0.35)	0.31 (0.28-0.34)	0.34 (0.31-0.35)	0.31 (0.28-0.36)	0.32 (0.29-0.37)	0.32 (0.29-0.35)	0.32±0.03		17.91	NS
LC	0.53 (0.50-0.55)	0.51 (0.49-0.52)	0.51 (0.50-0.53)	0.52 (0.49-0.54)	0.53 (0.51-0.55)	0.48 (0.46-0.50)	0.48 (0.45-0.51)	0.52 (0.51-0.53)	0.49 (0.47-0.51)	0.50 (0.48-0.52)	0.50 (0.49-0.52)	0.51±0.01		5.97	NS

For expansion of the row abbreviations, refer Appendix I.

Figures in the parenthesis are range values

For column abbreviations, refer Appendix III

NS p > 0.001

significantly highest in Shivamogga population (2.04 mm) which was statistically on par with Bagalkot (1.97 mm), Chikkaballapura (1.97 mm), Chamarajanagara (1.95 mm) and Chikkamagaluru (1.93 mm) populations and significantly lowest width was recorded from Kolar population (1.56 mm) which was statistically on par with Bengaluru rural (1.61 mm), Dharwad (1.68 mm) and Haveri (1.70 mm) population.

4.1.2.2 Leg morphometry

Fore femur length of male *B. tabaci* ranged from 0.92 mm (Chikaballapura) to 1.13 mm (Bagalkot) with mean of 1.05 mm. Also length of fore tarsi was ranged from 0.86 mm (Chikaballapura) to 1.07 mm (Bagalkot) with mean of 0.94 mm but, these two characters were found non significant among the different populations.

Fore tibial length (FTL) was significantly highest in Bengaluru rural (1.54 mm) population followed by Chikkamagaluru (1.36 mm), Bagalkot (1.33 mm), Dharwad (1.33 mm) and Chamarajanagara (1.32 mm) population. Significantly lowest FTL was recorded from Chikkaballapura population (1.12 mm) which statistically on par with Kolar (1.16 mm), Davanagere (1.21 mm), Haveri (1.21 mm) and Belagavi (1.22 mm) populations.

Hind femur length (HFeL) was significantly highest in Shivamogga population (1.28 mm) which was statistically on par with Bengaluru rural, Davanagere, Dharwad and Bagalkot populations. The significantly lowest length was recorded from Chikkaballapura (1.26 mm) population which was statistically on par with Kolar, Belagavi, Chikkamagaluru, Haveri and Chamarajanagara populations. The hind tibial length (HTiL) was significantly highest in Shivamogga population (2.34 mm) followed by Davanagere and Chikkamagaluru populations. The significantly lowest HTiL was recorded from Chikkaballapura population (1.54 mm) followed by Kolar, Belagavi and Chamarajanagara populations. Hind tarsal length was significantly highest in Shivamogga population (1.20 mm) which was statistically on par with Davanagere population and the least significant length was recorded from Belagavi population (0.93 mm) which was statistically on par with Bengaluru rural, Chikkaballapura, Dharwad, Kolar, Haveri and Chamarajanagara populations.

4.1.2.3 Antennal morphometry

Length of the antenna was significantly highest in Chikkaballapura population (1.97 mm) followed by Shivamogga (1.49 mm) and Bagalkot (1.31 mm) populations. The significantly lowest length was recorded from Bengaluru rural population (0.90 mm) followed by Chamarajanagara (1.08 mm) and Dharwad (1.14 mm) population.

4.1.2.4 Proboscis morphometry

Length of the proboscis was significantly highest in Bagalkot population (2.32 mm) followed by Dharwad (1.91 mm), Chikkaballapura (1.88 mm) and Belagavi (1.82 mm) populations. Significantly lowest proboscis length was recorded from Kolar population (1.27 mm) followed by Chamarajanagara (1.41 mm), Bengaluru rural (1.44 mm) and Chikkamagaluru (1.61 mm) populations.

4.1.2.5 Abdominal traits morphometry

Abdomen length was significantly highest in Chikkaballapura population (2.85 mm) which was statistically on par with Bagalkot (2.77 mm), Belagavi (2.73 mm) populations followed by Shivamogga (2.52 mm) population and significantly lowest abdominal length was recorded from Kolar (1.95 mm) population followed by Chikkamagaluru (2.16 mm) and Bengaluru rural (2.17 mm) populations.

Length of last abdominal segment ranged from 0.30 mm (Kolar) to 0.34 mm (Chikaballapura, Davanagere and Bagalkot population) with the mean value of 0.32 mm. The length of claspers ranged between 0.48 mm (Kolar and Bengaluru rural) to 0.53 mm (Chikaballapura and Davanagere) with the mean of 0.51 mm. Both the characters were found non significant among the different populations.

4.1.3 Morphometrics of female *Bemisia tabaci* from different locations

All the 14 morphological characters analyzed were statistically highly significant ($p \leq 0.001$) across different locations (Table 7) and found to be very helpful in differentiating the populations of *B. tabaci* from different locations.

Table 7. Morphometrics of *Bemisia tabaci* females on tomato from different agro climatic zones of Karnataka

Female Characters [#]	Measurements from different districts (mm) ^{##}											Mean± SE	C.D (0.05)	C.V %	Statistical significance
	DVN	HVR	DWD	BLV	CKBR	KLR	BR	BGK	CHA	CKM	SHI				
FWL	6.04 (5.59-6.45)	5.98 (5.50-6.47)	6.11 (5.67-6.55)	6.03 (5.67-6.50)	6.68 (6.09-7.44)	6.04 (5.25-6.47)	5.66 (4.98-6.18)	5.99 (5.59-6.43)	5.83 (5.31-6.27)	6.30 (5.90-6.87)	6.15 (5.87-6.55)	6.07±0.05	0.15	1.89	< 0.001
FWW	2.41 (2.15-2.90)	2.35 (1.90-2.79)	2.27 (2.06-2.49)	2.21 (2.06-2.40)	2.59 (2.41-2.90)	2.23 (1.99-2.38)	2.23 (1.97-2.57)	2.26 (2.06-2.60)	2.41 (1.98-2.70)	2.73 (2.34-2.99)	2.40 (2.16-2.84)	2.37±0.10	0.27	9.08	< 0.001
LFWV	4.97 (4.57-5.27)	4.95 (4.66-5.37)	3.91 (3.65-4.27)	4.36 (3.83-4.88)	5.86 (5.08-8.79)	4.61 (4.11-5.03)	4.43 (3.76-4.89)	4.71 (4.38-4.97)	4.75 (4.25-5.27)	5.22 (4.79-5.86)	5.15 (4.84-5.57)	4.81±0.07	0.19	3.04	< 0.001
LHW	5.34 (4.97-5.91)	5.32 (4.88-5.84)	5.49 (5.08-5.87)	5.44 (5.17-5.78)	5.79 (5.29-6.69)	5.22 (4.87-5.67)	4.89 (4.19-5.46)	5.40 (4.99-5.77)	5.08 (4.37-5.57)	5.62 (5.17-6.14)	5.33 (5.14-5.93)	5.36±0.04	0.10	1.51	< 0.001
WHW	2.14 (1.91-2.30)	2.09 (1.83-2.38)	2.14 (2.02-2.37)	2.13 (2.03-2.28)	2.25 (2.10-2.46)	1.91 (1.67-2.34)	1.88 (1.65-2.16)	2.18 (2.03-2.32)	2.13 (1.77-2.48)	2.15 (1.95-2.31)	2.25 (2.07-2.49)	2.11±0.08	0.24	8.75	< 0.001
LFFe	1.15 (0.93-1.29)	1.11 (0.94-1.28)	1.32 (1.21-1.47)	1.24 (1.08-1.36)	1.02 (0.74-1.31)	1.10 (0.92-1.27)	1.33 (1.24-1.48)	1.24 (1.05-1.34)	1.29 (1.07-1.47)	1.27 (1.16-1.39)	1.28 (1.16-1.39)	1.21±0.05	0.14	8.99	< 0.001
LFTi	1.38 (1.20-1.58)	1.33 (1.18-1.46)	1.59 (1.47-1.77)	1.47 (1.28-1.69)	1.25 (0.97-1.58)	1.32 (1.07-1.55)	1.75 (1.63-1.88)	1.45 (1.26-1.69)	1.55 (1.37-1.68)	1.51 (1.41-1.66)	1.57 (1.34-1.72)	1.47±0.04	0.12	6.21	< 0.001
LFTa	1.06 (0.82-1.22)	1.01 (0.83-1.17)	1.13 (1.07-1.18)	1.13 (0.96-1.27)	0.95 (0.72-1.28)	0.97 (0.67-1.18)	1.18 (0.96-1.38)	1.15 (0.96-1.27)	1.15 (0.96-1.27)	1.09 (0.96-1.22)	1.10 (0.89-1.27)	1.08±0.05	0.13	9.45	< 0.001
LHFe	1.35 (1.16-1.50)	1.26 (1.06-1.37)	1.46 (1.31-1.60)	1.37 (1.16-1.59)	1.30 (1.24-1.39)	1.26 (1.12-1.38)	1.48 (1.36-1.77)	1.32 (1.19-1.49)	1.38 (1.17-1.67)	1.42 (1.36-1.50)	1.50 (1.25-1.83)	1.37±0.04	0.12	6.87	< 0.001
LHTi	2.43 (2.17-2.67)	2.36 (2.17-2.55)	2.11 (2.01-2.18)	2.20 (1.96-2.48)	1.88 (1.47-2.85)	1.93 (1.40-2.26)	2.13 (0.22-2.69)	2.34 (2.17-2.66)	1.92 (1.35-2.46)	2.49 (2.37-2.67)	2.56 (2.16-2.86)	2.21±0.03	0.10	3.51	< 0.001
LHTa	1.22 (1.02-1.34)	1.16 (0.98-1.25)	1.25 (1.17-1.29)	1.20 (1.03-1.30)	1.22 (1.16-1.30)	1.17 (1.00-1.35)	1.23 (1.08-1.35)	1.19 (1.08-1.29)	1.24 (1.04-1.49)	1.35 (1.24-1.49)	1.54 (1.36-1.70)	1.25±0.05	0.13	9.15	< 0.001
LA	1.30 (1.01-1.49)	1.30 (1.21-1.43)	1.25 (1.16-1.38)	1.32 (1.22-1.38)	2.13 (2.01-2.27)	1.25 (1.14-1.35)	0.98 (0.81-1.18)	1.36 (1.27-1.47)	1.19 (1.06-1.33)	1.39 (1.27-1.56)	1.55 (1.48-1.61)	1.37±0.04	0.10	5.76	< 0.001
LP	1.77 (1.58-2.24)	1.98 (1.67-2.26)	2.21 (2.05-2.38)	2.17 (1.76-2.38)	2.12 (1.71-2.39)	1.52 (1.32-1.86)	1.70 (1.44-1.85)	2.38 (2.17-2.77)	1.54 (1.35-1.78)	1.80 (1.63-1.92)	1.68 (1.55-1.80)	1.90±0.04	0.11	4.56	< 0.001
Lab	2.70 (2.35-3.00)	2.58 (2.28-2.89)	3.13 (3.05-3.21)	3.20 (2.90-3.36)	3.23 (3.10-3.37)	2.36 (2.16-2.55)	2.50 (2.25-2.65)	3.09 (2.77-3.37)	2.45 (2.16-2.88)	2.38 (2.26-2.60)	2.87 (2.55-3.14)	2.77±0.05	0.15	4.18	< 0.001

For expansion of the row abbreviations, refer Appendix I.
Figures in the parenthesis are range values

For column abbreviations, refer Appendix IV
NS p > 0.001

4.1.3.1 Wing morphometry

Fore wing length was recorded significantly highest in Chikkaballapura population (6.68mm) followed by Chikkamagaluru (6.30 mm) and Shivamogga (6.15 mm) populations. Significantly lowest length was recorded from Bengaluru rural population (5.66 mm) followed by Chamarajanagara (5.83 mm), Haveri (5.98 mm) and Bagalkot (5.99) populations but were not statistically on par with each other. Fore wing width was significantly highest from Bengaluru rural (5.66 mm) which was on par with Chikkaballapura population (2.59 mm). Significantly least width was recorded from Belagavi population (2.21mm) which was on par with Bengaluru rural (2.23 mm), Kolar (2.23 mm), Bagalkot (2.26 mm) and Dharwad (2.27 mm) populations.

Fore wing vein length (FWVL) was significantly highest in Chikkaballapura population (5.86 mm) followed by Chikkamagaluru (5.22 mm) population and significantly least FWVL was recorded from Dharwad population (3.91 mm) followed by Belagavi population (4.36 mm).

Hind wing length was significantly highest in Chikkaballapura population (5.97 mm) followed by Chikkamagaluru (5.62 mm) and Dharwad (5.49 mm) populations. Significantly lowest length was recorded from Bengaluru rural population (4.89 mm) followed by Chamarajanagara (5.08 mm) and Kolar (5.22 mm) populations. Hind wing width was significantly highest from Shivamogga (2.25 mm) which was on par with Chikkaballapura (2.25 mm), Bagalkot (2.18 mm) and Chamarajanagara (2.13 mm) populations and significantly least width was recorded from Bengaluru rural (1.88 mm) population which was on par with Kolar (1.91 mm) population.

4.1.3.2 Leg morphometry

Fore femur length was significantly highest in Bengaluru rural population (1.33 mm) which was on par with Dharwad, Chamarajanagara, Shivamogga, Chikkamagaluru, Bagalkot and Belagavi populations. Significantly lowest length was recorded from Chikkaballapura population (1.02 mm) which was on par with Kolar, Haveri and Davanagere populations. The overall mean of fore femur length was 1.12

mm. The fore tibial length was significantly highest in Bengaluru rural (1.75 mm) population followed by Dharwad population. The least was recorded from Chikkaballapura population (1.25 mm) which was on par with Kolar and Haveri populations. Fore tarsal length was significantly highest in Bengaluru rural population (1.18 mm) which was on par with Chamarajanagara, Bagalkot, Dharwad, Belagavi, Shivamogga and Chikkamagaluru populations and significantly lowest length was recorded from Chikkaballapura population (0.95 mm) which was on par with Kolar and Haveri populations.

Hind femur length was significantly highest in Shivamogga population (1.50 mm) which was on par with Bengaluru rural and Dharwad populations. The significantly lowest length was recorded from Haveri (1.26 mm) population which was on par with Kolar, Chikkaballapura and Bagalkot populations. The hind tibial length was significantly highest in Shivamogga population (2.56 mm) which was statistically on par with Chikkamagaluru population. The significantly lowest length was recorded from Chikkaballapura population (1.88 mm) which was statistically on par with Chamarajanagara and Kolar populations. Significantly highest hind tarsal length was recorded from Shivamogga population (1.54 mm) followed by Chikkamagaluru and Dharwad populations and the least significant length was recorded from Haveri population (1.16 mm) which was statistically on par with Kolar, Bagalkot, Belagavi, Davanagere and Chikkaballapura populations.

4.1.3.3 Antennal morphometry

Length of the antenna was significantly highest in Chikkaballapura population (2.13 mm) followed by Shivamogga (1.55 mm), Chikkamagaluru (1.39 mm) and Bagalkot (1.36 mm) populations. The significantly lowest length was recorded from Bengaluru rural (0.98 mm) followed by Chamarajanagara (1.19 mm) population.

4.1.3.4 Proboscis morphometry

Proboscis length was significantly highest in Bagalkot population (2.38 mm) followed by Dharwad (2.21 mm), Belagavi (2.17 mm) and Chikkaballapura (2.12 mm) populations. Significantly lowest proboscis length was recorded from Kolar population (1.52 mm) which statistically on par with Chamarajanagara population (1.54 mm) followed by Shivamogga population (1.68 mm).

4.1.3.5 Abdominal trait morphometry

Abdomen length was significantly highest in Chikkaballapura population (3.23 mm) which was statistically on par with Belagavi (3.20 mm), Dharwad (3.13 mm) and Bagalkot (3.09 mm) populations and significantly lowest abdominal length was recorded from Kolar (2.36 mm) population which was statistically on par with Chikkamagaluru (2.38 mm), Chamarajanagara (2.45 mm) and Bengaluru rural (2.50 mm) populations.

4.1.4 Cluster analysis for *B. tabaci* adult (male and female) population

Cluster analysis was performed using software using Past 3.x software package for all quantitative features based on different morphological characters of adult *B. tabaci* (both male and female) populations collected from different agro climatic zones of Karnataka revealed the existence of two major clusters-Cluster 1 and Cluster 2 (Fig. 2). Cluster 1 consisted of single population from Chikkaballapura separate from other populations. Cluster 2 was further divided into two major sub clusters (Cl 2a and Cl 2b). Sub-cluster Cl 2a consisted of populations from Belagavi and Dharwad. On the other hand, Cl 2a consist of Bagalkot population which was deviated from other Cl 2a populations. The sub cluster Cl 2b consists of seven populations from Shivamogga, Chikkamagaluru, Davanagere, Haveri, Chamarajanagara, Bengaluru rural and Kolar. Whereas, populations from Shivamogga, Chikkamagaluru, Davanagere, Haveri and Chamarajanagara are grouped in one hand and remaining two populations *i.e.* Bengaluru rural and Kolar were grouped into another clutch deviating from rest of the populations.

4.1.5 Principal component analysis (PCA) for the estimated variables of *Bemisia tabaci* adult (male and female) populations

The results of principal component analysis based on 30 morphological characters of adult (female and male) collected from tomato ecosystems of various agro climatic zones of Karnataka are presented in Table 8. The principal component analysis divided these 30 traits into three major principal components. The first principal component (PC1) accounts for maximum variability in the data with respect to succeeding components.

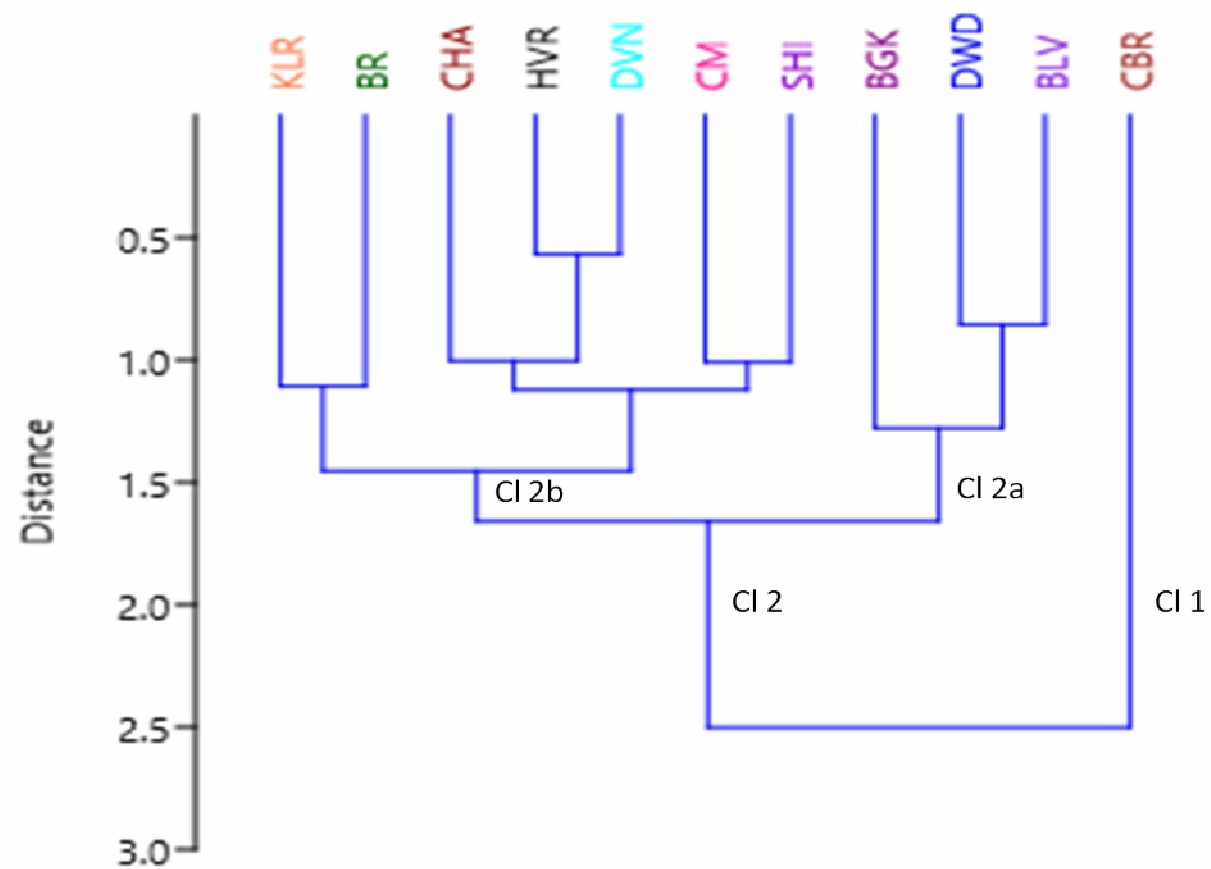


Fig 2. Cluster analysis for *Bemisia tabaci* adults (both male and female) from different agro climatic zones of Karnataka based on 30 quantitative characters

Table 8. Morphometrics of *Bemisia tabaci* adults (both male and female) based on 30 quantitative characters- proportion of contribution and variable coefficients of the first three eigenvectors for principal component analysis.

Characters*	Principal Component 1 (PC 1)	Principal Component 2 (PC 2)	Principal Component 3 (PC 3)
FWL¹	0.255	0.074	-0.150
FWW¹	0.137	-0.109	0.056
LFWV¹	0.541	-0.326	-0.052
LHW¹	0.210	0.163	-0.035
WHW¹	0.102	0.064	0.106
LFFe¹	-0.065	0.013	0.149
LFTi¹	-0.094	-0.007	0.171
LFTa¹	-0.045	0.025	0.115
LHFe¹	-0.024	0.001	0.113
LHTi¹	0.025	-0.035	0.532
LHTa¹	0.032	-0.044	0.152
LA¹	0.312	0.086	-0.170
LP¹	0.081	0.427	0.105
LAB¹	0.144	0.502	0.007
FWL²	0.197	-0.091	0.016
FWW²	0.194	-0.092	0.192
LFWV²	0.415	-0.272	0.171
LHW²	0.134	0.088	-0.059
WHW²	0.141	0.001	0.181
LFFe²	-0.030	-0.012	0.109
LFTi²	-0.069	-0.019	0.136
LFTa²	-0.023	0.032	0.073
LHFe²	-0.020	-0.016	0.105
LHTi²	-0.010	-0.093	0.536
LHTa²	0.027	-0.037	0.104
LA²	0.293	0.082	-0.139
LP²	0.118	0.380	0.246
LAB²	0.182	0.371	0.088
LLAB²	0.010	0.012	0.009
LC²	0.012	0.017	0.006
Proportion of variation (%)	50.383	25.283	10.761

* For expansion of the abbreviations, refer Appendix III and IV

¹Female characters

²Male characters

The scree plot analysis of the principal components (PC) (Fig. 3) considered totally ten principle components. The graph showed that, the first three eigen values correspond to most of the variances in the dataset. The major principal components were extracted, the total cumulative variance of these principal components amounted to 86.427 per cent variations. The principal component analysis grouped the estimated variables into three major groups, in which, PC1 accounted for 50.383 per cent, PC2 for 25.283 per cent, PC3 for 10.761 per cent of the total variation. Among the three principal components analyzed, PC1 which made the largest contribution of 50.383 per cent of the total variation, had shown highest positive contribution for female characters viz., fore wing length, fore wing vein length, hind wing length, length of antenna and male characters viz., fore wing length, fore wing width, fore wing vein length, length of antenna and length of abdomen. In case of PC2, highest positive contributions came from characters such as proboscis length and abdomen length in both male and female. In case of PC3, highest positive contributions came from characters such as hind tibial length in male and female and length of proboscis in male alone (Table 8).

The first two principal components contributing the major share of variances. In first and second principal components all the characters under consideration contributing diversity positively and up to second principal component 75.67 per cent diversities were observed. So, other principal components were not considered as major contributing principal components or they were already considered and measured in first two principal components.

4.1.6 Score plot of principal components for *B. tabaci* adults (both male and female) from different agro climatic zones of Karnataka

Scores for *B. tabaci* collected from different agro climatic zones of Karnataka, based on PC1 and PC2 are plotted in Fig. 4. The eleven districts were grouped into four major distinct clusters/ quarters. The distribution pattern revealed that, maximum number of entries (4) were included in quarter III, namely Bengaluru rural, Kolar, Chamarajanagara and Haveri whereas, quarter II, included Davanagere, Shivamogga and Chikkamagaluru. Quarter I shares two entries i.e. Bagalkot and Chikkaballapur whereas, quarter IV included entries viz., Dharwad and Belagavi (Fig. 4).

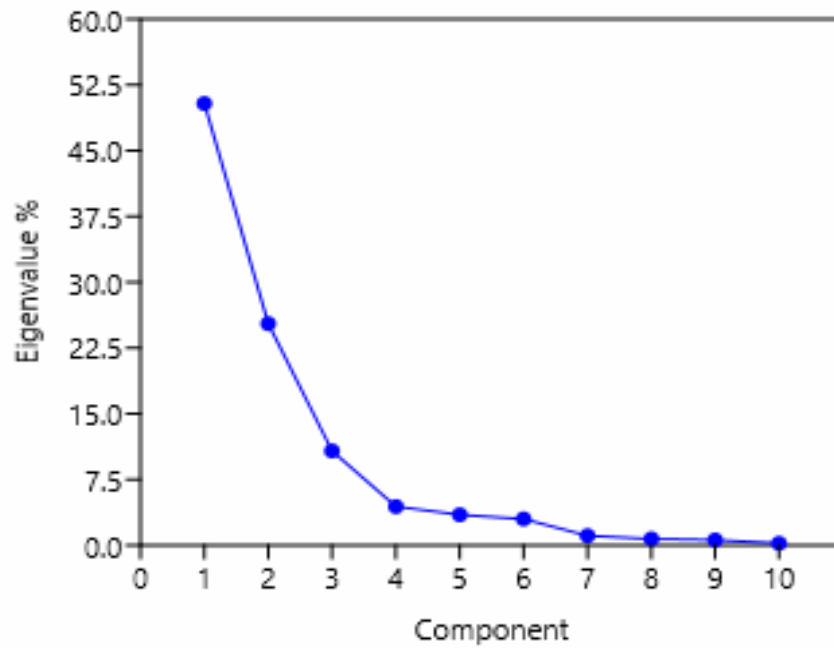


Fig 3. Scree plot analysis of the principal components for *Bemisia tabaci* adults (both male and female) based on 30 quantitative characters

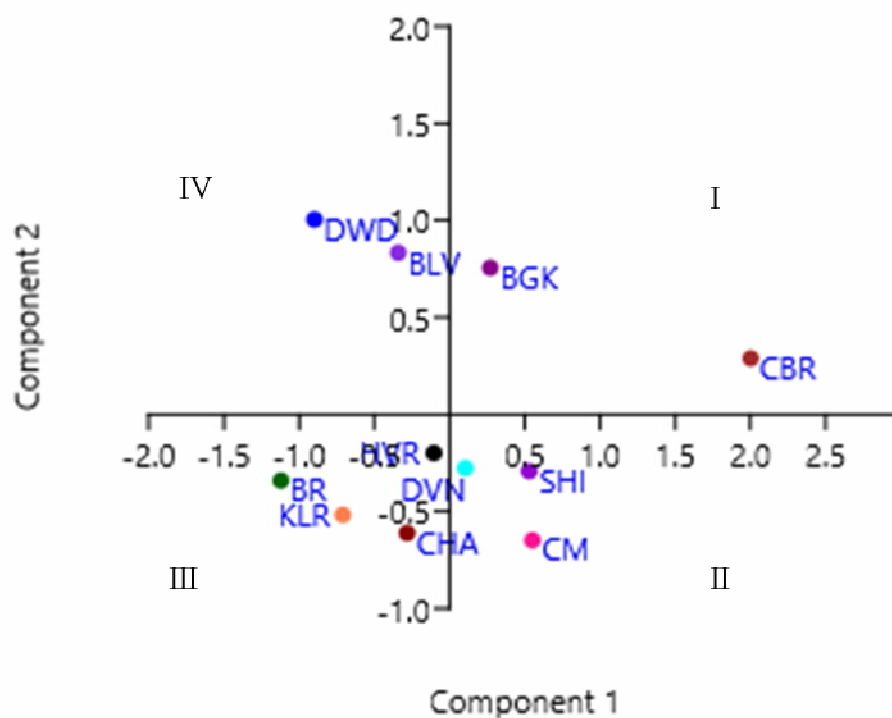


Fig 4. Score plot of principal components for *Bemisia tabaci* adults (both male and female) from different agro climatic zones of Karnataka based on 30 quantitative characters.

4.1.7 Cluster analysis for *B. tabaci* adult (both male and female) and puparia of different agro climatic zones of Karnataka

The cluster analysis of adult (male and female) and puparia of *B. tabaci* populations revealed the existence of two major clusters-Cluster 1 and Cluster 2 (Fig. 5). Cluster 1 consists of single population from Chikkaballapura which was deviated from all other populations forming out group. Cluster 2 was further divided into two major subclusters (Cl 2a and Cl 2b). Sub-cluster Cl 2a consisted of populations from Belagavi and Dharwad on one hand. On the other hand, population from Bagalkot which was deviated from other two populations of Cl 2a. The sub cluster Cl 2b consists of seven populations viz., Davanagere, Haveri, Shivamogga, Chikkamagaluru, Bengaluru rural, Chamarajanagara and Kolar. Whereas populations Davanagere, Haveri, Shivamogga and Chikkamagaluru formed single group whereas, Chikkamagaluru population was deviated. The remaining populations viz., Kolar Chamarajanagara and Bengaluru rural formed another group in which Bengaluru rural population was deviated from other two populations.

4.1.8 Principal component analysis (PCA) for the estimated variables of *Bemisia tabaci* adults (both male and female) and puparia

The results of principal component analysis based on 42 morphological characters of adult (female and male) and puparia from various agro climatic zones of Karnataka, are presented in Table 9. The principal component analysis divided these 42 traits into four major principal components. The first principal component (PC1) accounts for maximum variability in the data with respect to succeeding components.

The scree plot of the principal components (PC) (Fig. 6) showed that, eigenvalues of the first four PC correspond to most of the variances in the dataset and the total cumulative variance of these principal components amounted to 89.508 per cent variations. The principal component analysis grouped the estimated variables into four major groups, in which PC1 accounted for 44.181 per cent, PC2 for 23.935 per cent, PC3 for 12.682 per cent and PC4 accounts for 8.710 per cent (Table 9) of the total variation. Among them, PC1 had the largest contribution of 44.181 per cent of the total variation, shown highest positive contribution for female characters viz., fore

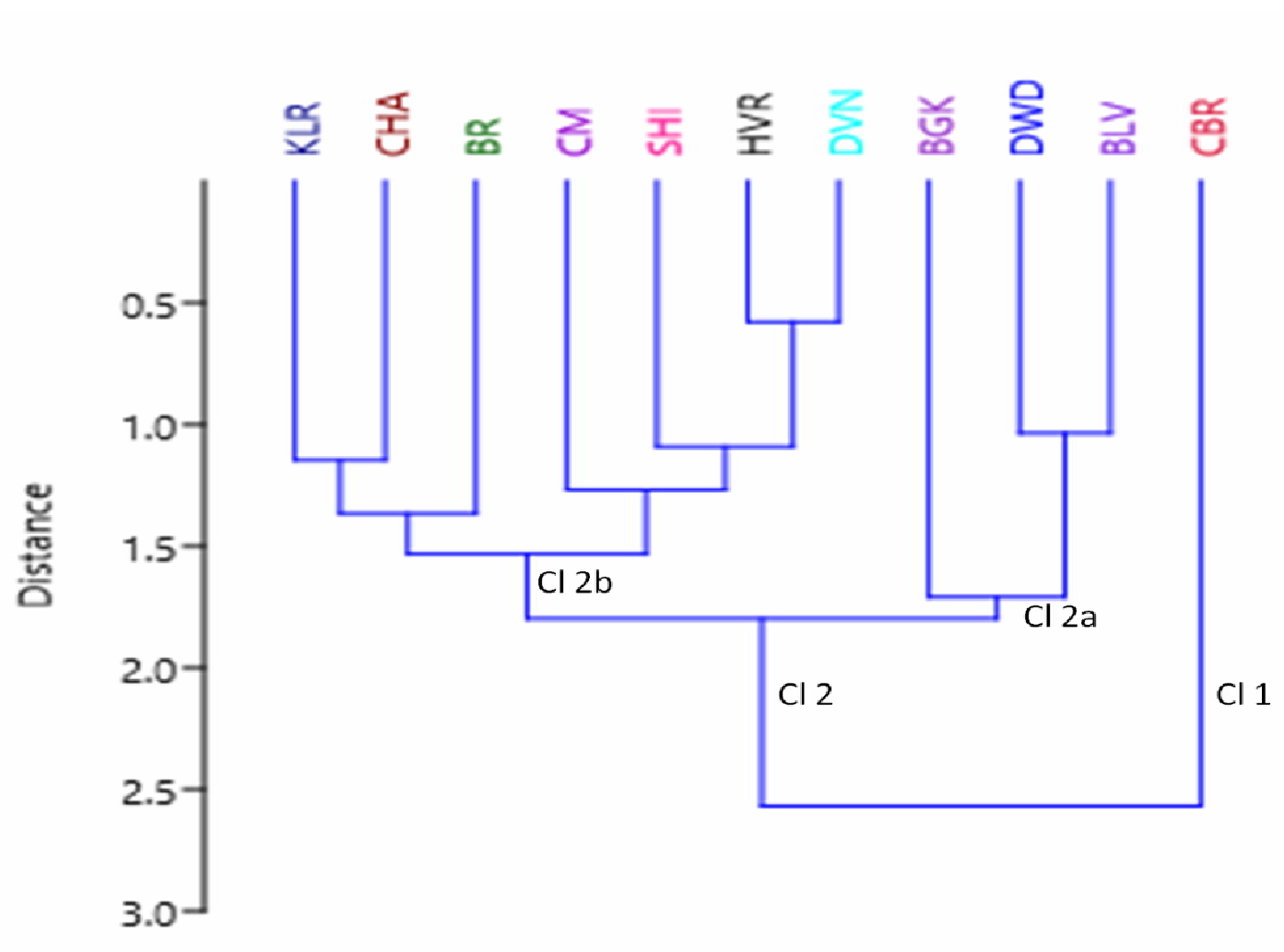


Fig 5. Cluster analysis for *Bemisia tabaci* adults (both male and female) and puparia from different agro climatic zones of Karnataka based on 42 quantitative characters.

Table 9. Morphometrics of *Bemisia tabaci* adults (both male and female) and puparia based on 42 quantitative characters- proportion of contribution and variable coefficients of the first four eigenvectors for principal component analysis

Characters*	Principal Component 1 (PC 1)	Principal Component 2 (PC 2)	Principal Component 3 (PC 3)	Principal Component 4 (PC 4)
FWL ¹	0.249	0.110	0.138	-0.064
FWW ¹	0.139	-0.093	0.032	0.075
LFWV ¹	0.543	-0.254	0.211	0.016
LHW ¹	0.205	0.165	-0.020	-0.024
WHW ¹	0.101	0.061	-0.052	0.099
LFFe ¹	-0.065	0.003	-0.059	0.142
LFTi ¹	-0.095	-0.004	-0.009	0.199
LFTa ¹	-0.044	0.011	-0.076	0.087
LHFe ¹	-0.026	0.013	0.032	0.160
LHTi ¹	0.027	-0.044	-0.155	0.526
LHTa ¹	0.030	-0.023	0.052	0.217
LA ¹	0.304	0.129	0.155	-0.086
LP ¹	0.074	0.373	-0.277	-0.012
LAB ¹	0.128	0.494	-0.075	0.025
FWL ²	0.200	-0.084	-0.011	-0.010
FWW ²	0.195	-0.077	-0.015	0.202
LFWV ²	0.423	-0.261	-0.064	0.097
LHW ²	0.136	0.056	-0.147	-0.168
WHW ²	0.143	-0.011	-0.111	0.135
LFFe ²	-0.027	-0.029	-0.091	0.063
LFTi ²	-0.068	-0.026	-0.050	0.123
LFTa ²	-0.022	0.013	-0.093	0.024
LHFe ²	-0.021	-0.007	0.015	0.133
LHTi ²	-0.006	-0.102	-0.144	0.532
LHTa ²	0.027	-0.027	0.017	0.132
LA ²	0.286	0.121	0.138	-0.062
LP ²	0.114	0.315	-0.356	0.091
LAB ²	0.172	0.353	-0.143	0.049
LLAB ²	0.010	0.010	-0.010	0.005
LC ²	0.012	0.016	-0.009	0.002
PL ³	-0.067	0.233	0.441	0.198
PD ³	-0.056	0.156	0.339	0.141
DVOAE ³	-0.066	0.239	0.437	0.159
DTMSAE ³	-0.009	0.094	0.201	0.140
LVD ³	-0.002	0.031	0.027	0.038
BVO ³	-0.003	0.014	0.022	0.008
LL ³	0.001	0.008	0.015	0.017
LD ³	-0.006	0.006	0.012	0.012
BO ³	0.000	0.012	0.019	0.018
LCF ³	-0.012	0.011	0.026	0.006
LCS ³	-0.021	-0.014	0.026	-0.007
DCS ³	0.002	0.004	0.015	0.013
Proportion of variation (%)	44.181	23.935	12.682	8.710

* For expansion of the abbreviations, refer Appendix II, III and IV

¹Female characters;

²Male characters;

³Puparia characters

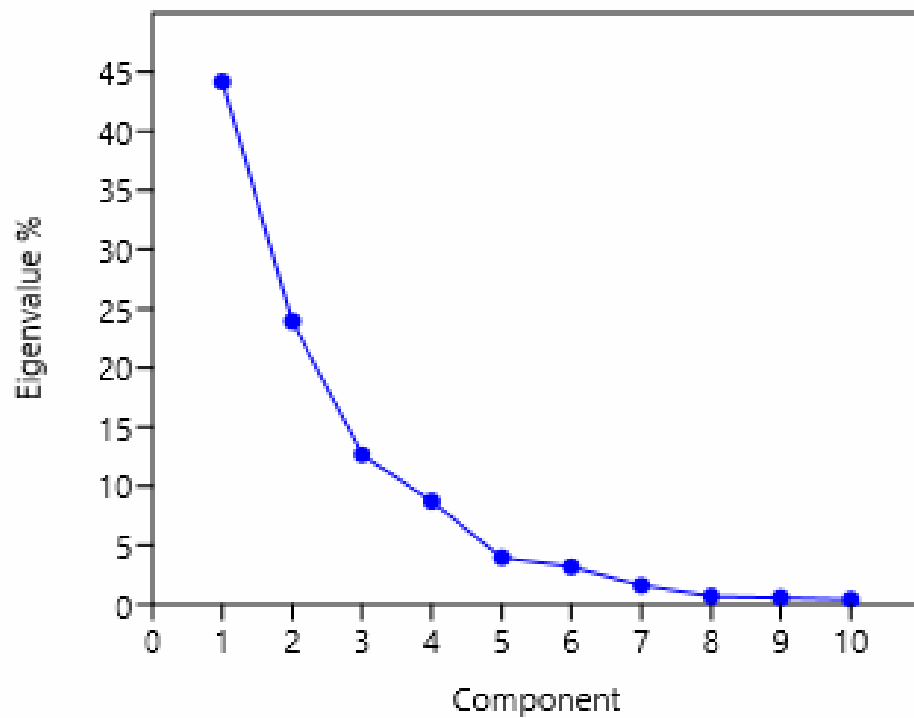


Fig 6. Scree plot analysis of the principal components for *Bemisia tabaci* adults (both male and female) and puparia based on 42 quantitative characters

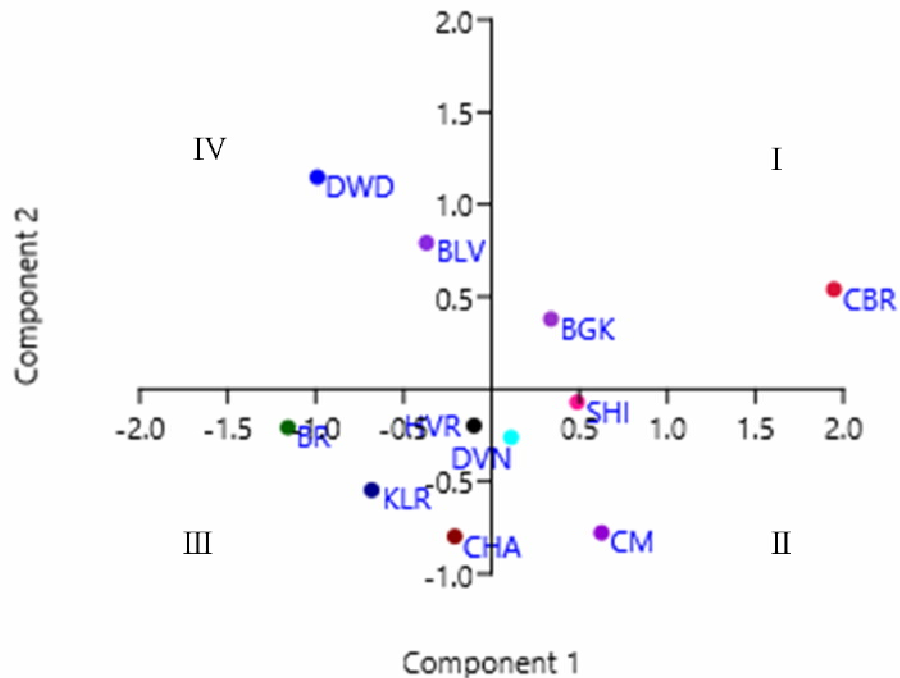


Fig 7. Score plot of principal components for *Bemisia tabaci* adults (both male and female) and puparia from different agro climatic zones of Karnataka based on 42 quantitative characters.

wing length, fore wing vein length, hind wing length, length of antenna and male characters viz., fore wing length, fore wing width, fore wing vein length and length of antenna. In case of PC2 highest positive contributions came from female characters such as length of proboscis, length of abdomen and male characters such as length of proboscis, length of abdomen also puparia characters like puparia length and distance of vasiform orifice from anterior end. In case of PC3 highest positive contributions came from female character such as fore wing vein length and puparia characters such as puparia length, puparia breadth and distance of transverse moulting suture from anterior end. In case of PC4 highest positive contributions came from female characters like hind tibial length, hind tarsal length and male characters like fore wing width, hind tibia length.

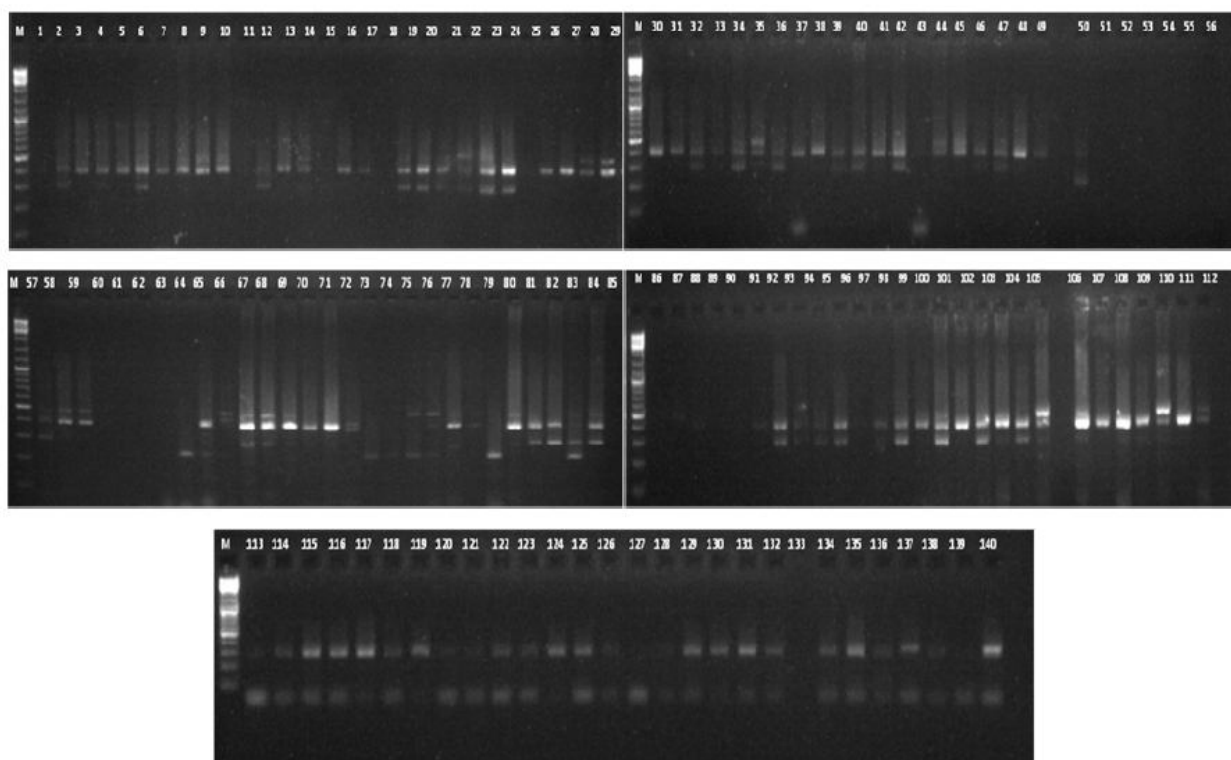
The first two principal components contributed the major share of variances. In first and second principal components, all the characters under consideration contributed for 68.12 per cent diversity.

4.1.9 Score plot of principal components for *B. tabaci* adults (both male and female) and puparia from different agro climatic zones of Karnataka

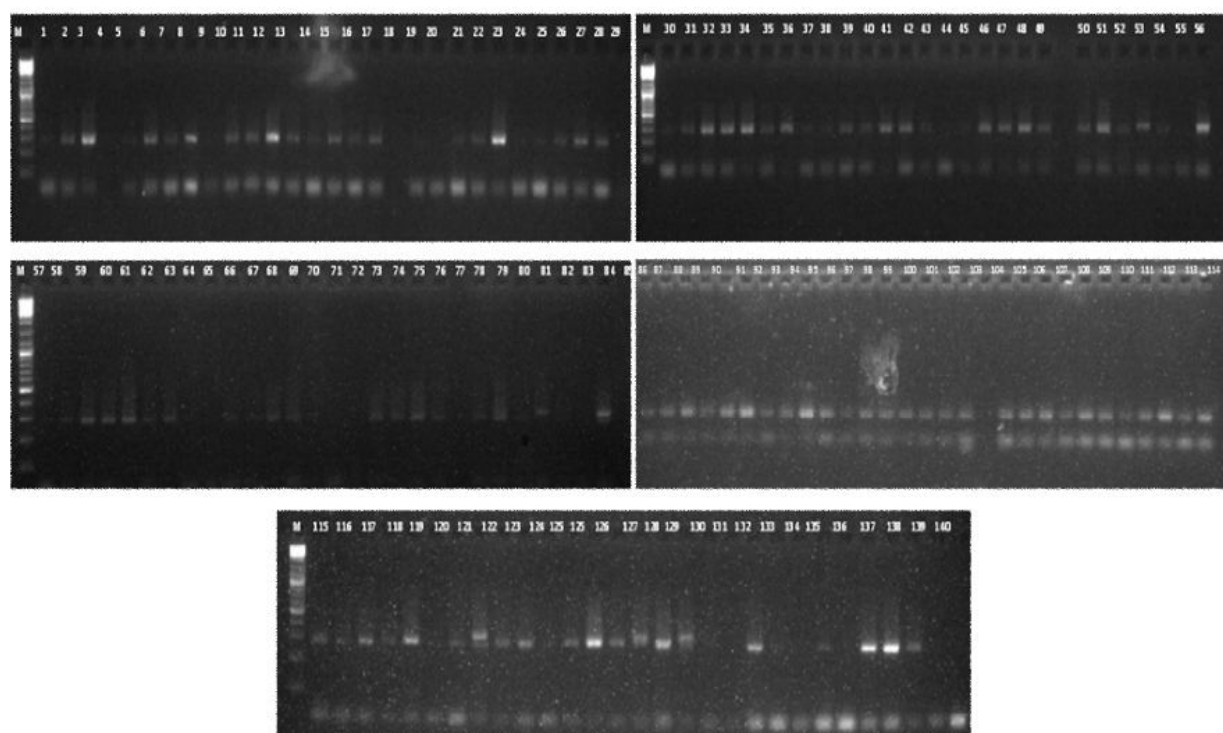
Scores for *B. tabaci* adults and puparia of different agro climatic zones of Karnataka, based on PC1 and PC2 are plotted in Fig. 7. The distribution pattern population of eleven districts revealed that, maximum number of entries were included in quarter III, namely Bengaluru rural, Kolar, Chamarajanagatra and Haveri whereas, quarter II included Davanagere, Shivamogga and Chikkamagaluru. Quarter I shared two entries such as Bagalkot and Chikkaballapur whereas, quarter IV included entries like Dharwad and Belagavi (Fig. 7).

4.2 Genomic flux and population genetic structure of whitefly populations of tomato ecosystems of Karnataka

Genetic diversity of whitefly, *Bemisia tabaci* collected from different agro climatic zones of Karnataka were assessed with Simple Sequence Repeats (SSR) markers (Plate 11).



a) Marker FbBEM31



b) Marker FbBEM15

Plate 11. Allele size variation for SSR markers a) FbBEM31 b) FbBEM31 in 140 *B. tabaci* individuals collected from different geographical areas

4.2.1 Population genetic diversity analysis using microsatellite markers

The genetic analysis was carried out for 140 whitefly DNA samples from eleven populations collected from different agro climatic zones of Karnataka. A set of 17 microsatellite primer pairs linked to *B. tabaci* with high polymorphic information content (PIC) was selected based on the literature available were used to understand the genomic flux and population genetic structure of *B. tabaci*. Primers that amplified products of the expected size were then used for the microsatellite screening of females from each of the collected populations. DNA samples were amplified by using the multiplex PCR method.

The data was analyzed for mean number of alleles (N_a), number of effective alleles (N_e), Shannon's Information Index (I), percentage of polymorphic loci (% P), mean unbiased estimates of observed (H_o) and expected (H_e) heterozygosity, number of effective migrants (N_m) and F-coefficients, population allele frequencies, genetic distance and pair wise population F_{ST} values were calculated using GenAEx V 6.41.

The microsatellite data was subjected to a hierarchical analysis of molecular variance (AMOVA) at individual, population and intrapopulation level using Arlequin V3.0. The principal coordinate analysis using genetic distance was plotted using GenAlex V6. The Neighbor Joining tree at population and individual levels was constructed using genetic distance matrix from GenAlex with 1000 bootstrap values was carried out using MEGA 5 software. Population structure was examined using the Bayesian cluster algorithm STRUCTURE V2.3.1.

4.2.1.1 Polymorphism and allelic frequency

The number of different alleles among the microsatellite loci (N_a) varied from 1.45 (FbBEM31) to 4.36 (FbBem23) across the regions with the mean of 2.257 alleles. The mean number of effective alleles (N_e) was 1.663 and ranged from 1.300 (FbBEM31) to 2.699 (FbBem23). An overall number of migrant (N_m) mean value for all loci was 0.281 with the locus FbBem23 recording the highest N_m (0.558) and the locus FbBEM39 recorded least N_m (0.073). High N_m values (>0.5) across all the populations for each loci indicated selection pressure acting on the loci (Table 10).

Table 10. Locus -wise information on the number of different alleles (Na), number of effective alleles (Ne), Shannon's Information Index (I), Observed Heterozygosity (Ho), Expected Heterozygosity (He), the number of migrants (Nm), Fixation Index (F) & F-statistics across populations of *Bemisia tabaci* in Karnataka

Locus	Na	Ne	I	Ho	He	Nm	F	Fis	Fit	Fst
FbBEM11	2.818	1.820	0.645	0.055	0.366	0.296	0.866	0.851	0.919	0.458
FbBEM14ii	2.636	1.570	0.539	0.100	0.304	0.172	0.633	0.671	0.866	0.592
FbBEM15	1.636	1.485	0.373	0.000	0.252	0.180	1.000	1.000	1.000	0.581
FbBEM22	2.455	1.593	0.558	0.064	0.335	0.472	0.725	0.810	0.876	0.346
FbBEM25	2.182	1.596	0.506	0.215	0.312	0.260	0.447	0.310	0.648	0.490
FbBEM31	1.455	1.300	0.229	0.000	0.144	0.169	1.000	1.000	1.000	0.596
FbBEM39	1.545	1.321	0.248	0.000	0.152	0.073	1.000	1.000	1.000	0.773
FbBEM40	1.727	1.564	0.413	0.000	0.278	0.174	1.000	1.000	1.000	0.590
FbBem15	2.364	1.808	0.635	0.018	0.396	0.317	0.964	0.954	0.974	0.441
FbBtIs1.17	2.091	1.547	0.476	0.000	0.294	0.288	1.000	1.000	1.000	0.465
FbBtIs1.4	2.182	1.758	0.635	0.000	0.415	0.460	1.000	1.000	1.000	0.352
FbBT-e49	2.182	1.740	0.563	0.000	0.347	0.468	1.000	1.000	1.000	0.348
FbBT-4	2.545	1.790	0.652	0.000	0.393	0.287	1.000	1.000	1.000	0.466
FbBT-b159	2.000	1.482	0.433	0.000	0.269	0.144	1.000	1.000	1.000	0.634
FbBem23	4.364	2.669	1.085	0.382	0.576	0.588	0.335	0.337	0.535	0.298
FbBem37	1.909	1.579	0.473	0.006	0.305	0.213	0.985	0.980	0.991	0.540
FbBT-83	2.273	1.650	0.571	0.000	0.353	0.221	1.000	1.000	1.000	0.531
Mean	2.257	1.663	0.531	0.049	0.323	0.281	0.880	0.877	0.930	0.500

Fis = (Mean He - Mean Ho) / Mean He, Fit = (Ht - Mean Ho) / Ht, Fst = (Ht - Mean He) / Ht, Nm = [(1 / Fst) - 1] / 4, Key: Mean He = Average He across the populations. Mean Ho = Average Ho across the populations, Ht = Total Expected Heterozygosity = 1 - Sum tpi² where tpi is the frequency of the ith allele for the total & Sum tpi² is the sum of the squared total allele frequencies,

The heterozygosity (gene diversity) is considered as a reliable parameter of genetic variation among the loci. The observed (H_o) and expected heterozygosity (H_e) ranged from zero to 0.382 (FbBem23) with an average of 0.049 and 0.144 (FbBEM31) to 0.576 (FbBem23) with an average of 0.323, respectively indicating a high degree of genetic diversity and possibility of a very high selection potential for the loci under study. Generally, a polymorphic loci should have a minimum heterozygosity value of 0.10. The fixation coefficient (F_{ST}) value of population measured with 17 microsatellite markers varied from 0.298 (FbBem23) to 0.773 (FbBEM39), with a mean of 0.500. The heterozygote's in F_{IT} was amounted to 0.93, while in F_{IS} amounted to 0.877 (Table 10).

Among the populations, number of different alleles of microsatellite loci (N_a) ranged between 1.824 and 2.647 across the regions with a mean of 2.257. The most diverse population, Bt_BR (Bengaluru rural), recorded 2.647 alleles followed by Bt_CKM (Chikkamagaluru) and Bt_KLR (Kolar) with 2.588 and 2.529 alleles, respectively. The least diverse population, Bt_BGK (Bagalkot) had 1.824 alleles followed by Bt_BLV (Belagavi) and Bt_SHI (Shivamogga) had 1.882 alleles each, respectively, preceded by Bt_DWD (Dharwad), Bt_CKBR (Chikkaballapura), Bt_DVN (Davanagere), Bt_HVR (Haveri), Bt_CHA (Chamarajanagara) with 2.176, 2.235, 2.294, 2.294, and 2.471 alleles, respectively (Table 11). Number of Effective alleles (N_e), that provides a good measure of genetic variation in accordance with population size was maximum for the population Bt_CKM (Chikkamagaluru) (1.985) followed by Bt_BR (Bengaluru rural) (1.867) and the population Bt_BLV (Belagavi) recorded the minimal value of 1.417. The observed heterozygosity (H_o) ranged between 0.00 in Bt_CKBR population (Chikkaballapura) to 0.124 in Bt_BGK population (Bagalkot). The mean expected heterozygosity ranged between 0.226 in Bt_SHI (Shivamogga) to 0.419 for Bt_BR (Bengaluru rural). The per cent polymorphism for the loci ranged between 58.82 per cent for Bt_SHI population (Shivamogga) to 100 per cent for Bt_BR population (Bengaluru rural) indicating the greater extent of polymorphism among the populations with these set of molecular markers used in the present study (Table 11).

Table 11. Population-wise information on the number of different alleles (Na), number of effective alleles (Ne), Shannon's Information Index (I), Observed Heterozygosity (Ho), Expected Heterozygosity (He), Fixation Index (F) & percentage polymorphism (% P) observed across 17 microsatellite loci in *Bemisia tabaci*.

Population	Na	Ne	I	Ho	He	F	%P
Bt_DVN	2.294	1.675	0.577	0.020	0.364	0.950	88.24
Bt_HVR	2.294	1.709	0.503	0.031	0.288	0.937	64.710
Bt_DWD	2.176	1.485	0.458	0.088	0.273	0.759	82.35
Bt_BLV	1.882	1.417	0.382	0.029	0.242	0.802	70.59
Bt_CKBR	2.235	1.779	0.604	0.000	0.379	1.000	88.24
Bt_KLR	2.529	1.592	0.518	0.027	0.297	0.925	76.47
Bt_BR	2.647	1.867	0.692	0.043	0.419	0.909	100.00
Bt_BGK	1.824	1.555	0.448	0.124	0.300	0.622	70.59
Bt_CHA	2.471	1.758	0.604	0.071	0.357	0.856	82.35
Bt_CKM	2.588	1.985	0.682	0.063	0.407	0.863	82.35
Bt_SHI	1.882	1.472	0.376	0.047	0.226	0.101	58.82
Mean	2.257	1.663	0.531	0.049	0.323	0.859	78.61

Shannon's Information Index (I) was considered as a parameter for genetic variation among 11 populations. Among the total populations, the I value ranged from 0.376 (Bt_SHI) to 0.692 (Bt_BR) with a mean index value of 0.531 (Table 11). Among the loci, the Shannon's Information Index value ranged from 0.229 (FbBEM31) to 1.085 (FbBem23) with a mean of 0.531 (Table 10).

4.2.1.2 F co-efficient analysis

The major components of F-statistics are F_{IS} , F_{IT} and F_{ST} where, 'I' represent individuals, 'S' represents sub-population and 'T' represents total population were calculated for the whitefly populations. The F_{IS} and F_{IT} values indicate the inbreeding coefficient among the sub-populations and among the total populations, respectively.

In the present study, mean F_{IS} value of 0.877 across all the loci was recorded. The F_{IS} value ranged between 0.31 for FbBEM25 to 1.00 for FbBEM15, FbBEM31, FbBEM39, FbBEM40, FbBtIs1.17, FbBem15, FbBT-e49, FbBT-4, FbBT-b159 and FbBT-83. The F_{IT} mean value was 0.93 which ranged between 0.535 for FbBem23 and 1.00 for FbBEM15, FbBEM31, FbBEM39, FbBEM40, FbBtIs1.17, FbBem15, FbBT-e49, FbBT-4, FbBT-b159 and FbBT-83. The significant F_{IS} and F_{IT} indicated the deficiency of heterozygosity among the sub-populations and the total populations. Generally, positive F_{IS} values indicate a significant lower heterozygotes, while the negative values indicate an abundance of heterozygotes. In the present study, all loci showed positive values, which indicated the significant deficit of heterozygotes which may be due to selection pressure and presence of null alleles. The significant mean F_{ST} value was 0.500 for all the populations and the individual values ranged between 0.298 for FbBem23 to 0.773 for FbBEM39 indicating the presence of significant genetic differentiation among the populations (Table 10).

The pair wise population F_{ST} values ranged from a minimum of 0.180 between Bt_BR and Bt_CHA and maximum of 0.530 between Bt_HVR and Bt_CKBR (Table 12). The pairwise genetic distance varied with a minimum value of 0.280 between the populations Bt_DVN and Bt_HVR and the maximum of 1.334 between the populations Bt_HVR and Bt_CKBR (Table 13). The pair wise F_{ST} values indicated the presence of moderate to high genetic differentiation among the sampled populations (Table 12).

Table 12. Pair-wise F_{ST} value for population of *Bemisia tabaci* across the sampling regions of Karnataka

Bt_DVN	Bt_HVR	Bt_DWD	Bt_BLV	Bt_CKBR	Bt_KLR	Bt_BR	Bt_BGK	Bt_CHA	Bt_CKM	Bt_SHI
0.000										Bt_DVN
0.185	0.000									Bt_HVR
0.271	0.451	0.000								Bt_DWD
0.263	0.372	0.215	0.000							Bt_BLV
0.360	0.530	0.457	0.474	0.000						Bt_CKBR
0.388	0.451	0.360	0.454	0.407	0.000					Bt_KLR
0.289	0.410	0.353	0.344	0.226	0.270	0.000				Bt_BR
0.288	0.421	0.335	0.299	0.443	0.435	0.315	0.000			Bt_BGK
0.293	0.399	0.395	0.344	0.288	0.346	0.180	0.331	0.000		Bt_CHA
0.242	0.346	0.215	0.267	0.254	0.312	0.228	0.273	0.311	0.000	Bt_CKM
0.257	0.293	0.248	0.327	0.399	0.309	0.326	0.400	0.357	0.223	0.000 Bt_SHI

Table 13. Pair-wise genetic distance of population for *Bemisia tabaci* across the sampling regions of Karnataka

Bt_DVN	Bt_HVR	Bt_DWD	Bt_BLV	Bt_CKBR	Bt_KLR	Bt_BR	Bt_BGK	Bt_CHA	Bt_CKM	Bt_SHI
0.000										Bt_DVN
0.280	0.000									Bt_HVR
0.497	1.096	0.000								Bt_DWD
0.484	0.808	0.291	0.000							Bt_BLV
0.762	1.334	0.940	1.028	0.000						Bt_CKBR
1.034	1.250	0.832	1.002	0.989	0.000					Bt_KLR
0.801	1.270	0.990	0.826	0.366	0.628	0.000				Bt_BR
0.596	0.905	0.593	0.519	0.907	1.113	0.735	0.000			Bt_BGK
0.689	1.041	1.033	0.738	0.442	0.880	0.330	0.708	0.000		Bt_CHA
0.629	0.930	0.467	0.553	0.484	0.777	0.609	0.668	0.882	0.000	Bt_CKM
0.585	0.650	0.452	0.634	0.926	0.695	1.113	1.125	1.123	0.538	0.000 Bt_SHI

4.2.1.3 Analysis of Molecular variance (AMOVA)

The AMOVA results revealed that, the per cent variation among the populations was 49.79 and within populations was 50.21. The variation within populations was higher than that of among populations, indicating the existence of differentiation between the two populations (Table 14). Even though significant variance among populations was detected, it was relatively high (49.79) considering the expectations of high gene flow among some of the populations. However, significant and high variation (50.21) obtained within populations, which is a characteristic feature of microsatellite markers because of their high polymorphic nature, thus resulting in increased genetic diversity within a population and eventually may reduce the power of differentiation among populations.

4.2.1.4 Phylogenetic analysis

Allele frequencies were used to generate the pair wise genetic distances between pairs of populations and the resulting distance matrix was used to build phylogenetic tree using Neighbour Joining (NJ) algorithms. In this present study, the Neighbor Joining (NJ) phylogenetic tree constructed across the samples of *B. tabaci* revealed the existence of two major clusters-Cluster 1 and Cluster 2 (Fig. 8). Cluster 1 consisted of populations from Davanagere, Haveri and Shivamogga. The cluster 2 was further sub-divided into two sub-clusters (Cl 2a and Cl 2b). Sub-cluster Cl 2b consisted of populations from Bengaluru rural, Chamarajanagara, Chikballapura, Kolar and Chikkamagaluru sampling regions, whereas the sub-cluster Cl 2a consisted of samples from Belagavi, Dharwad and Bagalkot..

Careful observations revealed that, populations from sub clusters Cl 2a and sub clusters Cl 2b though formed separate groups, they shared close genetic proximity. The populations from Shivamogga, Davanagere and Haveri formed separate cluster. The populations from Bengaluru rural, Chamarajanagara and Chikballapur, Kolar and Chikkamagaluru were intermixed with each other.

The phylogenetic analysis of all the 140 individuals across sub-populations resulted in formation of 2 major clusters (Fig. 9). Further, clusters 1sub divided into two sub-cluster (C 1a and C 1b). Individuals collected from Haveri, Davanagere, Dharwad, Bagalkot, Kolar, Chikkamagaluru, Shivamogga and Belagavi are distributed

Table 14. Summary of Analysis of Molecular Variance (AMOVA) and mean F-coefficients calculated over 11 populations of *Bemisia tabaci*

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Among populations	10	763.371	2.895 Va	49.79
Within populations	269	785.300	2.919 Vb	50.21
Total	279	1548.671	5.81468	
Fixation Index	FST	0.498		

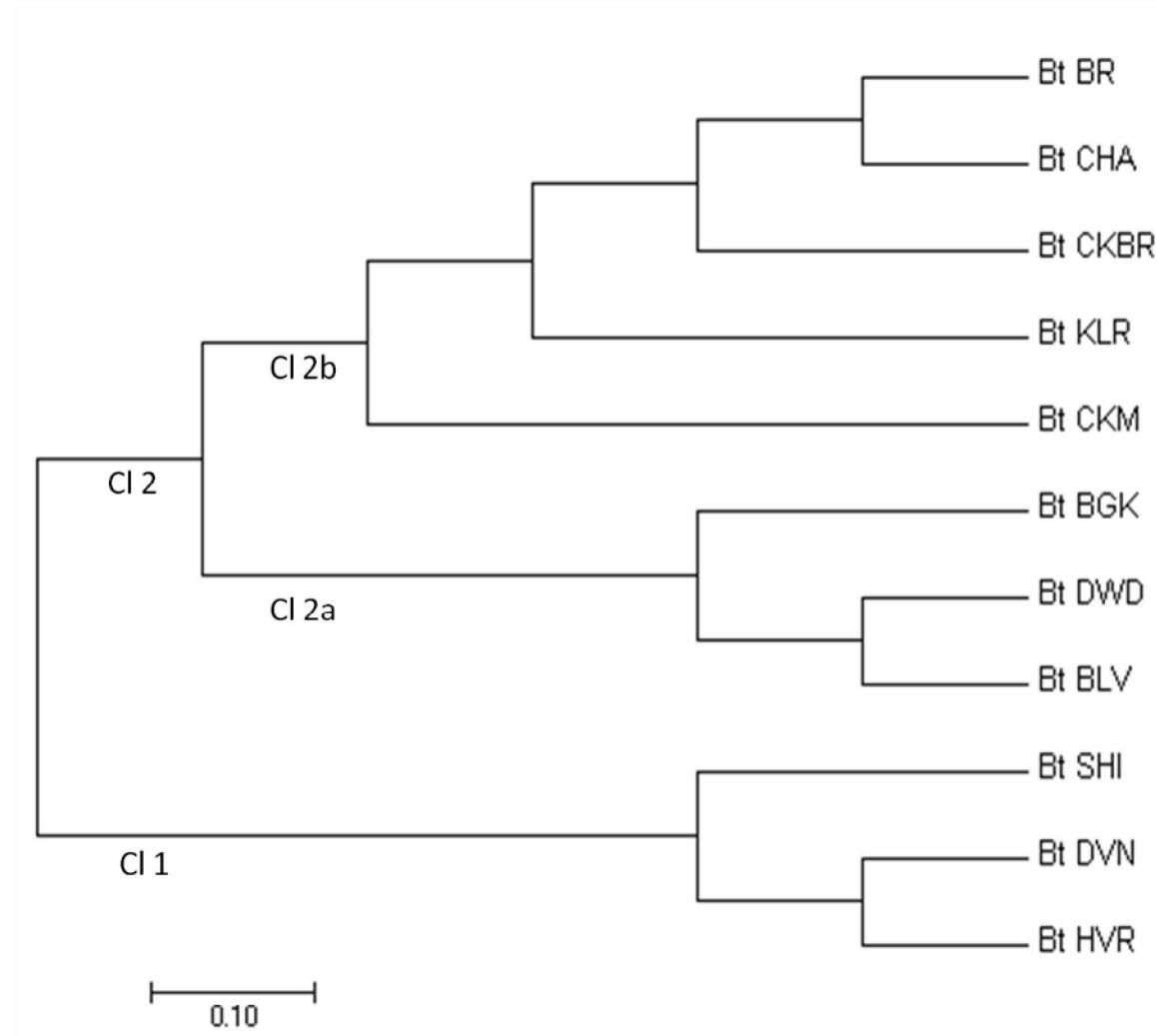


Fig 8. Neighbour Joining (NJ) tree constructed using MEGA 7 based on pair-wise genetic distance across *Bemisia tabaci* populations

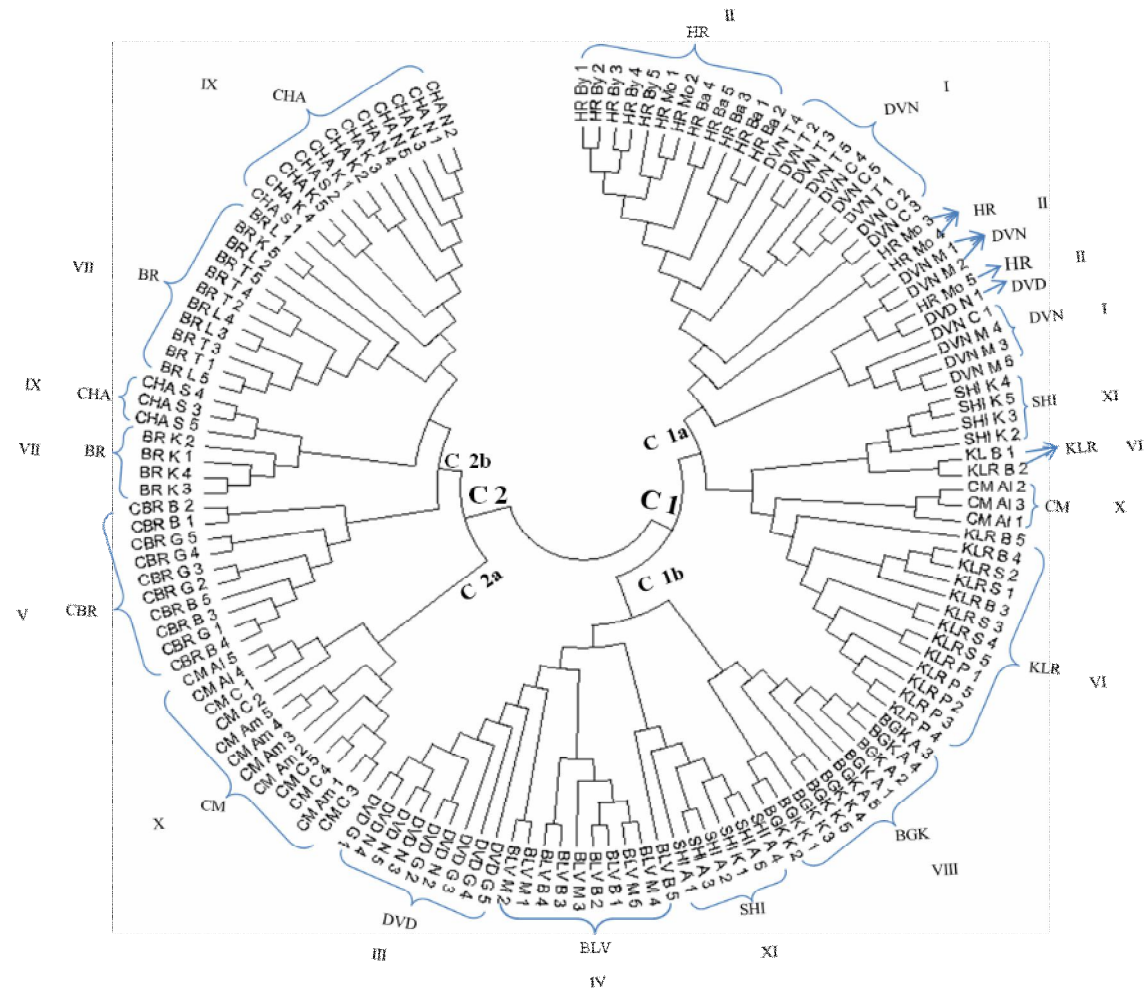


Fig 9. Neighbour joining (NJ) tree constructed using MEGA 7 based on pair-wise genetic distance across *Bemisia tabaci* individuals

Note: DWD= DVD, CKBR=CBR, CKM=CM, HVR=HR

across cluster 1. Sub cluster C 1a consisted of individuals from Haveri, Davanagere, Kolar and few individuals from Dharwad, Shivamogga and Chikkamagaluru regions. Sub cluster C 1b consisted of individuals from Bagalkot, Belagavi, Dharwad and few individuals from Shivamogga regions. Cluster 2 also sub divided into two sub clusters C 2a and C 2b which consists of individuals from Chikkamagaluru, Chikkaballapur, Bengaluru rural and Chamarajanagara. Individuals from Chikkamagaluru formed separate sub cluster as C 2a whereas, individuals from Chikkaballapur, Bengaluru rural and Chamarajanagara formed another sub cluster C 2b. Majority of individuals are distributed across the major clusters and sub clusters, possibly due to high rate of gene flow/genetic drift across the populations/regions.

4.2.1.5 Principal Coordinate Analysis

The results obtained by the cluster analysis was confirmed by Principal Coordinate Analysis (PCA). PCA shows the distribution and relationships between the populations based on the bidimensional plot of the genetic distance. The position of the populations is depicted in the Fig. 10, in upper right quadrant, the populations from Dharwad and Shivamogga were grouped together, while in the downside right quadrant populations from Belagavi, Davanagere, Bagalkot and Haveri were grouped together. The upper left quadrant had populations from Kolar and Chikkamagaluru whereas, downside left quadrant, the populations from Chikballapur, Bengaluru rural and Chamarajanagara were present. The relative position of 140 individuals of eleven populations is illustrated in Fig. 11. The whitefly individuals which are distributed across different quadrant based on their genetic distance matrix were depicted in the Table 15.

Principal component analysis revealed the separation of samples more clearly between populations of different geographical locations. Some populations that showed a close phylogenetic relationship were separated more clearly by the PCA plot.

4.2.1.6 Structure analysis

The population genetic structure was investigated using the 140 individuals of *B. tabaci* sampled across the populations using STRUCTURE v2.3.4 based on the genotyping data of 17 SSR markers. The posterior probability [$\ln P(D)$] of the data

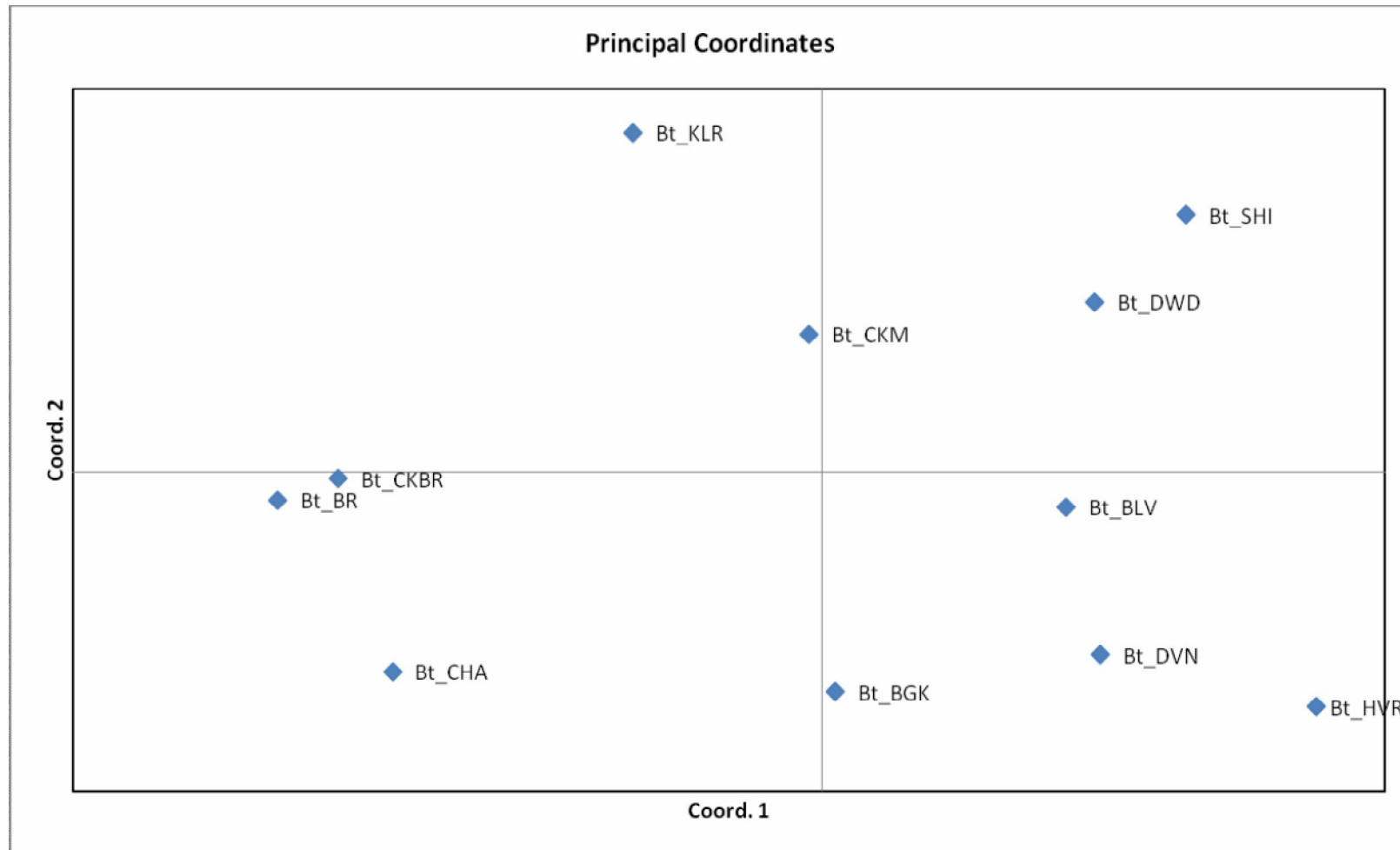


Fig 10. Principle coordinates analysis (PCA) using pair-wise genetic distance matrix of eleven *Bemisia tabaci* populations sampled across Karnataka

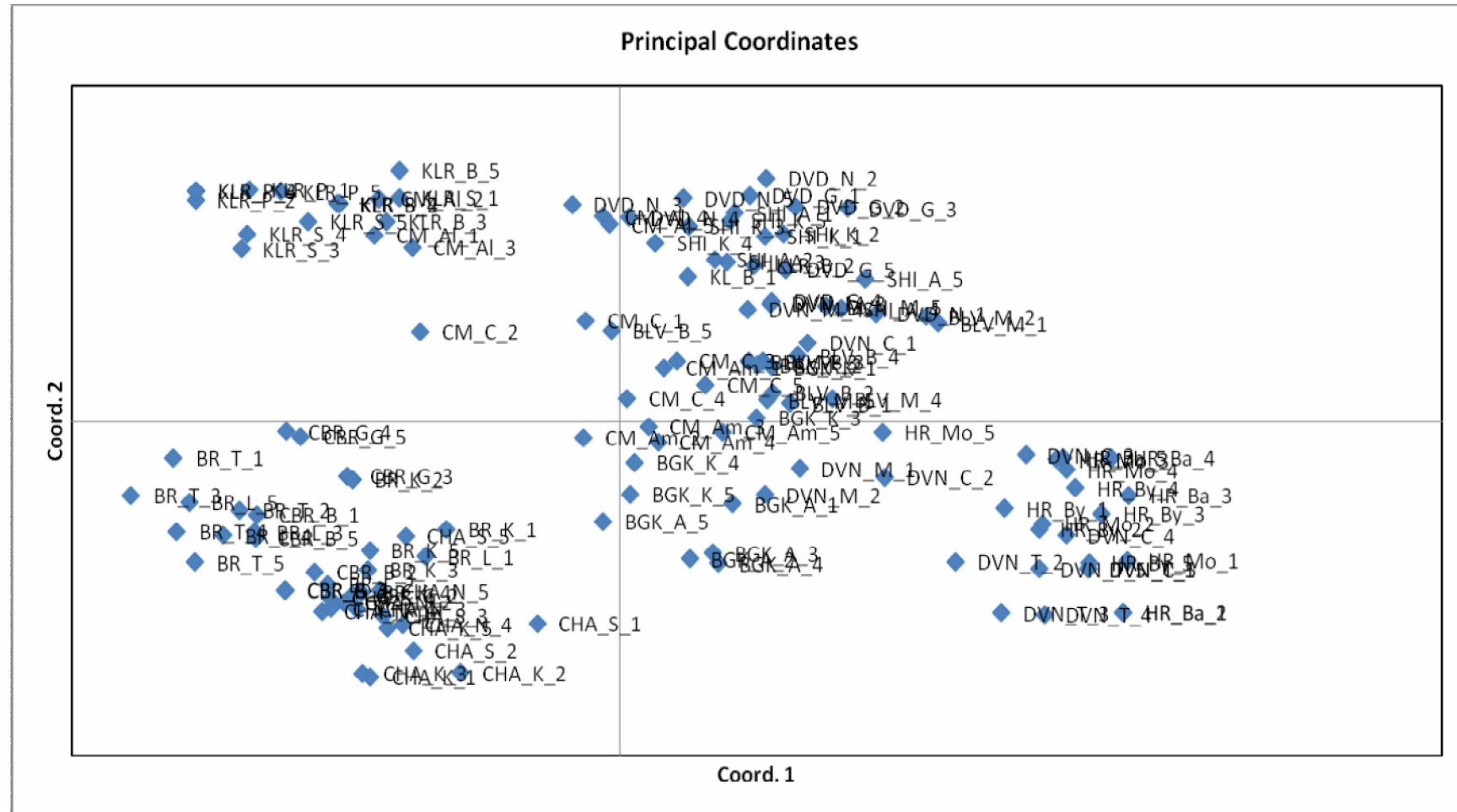


Figure 11. Principle coordinates analysis (PCA) using pair-wise genetic distance matrix of 140 *Bemisia tabaci* populations sampled across Karnataka

Note: DWD= DVD, CKBR=CBR, CKM=CM, HVR=HR

Table 15. Distribution of whitefly individuals distributed across different quadrant based on their genetic distance matrix

Sl. No.	Quadrant	Individuals
1	Quadrant 1	KLR_P_1, KLR_P_2, KLR_P_3, KLR_P_4, KLR_P_5, KLR_S_1, KLR_S_2, KLR_S_3, KLR_S_4, KLR_S_5, KLR_B_3, KLR_B_4, KLR_B_5, CKM_A1_1, CKM_A1_2, CKM_A1_3, CKM_A1_4, CKM_A1_5, CKM_C_2, CKM_C_1, DWD_N_3, BLV_B_5
2	Quadrant 2	DWD_N_1, DWD_N_2, DWD_N_4, DWD_N_5, DWD_G_1, DWD_G_2, DWD_G_3, DWD_G_4, DWD_G_5, SHI_K_1, SHI_K_2, SHI_K_3, SHI_K_4, SHI_K_5, SHI_A_1, SHI_A_2, SHI_A_3, SHI_A_4, SHI_A_5, BLV_M_1, BLV_M_2, BLV_M_3, BLV_M_4, BLV_M_5, BLV_B_1, BLV_B_2, BLV_B_3, BLV_B_4, BGK_K_1, BGK_K_2, BGK_K_3, DVN_M_3, DVN_M_4, DVN_M_5, DVN_C_1, KL_B_1, KL_B_2, CKM_C_3, CKM_C_4, CKM_C_5, CKM_Am_1
3	Quadrant 3	CKBR_B_1, CKBR_B_2, CKBR_B_3, CKBR_B_4, CKBR_B_5, CKBR_G_1, CKBR_G_2, CKBR_G_3, CKBR_G_4, CKBR_G_5, BR_L_1, BR_L_2, BR_L_3, BR_L_4, BR_L_5, BR_T_1, BR_T_2, BR_T_3, BR_T_4, BR_T_5, BR_K_1, BR_K_2, BR_K_3, BR_K_4, BR_K_5, CHA_K_1, CHA_K_2, CHA_K_3, CHA_K_4, CHA_K_5, CHA_N_1, CHA_N_2, CHA_N_3, CHA_N_4, CHA_N_5, CHA_S_1, CHA_S_2, CHA_S_3, CHA_S_4, CHA_S_5, CKM_Am_2, BGK_A_5
4	Quadrant 4	DVN_T_1, DVN_T_2, DVN_T_3, DVN_T_4, DVN_T_5, DVN_C_2, DVN_C_3, DVN_C_4, DVN_C_5, DVN_M_1, DVN_M_2, CKM_Am_3, CKM_Am_4, CKM_Am_5, BGK_A_1, BGK_A_2, BGK_A_3, BGK_A_4, BGK_K_4, BGK_K_5, HVR_Ba_1, HVR_Ba_2, HVR_Ba_3, HVR_Ba_4, HVR_Ba_5, HVR_By_1, HVR_By_2, HVR_By_3, HVR_By_4, HVR_By_5, HVR_Mo_1, HVR_Mo_2, HVR_Mo_3, HVR_Mo_4, HVR_Mo_5

took peak probability at 14 in the range of 1 to 15 subpopulations. The model with $K=14$ clusters showed a higher likelihood than all other K s indicating the presence of 14 population clusters across the sampled populations (Fig. 12). Each vertical line represents an individual's probability of belonging to one of K clusters (represented by the various colors) or a combination thereof if ancestry is mixed. Site order left to right: 1 Davanagere, 2 Haveri, 3 Dharwad, 4 Belagavi, 5 Chikkaballapur, 6 Kolar, 7 Bengaluru rural, 8 Bagalkot, 9 Chamarajanagara, 10 Chikkamagaluru, 11 Shivamogga (Fig. 13).

The analysis distinguished 14 population clusters with fairly homogenous population (Belagavi, Chikaballapura, Bagalkot, Chamarajanagara and Chikkamagaluru). The remaining clusters showed populations with a smaller proportion of individuals with mixed ancestry (Davanagere, Haveri, Dharwad, Kolar, Bengaluru rural and Shivamogga). The analysis also indicated that populations from Davanagere, Kolar, and Shivamogga with larger proportion of individuals with mixed ancestry.

4.3 Frequency of mono and bipartite virus particle in *B. tabaci* populations across tomato growing ecosystems of Karnataka

4.3.1 Tomato Leaf Curl disease incidence.

Disease incidence of ToLCV was recorded during the survey in each field on randomly selected 10 tomato plants by counting number of infested leaves out of total number of leaves per plant during the sample collection. The details of the places surveyed, ToLCV incidence in percentage, mean per cent disease incidence (PDI) and category of infection at each location are presented in Table 16.

The symptoms of naturally infected plants of tomato were upward curling of the lower leaves, reduction in size of newly emerged leaves, crinkling, puckering and slight chlorosis followed by severe reduction of internodal length which leads to stunting of plants. The mean per cent disease incidence of tomato leaf curl virus (ToLCV) on tomato in the surveyed areas ranged from 4.41 to 19.26 per cent. Among the districts surveyed, the highest disease incidence of ToLCD on tomato was recorded in Chikballapura district (19.26 %), followed by Davanagere (17.41 %), Bengaluru rural (16.11 %), Kolar (15.81 %), Haveri (9.58 %), Belagavi (8.55 %),

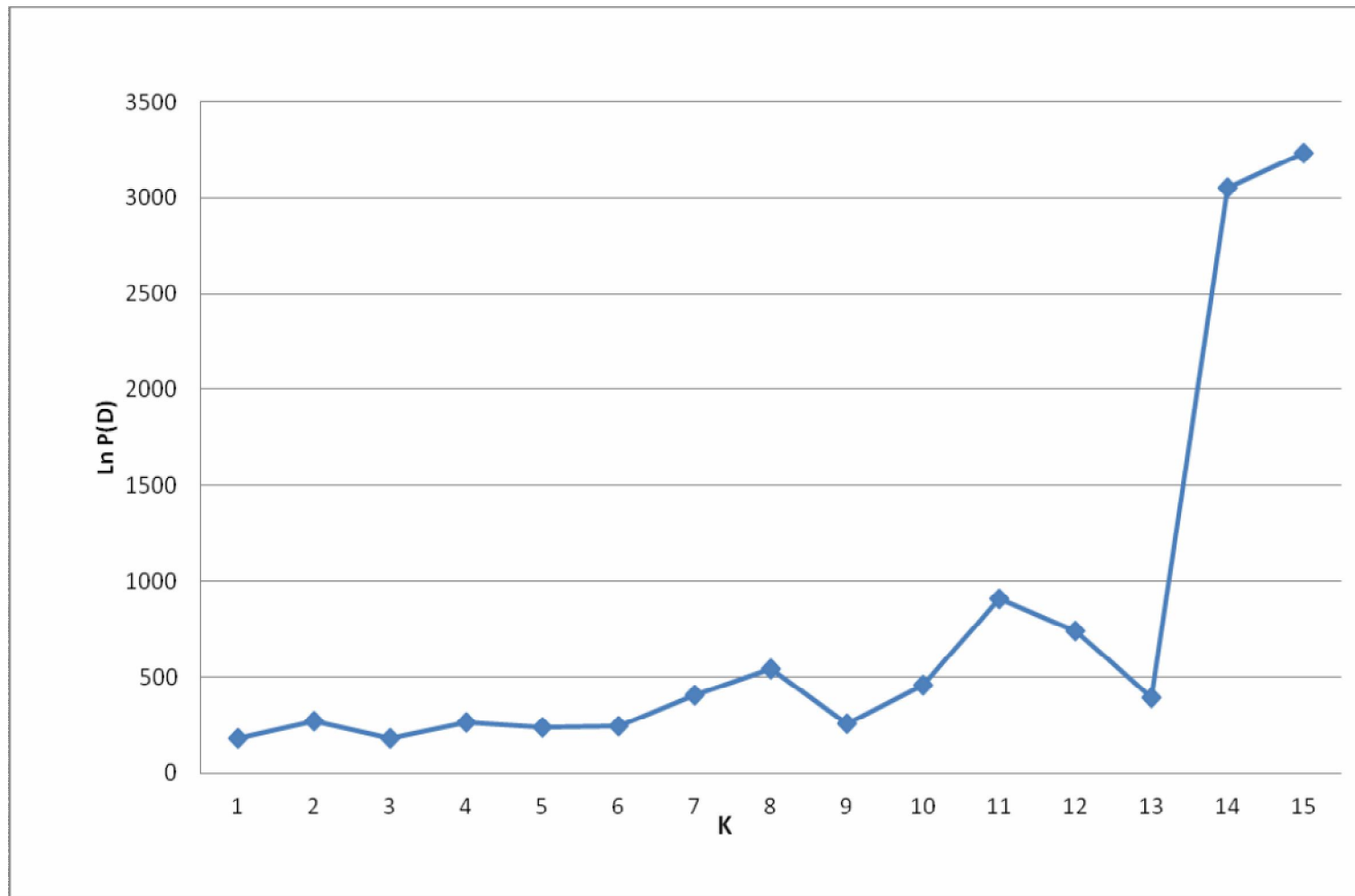


Fig. 12. $\ln P(D)$ values presented as a function of the number of clusters. The largest $\ln P(D)$ values were found for $K=14$ (among 1000 runs)

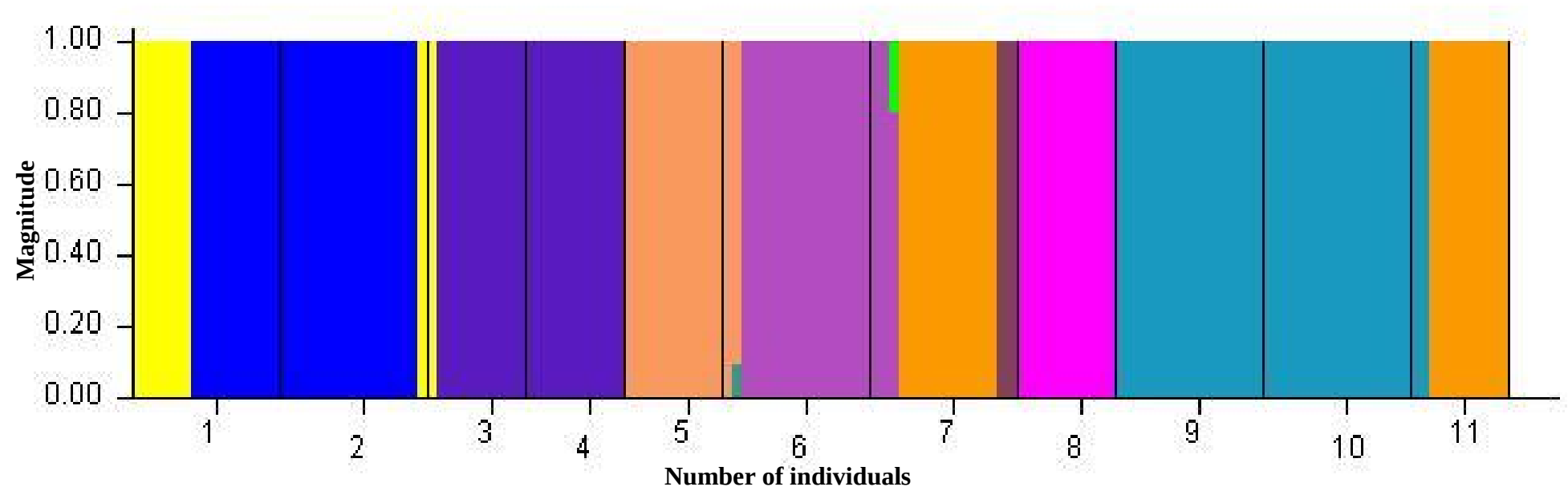


Fig 13. Population genetic structure of 140 individuals of *Bemisia tabaci* at K=14 sampled across Karnataka

Table 16. Tomato leaf curl virus (ToLCV) disease incidence across the sampling regions of Karnataka

Sampling Districts/Locations	Per cent ToLCV incidence	Mean PDI	Infection Category *
1. Davanagere			
Mayakonda	18.40	17.41	R
Tholahunase	14.18		R
Channapura	19.64		R
2. Haveri			
Battikoppa	13.56	9.58	R
Byadagi	7.29		R
Motebennur	7.91		R
3. Dharwad			
Narendra	5.34	4.84	R
Garag	4.35		R
4. Belagavi			
Muttaga	3.79	8.55	R
Banakatti	13.31		R
5. Chikkaballapura			
Buragamakalahalli	23.99	19.26	MR
Gollahalli	14.53		R
6. Kolar			
Balageri	19.83	15.81	R
Sugaturu	13.27		R
Pathapalli	14.32		R
7. Bengaluru rural			
Kelaginanaikarahalli	21.49	16.11	MR
Lakshmidevipura	12.65		R
Tubagere	14.21		R
8. Bagalkot			
Kaladagi	3.26	4.41	R
Hiresamsi	5.57		R
9. Chamarajanagara			
Nanjedevanapura	7.87	6.51	R
Kengaki	5.40		R
Sattegala	6.25		R
10. Chikkamagaluru			
Allampura	5.36	5.76	R
Chikkagouja	5.61		R
Amble	6.32		R
11. Shivamogga			
Alada halli	5.40	6.25	R
Kunchenahalli	7.09		R

* R= Resistant, MR= Moderately Resistant

Chamarajanagara (6.51 %), Shivamogga (6.25 %), Chikkamagaluru (5.76 %), Dharwad (4.84 %) and the least incidence was recorded in Bagalkot district (4.41 %). The infection category for all locations surveyed was also presented (Table 16).

4.3.2 Determination of frequency of mono and bipartite virus particle distribution

Frequency of mono and bipartite particle in *B. tabaci* collected from different agro climatic zones of Karnataka was determined by PCR using mono and bipartite particle specific primers viz. Pm (F: GGCTAGGCTGTGTTGCACTT, R: GTCGAC CCGCATTATCTAAA) and Pb (F: TTGACGAGACCAATCGACG, R: CATCAA GATCTGTAGAGAGC). Testing of randomly selected 55 whitefly DNA samples from eleven populations (five from each district) revealed the occurrence of virus particles in the different locations. The monopartite virus particles were amplified at 270 bp region whereas, the bipartite virus particles were amplified at 477 bp region (Plate 12). The details of the results are presented in the Table 17.

The results revealed the occurrence of monopartite, bipartite and both virus particles in some individuals of whiteflies analysed. The presence (+) and absence (-) of virus particles was represented in the Table 17. Thirty one (31) individuals out of 55 individuals analysed did not carry any virus particle. In remaining 24 individuals, monopartite, bipartite and both mono and bi partite virus particles were detected in seventeen (17), one (1) and six (6) individuals respectively.

4.3.3 Distribution frequency of virus particles among the *B. tabaci* population

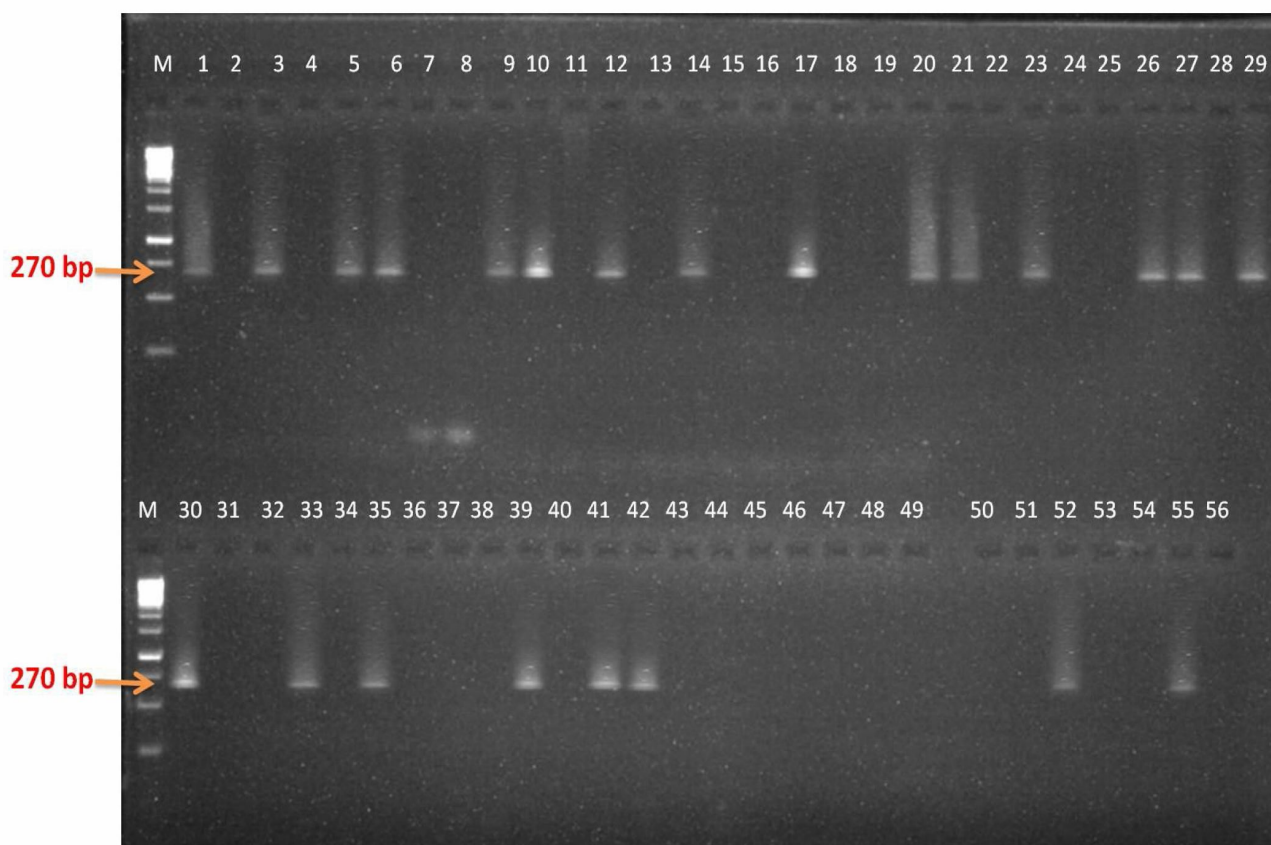
The distribution frequency of monopartite, bipartite and both mono and bipartite virus particles among the *B. tabaci* population analyzed from different districts are presented in the Table 18 and Fig. 14.

Among the districts surveyed, Davanagere district, depicted 60 per cent of individuals carrying monopartite virus particles alone whereas, remaining 40 per cent of the individuals did not carrying any virus particles. There were no record of presence of bipartite virus particles from Davanagere district. From Haveri, the result revealed 40 per cent of tested individuals carrying only monopartite virus particles, 20

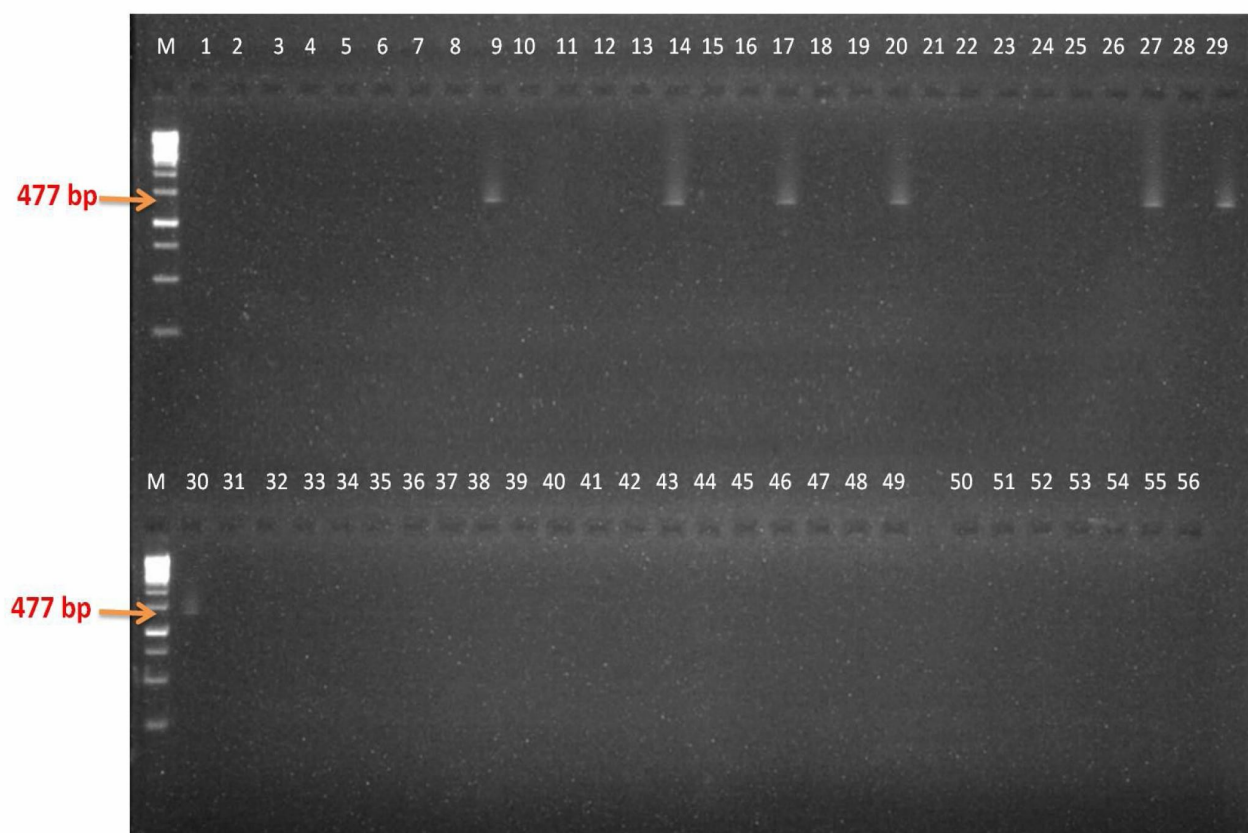
Table 17. PCR amplification status of monopartite and bipartite virus particles in populations of *Bemisia tabaci* across the sampling regions of Karnataka

Sl. No.	Sample Code	Monopartite	Bipartite	Sl. No.	Sample Code	Monopartite	Bipartite
1	DVN_M_1	+	-	29	KLR_P_1	+	+
2	DVN_M_4	-	-	30	KLR_P_5	+	+
3	DVN_C_2	+	-	31	BR_K_2	-	-
4	DVN_C_4	-	-	32	BR_K_5	-	-
5	DVN_T_3	+	-	33	BR_L_3	+	-
6	HVR_Ba_4	+	-	34	BR_T_1	-	-
7	HVR_Ba_5	-	-	35	BR_T_2	+	-
8	HVR_By_1	-	-	36	BGK_K_1	-	-
9	HVR_By_5	+	+	37	BGK_K_2	-	-
10	HVR_Mo_4	+	-	38	BGK_K_3	-	-
11	DWD_N_1	-	-	39	BGK_H_3	+	-
12	DWD_N_2	+	-	40	BGK_H_4	-	-
13	DWD_N_5	+	-	41	CHA_N_4	+	-
14	DWD_G_3	-	+	42	CHA_N_5	+	-
15	DWD_G_4	-	-	43	CHA_K_1	-	-
16	BLV_M_1	-	-	44	CHA_K_5	-	-
17	BLV_M_2	+	+	45	CHA_S_1	-	-
18	BLV_M_3	-	-	46	CKM_Al_1	-	-
19	BLV_B_3	-	-	47	CKM_Al_5	-	-
20	BLV_B_4	+	+	48	CKM_C_4	-	-
21	CKBR_B_1	+	-	49	CKM_C_5	-	-
22	CKBR_B_5	-	-	50	CKM_Am_2	-	-
23	CKBR_G_3	+	-	51	SHI_A_2	-	-
24	CKBR_G_4	-	-	52	SHI_A_3	+	-
25	CKBR_G_5	-	-	53	SHI_A_4	-	-
26	KLR_B_2	+	-	54	SHI_K_1	-	-
27	KLR_S_1	+	+	55	SHI_K_2	+	-
28	KLR_S_2	-	-				

+ : Presence of amplicon - : Absence of amplicon



a) Monopartite virus particles



b) Bipartite virus particles

Plate 12. PCR amplification patterns in a) Monopartite and b) Bipartite virus particle by the specific DNA markers in *B. tabaci* adults.

Table 18. Distribution frequency of virus particles among the *Bemisia tabaci* population

[illegible]

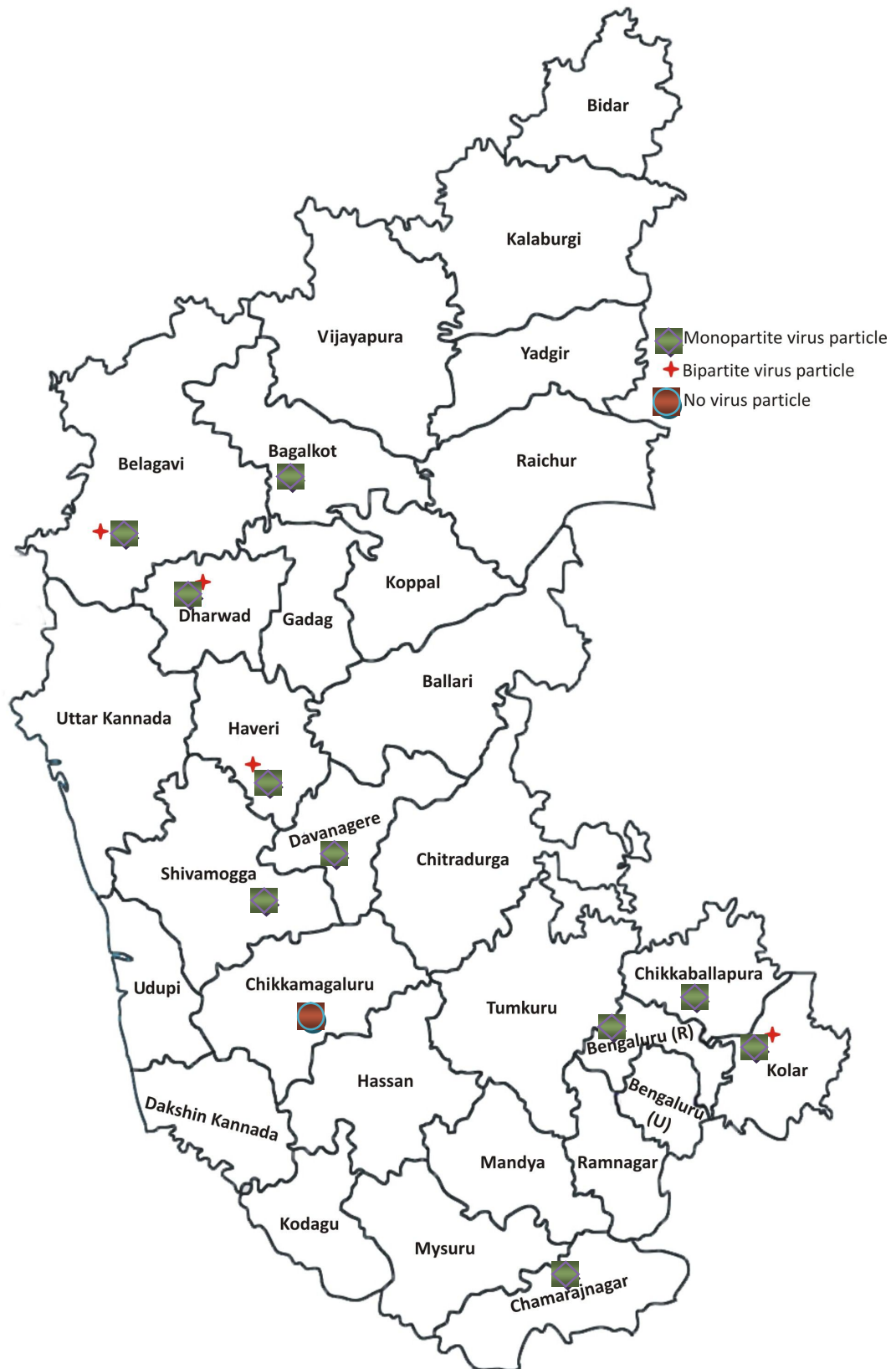


Fig 14. Distribution frequency of monopartite and bipartite virus particles in Karnataka

per cent of individuals carrying both mono and bipartite virus particles, remaining 40 per cent of tested individuals did not carrying any virus particles. Dharwad populations revealed that, out of total individuals tested, 40 per cent of individuals carrying only monopartite virus particles, 20 per cent of individuals carry only bipartite virus particles. Remaining 40 per cent of the individuals did not carry any virus particles. Among the individuals tested from Belagavi district, 40 per cent of the population detected with both mono and bipartite virus particles and no virus particle detected from remaining 60 per cent of the individuals tested. Forty per cent of only monopartite virus particles were detected from Chikkaballapura population tested and bipartite virus particles were absent among the individuals tested. Remaining 60 per cent of the population detected with no virus particles (Table 18).

Among the whiteflies analysed from Kolar district, 20 per cent of the individuals detected with only monopartite virus particles, 60 per cent with both mono and bipartite virus particles. Whereas, remaining 20 per cent of the individuals did not carry any virus particles. From Bengaluru rural population, 40 per cent of the individuals found with only monopartite virus particles and remaining 60 per cent free virus particles. Bagalkot population detected with 20 per cent of only monopartite virus particles and 80 per cent of population did not carry any virus particles. Individuals tested from Chamarajanagara and Shivamogga districts detected with 40 per cent of only monopartite virus particles each and remaining 60 per cent of the tested individuals free from virus particles. The result obtained from Chikkamagaluru district showed that, none of the individuals were detected with the virus particles (Table 18).

Overall frequency distribution of virus particles from tested *B. tabaci* population resulted that, among the individuals studied, 30.90 per cent of the individuals detected with only monopartite, 1.82 per cent of the individuals with only bipartite and 10.36 per cent with both mono and bipartite virus particles all together with 43.64 per cent of the total population detected with virus particles studied. The remaining 56.36 per cent of the population, among the total tested population were free from virus particles (Table 18).

4.4 Variation for traits related to whitefly resistance in tomato association mapping panel (TAMP)

A set of 260 tomato accessions from diverse sources were subjected to field evaluation against *Bemisia tabaci* resistance. Further, accessions were assessed for biochemical parameters like chlorophyll, phenols, tannin, terpenoid and biophysical parameters such as trichome type and trichome density to understand the variation for traits related whitefly resistance.

4.4.1 Field evaluations of tomato accessions

Field trial was conducted at College of Horticulture (COH), UHS, campus GKVK post, Bengaluru during *rabi* and summer of 2016-17. Seedling of 25 days old were transplanted in an Augmented Block Design with regular resistant and susceptible lines viz., Nandi, Sankranti and Pusa ruby as checks, spaced at 60 cm row to row and 45 cm plant to plant. The UHS packages of practices were followed except for the whitefly management.

Analysis of variance for whitefly population at two seasons are presented in Table 19 and for biochemical and biophysical parameters recorded in Table 20. The analysis of variance indicated highly significant differences among the accessions. The descriptive parameters viz., range, mean, variance, standard error, coefficient of variation for all the characters were presented in the Table 21 and Table 22. The genetic variability parameters viz., phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), heritability in broad sense (h^2), genetic advance and genetic advance mean (GAM) for all the all the characters were studied (Table 23). The correlation co-efficient for all component traits whitefly population and per cent disease incidence was presented in the Table 26. The mean values of different traits of tomato accessions is presented in Appendix IX.

4.4.2 Whitefly population

4.4.2.1 During *rabi* season

The variation observed for whitefly population ranged from 0.30 to 3.31 per plant with the overall mean of 1.57 ± 0.03 per plant during *rabi* field evaluation. Comparatively lower number of whitefly populations were observed during the

Table 19. Analysis of variance (ANOVA) for whitefly nymph population in minicore accessions field evaluated during *rabi* and summer seasons 2016-17 at COH, Bengaluru

Source of variation	Mean Sum of Squares		
	<i>Rabi</i>	Summer	Avg. of both season
Block	0.05	14.62*	5.24
Entries	0.28**	56.26**	14.42 **
Checks	1.87**	189.64**	63.30 **
Accessions	0.25*	55.14**	14.10 **
Checks vs. Accessions	4.61**	77.33**	1.04
Error	0.09	4.36	2.69

*Significant at 5 per cent probability level

**Significant at 1 per cent probability level

Table 20. Analysis of variance (ANOVA) for biochemical and biophysical traits in minicore accessions field evaluated during summer 2016-17 at COH, Bengaluru

Source of variation	Mean Sum of Squares					
	Df	Phenols	Tannins	Terpinoid	Chlorophyll	Trichome Density
Block	12	3.03**	4.72**	16020.58*	47.20*	128550.30**
Entries	262	5.55**	3.52**	21859.79**	32.69*	70117.78**
Checks	2	21.62**	0.02	252964.50**	75.90*	294352.90**
Accessions	259	4.97**	3.31**	18766.53**	32.47*	68656.55**
Checks vs. Accessions	1	124.16**	63.61**	360807.00**	1.02	105.78
Error	24	0.08	0.18	5907.18	11.16	3985.19

*Significant at 5 per cent probability level **Significant at 1 per cent probability level

experiment (Table 21). ANOVA has shown significant variation for whitefly across tomato minicore accessions but highly significant differences between checks and accessions (Table 19).

4.4.2.2 During summer season

Summer field evaluation recorded wide variation for whitefly population. ANOVA has shown highly significant variation across tomato minicore accessions and also between checks and minicore accessions (Table 19). The population was gradually decreased over the different days interval. 30 days after transplanting (DAT), the whitefly population was ranged from 19.80 to 62.20 nymphs/ plant with the mean 38.27 nymphs/ plant. At 45 DAT, whitefly population was ranged from 19.60 to 53.00 nymphs/ plant with the mean of 34.31 nymphs/ plant. Comparatively lesser population was recorded at 60 DAT with the population ranged from 12.00 to 52.60 nymphs/ plant and mean of 29.20 nymphs/ plant (Appendix X). The mean whitefly population was ranged from 20.13 to 54.60 nymphs/ per plant with a mean of 34.35 ± 0.47 nymphs/ per plant. Summer season favored the multiplication of whitefly population (Table 21).

4.4.2.3 Per cent Disease Incidence (PDI)

Per cent disease incidence was recorded 60 days after transplanting during summer season 2016-17. The PDI was ranged from zero per cent to 66.67 per cent with the mean PDI of 22.50 (Appendix X). The tomato accessions with disease incidence were categorized into six groups viz., immune, resistant, moderately resistant, moderately susceptible, susceptible and highly susceptible. Among 260 tomato accessions, 68 accessions were recorded as immune with zero per cent infection, 29 accessions were moderately resistant, 66 were moderately susceptible, 73 were susceptible and remaining 24 accessions were highly susceptible to ToLCV disease (Appendix XI).

4.4.3 Biochemical analysis in tomato accessions

4.4.3.1 Phenol Content

A wide variation was observed for phenol content across the accessions and the mean values ranged from 1.77 to 14.67 mg with a mean of 6.57 ± 0.14 mg (Table

Table 21. Descriptive statistics of whitefly populations in 260 tomato minicore accessions.

Seasons	Range		Mean	Std. Error	C.V. (%)
	Minimum	Maximum			
Rabi (No. of nymph/ plant)	0.30	3.31	1.57	0.03	32.84
Summer (No. of nymph/ plant)	20.13	54.6	34.35	0.47	20.25
Avg. of both seasons (No. of nymph/ plant)	10.22	28.96	17.96	0.24	19.59

Table 22. Descriptive statistics of biochemical and biophysical component traits in 260 tomato minicore accessions.

Component traits	Range		Mean	Std. Error	C.V. (%)
	Minimum	Maximum			
Phenol (mg)	1.77	14.67	6.57	0.14	33.99
Tannin (g)	2.58	12.10	5.70	0.11	32.33
Terpinoid(mg)	145.52	913.86	510.25	8.47	26.90
Chlorophyll	23.76	63.67	45.63	0.38	13.43
Trichome density (mm²)	151.15	1500.50	861.35	16.17	30.45

22). Analysis of variance (ANOVA) shown highly significant (<1% probability) variation across the tomato accessions and also for checks and accessions (Table 20). Higher PCV (32.22 %) and GCV (31.90 %) values along with high heritability (98.00 %), genetic advance (4.30 %) and expected genetic advance mean (65.18 %) were observed (Table 23).

4.4.3.2 Tannin

The tannin content ranged between 2.58 to 12.10 g with the mean of 5.70 ± 0.11 g, (Table 22). ANOVA has shown highly significant differences across tomato accessions and also checks vs. accession analysis (Table 20). Higher GCV (29.45 %), PCV (30.37 %), heritability (94 %) with genetic advance of 3.36 per cent and 58.82 per cent of expected genetic advance mean were observed (Table 23).

4.4.3.3 Terpenoid

The terpenoid content ranged from 145.52 to 913.86 mg with a mean of 510.25 ± 8.47 mg (Table 22). ANOVA has shown highly significant differences across tomato accessions and also checks vs. accession analysis (Table 20). High GCV (21.10 %) and PCV (25.90 %), moderate heritability of 66.00 per cent and expected genetic advance of 35.40 per cent were observed for this trait (Table 23).

4.4.3.4 Chlorophyll

Chlorophyll content varied across the tomato accessions. The chlorophyll content ranged from 23.76 to 63.67 with a mean of 45.63 ± 0.38 (Table 22). ANOVA has shown significant differences across tomato accessions but non significant differences between checks and accessions (Table 20). Genetic variability parameters showed low GCV (12.10 %) and PCV (9.63 %) along with moderate heritability (63.00 %) and moderate expected genetic advance mean (15.80 %) (Table 23).

4.4.4 Biophysical analysis in tomato accessions

4.4.4.1 Trichome density

Trichome density varied across the tomato accessions, ranged from 155.15 to 1500.50 per mm^2 with the mean of 861.35 ± 16.17 per mm^2 (Table 22). ANOVA has

Table 23 . Genetic variability parameters of biochemical and biophysical component traits in 260 tomato minicore accessions

Component traits	GCV (%)	PCV (%)	h² (%)	GA	GAM
Phenol	31.90	32.22	98.00	4.30	65.18
Tannin	29.45	30.37	94.00	3.36	58.82
Terpinoid	21.10	25.90	66.00	181.07	35.40
Chlorophyll	9.63	12.10	63.00	7.21	15.80
Trichome density	28.09	29.03	94.00	482.39	55.99

GCV= Genotypic coefficient of variability, **PCV**= Phenotypic coefficient of variability, **h²**= Heritability, **GA**= Genetic advance, **GAM**= Genetic Advance Mean

shown highly significant differences across tomato accessions but non significant differences between checks and accessions (Table 20). Genetic variability parameters showed high GCV (28.09 %), PCV (29.03 %), heritability (94.00 %), genetic advance (482.39 %) and expected genetic advance mean (55.99 %) (Table 23).

4.4.4.2 Influence of trichome type on *B. tabaci* population

Different types of trichomes were recorded from 260 tomato accessions the data are analyzed and presented in the Appendix XII. It was clear from the tomato accessions having different types of trichomes were grouped into 12 groups (X_1 to X_{12}) and its effect was compared with the *B. tabaci* population recorded during *rabi* and summer season 2016-17 at COH, Bengaluru. Results are presented in the Table 24.

4.4.4.2.1 Whitefly population during *rabi* season

Rabi field evaluation recorded significantly lower number of whitefly population in accession group, X_4 (Type III, V, VII) (1.52/ plant) followed by X_1 (Type III, V) (1.53/ plant), X_{12} (Type I, II, III, IV, V, VII) (1.53/ plant) and X_8 (Type I, III, IV, V, VII) (1.62/ plant) were statistically on par with each other. Accession group, X_3 (Type III, IV, V) has recorded significantly higher number of whiteflies (1.77/ plant) as compared to all other and was followed by X_7 (Type III, IV, V, VII) (1.72/ plant) which was on par with X_{10} (Type I, II, III, V, VII) (1.67/ plant) and X_9 (Type I, III, IV, V, VII) (1.66/ plant) (Table 24).

4.4.4.2.2 Whitefly population during summer season

During summer season evaluation, *B. tabaci* population significantly lowest in accession group, X_{12} (Type I, II, III, IV, V, VII) with 26.50 whiteflies per plant and followed by X_{10} (Type I, II, III, V, VII) (29.73/ plant) which was on par with X_5 , X_7 , X_{11} and X_9 . Significantly higher number of whiteflies were recorded from accession group, X_2 (Type I, III, V) with 41.75 whiteflies per plant which was on par with X_1 (Type III, V) with 40.95 whiteflies (Table 24).

The 260 tomato accessions were categorized based on presence of different trichome type viz., Type I, II, III, IV, VI and VII. Type I trichome was recorded in

Table 24. Effect of trichome type on *Bemisia tabaci* population in tomato accessions during *rabi* and summer season 2016-17 at COH, Bengaluru

Accessions group*	Whitefly population (Nymphs/ plant)	
	<i>Rabi</i>	Summer
X ₁	1.53 (0.73-2.33)	40.95 (33.8-54.6)
X ₂	1.63 (0.80-2.13)	41.75 (36.67-49.73)
X ₃	1.77 (1.00-3.07)	31.62 (25.07-36.33)
X ₄	1.52 (0.27-2.80)	37.17 (22.60-51.13)
X ₅	1.63 (1.07-2.07)	30.67 (25.27-37.13)
X ₆	1.61 (0.60-3.13)	33.45 (25.73-48.93)
X ₇	1.72 (0.80-2.53)	30.98 (25.13-40.40)
X ₈	1.62 (0.93-2.73)	32.95 (26.53-36.47)
X ₉	1.66 (0.93-2.27)	31.18 (24.33-37.33)
X ₁₀	1.67 (0.73-3.53)	29.73 (20.53-46.53)
X ₁₁	1.62 (1.53-1.73)	30.98 (29.67-32.33)
X ₁₂	1.53 (0.60-2.73)	26.50 (20.13-43.40)
SEm ±	0.03	0.62
C. D @ 5 %	0.09	1.83

*Tomato accessions with different trichome types

X₁= Type III, V

X₅= Type I, III, IV, V

X₉= Type I, III, IV, V, VII

X₂= Type I, III, V

X₆= Type I, III, V, VII

X₁₀= Type I, II, III, V, VII

X₃= Type III, IV, V

X₇= Type III, IV, V, VII

X₁₁= Type II, III, IV, V, VII

X₄= Type III, V, VII

X₈= Type I, III, IV, V, VII

X₁₂= Type I, II, III, IV, V, VII

101 tomato accessions, Type II recorded in all 43 accessions, Type III in 258 accessions, Type IV in 50 accessions, Type V in 260 accessions and Type VII were recorded in 229 accessions (Table 25 and Appendix XIII). The mean whitefly population was recorded non significant result among the trichome types during the *rabi* season. The whitefly population during summer season has shown significant difference among the trichome type. Forty five days after transplanting (DAT), significantly lesser population was recorded in the populations with Type VII trichomes (29.36 nymphs/ plant) which was on par with the accessions having Type IV trichomes (29.43 nymphs/ plant), followed by Type I (31.63 nymphs/ plant), Type V, Type II and Type III. Same trend was followed during 60 DAT also, accessions with Type VII trichomes has recorded significantly lesser population (25.19 nymphs/ plant), which was on par with the accessions having Type IV trichomes (25.80 nymphs/ plant), followed by Type I (27.57 nymphs/ plant). Mean whitefly population from 30, 45 and 60 DAT also followed with the same trend *i.e.*, Trichome Type VII containing accessions were recorded significantly lesser whitefly population (29.37 nymphs/ plant) and on par result were observed in populations with Trichome IV (29.37 nymphs/ plant) which were followed by Type I (Table 25 and Appendix XIII).

4.4.5 Correlation co-efficient for biochemical, biophysical traits, whitefly population and per cent disease incidence (PDI).

The simple correlation studies were carried out to know the nature of relationship existing among biochemical and biophysical parameters and their influence on whitefly population during summer season (Table 26).

Phenol content exhibited highly significant and positive association only with tannin (0.340) and positive association with terpenoid content (0.002) trichome density (0.008) and negatively correlated with chlorophyll. Whereas, phenol content was significantly and negatively correlated with whitefly population (0.018) 60 days after transplanting (DAT) and negatively correlated with total whitefly population during the summer (-0.020) and positive correlation observed with per cent disease incidence (0.100) (Table 26).

The correlation with tannin content was positively correlated with terpenoid content (0.017), chlorophyll content (0.075) and negatively correlated with trichome

Table 25. Influence of glandular and non glandular trichomes on whitefly population

Sl. No.	Trichome type	No. of accessions	Whitefly population during <i>Rabi</i> season	Whitefly population during summer season		
				45 DAT	60 DAT	Mean
Glandular trichomes						
1	Type I	101	1.63	31.63	27.57	31.64
2	Type IV	50	1.65	29.43	25.80	29.86
3	Type VII	229	1.64	29.36	25.19	29.37
Non- glandular trichomes						
4	Type II	43	1.58	34.33	29.28	33.93
5	Type III	258	1.58	34.36	29.31	33.96
6	Type V	260	1.58	33.83	29.04	33.49
SEm			NS	0.31	0.36	0.25
CD @ 5 %				0.98	1.15	0.80

DAT: Days After Treatment,

NS: Non Significant

Table 26. Correlation co-efficient for component traits and whitefly population in minicore accessions field evaluated during summer season, 2016-17 at COH, Bengaluru

Component traits	Phenols	Tannins	Terpinoid	Chlorophyll	Trichome density	Whitefly Population				PDI
						30 DAT	45 DAT	60 DAT	Mean population	
Phenols	1	0.340**	0.002	-0.006	0.008	0.075	0.079	-0.018*	-0.020	0.100
Tannins		1	0.017	0.075	-0.010	0.114	0.096	-0.083	0.115	0.090
Terpinoid			1	0.096	0.025	-0.041	-0.124*	-0.057	-0.094	0.016
Chlorophyll				1	0.112*	0.022	-0.021	-0.018	0.030	0.026
Trichome density					1	0.047	-0.052	-0.014	0.000	0.007
30 DAT						1	0.752**	0.260**	0.805**	0.272**
45 DAT							1	0.579**	0.926**	0.334**
60 DAT								1	0.744**	0.364**
Mean population									1	0.395**
PDI										1

**₁. Correlation is significant at the 0.01 level

*₁. Correlation is significant at the 0.05 level

DAT= Days After Transplanting

density (-0.010). It was also negatively correlated with whitefly population 60 DAT (0.083) whereas, positively correlated with whitefly population at 30 and 45 DAT and total whitefly population (0.115) and PDI (0.090) (Table 26).

Terpenoid content was positively correlated with chlorophyll content (0.096) and trichome density (0.025). It has exhibited significant and negative correlation with whitefly population at 45 DAT (-0.124) and negative correlation with whitefly population at 30 DAT (-0.041), 60 DAT (-0.057) and total population (-0.094). Whereas, it has recorded positive correlation with per cent disease incidence (0.016) (Table 26).

Correlation with chlorophyll content showed significant and positive association with trichome density (0.112) and negative correlation with whitefly population at 45 DAT (-0.021) and 60 DAT (-0.018). It was positively correlated with whitefly population at 30 DAT (0.022) and total population (0.030). Whereas, it has recorded positive correlation with per cent disease incidence (0.026) (Table 26). Further, trichome density was significantly and negatively correlated with whitefly population 60 DAT (-0.014) and negatively correlated with 45 DAT (-0.052) but positively correlated with whitefly population at 30 DAT (0.047), total population (0.000) and PDI (0.007) (Table 26).

Whitefly population at 30 days after transplanting was highly significant (<0.001) and positive correlation with whitefly population at 45 DAT (0.752), 60 DAT (0.260), total population (0.805) and per cent disease incidence (0.272) (Table 26). The correlation with whitefly population at 45 DAT was highly significant (<0.001) and positive with whitefly population at 60 DAT (0.579), total population (0.926) and per cent disease incidence (0.334) (Table 26).

Correlation with whitefly population at 60 DAT was highly significant and positive with total whitefly population (0.744) and per cent disease incidence (0.364). Total whitefly population was highly significant and positively correlated with PDI (0.395) (Table 26).

During summer season 2016-17, biochemical parameters viz., phenols and terpenoids have shown significant negative correlation with whitefly population at 60 and 45 DAT, respectively. Whereas negatively correlated with total population and 30

DAT, 60 DAT and total population. Tannin and chlorophyll was negatively correlated with whitefly population 60 DAT and 45, 60 DAT. Biophysical parameter, trichome density has shown significant negative correlation with whitefly population, 60 DAT and negatively correlated at 45 DAT.

4.4.6 Molecular analysis of tomato accessions

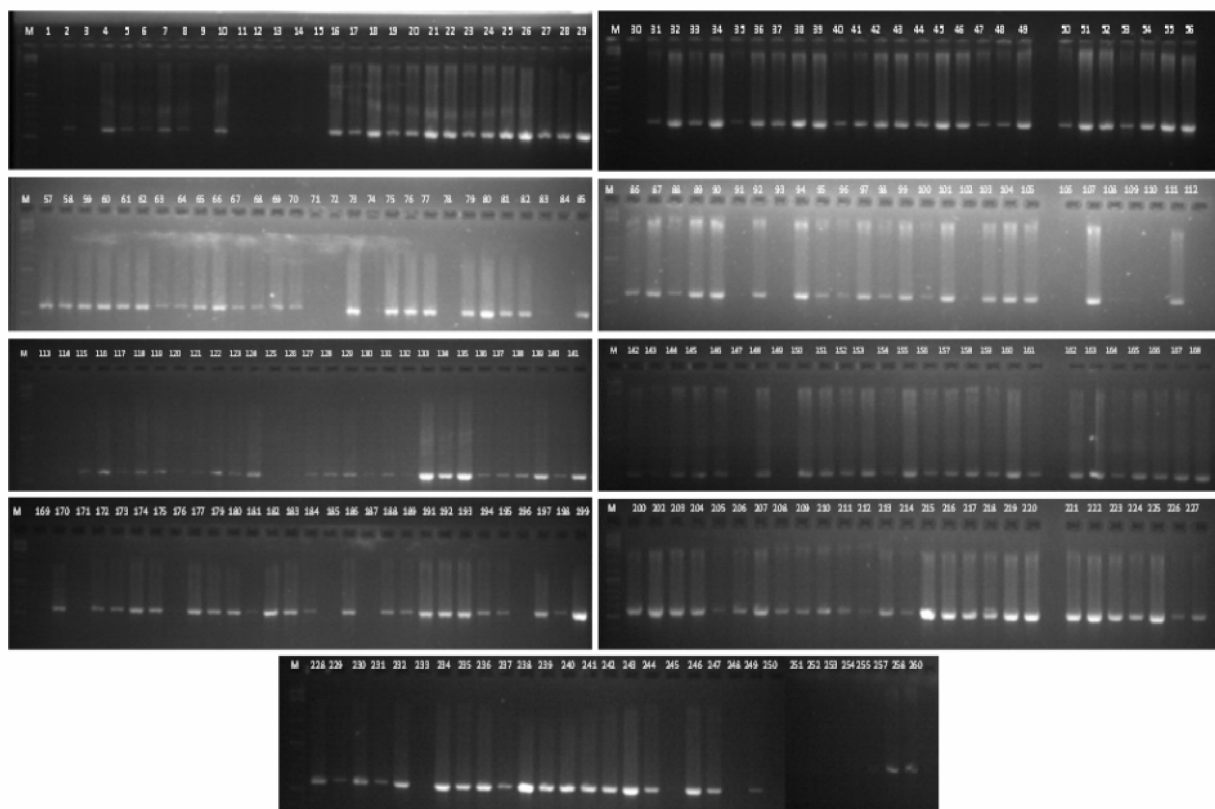
4.4.6.1 Population genetic analysis using microsatellite markers

Genetic diversity of tomato association mapping panel was assessed with Simple Sequence Repeats (SSR) markers. A total of 260 tomato minicore accessions were arranged in five different groups based on their source of collections and DNA samples from these five groups (populations) were genotyped using SSR markers (Appendix XIV). A set of 40 microsatellite primer pairs were chosen through an initial screening of larger set used to understand the structure and genetic variability of populations of tomato accessions (Appendix VIII). DNA samples were amplified by using the multiplex PCR wherever possible and rest were amplified singly (Plate 13).

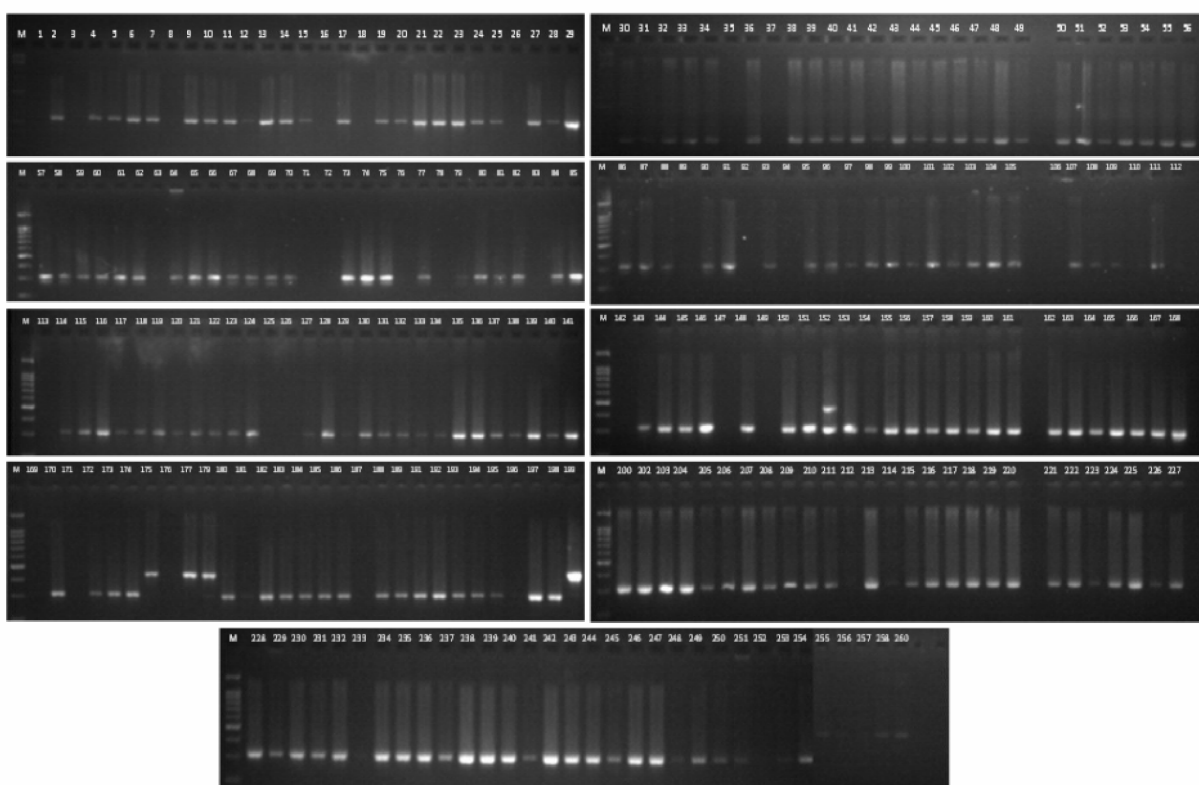
4.4.6.2 Polymorphism and allelic frequency

Number of alleles (N_a) among the polymorphic microsatellite loci ranged between 2.0 and 4.60 across the samples. A total of 122 alleles were recorded for the 40 microsatellite loci screened across 5 populations of tomato. The most diverse locus, BF-CHVR-2-616 recorded 4.6 alleles followed by Mi23 and FBTGS0318 with 4.0 alleles each and the least diverse locus, Pb had 2.0 alleles preceded by CD2, BW3 and BF-CHVR-08-2155 with 2.20 alleles each across the populations. The average number of alleles across all the microsatellite loci stood at 2.60, indicating the validity of the sample size selected for the present study. Effective number of alleles (N_e) that provides a good measure of genetic variation in accordance with population size, was maximum for the locus BF-CHVR-12-616 (3.595) followed by LEaat1 (2.898) and BF-CHVR-10-3817 (2.839). The loci BW3 recorded the minimal value of 1.445 (Table 27).

The heterozygosity (gene diversity) is considered as a reliable parameter of genetic variation among the loci. Among all the loci screened across 260 accessions,



a) Marker T0800



b) Marker P6-25

Plate 13. Allelic variation for the SSR markers across 260 tomato TAMP accessions
a) marker T0800 b) Marker P6-25

Table 27. Locus -wise information on the number of different alleles (Na), number of effective alleles (Ne), Shannon's Information Index (I), Observed Heterozygosity (Ho), Expected Heterozygosity (He), the number of migrants (Nm), Fixation Index (F) & F-statistics across tomato minicore accessions

Primer name	Na	Ne	I	Ho	He	Nm	F	Fis	Fit	Fst
P6-25	2.600	1.815	0.609	0.003	0.390	0.664	0.993	0.994	0.995	0.274
Mi23	4.000	2.583	1.044	0.014	0.586	2.112	0.982	0.979	0.981	0.106
TES0344	3.600	2.285	0.772	0.004	0.422	0.660	0.996	0.994	0.996	0.275
Pb	2.000	1.738	0.605	0.000	0.416	1.320	1.000	1.000	1.000	0.159
T0800	2.800	1.918	0.679	0.012	0.420	0.902	1.000	1.000	1.000	0.217
SINAC1 (TAQ I)	3.400	2.456	0.883	0.011	0.498	0.527	1.000	1.000	1.000	0.322
TG178	3.400	2.754	0.996	0.006	0.542	0.850	1.000	1.000	1.000	0.227
T0302	2.800	2.188	0.801	0.004	0.476	0.950	1.000	1.000	1.000	0.208
PM3	3.800	2.306	0.895	0.003	0.479	2.302	0.995	0.995	0.996	0.098
TY-1/3	3.200	2.216	0.822	0.003	0.459	0.548	1.000	0.995	0.996	0.313
CD2	2.200	2.007	0.616	0.005	0.374	0.509	1.000	1.000	1.000	0.330
BW3	2.200	1.445	0.460	0.004	0.282	0.343	1.000	1.000	1.000	0.421
BW4	2.600	1.575	0.537	0.010	0.290	0.581	1.000	1.000	1.000	0.301
AVRDC-TM719	2.400	2.208	0.758	0.011	0.470	0.296	1.000	1.000	1.000	0.458
AVRDC-TM273	2.600	2.186	0.831	0.005	0.530	0.699	1.000	1.000	1.000	0.264
AVRDC-TM947	3.000	2.200	0.858	0.003	0.513	2.711	1.000	1.000	1.000	0.084
BF-CHO3	2.600	2.012	0.714	0.012	0.441	1.134	1.000	1.000	1.000	0.181
BF-CHVR-12-542	2.200	1.583	0.534	0.013	0.331	0.868	1.000	1.000	1.000	0.224
BF-CHVR-01-182	2.600	2.230	0.797	0.003	0.484	0.587	1.000	1.000	1.000	0.299
BF-CHVR-10-3817	3.400	2.839	1.084	0.013	0.632	1.369	0.983	1.000	1.000	0.154
BF-CHVR-08-2155	2.200	1.575	0.467	0.012	0.290	2.331	1.000	0.982	0.983	0.097
BF-CHVR-11-219	3.000	1.988	0.739	0.015	0.423	1.099	1.000	1.000	1.000	0.185

Contd....

Primer name	Na	Ne	I	Ho	He	Nm	F	Fis	Fit	Fst
BF-CHVR-11-648	3.000	2.131	0.841	0.021	0.504	0.876	0.992	1.000	1.000	0.222
BF-CHVR-12-616	4.600	3.595	1.313	0.027	0.698	0.720	0.833	0.991	0.994	0.258
BF-CHVR-05-290	3.000	1.872	0.673	0.058	0.417	2.783	1.000	0.822	0.837	0.082
BF-CHVR-03-3095	3.400	2.549	0.923	0.013	0.525	1.224	0.991	1.000	1.000	0.170
BF-CHVR-02-378	3.600	2.404	0.935	0.014	0.543	0.685	0.996	0.992	0.994	0.267
LEaat8	3.600	2.101	0.822	0.014	0.457	1.356	0.913	0.995	0.996	0.156
LEaat1	3.600	2.898	1.023	0.054	0.555	1.046	1.000	0.921	0.936	0.193
LEaat7	3.600	2.238	0.799	0.004	0.426	0.770	0.995	1.000	1.000	0.245
LEgata2	2.600	1.791	0.589	0.003	0.335	0.753	0.835	0.994	0.995	0.249
LEaat3	3.000	1.955	0.658	0.058	0.367	0.972	1.000	0.840	0.873	0.205
LEat18	2.800	1.880	0.613	0.013	0.335	0.261	1.000	1.000	1.000	0.489
FBTGS0321	2.600	2.013	0.784	0.002	0.496	0.237	1.000	1.000	1.000	0.513
FBTGS0244	2.400	2.014	0.695	0.003	0.443	0.969	0.994	1.000	1.000	0.205
FBTGS0318	4.000	2.532	0.958	0.004	0.520	1.197	0.926	0.994	0.995	0.173
FBTGS0289	2.600	2.077	0.737	0.061	0.453	0.775	1.000	0.924	0.943	0.244
FBTGS0209	2.600	2.238	0.804	0.024	0.482	0.800	1.000	1.000	1.000	0.238
SSR241	3.200	1.986	0.802	0.006	0.479	0.733	1.000	1.000	1.000	0.254
SSR45	2.995	2.164	0.781	0.012	0.456	1.240	0.985	1.000	1.000	0.168
Mean	2.600	1.815	0.609	0.014	0.390	1.019	0.993	0.985	0.988	0.238

Fis = (Mean He - Mean Ho) / Mean He, Fit = (Ht - Mean Ho) / Ht, Fst = (Ht - Mean He) / Ht, Nm = [(1 / Fst) - 1] / 4, Key: Mean He = Average He across the populations. Mean Ho = Average Ho across the populations, Ht = Total Expected Heterozygosity = 1 - Sum tpi² where tpi is the frequency of the ith allele for the total & Sum tpi² is the sum of the squared total allele frequencies,

the grand mean of observed heterozygosity (H_o) was 0.014, indicating a high degree of genetic diversity and possibility of a very high selection potential for the loci under study. The mean value among the loci was between 0.00 for Pb and 0.061 for FBTGS0289. The grand mean of expected heterozygosity (H_e) was 0.390. The mean heterozygosity values for loci ranged between 0.282 for BW3 and 0.698 for BF-CHVR-12-616 loci (generally, a polymorphic loci should have a minimum heterozygosity value of 0.10). The N_m values that indicate an overall number of migrants and possible divergence among the microsatellite loci was computed. The grand mean for the N_m stood at 1.019 with locus BF-CHVR-05-290 having maximum N_m value of 2.783 and the locus FBTGS0321 recorded the minimum N_m value of 0.237 (Table 27). The fixation coefficient (F_{ST} value) of population measured with 40 microsatellite markers varied from 0.082 (BF-CHVR-05-290) to 0.513 (FBTGS0321) with the mean of 0.238. The heterozygotes in F_{IT} was amounted to 0.988. Mean F_{IS} was recorded at 0.985 (Table 27).

Genetic parameters across populations based on microsatellite analysis were determined and the details of these parameters are presented in the Table 28. The number of different alleles of microsatellite loci (N_a) ranged between 1.375 and 4.150 across the populations. The most diverse population, Group 4 recorded 4.150 alleles followed by Group 1 with 3.975 alleles. The least diverse population, Group 5 had 1.375 alleles, preceded by Group 3 and Group 2 with 2.200 and 3.400 alleles, respectively. The average number of alleles across all the microsatellite loci stood at 3.020 (Table 28). Number of effective numbers of alleles (N_e), that provided a good measure of genetic variation in accordance with population size was maximum for the population Group 4 (2.692) followed by Group 1 (2.611). The population Group 5 recorded the minimal value of 1.303 (Table 28). The observed and expected heterozygosity were indicative measures of heterozygosity. The grand mean of observed heterozygosity (H_o) across all the populations was 0.008 and varied between 0.00 (Group 5) to 0.012 (Group 4). Mean expected heterozygosity (H_e) was 0.461 which was varied between 0.143 (Group 5) and 0.604 (Group 4) (Table 28). The maximum expected and observed heterozygosity among population indicated that the populations were genetically diverse. The per cent polymorphism for the loci ranged between 30.00 per cent for Group 5 and 100 per cent for Group 1, 2 and 4.

Table 28. Population-wise information on the number of different alleles (Na), number of effective alleles (Ne), Shannon's Information Index (I), Observed Heterozygosity (Ho), Expected Heterozygosity (He), Fixation Index (F) & percentage polymorphism (% P) observed across 40 microsatellite loci

Population	Na	Ne	I	Ho	He	F	%P
Group 1	3.975	2.611	1.058	0.010	0.592	0.982	100.00
Group 2	3.400	2.388	0.939	0.008	0.545	0.988	100.00
Group 3	2.200	1.961	0.661	0.008	0.423	0.986	82.50
Group 4	4.150	2.692	1.083	0.012	0.604	0.983	100.00
Group 5	1.375	1.303	0.218	0.000	0.143	1.000	30.00
Mean	3.020	2.191	0.792	0.008	0.461	0.986	82.50

Shannon's Information Index (I) was considered as a parameter for genetic variation among five populations. The I value ranged from 0.218 (Group 5) to 1.083 (Group 4). The overall mean of I was 0.792 (Table 28). Among the loci, the I value ranged from 0.460 (BW3) to 1.313 (BF-CHVR-12-616) with the mean of 0.609. (Table 27).

4.4.6.3 F co-efficient analysis

F-statistics (F-coefficients), also known as fixation indices describe the extent of inbreeding in a given population. The major components of F-statistics are F_{IS} , F_{IT} and F_{ST} ; where, 'I' represent individuals, 'S' represents sub-population and 'T' represents total population and were calculated for the tomato accessions and the results are presented in Table 27. The significant mean F_{IS} value across the population was 0.985. The values ranged between 0.822 for BF-CHVR-05-290 and 1.000 for 25 loci. The F_{IT} mean value across all the loci and populations was 0.988 which ranged between 0.837 for BF-CHVR-05-290 and 1.000 for 25 loci. The non significant F_{IS} and F_{IT} values indicated the deficiency of heterozygosity among the population for the screened microsatellite loci. The F_{ST} values in the range of 0.082 to 0.513 indicated high genetic differentiation with the mean F_{ST} value observed was 0.238 (23.8%) among all the populations spread over sampled regions (Table 27).

The pairwise population F_{ST} values ranged from a minimum of 0.029 between Group 1 and Group 4 whereas, maximum of 0.448 between Group 3 and Group 5 (Table 29). The pairwise genetic distance varied a minimum value of 0.092 between the populations, Group 1 and Group 4 whereas, maximum of 0.971 between the populations, Group 3 and Group 5 (Table 30). The pair-wise F_{ST} values and genetic distance for all the populations of *B. tabaci* are presented in Table 29 and 30.

4.4.6.4 Analysis of Molecular Variance (AMOVA)

The AMOVA revealed significant variation at each hierarchical level in the populations (Table 31). The variation observed among groups was at 3.53 per cent. A variance of 4.15 per cent ($F_{ST}=0.0768$) was observed among populations and within groups, whereas the variance within populations was observed at 92.31 per cent. The significant observed variation and the F-coefficients clearly indicated the presence of definite structure at each level of the population hierarchy.

Table 29. Pair-wise F_{ST} value for population of tomato minicore accessions

Group 1	Group 2	Group 3	Group 4	Group 5	
0.000					Group 1
0.051	0.000				Group 2
0.138	0.142	0.000			Group 3
0.029	0.037	0.107	0.000		Group 4
0.281	0.255	0.448	0.254	0.000	Group 5

Table 30. Pair-wise genetic distance of population for tomato minicore accessions

Group 1	Group 2	Group 3	Group 4	Group 5	
0.000					Group 1
0.154	0.000				Group 2
0.374	0.347	0.000			Group 3
0.092	0.104	0.260	0.000		Group 4
0.547	0.430	0.971	0.451	0.000	Group 5

Table 31. Summary of Analysis of Molecular Variance (AMOVA) and mean F-coefficients calculated over 260 tomato accessions

Source of variation	d.f.	Sum of squares	Variance components	Percentage of variation
Among groups	1	23.783	0.05049 Va	3.53
Among populations within groups	3	15.186	0.05935 Vb	4.15
Within populations	515	679.460	1.31934 Vc	92.31
Total	519	718.429	1.42918	
Fixation Indices	F _{ST} :	0.0768		

4.4.6.5 Phylogenetic analysis

Allele frequencies were used to generate the pairwise genetic distances between pairs of populations and the resulting distance matrix was used to build phylogenetic tree using Neighbour Joining (NJ) algorithms. The Neighbor Joining (NJ) phylogenetic tree constructed across the samples of *S. lycopersicum* revealed the existence of two major clusters-Cluster 1 and Cluster 2 (Fig. 15). Cluster 1 consisted of single group of population *i.e.* Group 5 which was cluster separately forming out group. The cluster 2 was further sub-divided into two sub-clusters (Cl 2a and Cl 2b). Sub-cluster Cl 2a consisted of single populations from Group 2 individuals separated from all other populations of cluster 2 on one hand. On the other hand, the sub cluster Cl 2b includes populations from Group 1, Group 4 and Group 3, among them individuals of Group 4 and Group 3 were closely related to each other whereas, individuals of Group 1 were separated from those two even though they share close genetic proximity (Fig. 15).

The phylogenetic analysis of all the 260 tomato accessions across sub-populations resulted in formation of 2 major clusters (Fig.16). Further, clusters 1 sub divided into two sub-cluster (Cl 1a and Cl 1b). Sub cluster Cl 1a consisted of individuals from Group 1, Group 2, Group 3, Group 4 and Group 5. whereas sub cluster Cl 1b consisted of individuals from Group 2, Group 3 and Group 4. Cluster 2 also sub divided into two sub clusters Cl 2a and Cl 2b.). Sub cluster Cl 2a consisted of individuals from Group 1, Group 2 and Group 5 whereas sub cluster Cl 2b consisted of individuals from Group 1, Group 2, Group 3 and Group 4 (Fig. 16). The phylogenetic tree shows that, there was high rate of gene flow/ genetic drift across the populations among the individuals because of its cross pollination or due to human intervention for breeding activity.

4.4.6.6 Principal Coordinate Analysis

The results obtained by the cluster analysis was confirmed by Principal Coordinate Analysis (PCA). PCA shows the distribution and relationships between the populations based on the bidimensional plot of the genetic distance. The position of the populations is depicted in the Figure 17, the distribution pattern of five groups revealed that, maximum number of entries were included in quarter III, namely Group 1 and Group 4, quarter 1 and IV included Populations from Group 5 and Group 3,

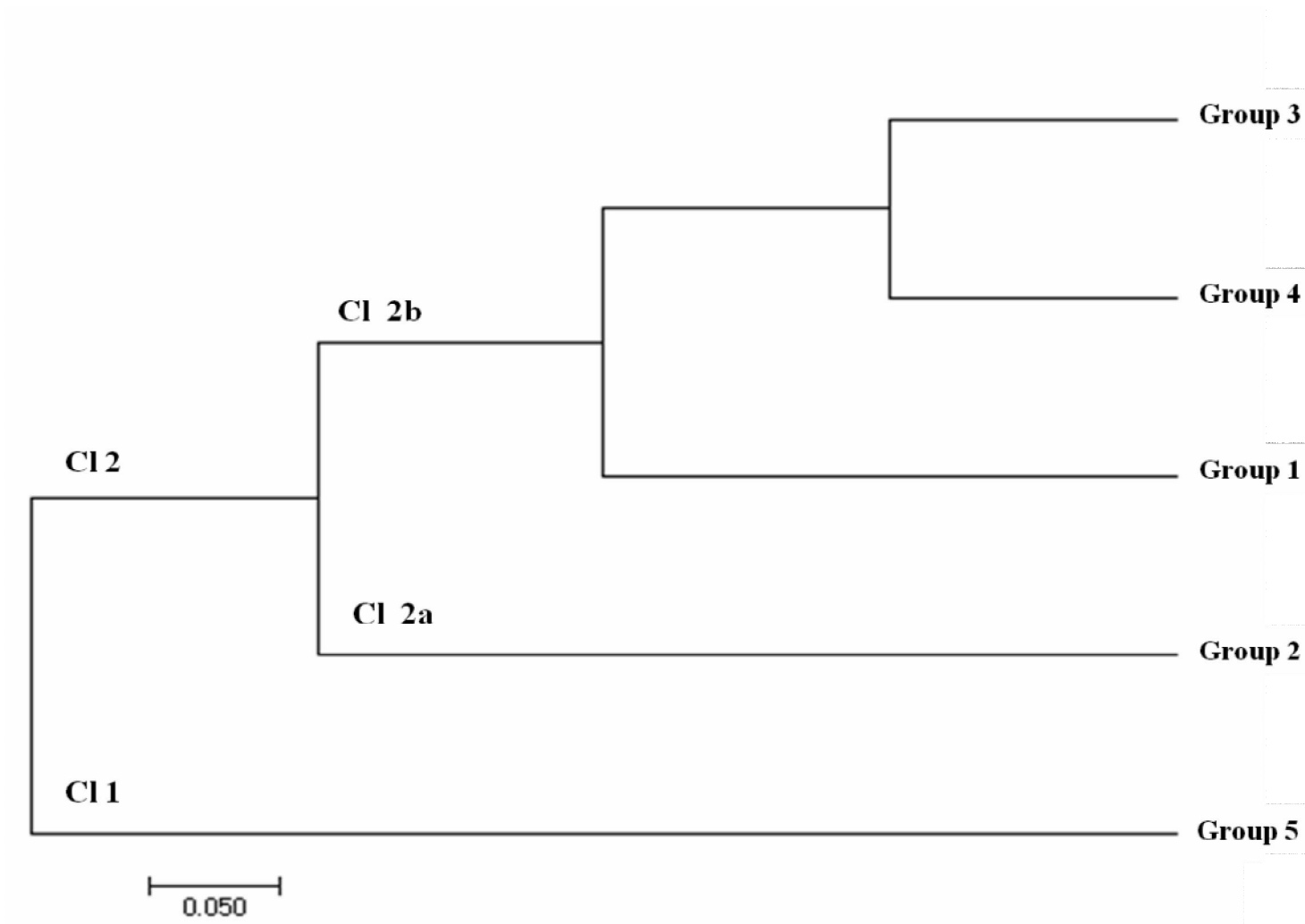


Figure 15. Neighbour Joining (NJ) tree constructed using MEGA 7 based on pair-wise genetic distance across tomato sub populations

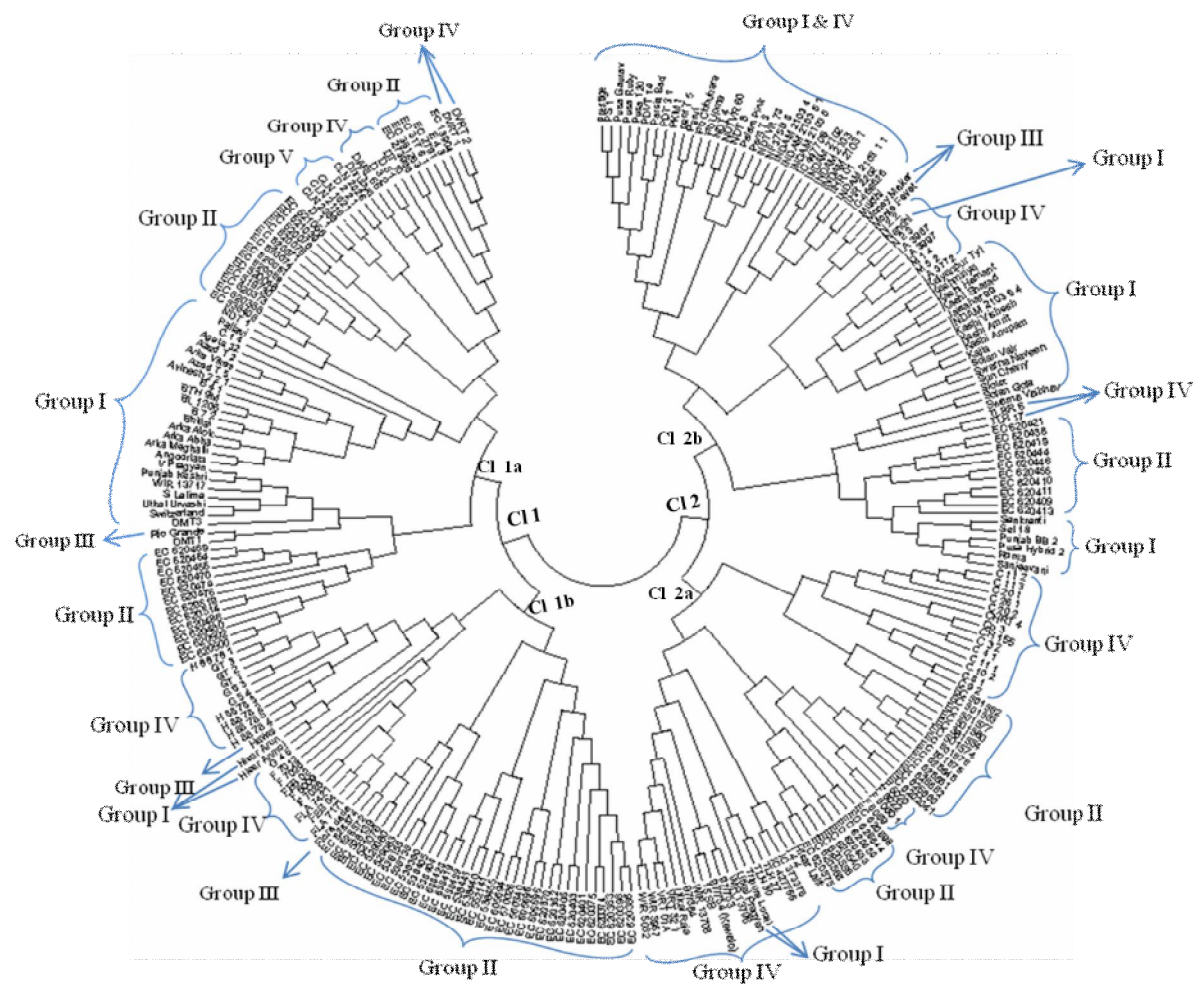


Figure 16. Neighbour joining (NJ) tree constructed using MEGA 7 based on pair-wise genetic distance across 260 tomato minicore accessions accessions.

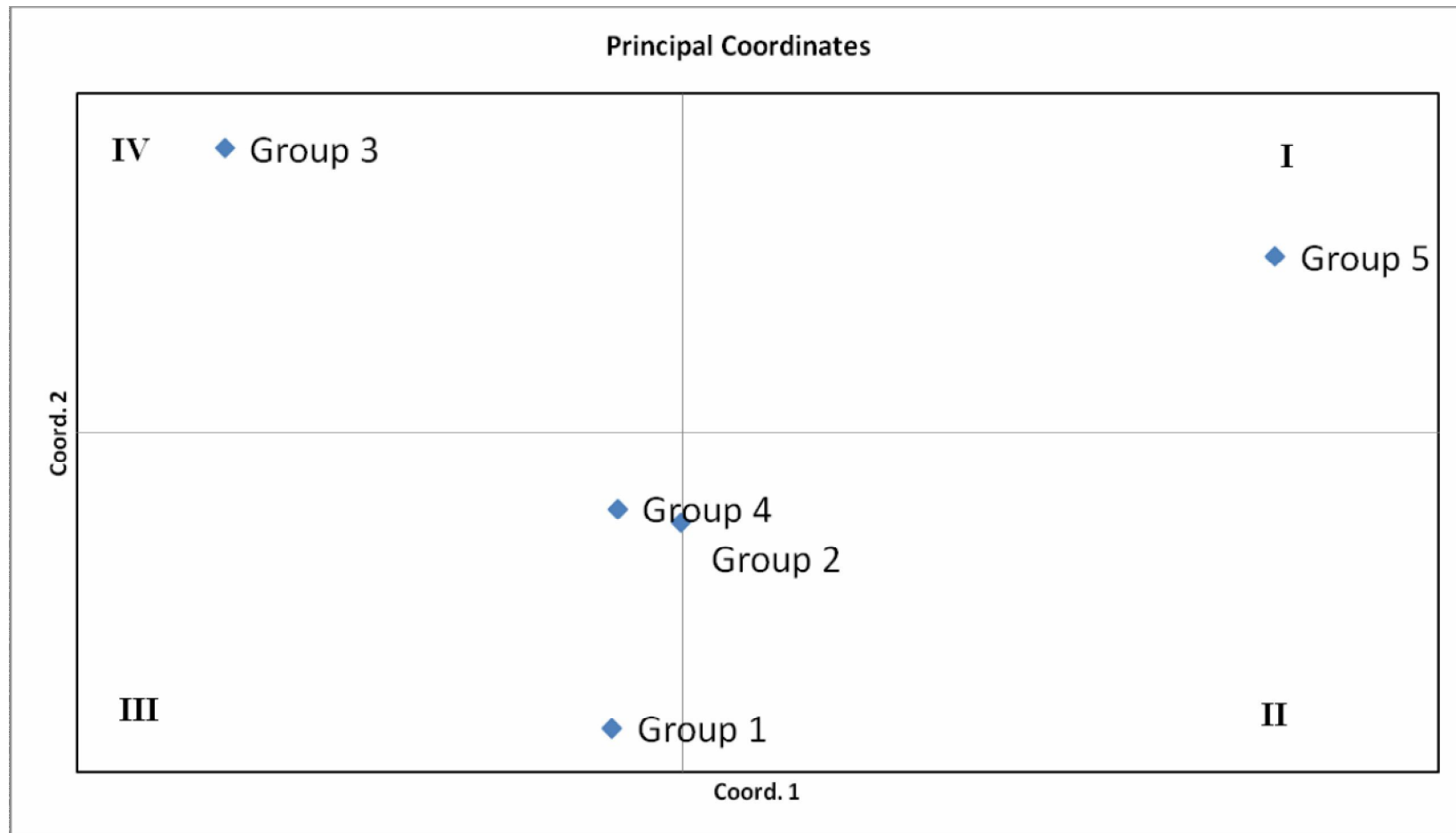


Figure 17. Principle coordinates analysis (PCA) using pair-wise genetic distance matrix of five tomato populations

respectively. The populations from Group 2 does not fall either on quarter II or quarter III, but it was distributed at the centre. The result shows that, populations of Group 2, Group 4 and Group 1 shares close genetic distance whereas, Group 3 and Group 5 are genetically different. The relative position of 260 accessions of five populations is illustrated in Figure 18. The 260 tomato accessions which are distributed across different quadrant based on their genetic distance matrix were exhibited in the Table 32.

Principal component analysis revealed the separation of samples more clearly between populations of different geographical locations. Some populations that showed a close phylogenetic relationship were separated more clearly by the PCA plot.

4.4.6.7 Structure analysis

The population genetic structure was investigated using the 260 accessions of *S. lycopersicum* using STRUCTURE v2.3.4 based on the genotyping data of 40 SSR markers. The posterior probability [$\ln P(D)$] of the data took peak probability at seven in the range of 1 to 15 subpopulations (Fig. 19). The structure analysis revealed that, there was high rate of intermixing populations with larger proportion of gene flow/ genetic drift/ mixed ancestry across the populations because of its cross pollination or due to human intervention for crop improvement activity. Each vertical line represents an individual's probability of belonging to one of K clusters (represented by the various colors) or a combination thereof if ancestry is mixed. Site order (left to right) is: 1 Group I, 2 Group II, 3 Group III, 4 Group IV and Group V (Fig. 20).

4.5 Association analysis of component traits of whitefly resistance in tomato

Decay of Linkage Disequilibrium (LD) and the corresponding significance level (P-value) were calculated using Trait Analysis by aSSociation, Evolution and Linkage, TASSEL 3.0 software (Bradbury *et al.*, 2007). Associations between biochemical, biophysical traits and DNA markers were calculated using TASSEL 3.0 software. Mixed Linear Model (MLM) was used in order to reduce false positive associations. Probability, $P < 0.005$ was taken as the value to detect associations and P

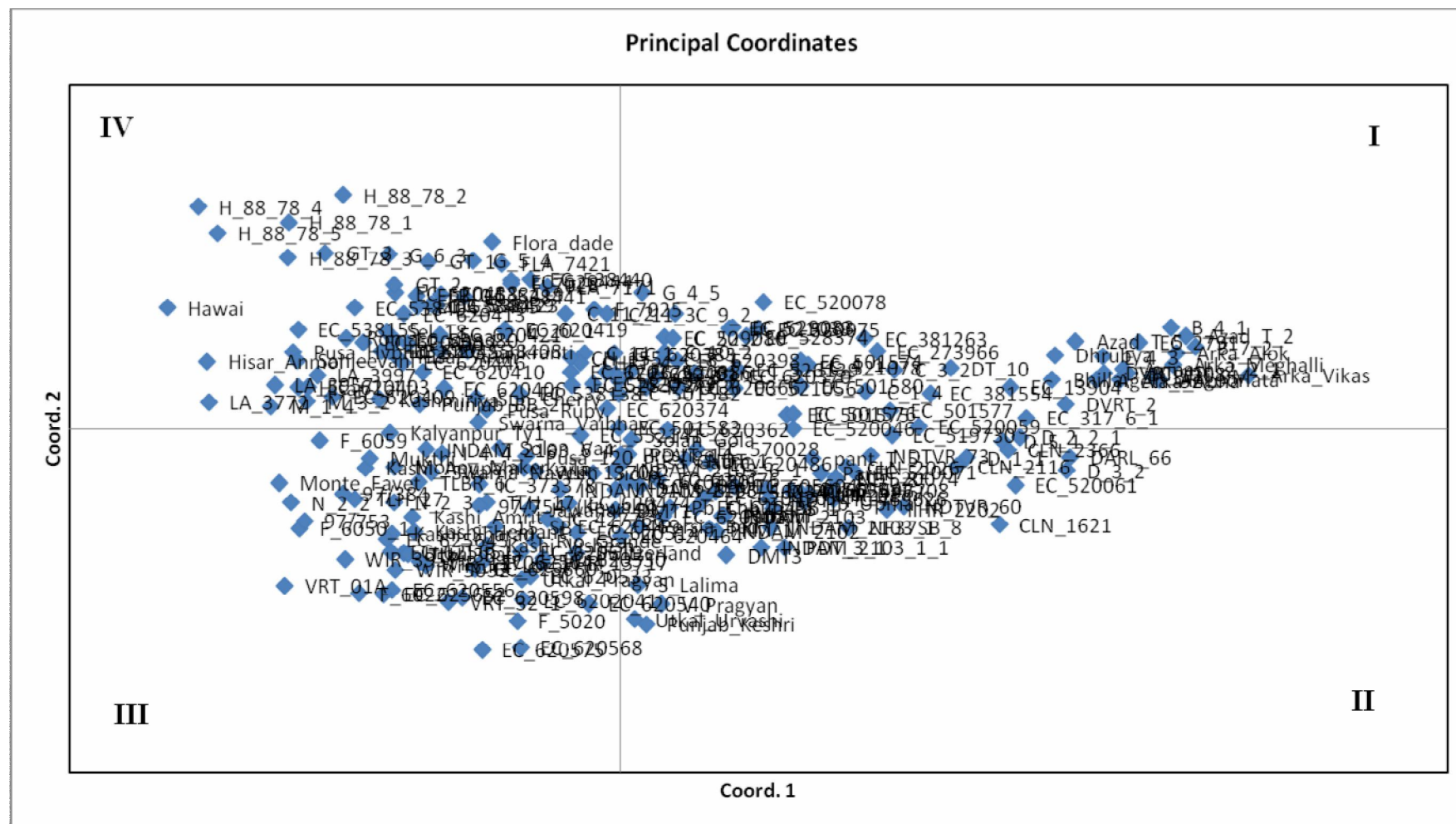


Figure 18. Principle coordinates analysis (PCA) using pair-wise genetic distance matrix of 260 tomato minicore accessions

Table 32. List of minicore accessions distributed across different quadrant based on their genetic distance matrix

Sl. No.	Quadrant	Individuals
1	Quadrant 1	H_88_78_4, H_88_78_2, H_88_78_5, H_88_78_3, H_88_78_1, FEB_02, FEB_04, F_6009, Sanjeevani, Hisar_Anmol, Hisar_Arun, Hisar_Lalit, GT_3, G_5_4, GT_2, C_20_1, Pusa_Hybrid_2, Roma, Sel_18, LA_3772, Sankranti, Swarna_Vaibhav, Kashmiriya, F_7025, CHVRT_4, Pusa_Ruby, M_3_2, Punjab_BB_2, M_1_4, LA_3997, Hawai, Flora_dade, G_6_3, FLA_7421, GT_1, F_7028, C_11_2, Sun_Cherry, CH_155, FLA_7171, LA_3957, C_11_1, C_11_3, C_26_1, EC_538138, EC_620444, EC_620438, EC_538441, EC_538440, EC_538404, EC_538439, EC_620413, EC_538423, EC_620373, EC_620375, EC_620421, EC_538419, EC_620455, EC_620411, EC_538405, EC_538155, EC_620409, EC_620401, EC_538380, EC_620419, EC_620446, EC_620406, EC_620383, EC_620410, EC_538408, EC_620403, EC_528372, EC_620374
2	Quadrant 2	DVRT_1, G_4_5, C_20_2, C_9_2, C_10_2, C_8_1, F_7012, Co_3, C_3_2, B_4_1, C_4_1, C_1_4, DT_10, E_4_3, DVRT_2, Azad_T_5, Pant_T_3, DHVRuby, Bhillai, Avinash_2_2_1, BL_1208, Azad_T_2, Ageta_32, Angoorlata, B_7_2, BTH_9M, Arka_Alok, Arka_Meghalli, Arka_Vikas, Arka_Abha, EC_520059, EC_317_6_1, EC_381554, EC_13904, EC_2791, EC_501583, EC_501576, EC_381263, EC_620370, EC_620386, EC_273966, EC_273966, EC_521056, EC_620398, EC_529080, EC_501577, EC_501580, EC_526139, EC_520075, EC_529083, EC_520078, EC_538455, EC_521039, EC_620366, EC_520046, EC_501574, EC_521078, EC_501575, EC_528374, EC_501582
3	Quadrant 3	Switzerland, Jawahar_99, Sioux, Kajla, F_6022, F_6059, N_2_2, Monte_Favet, 97/753, F_6050_1, VRT_01A, I_4_4, Mukthi, TLBR_6, WIR_5032, VRT_32_1, DMT1, INDAM_2103_6_1, Swarna_Naveen, INDAM_2103_6_4, IC_427766, Solan_Vajr, 97/754_(Kewalo), IC_373378, 15_SB, Rio_Grande, Tripura_Local, Pusa_120, INDAM_2103_6, Utkal_Pragyan, N, Kashi_Amrit, Utkal_Raja, Kashi_Hemant, Kashi_Sharad, Kashi_Vishesh, Kashi_Anupam, Kalyanpur_Ty1, Money_Maker, 97/384, TLH_27, N_2_3, F_5020, TLH_30, TLH_17, WIR_13708, WIR_3957, WIR_13717, WIR_13706, EC_625644, EC_620533, EC_625652, EC_620556, EC_620598, EC_620575, EC_620568, EC_625651, EC_625660, EC_625645, EC_6202041, EC_620469, EC_620514, EC_620519, EC_620530, EC_620540, EC_620474, EC_552141
4	Quadrant 4	NDTVR_73, D_1_1, D_2_2_1, V_Pragyan, Punjab_KesHVRi, Utkal_Urvashi, S_Lalima, NF37SB_8, NDT_1, Nandhi, D_5_1, D_3_2, PDT_3_1, PS_1, NDT_4, DMT3, Pallavi, IIHVR_2202, PKM_1, NDTV_60, DARL_66, Persia_Bed, Pb_Upma, Parul, IIHVR_01, PDVT_14, NDT_8, Palam_Pink, Solan_Gola, Prestige, pant_T_5, Pusa_Gaurav, INDAM_2103_4, INDAM_2102, INDAM_2103, INDAM_2103_1_1, INDAM_2103_1, Pb_Chuhara, IC_447708, IC_469626, CLN_2026, CLN_2366, CLN_1621, CLN_2116, EC_605696, EC_620464, EC_520074, EC_605695, EC_620500, EC_620362, EC_570028, EC_519730, EC_620486, EC_605694, EC_620470, EC_520071, EC_620456, EC_620502, EC_620480, EC_620476, EC_560340, EC_520061

< 0.001 as the significant value to reduce false positive associations. The amount of phenotypic variation explained by each marker was estimated by R^2 .

The biophysical, biochemical data were analyzed separately. In all, a set of 24 marker-trait associations (MTAs) on five selected traits were detected at $P < 0.005$ (Table 33). Position of selected associated SSR markers on respective chromosomes are presented in the Figure 21. Phenol content in leaves was associated with three markers viz., LEaat7, TG178, TY-1/3 with the phenotypic variation (R^2 value) of 6.30, 2.14 and 2.51, respectively, explaining overall 10.95 per cent of the variation. For tannins, nine SSR markers viz., Pb, FBTGS0321, BF-CHO3, BF-CHVR-12-542, FBTGS0318, LEaat7, SINAC1 (TAQ 1), FBTGS0209 and PM3 showed association with the phenotypic variation of 2.56, 2.31, 2.15, 2.60, 2.01, 4.28, 2.23, 2.20 and 2.66, respectively, explaining overall 23 per cent of the variation. SSR markers, BF-CHVR-10-3817 ($2.466 R^2$) and BW4 ($2.72 R^2$) were found associated with terpenoid content explaining overall 5.18 per cent of the variation. The chlorophyll content was associated with the seven markers viz., AVRDC-TM719 ($2.37 R^2$), P6-25 ($2.03 R^2$), BF-CHO3 ($4.62 R^2$), LEaat1 ($3.67 R^2$), BF-CHVR-05-290 ($2.43 R^2$), PM3 ($2.71 R^2$) and LEat18 ($2.10 R^2$) explaining overall 19.93 per cent of the variation. Three markers, AVRDC-TM947, Pb and BF-CHVR-05-290 were associated with trichome with the R^2 value of 3.40, 4.02 and 2.84, respectively, and explained 10.26 per cent of the overall variation.

It was clear from the results that, a few DNA markers were associated with multiple traits marker LEaat7 (Chr05) associated with phenols and tannins, marker, Pb (Chr04) associated with tannins and trichomes. Both the tannins and chlorophylls were found associated with the marker BF-CHO3 (Chr07). Marker BF-CHVR-05-290 (Chr05) was associated with two chlorophyll and trichomes.

A set of three markers were detected to be significantly associations ($P < 0.001$). The marker on LEaat7 (Chr05) explained 6.30 per cent of the phenotypic variation. The other most significant MTA was detected was for tannins. This MTA was also detected through marker LEaat7 (Chr05), explaining 4.28 per cent of the phenotypic variation. The marker BF-CHO3 on chromosome 7 (Chr07) recorded significant MTA for chlorophyll content, explaining 4.62 per cent of phenotypic variation.

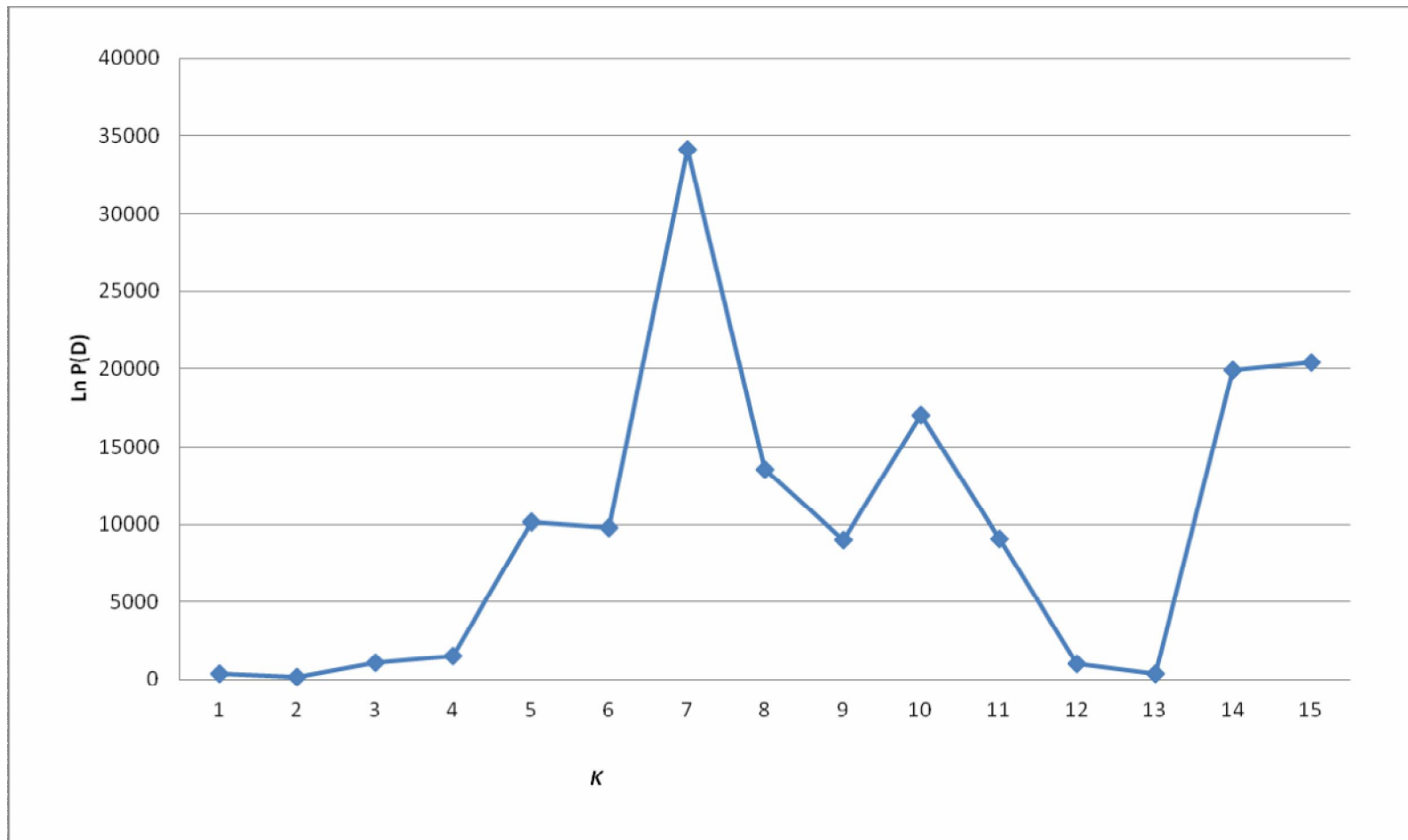


Fig 19. $\ln P(D)$ values presented as a function of the number of clusters. The largest $\ln P(D)$ values were found for $K=7$ (among 1000)

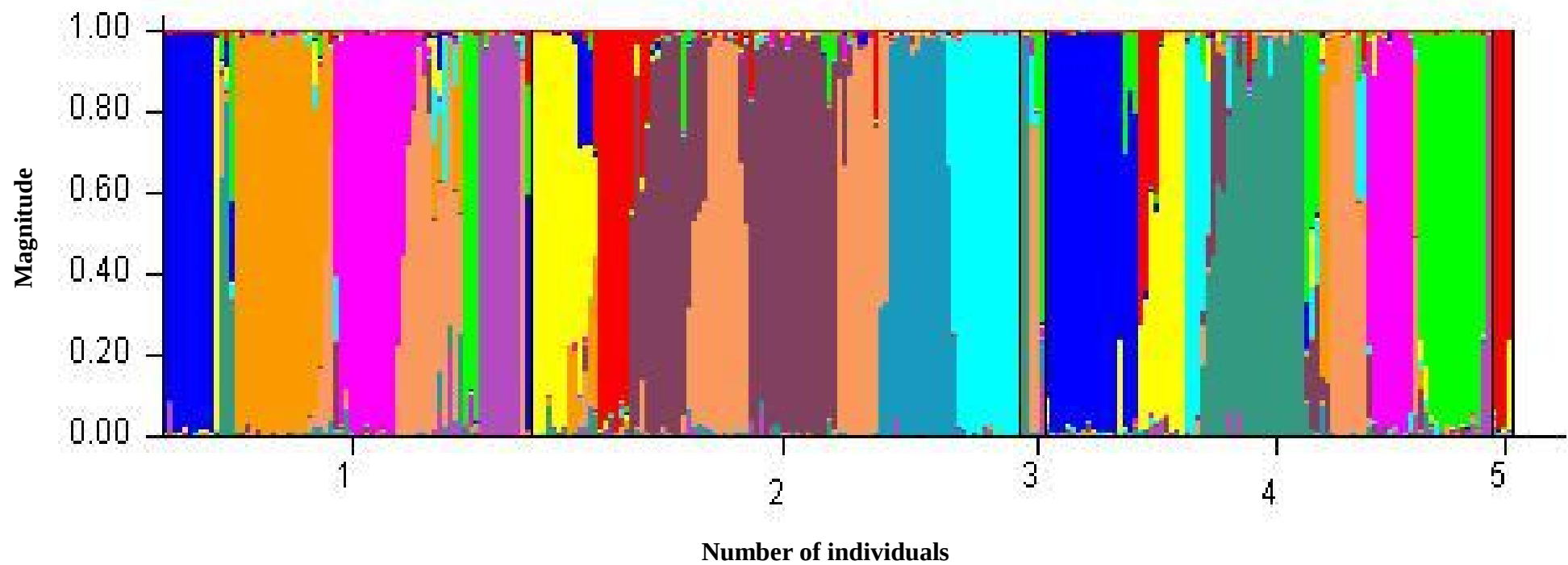
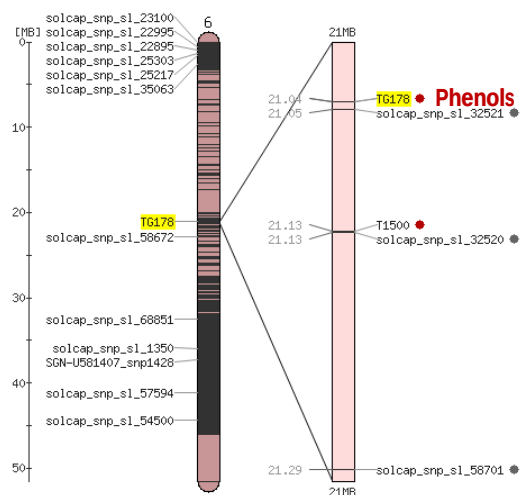


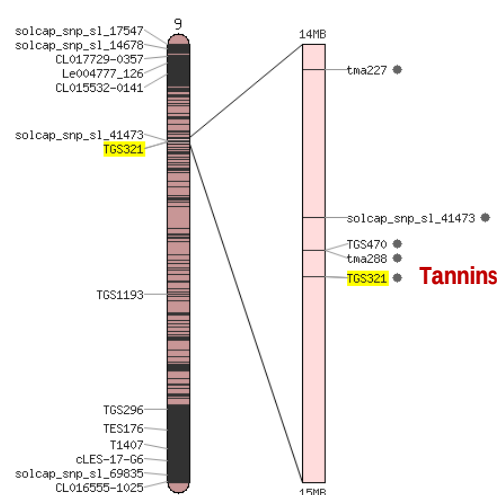
Fig 20. Population genetic structure of 260 tomato minicore accessions at K=7

Table 33. Markers associated with biophysical and biochemical traits and their position on chromosomes.

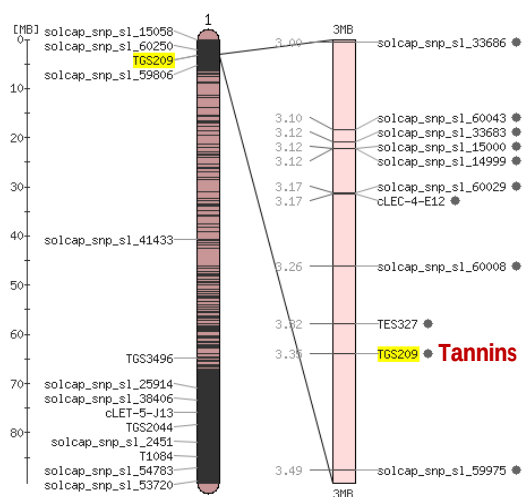
Trait	Marker	Chromosome	Position	F- marker	p- value	R ²
Phenols	LEaat7	chr05	104	17.34	0.000043	6.30
	TG178	chr06	123	5.64	0.01824	2.14
	TY-1/3	chr06	169	6.65	0.01045	2.51
Tannins	Pb	chr07	31	6.77	0.00981	2.56
	FBTGS0321	chr09	48	6.09	0.01425	2.31
	BF-CHO3	chr07	49	5.66	0.01809	2.15
	BF-CHVR-12-542	chr012	58	6.90	0.00915	2.60
	FBTGS0318	chr12	88	5.28	0.02236	2.01
	LEaat7	chr05	104	11.52	0.00080	4.28
	SINAC1 (TAQ 1)	chr04	122	5.88	0.01599	2.23
	FBTGS0209	chr01	143	5.81	0.0166	2.20
	PM3	chr06	147	7.06	0.00839	2.66
Terpinoid	BF-CHVR-10-3817	chr012	62	6.51	0.01133	2.46
	BW4	chr10	133	7.21	0.00771	2.72
Chlorophyll	AVRDC-TM719	chr04	4	6.27	0.01293	2.37
	P6-25	chr06	15	5.35	0.02156	2.03
	BF-CHO3	chr07	49	12.51	0.00048	4.62
	LEaat1	chr01	75	9.82	0.00193	3.67
	BF-CHVR-05-290	chr05	97	6.44	0.01177	2.43
	PM3	chr06	147	7.18	0.00783	2.71
	LEat18	chr04	157	5.53	0.01943	2.10
Trichome	AVRDC-TM947	chr04	27	9.07	0.00286	3.40
	Pb	chr04	33	10.79	0.00116	4.02
	BF-CHVR-05-290	chr05	100	7.55	0.00642	2.84



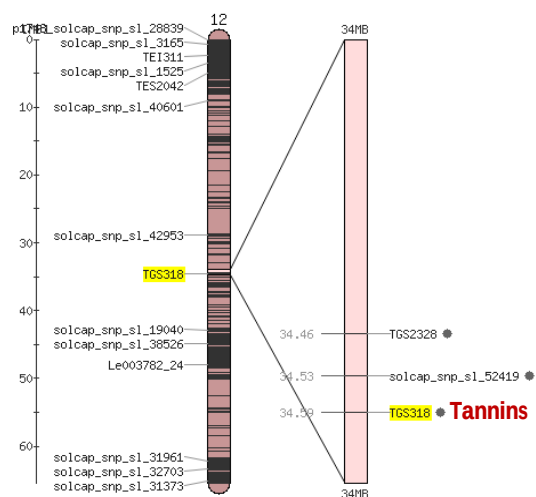
a. TG178



b. TGS321



c. TGS209



d. TGS318

Fig 21. Position of trait-wise associated markers on different linkage groups

5. DISCUSSION

Population parameters and their relative dynamics play critical role in deeper understanding of the whitefly populations prevailing in the tomato ecosystems. These parameters directly useful in formulation of strategies to manage whiteflies as pest and the viruses they transmit in tomato crop. Morphometric and biochemical traits in tomato manifest the resistance/ susceptibility to both whitefly and the viral diseases. Hence, a deeper understanding of plant traits that confer insect and viral resistance at genetic level is expected to elucidate their genome-wide landscape and identification of DNA markers linked to these traits for their further use in marker assisted selection (MAS). The results obtained from the present study on “Genetic diversity of whitefly, *Bemisia tabaci* (Genn.) (Hemiptera: Aleyrodidae) populations and molecular analysis for its resistant traits in tomato (*Solanum lycopersicum* L.)” are discussed here in the context of earlier reports and justifications.

5.1 Plasticity for morphological traits among the populations of whiteflies prevailing in tomato ecosystems of Karnataka

The morphometric analysis of randomly selected 140 whitefly male, female and puparia samples representing different agroclimatic zones of 11 districts of Karnataka, covering tomato crop ecosystem are discussed in this chapter (Fig. 22 to Fig. 24).

The puparia characters such as puparial length and breadth from Dharwad district recorded significant higher values of the puparia size, distance of vasiform orifice from anterior end (DVOAE), distance of transverse moulting suture from anterior end (DTMSAE), length of lingula (LL) and length of caudal furrow (LCF) and in addition, recorded comparatively higher values for the characters like length of vasiform orifice (LVO), breadth of vasiform orifice (BVO), length of operculum (LO), breadth of operculum (BO) and distance between caudal setae (DCS) (Fig. 22). Significantly lower values for PL, PB, DTMSAE, LL and LCF and numerically lowest values for LVO, BVO, LO, BO, DCS and Length of caudal setae (LCS) were recorded for the Bagalkot district population followed by the population from Chamarajanagara districts (Fig. 22). Populations from remaining eight districts were on par with each other for the majority of the traits studied.

Whitefly adults recorded slightly different trend for most of the traits. The characters of male *B. tabaci* individuals from the Chikaballapura population recorded significantly higher values for fore wing length (FWL), fore wing width (FWW), length of fore wing vein (LFWV), length of hind wing (LHW), length of antenna (LA), length of proboscis (LP) and length of abdomen (LAb), whereas, comparatively higher numerical values for length of last abdominal segment (LLAb) and length of claspers (LC). On the other hand, lower numerical values were recorded for length of fore femur (LFFi), length of fore tibia (LFTi), length of fore tarsus (LFTa), length of hind femur (LHF) and length of hind tibia (LHTi). Populations from remaining districts were on par with each other for some characters and some recorded higher or lower numerical values for different characters studied (Fig. 23).

In case of adult females, populations collected from Chikkaballapura district recorded significantly higher values for fore wing length (FWL), fore wing width (FWW), length of fore wing vein (LFWV), length of hind wing (LHW), width of hind wing (WHW), length of antenna (LA), length of abdomen (LAb) and length of proboscis (LP) and significantly lowest values recorded for the characters viz., length of fore femur (LFFe), length of fore tibia (LFTi), length of fore tarsus (LFTa) and length of hind tibia (LHTi). Whereas, populations from Shivamogga district recorded significantly higher values for the characters viz., width of hind wing (WHW), length of hind femur (LHFe), length of hind tibia (LHTi) and length of hind tarsus (LHTa). The remaining populations from other districts recorded on par values for majority of the characters studied (Fig. 24).

The results obtained from morphometric analysis of adult whiteflies revealed that, Chikkaballapura population showed significant differences for majority of the characters studied. Significant variation in wing and leg morphometry may be attributable to the presence of natural variation in geographically distinct populations. Host and geographical zones related to cropping pattern have known to influence on the traits that determine their immediate fitness such as wings and legs. These results were similar to the study conducted by Mound (1963) and Yan (1991), who reported that, the morphological variations of *B. tabaci* populations on different host plants and the variation in morphometrics corresponds to leaf surface features of host plants, environmental conditions and this was supported by Mound and Halsey (1978) and

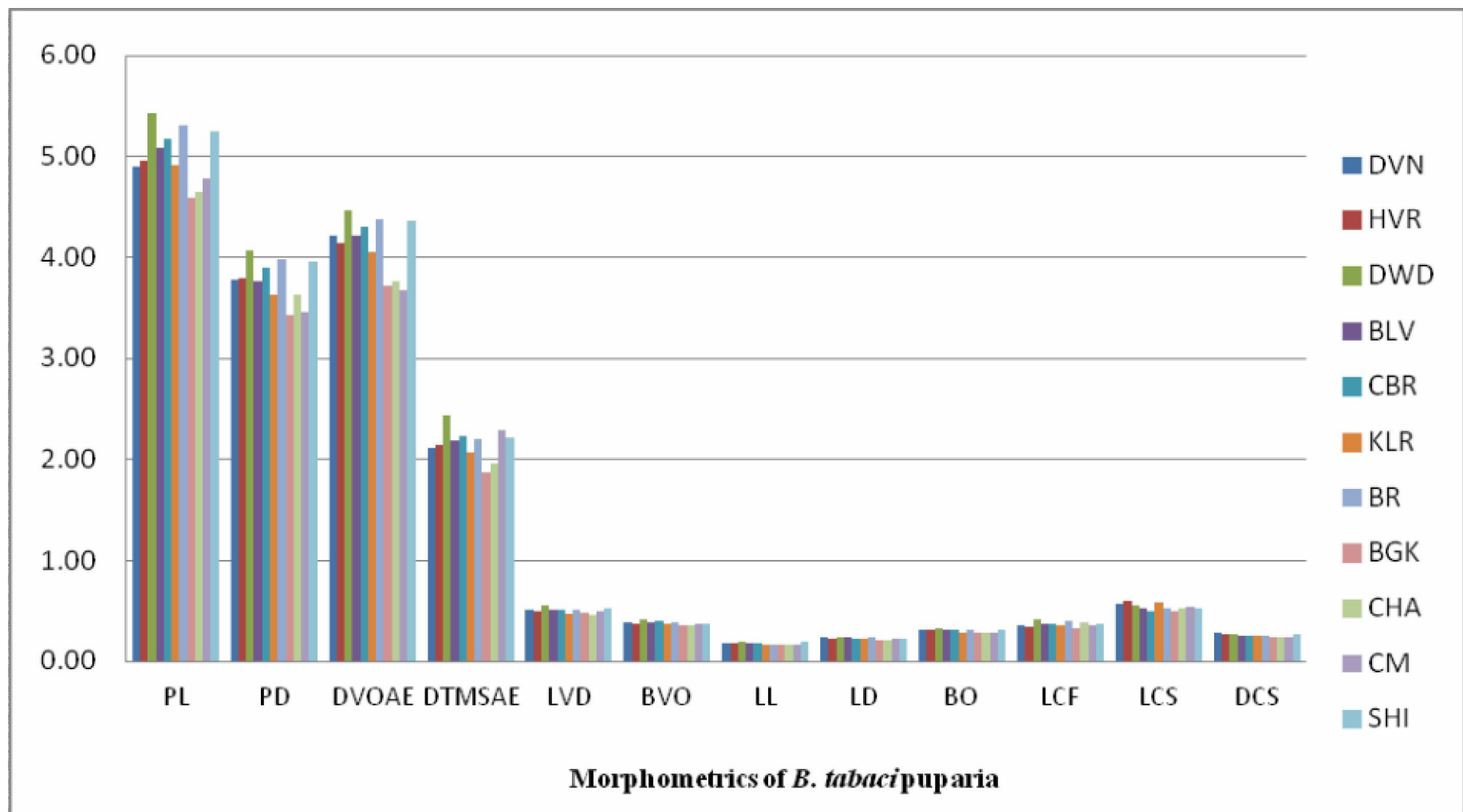


Fig 22. Morphometrics of *Bemisia tabaci* puparia on tomato from different agro climatic zones of Karnataka

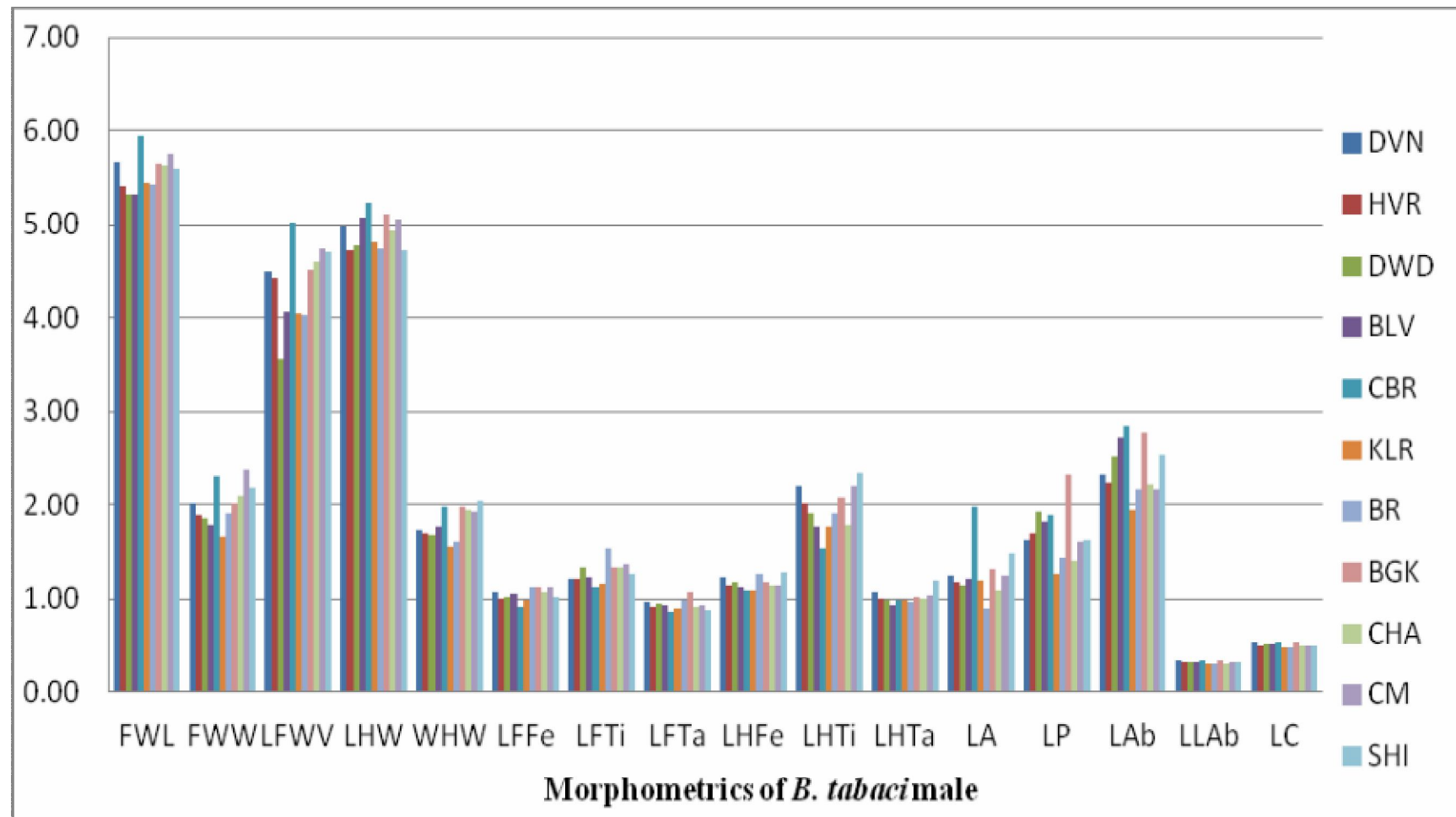


Fig 23. Morphometrics of *Bemisia tabaci* males on tomato from different agro climatic zones of Karnataka

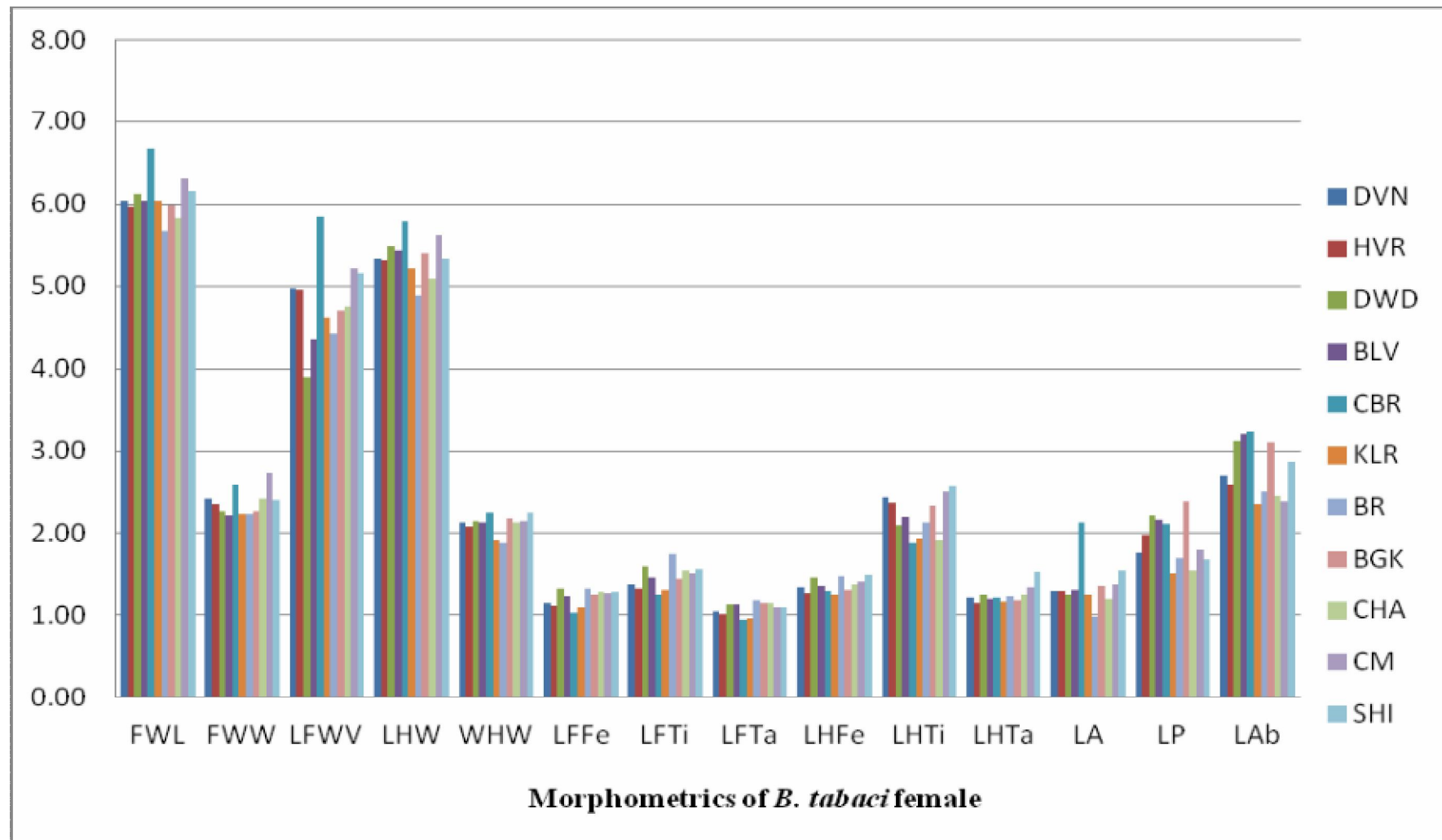


Fig 24. Morphometrics of *Bemisia tabaci* females on tomato from different agro climatic zones of Karnataka

Jing-jing *et al.* (2013). Similar host associated variation in fruit borer *Helicoverpa armigera* (Hubner) has also been reported by Patil *et al.* (2012). The host plant-associated morphological variations in *B. tabaci* resulted in very few stable morphological characters which can be used for taxonomy or identifications (Lee *et al.*, 2013). In fact, morphological variations across *B. tabaci* populations has confusions and resulted in more than 20 synonyms for this species (Mound and Halsey, 1978). The sex also can be reliably identified in puparia in *B. tabaci* species based on a combination of character such as the length and width of puparia, length of vasiform orifice (LVO) and the combination of some of their ratios (Baig *et al.*, 2016).

Present results pertaining to morphometric analysis were similar to the study conducted by Thomas *et al.* (2011), who reported significant differences in the length of egg, second, third and fourth instars. Out of 62 measurements of the puparia analysed, 70 per cent of the head, 44 per cent of the thorax and 51 per cent of the abdomen showed significant differences between the cotton and *Leucaena* populations. Positive correlation between body length and width of the nymphal instars and body sizes of males and females of *B. afer* singly and collectively recorded by Maruthi *et al.* (2004). This was similar to the kind of growth pattern observed for *B. tabaci* nymphal instars on cassava (Fishpool *et al.*, 1996; Thompson, 2000). A difference in size between male and female *B. tabaci* has also been reported by many workers (Lopez-Avilla, 1986; Bethke *et al.*, 1991; Fishpool *et al.*, 1996). Male and female body sizes for *B. afer* were significantly different and they were distinguishable on the basis of overall body length and width. However, identification based on body size alone was not always reliable because of overlap in the upper size range of males and lower size range of females. Instead, presence of claspers at the tip of the abdomen in males is quite reliable.

Morphometric characters of female was higher than those of the male individuals making females to be relatively larger than males. This may be because of feeding behavior and also developmental period (Baig *et al.* 2015) *i.e.* males are developing faster than females, indicating protandry that increases the chances of male mating success. Adult females are larger than males, which may be the result of a longer developmental time which shows a positive relationship between

developmental time and body size in these species. Jing *et al.* (2013) reported that, the sizes of all characters investigated from both male and female adults of invading biotypes B and Q were much larger than those of the indigenous ones viz., Cv, ZHJ-1, ZHJ-2 and ZHJ-3.

Cluster analysis for *B. tabaci* adult (male and female) population based on different morphological characters collected from different agro climatic zones of Karnataka revealed the existence of two major clusters-Cluster 1 and Cluster 2 (Fig. 2). Similar results observed when cluster analysis for *B. tabaci* adult (both male and female) and puparia population were studied (Fig. 5). In both the cases, cluster 1 consisted of single population from Chikkaballapura district which deviated from all other populations forming an out group. Cluster 2 was further divided into two subclusters (Cl a and Cl b). Sub-cluster C1a consisted of populations from Belagavi, Dharwad and Bagalkot population. The sub cluster Cl b consists of seven populations from Shivamogga, Chikkamagaluru, Davanagere, Haveri, Chamarajanagara, Bengaluru rural and Kolar in case of adults cluster analysis (Fig. 2). Whereas, in case of adults and puparia cluster analysis sub-cluster C1a consisted of populations from Belagavi, Dharwad and Bagalkot. The sub cluster Cl b consists of seven populations viz., Davanagere, Haveri, Shivamogga, Chikkamagaluru, Bengaluru rural, Chamarajanagara and Kolar (Fig. 5). However, in the present study, existence of biotypes has not been tested but, distinct clusters like Chikkaballapura population give evidence for existence of biotypes. The results were similar to Chaubey and Andrew (2015) reports where, overlapped clustering was observed in six populations analyzed with 91.11 per cent of the classifications which were correctly attributable and confirm the distinctiveness of populations. Present results are in agreement with those of Jayasekera *et al.* (2010) and Thomas *et al.* (2014). Present conclusions are also corroborated with the previous conclusions of Mound (1963); David and Ananthakrishnan (1976) and Mohanty and Basu (1986).

The principal component analysis (PCA) based on 30 morphological characters of adult (female and male) divided these 30 traits into major three principal components whereas, PCA based on 42 morphological characters of adult (female and male) and puparia resulted into four major principal components. In both the

cases, first two principal components contributed the major share of variances with 75.67 and 68.12 per cent diversities, respectively (Table 8 and Table 9). The score plot analysis based on PC1 and PC2 are plotted in Fig. 4 and Fig. 7 also exhibited distribution pattern of eleven district populations into four major distinct clusters/quarters. Similar results were observed by Thomas *et al.*, (2011) who stated that, principal component analysis separated whitefly population significantly according to host plants, with the first three principal components accounting for 66 per cent of the total variation. Whereas, 73.6 per cent of total variation was observed by Chaubey and Andrew (2015) where in, out of the 62 morphometrics characters, 30 characters vary significantly ($P < 0.05$), which reinforce the complexity of *B. tabaci* species. Present results are also in agreement with those of Mound (1963); David and Ananthakrishnan (1976); Mohanty and Basu (1986); Jayasekera *et al.* (2010) and Thomas *et al.* (2014).

Similar results were also reported by Harish *et al.* (2016) who revealed the presence of different genetic groups among whitefly populations of agro-ecological zones of Kerala using morphometric variations, with fourteen different puparia characters and nine different adult characters. The principal component analysis revealed the presence of more variations in populations collected from Sulthan Bathery region compared to others.

Bemisia tabaci may consist of many cryptic species. Morphological variations in *B. tabaci*, may imply its genetic differentiations among populations or biotypes. The variations might provide a support for distinguishing other populations as well. However, in the present study, existence of biotypes has not been tested, but, distinct clusters like Chikkaballapura population give evidence for existence of biotypes based on morphological characters. Cluster analysis indicated distinctness of Chikkaballapura population both in morphological and molecular analysis. Similarly, two sub clusters within Cl-2 divide and place northern district population viz., Belagavi, Dharwad and Bagalkot in Cl 2a cluster and southern Karnataka population comprising Kolar, Bengaluru and Chamarajanagara in another subcluster, Cl 2b which indicates initial evidence of evolution of potential biotypes or ecotypes within tomato growing regions of Karnataka.

5.2 Genomic flux and population genetic structure of whitefly populations of tomato ecosystems of Karnataka

The genetic analysis was carried out with randomly selected 140 whitefly DNA samples from eleven populations collected from different agro climatic zones of Karnataka. The level of polymorphism among the samples of *B. tabaci* was assessed with the shortlisted 17 microsatellites markers. DNA samples were amplified by using the multiplex PCR method.

The number of different alleles among the microsatellite loci (N_a) varied from 1.45 (FbBEM31) to 4.36 (FbBem23) across the regions with average number of 2.257. The average number of effective allele (N_e) was 1.663 in loci FbBem23 and it ranged from 1.300 (FbBEM31) to 2.699 (FbBem23). An overall number of migrant (N_m) mean value for all loci was 0.281 with the locus, FbBem23 recording the highest N_m (0.558) and the locus, FbBEM39 the least N_m (0.073). High N_m values (>0.5) across all the populations for each loci indicated the selection pressure acting on the loci (Table 10).

The heterozygosity (gene diversity) is considered as a reliable parameter of genetic variation among the loci. The observed (H_o) and expected heterozygosity (H_e) ranged from zero to 0.382 (FbBem23) with an average of 0.049 and ranged from 0.144 (FbBEM31) to 0.576 (FbBem23), respectively, indicating a high degree of genetic diversity and possibility of a very high selection potential for the loci under study. Generally, a polymorphic loci should have a minimum heterozygosity value of 0.10 (Ott, 2001). The fixation coefficient (F_{ST} value) of population measured with 17 microsatellite markers varied from 0.298 (FbBem23) to 0.773 (FbBEM39), with a mean of 0.500. The heterozygotes in F_{IT} was amounted to 0.93 with a mean F_{IS} of 0.877 (Table 10). There were three levels of gene flow viz., high ($N_m > 1$), intermediate ($0.25 < N_m < 0.99$) and low ($N_m < 0.25$) (Govindajaru, 1989). Similar results were observed by Govindajaru (1989) who reported, the mean number of migrants (N_m) across the populations for all the loci screened was 1.023, indicating a high migration rate in the populations. The population mix-up observed might be attributed to high migration rate among the populations. The estimated effective number of migrants per generation (N_m) between regions and between aggregations and strengthened such an interpretation, as there were significantly more migrants

between regions than between aggregations. These findings have direct bearing on the management eventualities through modeling the parameters in tomato ecosystems.

Among the populations, number of different alleles of microsatellite loci (N_a) ranged between 1.82 (Bt_BGK) and 2.647 (Bt_BR) across the regions. The average number of alleles across all the microsatellite loci stood at 7.33 (Table 11). The population size was maximum for the population, Bt_CKM (Chikkamagaluru) (1.985) while, the population, Bt_BLV (Belagavi) recorded the minimal value of 1.417 (Table 11). The effective number of alleles is also a good measure of the genetic variation, especially in conservation genetics study. Often, its effect on populations is more emphasised, but effective number of alleles is easily affected by sample size (Maudet *et al.*, 2002).

The observed heterozygosity (H_o) ranged between zero in Bt_CKBR population (Chikkaballapura) to 0.124 in Bt_BGK population (Bagalkot). The mean expected heterozygosity ranged between 0.226 in Bt_SHI (Shivamogga) to 0.419 for Bt_BR (Bengaluru rural). The polymorphism for the loci ranged between 58.82 per cent for Bt_SHI population (Shivamogga) to 100 per cent for Bt_BR population (Bengaluru rural) indicating the greater extent of polymorphism among the populations with set of molecular markers used in the present study (Table 11). An earlier study conducted by Valle *et al.* (2012) found a low level of polymorphism among 20 individuals analyzed. Among thirteen loci, only four were polymorphic with two alleles per locus. The results showed a low level of polymorphism in the genotypes evaluated. The expected heterozygosity ranged from zero to 0.505. For all loci, the observed heterozygosity was lower than or equal to the expected heterozygosity. The low polymorphism found in these molecular markers is probably associated with homology to the genes expressed in all these markers.

Among the total populations, the Shannon's Information Index (I) value ranged from 0.376 (Bt_SHI) to 0.692 (Bt_BR) with an average index value of 0.531 (Table 11). Among the loci, the Shannon's Information Index value ranged from 0.229 (FbBEM31) to 1.085 (FbBem23) with an average mean of 0.531 (Table 10). Shannon's Information Index is commonly used to characterize species diversity in a community. Shannon's index accounts for both abundance and evenness of the species

present. Equitability assumes a value between zero and one with one (1) being complete evenness (Hennink and Zeven, 1991).

The major components of F-statistics are F_{IS} , F_{IT} and F_{ST} , where, 'I' represent individuals, 'S' represents sub-population and 'T' represents total population and were calculated for the whitefly populations. The F_{IS} and F_{IT} values indicate the inbreeding coefficient among the sub-populations and among the total populations, respectively.

In the present study, mean F_{IS} value of 0.877 across all the populations was recorded. The F_{IS} value ranged between 0.31 to 1.00. The F_{IT} mean value was 0.93, which ranged between 0.535 and 1.00. The significant F_{IS} and F_{IT} indicated the deficiency of heterozygosity among the sub-populations and the total populations. Generally, positive F_{IS} values indicate a significant lower heterozygotes, while the negative values indicate an abundance of heterozygotes (Balloux and Lugon-moulin, 2002). In the present study, all loci showed positive values, which indicated the significant deficit of heterozygotes which may be due selection pressure and presence of null alleles (Table 10). The significant mean F_{ST} value was 0.500 for all the populations and the individual F_{ST} values ranged between 0.298 for FbBem23 to 0.773 for FbBEM39 indicating the presence of significant genetic differentiation across the populations (Table 10). The results were similar to the study conducted by Chu *et al.* (2014) which exhibited significantly high and positive mean values of F_{IS} (0.287-0.552) in *B. tabaci* population, indicating the existence of heterozygote deficiency. With respect to pairwise comparisons between collections, 841 of 990 F_{ST} (84.8%) values were associated with a significant structure analysis.

F_{ST} values for pair wise population ranged from a minimum of 0.180 between Bt_BR and Bt_CHA and a maximum of 0.530 between Bt_HVR and Bt_CKBR (Table 12). The pairwise genetic distance varied with a minimum value of 0.280 between the populations of Bt_DVN and Bt_HVR and the maximum value of 1.334 between the populations of Bt_HVR and Bt_CKBR (Table 13). The pair wise F_{ST} values indicated the presence of moderate to high genetic differentiation among the sampled populations.

The AMOVA results revealed that, the per cent variation across the populations was 49.79 and within populations was 50.21. The variation within populations was higher than that of across populations, indicating the existence of differentiation between the two populations (Table 14). Even though significant variance among populations was detected, it was relatively high (49.79) considering the expectations of high gene flow among some of the populations. However, significant and high variation (50.21) obtained within populations, which is a characteristic feature of microsatellite markers because of their high polymorphic nature (Carreras-Carbonell *et al.*, 2008), thus resulting in an increased genetic diversity within a population and eventually may reduce the power of differentiation among populations. A F_{ST} value between zero and 0.05 indicates little genetic differentiation, value between 0.05 and 0.15 indicates moderate differentiation, 0.15 and 0.25 indicates great differentiation and the value >0.25 considered a very great genetic differentiation and F_{ST} of 0.05 will generally be considered as reasonably low and structuring between sub populations would be weak (Balloux and Lugou-Moulin, 2002).

In present study, the average F_{ST} value for *B. tabaci* population was 0.498, which indicated a very great genetic differentiation among the *B. tabaci* populations (Table 14). Greatest genetic differentiation being exhibited between Chikkaballapura and Haveri population as evidenced by highest F_{ST} values and genetic distance (Table 13). Results of study conducted by Lima *et al.* (2002b) showed that, populations of the *B. tabaci* B biotype have considerable genetic variability. An average Jaccard similarity of 0.73 was observed among the B biotype individuals analyzed. AMOVA showed that, most of the total genetic variation is found within populations (56.70%), but a significant portion of the variation is found between crops (22.73%). Whereas, the variation percentage between groups was 62, similar to the result of Valle *et al.* (2011), which indicated a great difference between the localities. A previous study with other molecular markers (SSRs) for *B. tabaci* also showed a low level of polymorphism. A recent tool for genetic analysis was developed by Nazereno and Reis (2011), which considered in evaluating monomorphic microsatellites. Microsatellite markers used in the present study also showed a greater difference between geographic localities.

Allele frequencies were used to generate the pair wise genetic distances between pairs of populations and the resulting distance matrix was used to build phylogenetic tree using Neighbour Joining (NJ) algorithms. In the present study, the Neighbor Joining (NJ) phylogenetic tree constructed across the samples of *B. tabaci* revealed the existence of two major clusters-Cluster 1 and Cluster 2 (Fig. 8). The cluster 2 was further sub-divided into two sub-clusters (Cl 2a and Cl 2b). Sub-cluster Cl 2a consisted of samples from Belagavi, Dharwad and Bagalkot populations, whereas the sub-cluster, Cl 2b consisted of populations from Bengaluru rural, Chamarajanagara, Chikballapur, Kolar and Chikkamagaluru. Cluster 1 consisted of populations from Davanagere, Haveri and Shivamogga. Though, sub cluster Cl 2a and Cl 2b formed separate groups, they shared close genetic proximity. The populations from Shivamogga, Davanagere and Haveri formed separate cluster. The populations from Bengaluru rural, Chamarajanagara, Chikkaballapura, Kolar and Chikkamagaluru were intermixed with each other.

The phylogenetic analysis of all the 140 individuals across sub-populations also resulted in formation of 2 major clusters (Fig. 9). Further, clusters 1 was sub divided into two sub-clusters (C 1a and C 1b). Individuals collected from Haveri, Davanagere, Dharwad, Bagalkot, Kolar, Chikkamagaluru, Shivamogga and Belagavi are distributed across cluster 1. Sub cluster, C 1a consisted of individuals from Haveri, Davanagere, Kolar and few individuals from Dharwad, Shivamogga and Chikkamagaluru regions. Sub cluster, C 1b consisted of individuals from Bagalkot, Belagavi, Dharwad and few individuals from Shivamogga regions. Cluster 2 also sub divided into two sub clusters viz., C 2a and C 2b which consisted of individuals from Chikkamagaluru, Chikkaballapur, Bengaluru rural and Chamarajanagara. Individuals from Chikkamagaluru formed separate sub cluster as C 2a whereas, individuals from Chikkaballapur, Bengaluru rural and Chamarajanagara formed another sub cluster C 2b. Majority of individual distributed across the major clusters and sub clusters, possibly due to high rate of gene flow/genetic drift across the populations/ regions. Which is possibly a result of ready shift in populations especially adults, which have greater mobility within sub-clusters. In addition, ready and frequent exchange of seedlings or planting materials across geographical zones may be contributed for intermix of individuals among different clusters. The results were similar to the cluster analysis demonstrated by Lima *et al.* (2002b) who observed that, biotype B

individuals are scattered independently in the localities where samples were collected. Nevertheless, some clusters were evident, joining individuals according to the host plants.

Principal component analysis (PCA) was carried out to show the distribution and relationships between the populations based on the bidimensional plot of the genetic distance. The populations collected from different locations are distributed in four quadrants (Fig. 10). PCA revealed the separation of samples more clearly between populations of different geographical locations. Some populations that showed a close phylogenetic relationship were separated more clearly by the PCA plot.

Similar results are in agreement with results of Gocmen and Devran (2002) who reported that, eleven AFLP primer pairs detected a total of 547 AFLP fragments in *B. tabaci* populations and 389 of these showed polymorphism. Cluster analyses of AFLP data clearly separated these populations into two groups with a genetic variability between 42 and 81 per cent. The results indicated that, *B. tabaci* may have biotypes based on adaptation to certain host plant species.

The genetic differentiation estimated among three cryptic species was very high despite the overlapping distribution in the surveyed locations (Prasanna *et al.*, 2015). The high genetic differentiation indicates absence of gene flow between the species. Indeed, absence of gene flow has been observed between clades separated by 3.5 per cent divergence threshold (Elbaz *et al.* 2010; Xu *et al.* 2010). The reproductive incompatibility between the populations indicates strong reproductive isolation among the cryptic species (Liu *et al.* 2012).

Gene flow depends on the migration rate between populations. Migration rate, in turn, depends on the number of populations within a region, their geographic distribution, spatial pattern, distance between them and dispersal ability of the species. Gene flow between groups homogenizes the genetic variation between them. When gene flow rate is low or null, drift effects can become more easily visible in the differentiation of populations (Liu *et al.*, 2012). Rossel *et al.* (1997) analyzed the mitochondrial DNA of *B. tabaci* individuals from several countries and found a separation in *B. tabaci* due to its geographic origin. Therefore, the genetic

differentiation between *B. tabaci* populations seems to occur by gene flow restrictions between them, not by adaptation to a given host plant species.

The population genetic structure was investigated and the posterior probability [$\ln P(D)$] of the data took peak probability at 14 in the range of 1 to 15 subpopulations. The model with $K=14$ clusters, showed a higher likelihood than all other K s indicating the presence of 14 population clusters across the sampled populations (Fig. 12). Each vertical line represented an individual's probability of belonging to one of K clusters (represented by the various colors) or a combination thereof if ancestry is mixed (Fig. 13). The analysis also indicated that, populations from Davanagere, Kolar and Shivamogga are possibly from diverse ancestry as indicated by larger proportion of individuals with mixed ancestry. The high genetic divergence within the species when a broader geographical area was considered in the Mediterranean basin (Simon *et al.*, 2007). The results, with respect to degree of population structuring were similar to some other studies of *B. tabaci* within Latin America namely those of Valle *et al.* (2011) and Fontes *et al.* (2012).

The results were in accordance with the study conducted by Chu *et al.* (2014), who revealed substantial genetic structure in the collections of *B. tabaci* at the different locations, which indicates low gene flow between locations and that inbreeding was prevalent at most locations, which is concurrence with Tsagkarakou *et al.* (2007), who documented low gene flow between *B. tabaci* populations in Greece that were separated by only a few kilometres. These data suggest that, gene flow between whitefly populations may be minimal and that dispersal by *B. tabaci* is usually limited. Low gene flow between populations may contribute to the genetic differentiation of the populations across the region.

In the present study, populations of South and North Karnataka showed greater level of genetic variability. The results are corroborated with studies conducted by Bouktila *et al.* (2013) from which, AMOVA revealed that, diversity between geographical domains (North vs. South) and between individuals within populations were the most determining factors in the partitioning of the total genetic diversity (50.19% and 44.85%, respectively). Genetic distances between the populations indicated that, the populations of *B. tabaci* were structured according to their geographical origin. Ecological selection pressure should be considered as a key

parameter for the development of an integrated controlling strategy. This result is in agreement with most studies on *B. tabaci* populations across the world, where relatively high levels of genetic variability were detected (Moya *et al.*, 2001; Lima *et al.*, 2002b)

Significant genetic differentiation among *B. tabaci* populations from Colombia (Díaz *et al.*, 2015) and higher levels of population structure detected in previous studies, were associated mostly with variation among the species or biotypes (De Barro, *et al.*, 2005; Delatte *et al.*, 2006; Tahiri *et al.*, 2013) rather than within them. Most studies within species have been carried out on the invasive cryptic species. These studies indicated low or undetectable population structure, when evaluated across short geographic distances, even when physical barriers were suspected (Delatte *et al.*, 2006; Dalmon *et al.*, 2008; Tsagkarakou *et al.*, 2012; Tahiri *et al.*, 2013). Population structure was apparent at the level of the geographic region rather than within regions. Díaz *et al.* (2015) found an isolation by distance (IBD) effect when all distances were considered, but not within regions. This reflects lower gene flow between regions than within them. The genetic structure of *B. tabaci* to be dominated by region effects that, likely reflect a recent invasion during the late 90s (Quintero *et al.*, 2001).

In the present study, there is a high gene flow between the populations of *B. tabaci* collected from different geographical areas of Karnataka, which was predicted in the cluster analysis, AMOVA and structure analysis. Gene flow depends on the migration rate between the populations because of high mobility of *B. tabaci* adults. Migration rate, in turn, depends on the number of populations that are within a region, their geographic distribution, spatial pattern, distance between them and dispersal ability of the species.

5.3 Frequency distribution of mono and bipartite particle in populations of whitefly

5.3.1 Tomato Leaf Curl disease incidence

Begomo viruses have only one vector that is *B. tabaci* (Gottlieb *et al.*, 2010) because of a chaperone GroEL protein that binds the virus particles and protects them from degradation in gut and hemolymph. Gennadius during 1889 first identified the

holotype specimen of whitefly *B. tabaci* Genn. in tobacco from Greece. Insect classified under the order Hemiptera, family Aleyrodidae and sub family Aleyrodinae reported as the only known vector of ToLCV (Castellani *et al.*, 1981).

During survey, symptoms of naturally infected plants of tomato have shown that, mean percentage of disease incidence of ToLCV ranged from 4.41 to 19.26. Among the districts surveyed, the highest disease incidence of ToLCV on tomato was recorded in Chikballapura district (19.26 %), followed by Davanagere (17.41 %), Bengaluru rural (16.11 %), Kolar (15.81 %), Haveri (9.58 %), Belagavi (8.55 %), ChamaraJanagara (6.51 %), Shivamogga (6.25 %), Chikkamagaluru (5.76 %), Dharwad (4.84 %) and the least incidence was recorded in Bagalkot district (4.41 %). The infection category for all locations surveyed was also presented (Table 16 and Fig. 25).

Prevalence of B-biotype of *B. tabaci* has also been considered to be one of the major contributing factor for the disease to assume epidemic proportion (Banks *et al.*, 2001). B-biotype is potent vector of begomovirus and capable of transmitting many viruses efficiently. Reddy (1978) observed six to 38 per cent ToLCV incidence during winter months and 25 to 86 per cent during summer months. ToLCV disease incidence ranging from 24 to 100 per cent has also been reported from north Karnataka by Raghavendra (2002). On the contrary, disease incidence in the present study was low to moderate, especially lower incidence in Northern Karnataka.

The main reasons for the differences in the incidence level of the disease between districts might be due to difference in the cropping pattern and the abundance of virus inoculum, vector population and the biotype of whitefly. The main probable reason for comparatively high incidence of disease in Chikballapura, Davanagere, Bengaluru rural and Kolar districts could be extensive and continuous cultivation of tomato crop by the farmers and the prevalence of *B. tabaci* B-biotype vector. The results were similar to the study conducted by Jyothi (2015), who reported, highest incidence (76.46%) in Kolar district and least incidence of 21.64 per cent in Ramanagar district. Incidence of begomovirus has been found to be dependent on the population and biotype of the whitefly vector (Jyothi, 2015; Das *et al.*, 2017).

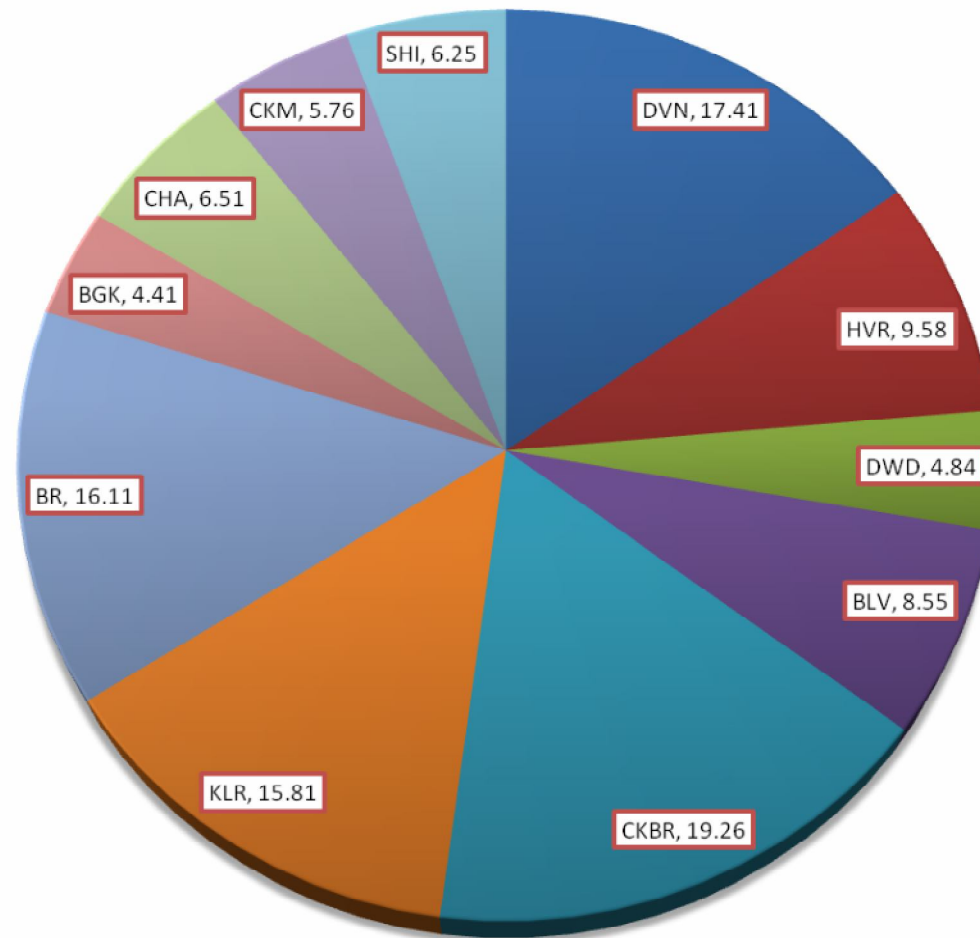


Fig 25. Mean per cent disease incidence (PDI) for ToLCVD incidence across the sampling regions of Karnataka

5.3.2 Destribution frequency of virus particles among the *B. tabaci* population

Frequency of mono and bipartite virus particles in *B. tabaci* collected from different agro climatic zones of Karnataka was determined by PCR using mono and bipartite particle specific primers. The results revealed the occurrence of virus particles in the different surveyed locations. The monopartite virus particles were amplified at 270 bp region, whereas, the bipartite virus particles were amplified at 477 bp region. The results revealed the occurrence of monopartite, bipartite and also presence of both mono and bipartite virus particles in some individuals of whiteflies analyzed (Table 17).

The distribution frequency of monopartite, bipartite and both mono and bipartite virus particles among the *B. tabaci* population were analyzed from different districts. Among the individuals analyzed, Davanagere population carried 60 per cent monopartite virus particles, the populations from Haveri, Dharwad, Chikkaballapura, Bengaluru rural, Chamarajanagara and Shivamogga were detected with 40 per cent each and populations from Kolar and Bagalkot carried 20 per cent of monopartite virus particles. Twenty per cent of the populations from Dharwad detected with bipartite virus particles whereas, populations from Haveri (20%), Belagavi (40%) and Kolar (60 %) were detected with both mono and bi partite virus particles (Table 18).

Overall frequency distribution of virus particles in *B. tabaci* population indicated 30.90 per cent monopartite, 1.82 per cent bipartite and 10.36 per cent of the populations with both mono and bipartite virus particles with overall occurrence of 43.64 per cent. The remaining 56.36 per cent of the population, were free from virus particles (Table 18 and Fig. 26).

Monopartite virus particle prevalence was thrice (41.26 %) compared to bipartite virus particles (12.16 %). Similar results of higher frequency of monopartite virus particle were also reported by Muniyappa *et al.* (2000), who reported occurrence of monopartite genome (DNA A) having a single genomic component from Australia, Taiwan and Southern India, while, bipartite genome (designated as DNA A and DNA B) was more prevalent in northern India (Pandey *et al.*, 2010)

The study conducted by Gotz *et al.* (2012) using microarray, real-time PCR and Western blot analyses indicated that, *B. tabaci* heat shock protein 70 (HSP 70)

specifically responded to the presence of the monopartite ToLCV and the bipartite Squash leaf curl virus. Fluorescence in situ hybridization and immuno localization showed co-localization of ToLCV and the bipartite Watermelon chlorotic stunt virus virions and HSP70 within midgut epithelial cells (Czosnek *et al.*, 2002; Brown, 2010).

The whitefly, *B. tabaci* with piercing and sucking type of mouth parts was reported to carry plant viruses on the stylet (Das *et al.*, 2017). Varma (1955) was the first to report successful transmission of begomovirus by *B. tabaci*, which was later confirmed by Capoor and Ahmad (1975) and Jayashree *et al.* (1999). The whiteflies remained infective throughout their life span but virus was not transmitted to its progeny (Reddy *et al.*, 1981).

In the present study, it is concluded that, *B. tabaci* is a sole and major vector for the transmission of tomato leaf curl virus (ToLCV). The transmission rate across the surveyed area ranged from 4.84 to 19.26 per cent, which was categorized under resistant to moderately resistant. The frequency distribution of virus particle also varied in the individuals of different agro climatic zones. The difference in the distribution of virus particles may be due to difference in acquisition time of virus particles or presence of disease symptoms in the surveyed area.

5.4 Variations for traits related to whitefly resistance in tomato association mapping panel (TAMP)

5.4.1 Variation for trait related to whitefly resistance

Field evaluation of tomato minicore accessions was conducted to access the resistant traits related to whitefly resistance and to find out the resistant accessions to *B. tabaci*. The experiment was conducted during *rabi* and summer seasons of 2016-17 at College of Horticulture, Bengaluru. Further, evaluation for biochemical parameters like chlorophyll, phenols, tannin, terpinoid and biophysical parameters such as trichome type and density were done in laboratory to understand the variation for traits related whitefly resistance. The whitefly population on tomato accessions were recorded during both the seasons. The analysis of variance for all the parameters have indicated highly significant differences among the accessions and also for the *B. tabaci* population during both the seasons (Table 19 and Table 20).

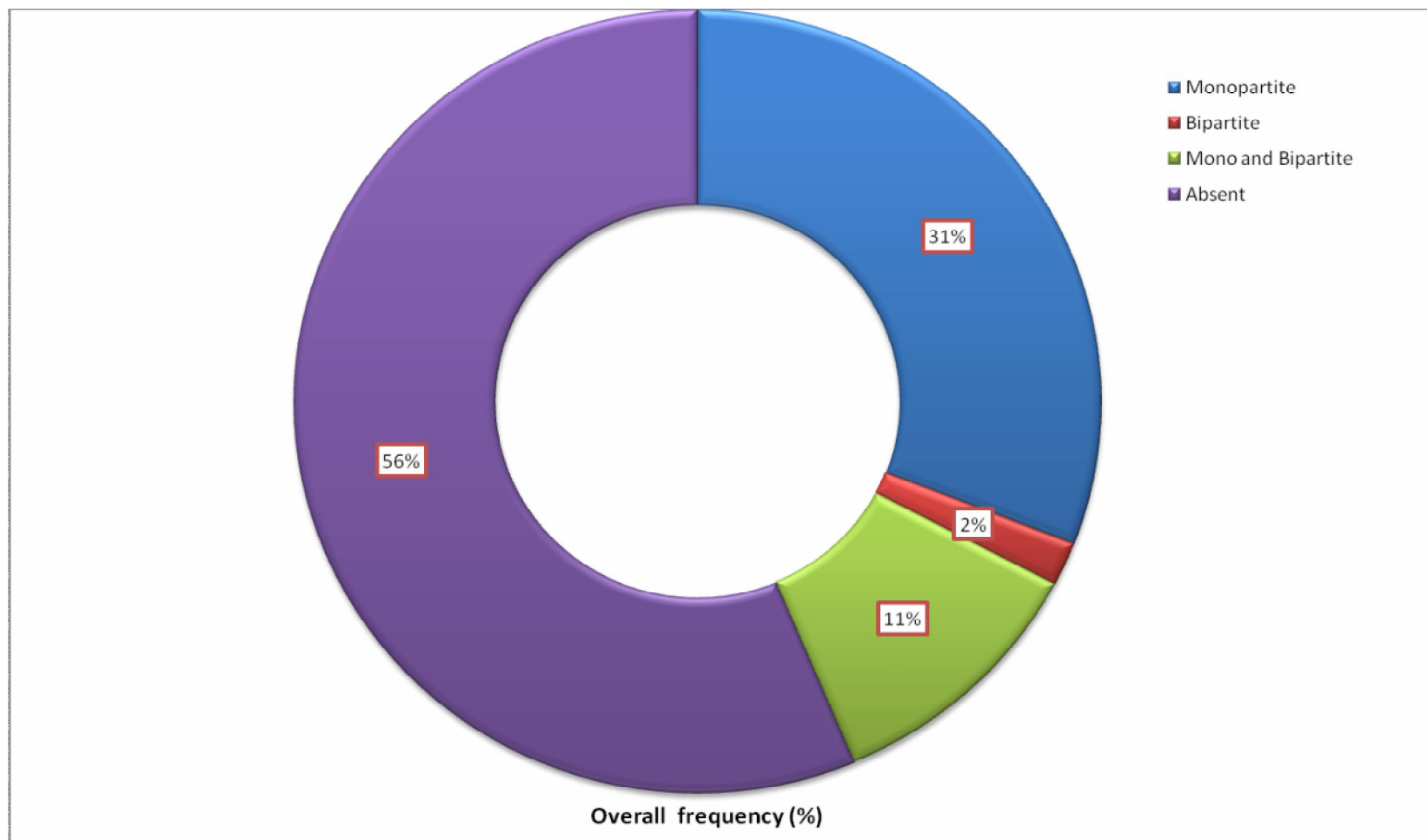


Fig 26. Overall frequency of virus particles among the *Bemisia tabaci* population

Whitefly population during *rabi* season were comparatively less and ranged from 0.30 to 3.31 nymphs per plant with the overall mean of 1.57 ± 0.03 nymphs per plant (Table 21). Whereas, during summer season, whitefly population ranged from 12.00 to 52.60 nymphs per plant with a mean of 29.20 ± 0.47 nymphs per plant. Which indicated that, summer season favoured the multiplication of whitefly population (Table 21 and Appendix X). The results are supported by Mwila *et al.* (2017) who indicated increased temperature has favoured increase in *B. tabaci* development, as it reduces the mean number of days for a nymph to change into adult. Similar results were also drawn by Zeshan *et al.* (2015) who stated that, whitefly count and leaf damage were dependent on varying environmental conditions.

Higher population of *B. tabaci* during summer compared to winter may be attributed to high temperature. Reports of Lal and Pillai (1982) indicated positive correlation between temperature and whitefly population also supports the present findings. Increased temperature has a favourable factor for increase in population is also in close agreement with EI-Sayed *et al.* (1991) and Abasse *et al.* (2018). But contrary to the present findings, Bharadia and Patel (2005) reported maximum population of whitefly in the 4th week of October which was attributed to variable climatic conditions of that particular region and time of cultivation.

During summer season 2016-17, the per cent disease incidence (PDI) was recorded at 60 days after transplanting. The PDI ranged from zero to 66.67 per cent with the mean PDI of 22.50. Among 260 tomato accessions, 68 accessions were recorded as immune with zero per cent infection, 29 accessions were moderately resistant, 66 were moderately susceptible, 73 were susceptible and remaining 24 accessions were highly susceptible to ToLCV disease incidence as per the disease rating scale (Singh *et al.*, 2014) (Appendix XI). These results were in accordance with Gaurav (2018) who reported that, the ToLCV incidence ranged from zero to 100.00 per cent at 60 days after transplanting (DAT).

Shankarappa *et al.* (2008) reported that, out of 20 genotypes, 11 were found resistant to ToLCV in the field condition. There were five wild relatives of tomato (*S. habrochaites*, *S. chilense*, *S. pimpnellifolium*, *S. cheesmanii* and *S. peruvianum*) that possessed high level of resistance to various Begomoviruses (Zamir *et al.*, 1994;

Chague *et al.*, 1997; Giordano *et al.*, 2005; Ji and Scott, 2005; Agrama and Scott, 2006; Hanson *et al.*, 2006 and Ji *et al.*, 2007).

In the present study, the chlorophyll content varied significantly across the accessions of tomato. The chlorophyll content ranged from 23.76 to 63.67 with a mean of 45.63 ± 0.38 (Table 22). Result showed low per cent of GCV, PCV, moderate heritability and moderate expected genetic advance mean (Table 23 and Fig. 27). Correlation with chlorophyll content showed negative correlation with whitefly population at 45 DAT (-0.021) and 60 DAT (-0.018). Whereas, it has recorded positive correlation with per cent disease incidence (0.026) (Table 25). These results are in close agreement with Petro and Redak (2000) and Petro *et al.* (2002) who showed that, some light green leaf poinsettia varieties are more susceptible to *B. tabaci* than those with dark green leaves. Whiteflies are generally attracted to yellow or yellow-green (Berlinger, 1980; Mound, 1962; Hasanuzzaman *et al.*, 2016). Our result is also supported by Elsey and Farnham (1994) who observed less whitefly infestation in dark green leaf varieties of *Brassica oleracea* (Maskato *et al.*, 2014).

In the present investigation, a wide variation in phenol content for accessions was observed and it ranged from 1.77 to 14.67 mg with a mean of 6.57 ± 0.14 mg (Table 22). High per cent PCV, GCV, heritability, genetic advance and expected genetic advance mean were observed (Table 23 and Fig. 27). The tannin content ranged between 2.58 to 12.10 g with a mean of 5.70 ± 0.11 g (Table 22). Here also high per cent of GCV, PCV, heritability and expected genetic advance mean of 58.82 percentage with low genetic advance of 3.36 per cent were observed (Table 23). Similarly, terpinoid content ranged from 145.52 to 913.86 mg with a mean of 510.25 ± 8.47 mg (Table 22). High per cent of GCV and PCV with moderate heritability and expected genetic advance were observed for this trait. The tannin in the genotypes increased with decrease in terpinoid (Table 23). The results are in accordance with the study conducted by Gaurav (2018) who observed, moderate estimates of GCV (18.47%), PCV (19.85%) along with higher heritability (92.25%) and GAM (39.36%) for quality traits in summer season. Similar results were also observed for characters like total soluble solids (Henareh, 2015 and Rai *et al.*, 2016). The lower environment influence on the expression of these characters and hence, these characters can be relied upon for selection. Hence, there is an ample opportunity for important trait selection.

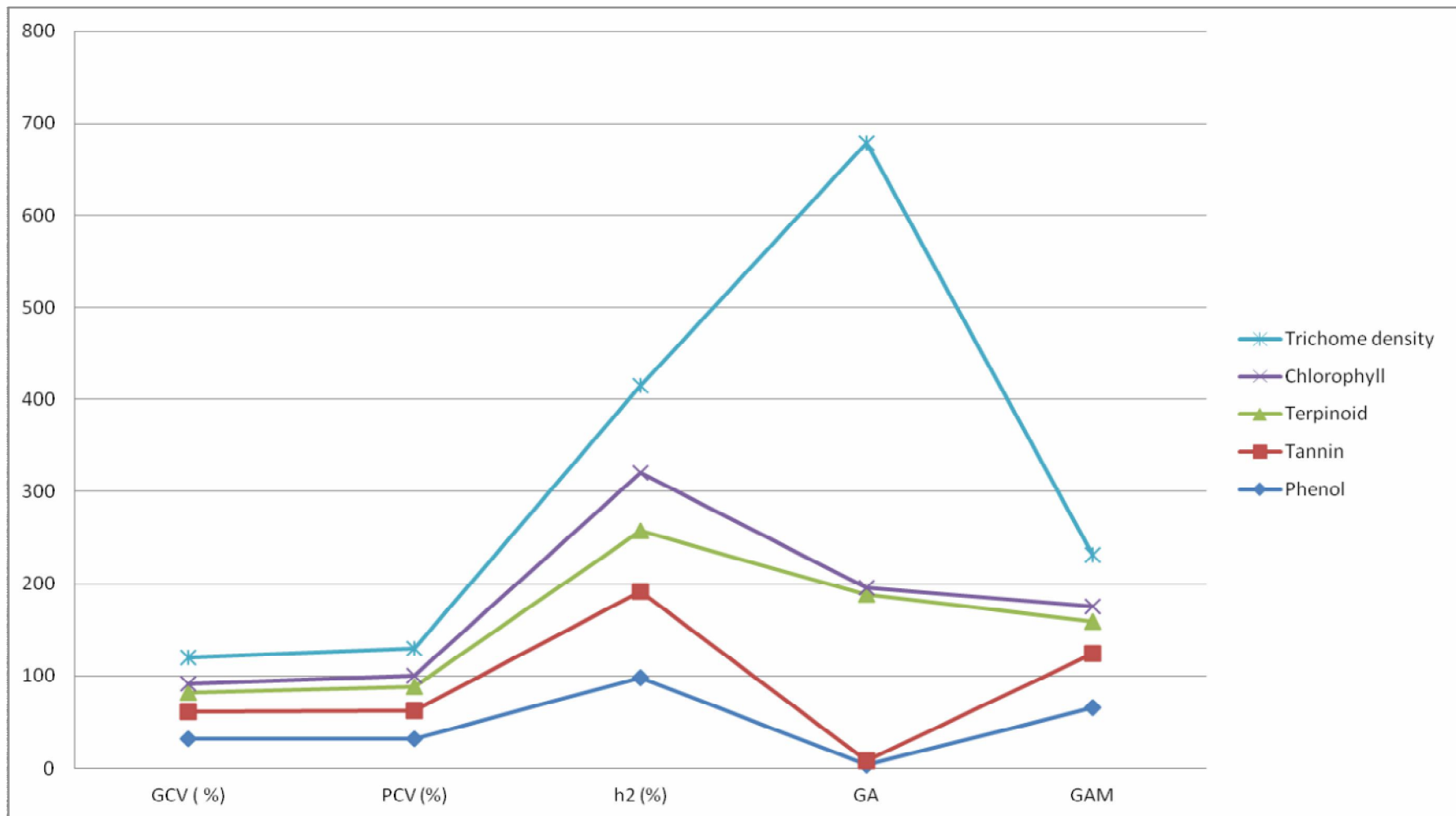


Fig 27. Genetic variability of biochemical and biophysical component traits in 260 tomato minicore accessions

Phenol content was significantly and negatively correlated with whitefly population at 60 days after transplanting (DAT) and negatively correlated with total whitefly population during summer. The correlation with tannin content was also negatively correlated with whitefly population at 60 DAT. Terpinoid content has exhibited significant and negative correlation with whitefly population at 45 DAT and negative correlation with whitefly population at 30 and 60 DAT and mean population (Table 26). It may be due to increase in phenol, tannin and terpenoids content after whitefly infestation has shown negative effect on population growth in subsequent days and resulted in decreased whitefly population among the tomato accessions.

The results are similar to Duffey and Stout (1996) who reported that, in tomato, phenolics and oxidative enzymes act together to affect insects during ingestion, digestion and metabolism. The tannin activity showed a significant negative correlation with the leaf damage, but were less effective than peroxidase, while flavonoid activity, though, showed negative association to damage, there was no significant correlation to damage (Mwila *et al.*, 2017). The tannins may decrease damage as they are bitter polyphenols that deter insect infestation (War *et al.*, 2012). They also reduce the nutritive availability by means of nonspecific protein precipitation and chelating of metal ions (Hagg *et al.*, 2013). Bellotti (2003) indicated that cassava resistance to the whitefly was based on antibiosis due to leaf containing lot of biochemical and anti-nutrient compounds, free sugars, protein and phenolic compounds (Koubala *et al.*, 2015), alkaloids, flavonoids and tannins (Anbuselvi and Balamurugan, 2014).

The results were in accordance with those of Taggar *et al.* (2012 and 2014) who found a negative correlation between tannins and flavonols with *B. tabaci* population, indicating that, increase in the activity of these biochemicals could contribute to the bioprotection of host plants against whiteflies by deterring the feeding and/or produce toxins that reduce the plant digestibility, which leads to nutrient deficiency in insects with drastic effects on their growth and development (Chen *et al.*, 2009). The expression of several defense metabolites is induced within minutes in damaged and hours in undamaged leaves, as a systemic response (Hagg *et al.*, 2013). In particular, peroxidase has been reported as a defense enzyme, which increases in various plants due to *B. tabaci* attack (Binu and Paliniswami, 2006) and

specific accumulation at the site of the attack (Kerchev *et al.*, 2012; Hagg *et al.*, 2013).

In the present study, it was observed that, terpinoid content was decreased while, the tannin content was increased in the tomato accessions. Similarly, the tannin in the tomato genotypes increased with decrease in terpinoid and flavenoid (Mwila *et al.*, 2017) which decreased damage. Terpinoid and flavonoid were reduced by tannin as they are produced in the same pathway in the defense system and have a similar mode of action, involving scavenging free radicals, including ROS (Treutter, 2006). Phenolics have also been documented to serve as defense compounds, through various means such as repelling from feeding by *B. tabaci* (Hagg *et al.*, 2013). Among the specific phenolics reported are the tannins and flavonoids (Engelberth *et al.*, 2007), both of which are the result of condensation of phenyl alanine derived compounds, with malonyl CoA (Hagg *et al.*, 2013). Tannins and flavonoids protect the plant against insect pests by influencing the behaviour, growth and development of the insects (Sulistyo and Inyati, 2016), by reducing the nutritive value of plant parts to the insect (War *et al.*, 2012; Hagg *et al.*, 2013). According to Selvanarayanan and Narayanasamy (2006), high phenol content could be contributed to the development of resistant variety. Annadurai *et al.* (1995) also reported that, high concentration of phenols and other secondary metabolites led to resistance against *B. tabaci*. Similarly, Banerjee and Kallo (1989) also found that, tomato varieties with high phenol content were resistant to insect pests infesting tomato (Usman *et al.*, 2015).

In the present study, it was observed that, trichome density varied across the accessions and ranged from 155.15 to 1500.50 per mm² with the mean of 861.35 ± 16.17 (Table 22). The results showed high per cent of GCV, PCV, heritability, genetic advance and expected genetic advance mean. (Table 23 and Fig. 27).

The correlation coefficients showed that, trichome density was significantly and negatively correlated with whitefly population at 60 DAT and negatively correlated at 45 DAT (Table 26). These results corroborate with the findings of Soundararajan and Baskaran (2001); Singh *et al.* (2002) and Ayyasamy and Baskaran (2005) who reported a negative correlation between trichome density in eggplant

leaves and resistance to *B. tabaci*. Similar results have also been found by Oriani *et al.* (2011) in tomato and Shibuya *et al.* (2009) in cucumber plant.

In accordance with the results of Baldin *et al.* (2012), most resistant varieties of tomato have shown oviposition non-preference against whitefly. The trichome density is associated with the variation in oviposition on the cultivars. Research has demonstrated that, leaf position on the plant can play an important role in the choice of oviposition location for *B. tabaci* (Chu *et al.*, 1995; Liu and Stansly, 1995; Baldin and Pereira, 2009). An experiment with *Cucurbita* spp. genotypes by Baldin and Beneduzzi (2010) showed that, there was less oviposition when the leaves were in a higher position on the plant. The same was reported by Cardoza *et al.* (1999), who observed less oviposition on the abaxial surface of upper leaves of the genotypes. Further, morphological aspects of the plant, such as trichome density and configuration (glandular or not), can represent as important resistance sources for whitefly oviposition (Toscano *et al.*, 2002).

Influence of trichome types on *B. tabaci* population during *rabi* season indicated significantly lower whitefly population on tomato accession group X₄ (trichome type III, V, VII) (1.52 nymphs/ plant) which was followed by X₁ (trichome type III, V) (1.53 nymphs/ plant), X₁₂ (trichome type I, II, III, IV, V, VII) (1.53 nymphs/ plant) and X₈ (trichome type I, III, IV, V, VII) (1.62 nymphs/ plant) and were statistically on par with each other. Accession group, X₃ (trichome type III, IV, V) has recorded significantly higher number of whiteflies (1.77) as compared to all other and was followed by X₇ (trichome type III, IV, V, VII) (1.72 nymphs/ plant) which was on par with X₁₀ (trichome type I, II, III, V, VII) (1.67 nymphs/ plant) and X₉ (trichome type I, III, IV, V, VII) (1.66 nymphs/ plant) (Table 24 and Fig. 28). Whereas during summer season, significantly least number of *B. tabaci* were recorded from accession group, X₁₂ (trichome type I, II, III, IV, V, VII) with 26.50 nymphs per plant and followed by X₁₀ (trichome type I, II, III, V, VII) (29.73 nymphs/ plant) which was on par with X₅, X₇, X₁₁ and X₉. Significantly higher number of whiteflies were recorded from accession group X₂ (trichome type I, III, V) with 41.75 nymphs per plant which was on par with X₁ (trichome type III, V) with 40.95 nymphs/ plant (Table 24). The results clearly indicate that, the tomato accessions with more types of trichome, hinders the population growth of *B. tabaci* compared to the accessions with

less number of trichome types. This shows the role of type of trichomes in growth and development of whiteflies.

Some of the earlier works carried out on plant resistance to *B. tabaci* showed that, this insect can be affected by leaf morphological characters such as leaf shape, hairiness and glandular trichomes (Berlinger, 1986). In solanaceous crops like tomato, there was a negative correlation between total number of trichomes and the attractiveness to the adults as well as number of eggs laid (Oriani *et al.*, 2005; Oriani *et al.*, 2011; Hasanuzzaman *et al.*, 2016).

In the present study, it was also observed that, tomato accessions having trichome Type VII, IV and Type I has recorded significantly lesser number of whitefly nymphs at 45 and 60 DAT and mean whitefly population as compared to accessions having other trichome types. All three trichome types are glandular trichomes with single or four lobes (Table 25). The glandular trichome may hinder the *B. tabaci* population. The presence of glandular trichomes is considered as one of the main causes of morphological resistance in plants and can affect oviposition and feeding of small sucking insects (Sippel *et al.*, 1987; Heinz and Zalom, 1995; McAuslane, 1996). The importance of these structures as resistance source against whitefly has been reported by earlier studies (Butler Junior *et al.*, 1986; Valle and Lourenção, 2002; Fancelli *et al.*, 2003; Lima and Lara, 2004; Baldin *et al.*, 2005). The potential effects of the trichomes on the whitefly can vary, depending on the trichome angle on the leaf surface, length and type. These factors potentially affect oviposition, fixing and juvenile feeding (Mound, 1965; Williams *et al.*, 1980; Channarayappa *et al.*, 1992; Baldin *et al.*, 2012).

Results are also in close argument with Hasanuzzaman *et al.* (2016) who reported that, morphological leaf characters like leaf trichome density and trichome length played important roles in attraction and oviposition choice of *B. tabaci*. The results proved that, the highly preferred eggplant varieties possessed the highest densities and the longest trichomes, indicating these two trichome characteristics may be a mechanism influencing the adult whitefly populations as well as oviposition. Trichome number, length and spatial arrangement also appear to influence the population density of whiteflies on different crops (Kishaba *et al.*, 1992; Heinz and

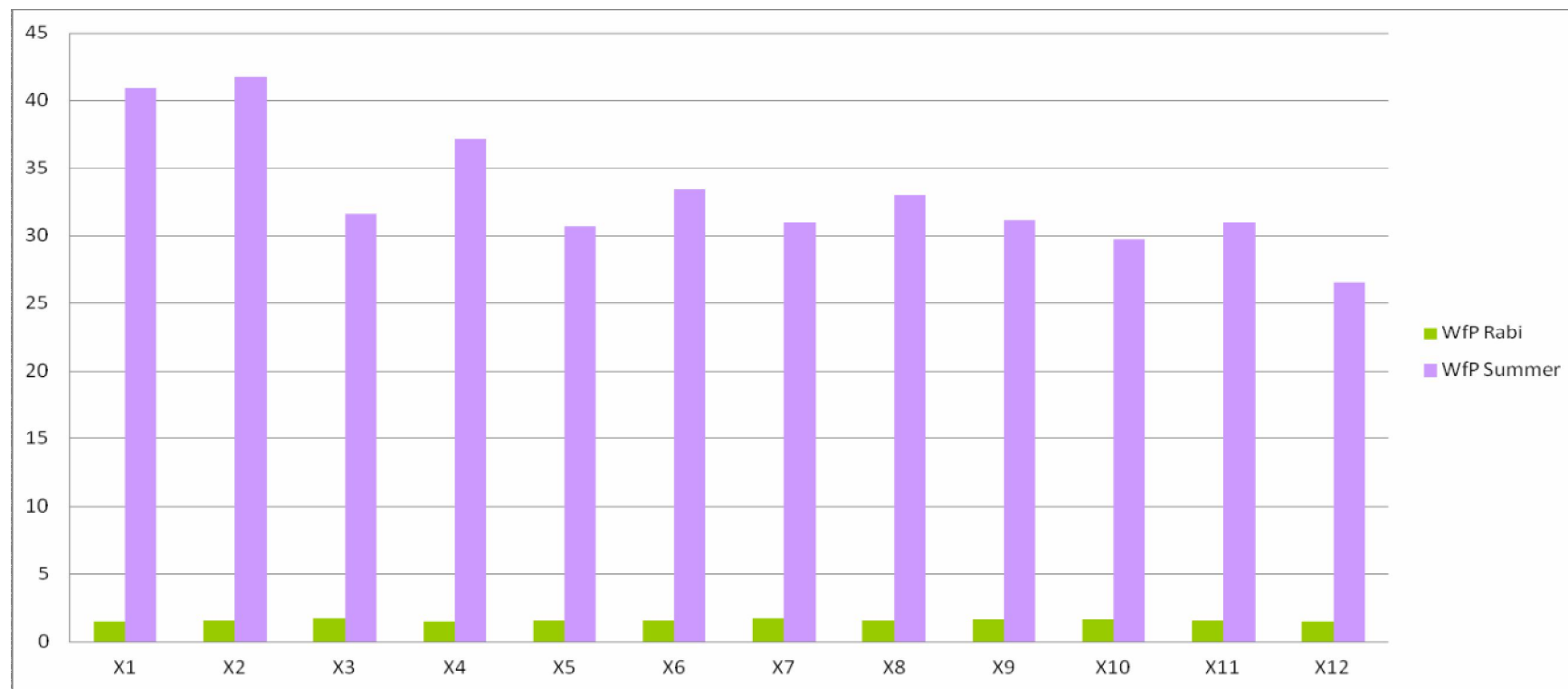


Fig 28. Effect of trichome type on *Bemisia tabaci* population in tomato accessions field evaluated during *rabi* and summer season 2016-17 at COH, Bengaluru

X₁= Type III, V

X₄= Type III, V, VII

X₇= Type III, IV, V, VII

X₁₀= Type I, II, III, V, VII

X₂= Type I, III, V

X₅= Type I, III, IV, V

X₈= Type I, III, IV, V, VII

X₁₁= Type II, III, IV, V, VII

X₃= Type III, IV, V

X₆= Type I, III, V, VII

X₉= Type I, III, IV, V, VII

X₁₂= Type I, II, III, IV, V, VII

Zalom, 1995). Eggplant varieties having higher trichome densities recorded lower numbers of whitefly adults and eggs than other varieties (Hasanuzzaman *et al.*, 2016).

5.4.2 Molecular analysis of tomato accessions

Molecular analysis of tomato accessions was undertaken by using a total of 260 tomato minicore accessions, DNA samples from five populations, which were screened across all the sampling locations were done using 40 SSR markers. SSR markers have been proved to be useful in genetic diversity studies because of their high reproducibility and great power for the detection of polymorphism (Guo *et al.*, 2012; Hamidi *et al.*, 2014; Abdein *et al.*, 2018). In the present study, our results showed that, there is a high genetic variation among the tested genotypes, which agrees with the results from previous studies carried out on tomato are discussed below.

Number of alleles (N_a) among the polymorphic microsatellite loci ranged between 2.0 and 4.60 across the samples. A total of 122 alleles were recorded for the 40 microsatellite loci screened across five groups (populations) of *Solanum lycopersicum*. The most diverse locus, BF-CHVR-2-616 recorded 4.6 alleles and the least diverse locus, Pb had 2.0 alleles across the populations. The average number of alleles across all the microsatellite loci stood at 2.60, indicating the validity of the sample size selected for the present study. Effective number of alleles (N_e) that provides a good measure of genetic variation in accordance with population size (Maudet *et al.*, 2002), was maximum for the locus BF-CHVR-12-616 (3.595) and minimum for the locus, BW3 (1.445).

Genetic parameters across populations indicated that, the number of different alleles of microsatellite loci (N_a) ranged between 1.375 and 4.150 across the populations. The most diverse population, Group 4 recorded 4.150 alleles. The least diverse population, Group 5 had 1.375 alleles. The average number of alleles across all the microsatellite loci stood at 3.020. Number of effective alleles (N_e), that provide a good measure of genetic variation in accordance with population size was maximum for the population, Group 4 (2.69) and minimum in Group 5 (1.303). The observed and expected heterozygosity are indicative measures of heterozygosity (Nei, 1987). The grand mean of observed heterozygosity (H_o) across all the populations was 0.008

and varied between 0.00 (Group 5) to 0.012 (Group 4). Mean expected heterozygosity (H_e) was 0.461, which varied between 0.143 (Group 5) to 0.604 (Group 4) (Table 28). The maximum expected and observed heterozygosity among population indicated that, the populations were genetically diverse. The percentage polymorphism for the loci ranged between 30 for Group 5 and 100 for Group 1, 2 and 4 with the mean per cent polymorphism of 82.50.

The results were similar in the context of Henareh *et al.* (2016) who recorded 100 per cent polymorphic loci among the tested markers. The number of total loci per primer ranged from 6 to 26 with an average of 13.2. The polymorphism percentage averaged to 47.27 across all the genotypes. In the same context, high level of polymorphism (100%) in tomato cultivars was also found by Mansour *et al.* (2010) and Henareh *et al.* (2016), while, 62 per cent polymorphism was recorded by Edris *et al.* (2014). On the contrary, low level of polymorphism was observed by Aguilera *et al.* (2011) (34%) and Shahlaei *et al.* (2014) (23.25%). In addition, Sharifova *et al.* (2017) reported high level of polymorphism ranging from 50 to 90 per cent, similarly by Abdein *et al.* (2018).

The current results are in agreement with the those obtained by Aguirre *et al.* (2017), who reported, the number of alleles observed in the introductions was between two and eight with an average of 4.92 alleles per locus. Muñoz *et al.* (2010) reported that, a significant number of alleles with microsatellite markers can be related to the origin of the material or its genetic nature, either because of its genetic diversity or geographical distance, so a low number of alleles found can be explained by a narrow geographical collecting area and the analysis of the materials. On the other hand, Kwon *et al.* (2009) evaluated 63 varieties of tomato with 33 SSR markers, finding eight SSRs with 2 alleles, six with 2 alleles, eight with 4 alleles and 11 markers with 5 alleles. In total, 132 alleles were identified with an average of 4 alleles, versus 64 found in present study with an average of 4.92 alleles per locus.

The heterozygosity (gene diversity) is considered as a reliable parameter of genetic variation among the loci. Among all the loci screened across 260 accessions, the grand mean of observed heterozygosity (H_o) was 0.014, indicating a high degree of genetic diversity and possibility of a very high selection potential for the loci under study. The mean value among the loci was between 0.00 for Pb and 0.061 for

FBTGS0289. The grand mean of expected heterozygosity (H_e) was 0.390. The mean heterozygosity values for loci ranged between 0.282 for BW3 and 0.698 for BF-CHVR-12-616 loci (generally, a polymorphic loci should have a minimum heterozygosity value of 0.10). The N_m values, that indicate an overall number of migrants and possible divergence among the microsatellite loci stood at 1.019 with locus, BF-CHVR-05-290 having maximum N_m value of 2.783 and the locus, FBTGS0321 recorded the minimum N_m value of 0.237 (Table 27). The fixation coefficient (F_{ST} value) of population measured with 40 microsatellite markers varied from 0.082 (BF-CHVR-05-290) to 0.513 (FBTGS0321) with the mean of 0.238 (Table 27). The heterozygotes in F_{IT} was amounted to 0.988 and mean F_{IS} was 0.985.

In the accordance with the result of Aguirre *et al.* (2017), the average number of observed heterozygotes was 0.1128, only three of the 13 microsatellites evaluated presented heterozygotes, indicating that, the species being evaluated has more diversity by being facultative self-pollinating wild introductions with PCN greater than 15 per cent (Rick, 1958) suggests that, the crossing of individuals, can lead to heterozygotes and the generation of genetic diversity (Aguirre *et al.*, 2017). Tomato and its ancestors are reported as predominantly autogamous plants, which have a percentage of cross pollination equal to or lower than 5 per cent and self-pollination of 95 per cent or greater, showing a very low percentage that results in crosses and heterozygotes formed naturally. Salmerón (2000) described that, if inbreeding is strict, there will be no heterozygotes. The average expected heterozygosity (H_e) was 0.6946, being higher in some microsatellites with values above 0.8. This indicated that, loci with high number of alleles are more likely to have heterozygotes. Further, Kwon *et al.* (2009) stated that, SSR markers as the most informative, which can be very useful for other studies evaluating tomato germplasm. These results allow generating groups with high genetic diversity from crosses of wild materials from a wide geographical distribution.

The 25 SSR markers analysis revealed the major allele frequency per locus varied from 0.4091 to 0.9091 with an average value of 0.6622 per marker (Choudhary *et al.*, 2018), which is corroborated to the present study results. Above SSR markers revealed 64 alleles among these tomato genotypes. Allelic richness per locus varied widely among the markers, ranging from 2 to 5 with an average of 2.72 alleles per

locus. In the present study, gene diversity per locus ranged from 0.1694 to 0.7025 with an average of 0.4548 per marker. Similar findings were also reported by earlier worker, Raveendar *et al.* (2016) who reported a total of 176 alleles with an average of ten alleles per SSR locus. Bredemeijer *et al.* (2002) have reported a mean number of 4.7 (range, 2-8) alleles per locus in 521 tomato accessions. Similarly, present findings are also in agreement with Benor *et al.* (2008) who have reported an average of 4.3 alleles per locus in 39 determinant and indeterminant tomato inbred lines. Smulders *et al.* (1997) have detected 3 alleles per locus from seven inbred lines of tomato. He *et al.* (2003) have identified 2.7 alleles per locus from 17 varieties and 2 parental lines of tomatoes.

Shannon's Information Index (I) was considered as a parameter for genetic variation among five populations. The I value ranged from 0.218 (Group 5) to 1.083 (Group 4). The overall mean I was 0.792 (Table 28). Among the loci, the I value ranged from 0.460 (BW3) to 1.313 (BF-CHVR-12-616) with the mean of 0.609 (Table 27).

F-statistics (F-coefficients), also known as fixation indices describe the extant of inbreeding in a given tomato population. The significant mean F_{IS} value across the population was 0.985. The F_{IT} mean value across all the loci and population was 0.988. The non significant F_{IS} and F_{IT} values indicated the deficiency of heterozygosity among the populations for the screened microsatellite loci. The F_{ST} values in the range of 0.082 to 0.513 indicated high genetic differentiation with the mean F_{ST} value of 0.238 (23.8%), across the populations spread over sampled regions (Table 27).

The pair wise population F_{ST} values ranged from a minimum of 0.029 between Group 1 and Group 4 to maximum of 0.448 between Group 3 and Group 5 (Table 29). The pairwise genetic distance varied from a minimum value of 0.092 between the Group 1 and Group 4 populations to maximum of 0.971 between the Group 3 and Group 5 populations (Table 30). The pair-wise F_{ST} values and genetic distance for all the populations of tomato are presented in Table 29 and 30. F_{ST} values ranged between zero and one, values close to one indicated that, majority of the total variation is distributed among populations, while values close to zero indicated a

dominant variation within the populations (Pérez-de-la-Vega and García, 2000; Aguirre *et al.*, 2017).

The present findings are also in close conformity with the results of Aguirre *et al.* (2017) where, Wright index (F_{ST}) values ($F_{ST} = 0.3474$; $DS = 0.0905$; 10,000 replications) showed a high genetic differentiation among the groups (Wright, 1978). The markers showing the highest F_{ST} values explain that, the total differentiation of the accessions, showing the accessions by country of origin, given their geographical remoteness, have no gene flow between groups and therefore they can be genetically differentiated. Nakazato *et al.* (2008) used 11 AFLP primer pairs to assess polymorphism among *S. lycopersicum* var. *cerasiforme*, *S. pimpinellifolium* and all entries. F_{ST} among all populations and all accessions was meaningful ($p < 0.01$) but small (0.052 and 0.023 between *S. lycopersicum* var. *cerasiforme* and *S. pimpinellifolium*, respectively), indicating little genetic differentiation among the accessions of the population assessed, despite the high phenotypic differentiation thereof. These estimates were low compared with those reported by Nuez *et al.* (2004) for six microsatellite markers in *S. pimpinellifolium* with $F_{ST} = 0.17$. In the present study, the F_{ST} values were quite higher than these and indicating that, the molecular markers used allowed for the detection of population structure and have a high power to differentiate groups and accessions of cherry tomato.

The AMOVA revealed significant variation at each hierarchical level in the populations. The variation observed among groups was 3.53 per cent. A variance of 4.15 per cent ($F_{ST}=0.0768$) was observed among populations and within groups, whereas, the variance within populations was 92.31 per cent. The significant observed variation and the F-coefficients clearly indicated the presence of definite structure at each level of the population hierarchy (Table 31). Similar to the present studies, Raveendar *et al.* (2016) estimated the distribution of molecular variance among and within clusters using AMOVA. The results revealed six per cent of the total variation among geographical groups while, 86 per cent of the variation among individuals within population clusters. Determination of F_{ST} for the polymorphic loci across all six geographical groups showed a F_{ST} of 0.064, indicating high genetic variations. The pairwise F_{ST} estimate value was 0.135 between the inferred clusters 1 and 2, indicating significant differences between the clusters two.

In this present study, the Neighbor Joining (NJ) phylogenetic tree constructed across the samples of tomato population revealed the existence of two major clusters, Cluster 1 and Cluster 2 (Fig. 15). Cluster 1 consisted of single group of population, Group 5 which was clustered separately forming an out group. The cluster 2 was further sub-divided into two sub-clusters (C 2a and C 2b). Sub-cluster, C 2a consisted of single population from Group 2 individuals separated from all other populations of cluster 2. The sub cluster, C 2b includes populations from Group 1, Group 4 and Group 3, (Fig. 15). The phylogenetic analysis of all the 260 tomato accessions across sub-populations resulted in formation of two major clusters (Fig.16). The phylogenetic tree shows that, there was high rate of gene flow/ genetic drift across the populations among the individuals because of its cross pollination or due to human intervention for breeding activity.

In the phylogenetic analysis, most of the tomato inbred lines were clustered together in respect to their geographical location and thus, might have a similar genetic background (Benor *et al.*, 2008). Those clustered within the same group or subgroups are mostly from the same origin and those, which are distantly grouped, were from different geographical locations. This finding was also supported by Song *et al.* (2006) where, clustering with the same growth habit was noticed in the case of determinate tomato inbred lines. The average genetic similarity matrix result was also consistent with clustering of the inbred lines with their growth habit.

The results are in close agreement with the results of Geethanjali *et al.* (2011) who reported that, 16 tomato genotypes were grouped into four major clusters based on 37 SSR markers specific to chromosome 12. The wild genotypes were well separated from the cultivated species and three distinct groups were observed. The cultivated genotypes were grouped into two subclusters. However, the bootstrap values were much lower at the nodes, except two, in these two clusters. This indicated relatively higher genetic similarity among the cultivated accessions. The present study results are in accordance with the results of Raveendar *et al.* (2016) who reported pairwise comparisons of Nei's genetic distance (D) between geographical groups by computing data from 18 primers (Nei, 1973). Nei's standard genetic distances (D) between pairs of geographical groups with SSR markers varied from 0.028 to 0.153. The genetic distance-based results observed in the unrooted neighbor-joining tree

revealed a similar trend to the genetic similarity analysis, revealing two possible subpopulations using model-based approach in Structure analysis. PCoA analysis was also consistent with the clustering results of the structure analysis.

The results of present findings are also in agreement with those of the results obtained by Aguirre *et al.* (2017) who's analysis of molecular variance indicated a variation percentage of 11 between the groups and of 89 within the groups. These differences between groups were associated with the geographical distances of the origins of the introductions and the difference within the groups may indicate genetic diversity originated from hybridization between plants of the var. *cerasiforme* and tomato cultivars introduced in the same region. After the initial crossing, successive backcrosses to the var. *cerasiforme* showed greater genetic diversity or variation within the same.

The genetic distance-based results observed in the dendrogram by Choudhary *et al.* (2018) revealed a similar trend to the genetic similarity analysis, revealing genotypes have been grouped into three clusters *i.e.*, I, II and III, but was not possible to distinguish among genotypes with different species

Principal Coordinate Analysis showed the distribution and relationships between the populations based on the bidimensional plot of the genetic distance (Figure 17). The result showed that, populations of Group 2, Group 4 and Group 1 shared close genetic distance, whereas, Group 3 and Group 5 were genetically different. Principal component analysis revealed the separation of samples more clearly between populations of different groups. Some populations that showed a close phylogenetic relationship were separated more clearly by the PCA plot.

The structure analysis revealed that, there was a high rate of intermixing populations with larger proportion of gene flow/ genetic drift/ mixed ancestry across the populations because of its cross pollination or due to human intervention for crop improvement activity. Each vertical line represented an individuals probability of belonging to one of K clusters (represented by the various colors) or a combination thereof if ancestry is mixed (Fig. 20).

Molecular markers have great potentiality to identify the structure and genetic diversity (GD) of accessions. GD analysis is important for collections, conservation and sustainable utilization of Genbank accessions (Suresh *et al.*, 2014). Various types of DNA markers have been utilized to estimate the GD and phylogenetic relationship among tomato genotypes (Klein-Lankhorst *et al.*, 1991; Kwon *et al.*, 2009; Geethanjali *et al.*, 2011). Various methods have been used for surveying population structures. The model-based approach implemented in the Structure software might be the most frequently used method (Falush *et al.*, 2003). The results of Raveendar *et al.* (2016) revealed two subpopulations (88%), including admixtures (11%) in the 355 Asian tomato accessions, consistent with clustering results based on genetic distance. The overall F_{ST} value was 0.135, indicating a moderate differentiation between the inferred subpopulations.

In the present study, the results indicated that, the summer season favoured the multiplication of *B. tabaci* population as compared to *rabi* season may be attributed to high temperature. Mean while, the biochemical (Phenol, tannin, terpinoid and chlorophyll) and biophysical (trichome type and density) characters analyzed were showed great impact on *B. tabaci* population by showing negative correlation. The molecular analysis resulted with high per cent polymorphism for loci studied and structure analysis revealed the presence of high rate of intermixing populations with larger proportion of gene flow/ mixed ancestry across the populations.

5.5 Association analysis of component traits of whitefly resistance in tomato

Associations between biochemical and biophysical traits that confer resistance to whitefly and DNA markers were calculated using mixed linear model (MLM) and ensured to reduce false positive associations following appropriate filters. Probability, $P < 0.005$ was taken as the value to detect associations and $P < 0.001$ as the significant value to reduce false positive associations. The amount of phenotypic variation explained by each marker was estimated by R^2 . The biophysical and biochemical data sets of 260 accessions of tomato constituting association mapping panel were analyzed separately.

In all, a total of 24 marker-trait associations (MTAs) were detected covering five plant traits ($P < 0.005$). Among them, three loci explained 10.95 per cent of the variation for phenol content, nine loci explained 23.00 per cent of the variation for tannin contents, three loci explained 5.18 per cent of the variation for terpenoid, seven loci explained 19.93 per cent of the variation in chlorophyll and three loci explained about 10.26 per cent of the variation in trichomes. Plant traits have different genetic architectures, in some cases, a few genes may explain a large proportion of the phenotypic variation (*i.e.* two loci explain 74.3% of the variation in fruit dehydroascorbate), while numerous genes may only explain a fraction of the phenotypic variation (*i.e.* five loci explain 33.2% of the ascorbate level variation) in tomato (Sauvage *et al.*, 2014). These results were supported by similar observations in rice, where, various genetic architectures were revealed using a GWAS approach for different traits of agronomic interest (Zhao *et al.*, 2011). However, significantly associated loci might contribute to a larger proportion of phenotypic variation, as many other small to medium effect loci were not detected due to the stringent threshold used in GWAS (false discovery rate) and the lack of statistical significance for the control of false negatives caused by small effect sizes (Visscher *et al.*, 2012).

Results of present study showed that some of the DNA markers were associated with multiple traits: LEaat7 (Chr05), Pb (Chr04), BF-CHO3 (Chr07) and BF-CHVR-05-290 (Chr05) were associated with the two traits each. The most significant MTA for all traits was detected for phenols and tannins through DNA marker, LEaat7 (Chr05), with 6.30 and 4.28 per cent of the phenotypic variation, respectively. The DNA marker, BF-CHO3 (Chr07) has recorded significant MTA for chlorophyll content, explaining 4.62 per cent of phenotypic variation.

The results of the present study were in close conformity with the results of Ruggieri *et al.* (2014) who identified 20 SNPs that were significantly associated with seven out of ten traits considered in tomato. Two DNA markers were associated with phenolic compounds, three with ascorbic acid, β -carotene and trans-lycopene, six with titratable acidity and one with pH and fresh weight. Moreover, 19 putative genes in linkage disequilibrium with markers were found. These genes might be involved in the biosynthetic pathways of the traits analyzed or might be implied in their transcriptional regulation (Xu *et al.*, 2013; Sauvage *et al.*, 2014).

The results of the present study were similar to the report of Zhang *et al.* (2015) who found six significant associations ($P < 0.005$) for 6-emthyl-5-hepten-2-one in *L. esculentum*. Among them, the most significant associations were detected on Chr11 (TES344) and Chr4 (SSR188). These two associations were also found in the near region of two QTLs for 6-emthyl-5-hepten-2-one in a previous study by Tieman *et al.* (2006). A total of 35 of the 44 associated loci (79.50%) were related to the metabolic traits (nine loci are associated with SSC) and accounted for between 16.2 (Asp) and 50.4 per cent (Rha) of the variation of these traits (Sauvage *et al.*, 2014). In a previous investigation of QTLs related to metabolic traits by Schauer *et al.* (2008) detected 104 metabolite QTLs for 22 distinct amino acids in tomato.

The 260 tomato accessions were subjected to various biochemical, biophysical and molecular profiling and also performed to identify the significantly linked markers. Greater diversity was seen for the biochemical, biophysical and molecular markers. The identified molecular markers may help in assisting selection (Marker Assisted Selection) for desirable traits of interest in tomato crop.

Future line of work

1. High genetic variation observed among the geographic populations of whitefly populations warrant a detailed barcode analysis to elucidate possible new biotypes
2. Detailed frequency distribution of New Delhi ToLCV type vis-à-vis prevalence of mono and bipartite ToLCV in different tomato growing regions of Karnataka.
3. Increasing the saturation of DNA markers on linkage map and fine mapping of different biochemical and biophysical characters governing *B. tabaci* resistance in tomato.
4. Validation of the identified DNA markers linked to companion traits conferring resistance to insects.
5. Detailed investigations on genome wide association studies through linkage disequilibrium approach for component trait of whitefly resistance to map the QTLs using the minicore accessions.

6. SUMMARY AND CONCLUSIONS

The present study on “Genetic diversity of whitefly, *Bemisia tabaci* (Genn.) (Hemiptera: Aleyrodidae) populations and molecular analysis for its resistant traits in tomato” was undertaken to study morphological traits plasticity, genomic flux and population genetic structure, occurrence of different virus particle frequency among whitefly populations collected from different districts of Karnataka and also screening of tomato minicore accessions at field and molecular screening for assessing whitefly resistance traits. The salient findings of the present study are summarized as below.

1. Detailed survey was undertaken to collect *Bemisia tabaci* puparia and adult samples from eleven districts of Karnataka which were distributed in seven agro climatic zones during the year 2016-17.
2. The morphometrics of *B. tabaci* puparia was recorded for 12 different characters and has recorded significantly higher values for 9 out of 12 characters in Dharwad population.
3. A set of 16 characters for adult male and 14 characters for female revealed that, the population of Chikkaballapura district was unique and recorded significantly higher values for the wing, antenna, proboscis and abdomen characters and lowest values for leg characters which was evident in cluster analysis. Morphometrics of *B. tabaci* adult (both male and female) revealed different trend compared to morphometrics of puparia.
4. The combined cluster analysis (both adult male, female and puparia) indicated similar trend. The principal component analysis (PCA) based on morphological characters of adult (female and male) + puparia, has divided all the characters into four major principal components with the diversity percentage of 68.12.
5. The genetic diversity and population structure of *B. tabaci* (140 female individuals) collected from different agro-climatic regions were accessed using 17 shortlisted microsatellite markers. The marker analysis revealed a significant observed and expected heterozygosity indicating the presence of significant genetic diversity among eleven populations of *B. tabaci*. The high mean number of migrants (N_m)

value of 0.281 across all the populations indicated the presence of significant migratory rate (gene flow) among the populations.

6. The significant mean values of F_{IS} (0.88), F_{ST} (0.50) and F_{IT} (0.93) for *B. tabaci* indicated the level of clustering across the populations and revealed the existence of distinct genetic clustering at each hierarchy of the population *i.e.*, individual, sub-population and total population, respectively.
7. The Analyses of Molecular Variance (AMOVA) across all the populations exhibited 49.79 per cent variation among the populations and 50.21 per cent within population with a mean fixation index of 0.498.
8. The combined results of Neighbour Joining tree and Principle Coordinate Analysis (PCA) revealed interesting clustering patterns with limited weight on geographic locations. Careful observations revealed that, subcluster populations formed separate groups and shared close genetic proximity. The clustering analysis from both morphometrics (adults + puparia) and molecular analysis revealed almost similar type of results.
9. The population genetic structure analyses of *B. tabaci* populations also indicated the presence of fourteen genetic clusters ($K=14$) which spread across all the sampled populations from eleven districts of Karnataka, forming genetically mixed populations.
10. The ToLCV incidence and whitefly infestation recorded during survey showed 4.41 to 19.26 per cent, which false into moderately resistance to resistance infection category. Among the districts surveyed, the highest disease incidence of ToLCD on tomato was recorded in Chikkaballapura district. This showed that the population of whiteflies from Chikkaballapura location may be highly virulent.
11. Mono and bipartite virus particles, amplified at 270 bp and 477 bp regions, respectively using SSR markers revealed an average of 56.36 per cent population, free from virus. Remaining populations showed the presence of virus particles and among them, 30.90 per cent of the individuals were detected with monopartite only, 10.36 per cent of the individuals with both mono and bipartite and 1.82 per cent with bipartite virus particles.

12. Field evaluation of 260 tomato minicore accessions during rabi and summer seasons revealed that, incidence of whitefly population was comparatively less (0.30 to 3.31 nymphs/ pl) with mean of 1.57 nymphs per pl in rabi season while, its population was higher (12.00 to 52.60 nymphs/ pl) and mean of 29.20 nymphs per pl. during summer season.
13. High GCV and PCV (>20 %) were observed for phenol, tannin, terpinoid and trichome density whereas moderate for chlorophyll. High estimates of broad sense heritability and genetic advance over mean for phenol, tannin, terpinoid and trichome density was observed among the minicore accessions.
14. Phenol was significantly and negatively correlated with whitefly population 60 days after transplanting (DAT). Terpinoid content exhibited significant and negative correlation with whitefly population at 45 DAT. While other parameters viz., tannins and chlorophyll showed non significant correlation with whitefly population.
15. The trichome density and trichome type played an important role in whitefly resistance on tomato. Trichome density was significantly and negatively correlated with whitefly population 60 DAT and negatively correlated with 45 DAT. The accessions with trichome types I, II, III, IV, V and VII have recorded significantly less number of whiteflies (26.50 nymphs/ pl) whereas, significantly higher number of whiteflies were recorded from the accessions with trichome type I, III, V (41.75 nymphs/ pl).
16. Tomato accessions having trichome type VII, IV and Type I have recorded significantly lesser number of whitefly nymphs at 45 and 60 DAT. All these trichome types are glandular trichomes with single or four lobes.
17. The molecular analysis of 260 tomato minicore accessions revealed significant observed and expected heterozygosity indicating the presence of significant genetic diversity among five clusters population.
18. The high mean Nm value of 1.091 across all the populations indicated the presence of significant gene flow among the populations. The significant mean values of F_{IS} (0.985), F_{ST} (0.238) and F_{IT} (0.988) indicated the clustering across

the populations and revealed the existence of distinct genetic clustering at each hierarchy of the population *i.e.*, individual, sub-population and total population.

19. The combined results of Neighbour Joining tree and Principle Coordinate Analysis (PCA) revealed interesting clustering patterns with limited weight on different populations.
20. On the other hand, population genetic structure analyses of tomato accessions indicated the presence of seven genetic clusters ($K=7$) which spread across all the populations from five groups, forming high level of genetically mixed population.
21. Association analysis between biochemical, biophysical traits and SSR markers were done using TASSEL 3.0 software by applying Mixed linear model (MLM) and results revealed 24 marker trait associations (MTAs) on five selected traits ($P < 0.005$). Among them, phenols were associated with three markers, tannins with nine markers, two markers with terpenoid, chlorophyll with seven markers and trichomes were associated with three markers.
22. Four markers [LEaat7 (Chr05), Pb (Chr04), BF-CHO3 (Chr07) and BFCHVR-05-290 (Chr05)] were associated with multiple traits (two traits each). The most significant marker trait associations (MTA) ($P < 0.001$) was detected for phenols and tannins on LEaat7 (Chr05), with 6.30 and 4.28 per cent of the phenotypic variation, respectively. The marker BF-CHO3 (Chr07) recorded significant MTA for chlorophyll content, explaining 4.62 per cent of phenotypic variation.
23. Morphological variations in *B. tabaci*, may imply its genetic differentiations among populations or biotypes. *Bemisia tabaci* exhibited phenotypic plasticity on tomato lead to conclusion that, *B. tabaci* may consist of many cryptic species. The variations might provide support for distinguishing other populations as well.

REFERENCES

- Abasse, A. A., Abd-El, W. A. H., Naema, A. A., Sawsan, M. A. and Enayat, M. M., 2018, Impact of biotic and abiotic factors on the population dynamics of *Bemisia tabaci* (Genn.) and *Tetranychus urticae* (Koch) infested tomato plant *Lycopersicon esculentum* L. at kafr El sheikh Governorate. *Egypt. Acad. J. Biolog. Sci.*, **11**(4): 41-50.
- Abdein, M. A., El-Moneim, A. D., Sahar, S., Al-Juhani, S. M. T. W. and Mohamed, S. E., 2018, Molecular characterization and genetic relationships among some tomato genotypes as revealed by ISSR and SCOT markers. *Egypt. J. Genet. Cytol.*, **47**:139-159.
- Abdelkrim, B. A., Hattab, T., Fakhfakh, H., Belkadhi, M. S., Gorsane, F., 2017, A landscape genetic analysis of important agricultural pest species in Tunisia: The whitefly *Bemisia tabaci*. *PLoS ONE*, **12**(10): 1-20.
- Abdullahi, I., Winter, S., Atiri, G. I. and Thottappilly, G., 2003, Molecular characterization of whitefly, *Bemisia tabaci* (Hemiptera: Aleyrodidae) populations infesting cassava. *Bull. Entomol. Res.*, **93**: 97-106.
- Agrama, H. A. and Scott, J. W., 2006, Quantitative trait loci for Tomato yellow leaf curl virus and Tomato mottle virus resistance in tomato. *J. American Soc. Hort. Sci.*, **131**: 267-276.
- Aguilera, J. G., Pessoni, L. A., Rodrigues, G. B., Elsayed, A. Y., Silva, D. J. H. and Barros, E. G., 2011, Genetic variability by ISSR markers in tomato (*Solanum lycopersicum* Mill.). *Rev. Bras. Cienc. Agrar.*, **6**: 243-252.
- Aguirre, N. C., Lopez, W., Orozco-Cardenas, M., Coronado, Y. M. and Vallejo-Cabrera, F., 2017, Use of microsatellites for evaluation of genetic diversity in cherry tomato. *Bragantia Campinas*, **76**(2): 220-228.
- Albert, E., Segura, V., Gricourt, J., Bonnefoi, J., Derivot, L. and Causse, M., 2016, Association mapping reveals the genetic architecture of tomato response to water deficit: focus on major fruit quality traits. *J. Exp. Bot.*, **67**(22): 6413-6430.

- Al-Shareef, L. A. H., 2011, Impact of whitefly, *Bemisia tabaci* (Gennadius) infestation on chlorophyll and carotene concentrations, as well as moisture content in some vegetable plants in a greenhouse. *Egypt. J. Exp. Biol. (Zool.)*, 7(1): 11-15.
- Anbuselvi, S. and Balamurugan, T., 2014, Phytochemical and antinutrient constituents of cassava and sweet potato. *World J. Pharma. Pharma. Sci.*, 3(3): 1440-1449.
- Annadurai, R. S., Murugesan, S., Senrayan, R., Bramanian, G. G. and Ananthakrishnan, T. N., 1995, Tritropic interaction in *Heliothis armigera* (Hub.) and its natural enemy systems: A chemical ecology approach. In: *Emerging trends in biological control of phytophagous insects* oxford IBM Publishers., New Delhi, pp 83-102.
- Anonymous, 2015, Data sheets on quarantine pests, *Bemisia tabaci*, *EPPO quarantine pest*, pp 1-6.
- Anonymus, 2018, Horticultural statistics at a glance-2018, Horticulture statistics division, Department of Agriculture, Cooperation & Farmers Welfare Ministry of Agriculture & Farmers. www.agricoop.nic.in, pp 140-220.
- Antonious, G. F., Kochhar, T. S. and Simmons, A. M., 2005, Natural products: seasonal variation in trichome counts and contents in *Lycopersicum hirsutum* f. *glabratum*. *J. Environ. Sci. Health.*, 40: 619-631.
- Ashfaq, M. P., Hebert, D. N., Mirza, M. S., Khan, A. M., Mansoor, S., Shah, G. S. and Zafar, Y., 2014, DNA barcoding of *Bemisia tabaci* complex (Hemiptera: Aleyrodidae) reveals southerly expansion of the dominant whitefly species on cotton in Pakistan, *PLoS One*, 9: 11-24.
- Atwell, S., 2010, Genome-wide association study of 107 phenotypes in *Arabidopsis thaliana* inbred lines. *Nature*, 465: 627-631
- Avidov, Z., 1956, Bionomics of the tobacco whitefly (*Bemisia tabaci*, Genn.) in Israel. *Ktavim*, 7: 25-41.

- Ayyasamy, R. and Baskaran, P., 2005, Influence of certain leaf characters of brinjal accessions with incidence of *Bemisia tabaci*. *J. Food Agric. Environ.*, **3**: 333-334.
- Azizi, A., Mozafari, J. and Shams-bakhsh, M., 2008, Phenotypic and molecular screening of tomato germplasm for resistance to tomato yellow leaf curl virus., *Iranian J. Biotech.*, **6**(4): 199-206.
- Baig, M. M., Dubey, A. K. and Ramamurthy, V. V., 2015, Biology and morphology of life stages of three species of whiteflies (Hemiptera: Aleyrodidae) from India. *The Pan-Pacific Entomol.*, **91**(2):168-183.
- Baig, M. M., Dubey, A. K. and Ramamurthy, V. V., 2016, Determination of sexual dimorphism in the puparia of four whitefly pest species from India (Hemiptera: Aleyrodidae). *Acta Entomol. Musei. Nat. Prag.*, **56**(2): 447-460.
- Baldin, E. L. L. and Beneduzzi, R. A., 2010, Characterization of antibiosis and antixenosis to the whitefly silverleaf *Bemisia tabaci* B biotype (Hemiptera: Aleyrodidae) in several squash varieties. *J. Pest Sci.*, **83**: 223-229.
- Baldin, E. L. L. and Pereira, J. M., 2009, Influencia da altura de foliolos na expressao da resistencia de genotipos de tomateiro a *Bemisia tabaci* (Genn.) biotipo B (Hemiptera: Aleyrodidae). *Bol. Sanid. Veg. Plag.*, **35**: 249-258.
- Baldin, E. L. L., Silva, J. P. G. F. and Pannuti, L. E. R., 2012, Resistance of melon cultivars to *Bemisia tabaci* biotype B. *Horti. Brasil.*, **30**: 600-606.
- Baldin, E. L. L., Vendramim, J. D. and Lourencao, A. L., 2005, Resistencia de genotipos de tomateiro a mosca-branca *Bemisia tabaci* (Gennadius) Biotipo B (Hemiptera: Aleyrodidae). *Neotrop. Entomol.* **34**: 435-441.
- Baldwin, I. T., 1998, Jasmonate-induced responses are costly but benefit plants under attack in native populations. *Proc. Nat. Acad. Sci. USA*, **95**: 8113-8118.
- Baldwin, I. T., 1999, Inducible nicotine production in native *Nicotiana* as an example of adaptive phenotypic plasticity. *J. Chem. Ecol.*, **25**: 3-30.

- Balloux, F. and Lugon-Moulin, N., 2002, The estimation of population differentiation with microsatellite markers. *Mol. Eco.*, **11**:155-165.
- Banerjee, M. K. and Kaloo, L., 1989, Role of phenols in resistance to tomato leaf curl virus (Fusarium wilt) and tomato fruit borer in *Lycopersicon*. *Curr. Sci.*, **58**: 575-576.
- Banks, G. K., Colvin, J., Chowda-Reddy, R. V., Maruthi, M. N., Muniyappa, V., Venkatesh, H. M., Kumar, K. M., Padmaja, A. S., Beitia, F. J. and Seal, S. E., 2001, First report of the *Bemisia tabaci* B-biotype in India and an associated tomato leaf curl virus disease epidemic. *Plant Dis.*, **85**: 231.
- Barbehenn, R. V., Maben, R. E. and Knoester, J. J., 2008, Linking phenolic oxidation in the midgut lumen with oxidative stress in the midgut tissues of a tree-feeding caterpillar *Malacosoma disstria* (Lepidoptera: Lasiocampidae). *Environ. Entomol.*, **37**: 1113-1118.
- Bedford, I. D., Briddon, R. W., Brown, J. K., Rossel, R. C. and Markham, P. G., 1994, Geminivirus transmission and biological characterisation of *Bemisia tabaci* (Genn.) biotypes from different geographic regions. *Ann. Appl. Biol.*, **125**: 311-325.
- Bedford, I. D., Briddon, R. W., Markham, P. G., Brown, J. K. and Rosell, R. C., 1992, *Bemisia tabaci* biotype characterisation and the threat of this whitefly species to agricolony. *Proceedings of the 1992 British Crop Prot. Conf. Pests Diseases.*, **3**: 1235-1240.
- Bel-Kadhi, M. S., Onillon, J. C. and Cenis, J. L., 2008, Molecular characterization of *Bemisia tabaci* biotypes in Southern Tunisia. *Tunisian J. Plant Protec.*, **3**: 79-85.
- Bellotti, A. C., 2003, Arthropod pests: In cassava: Biology, production and utilization Hillocks, R. J., Thresh, J. M. and Bellotti, A. C. (Eds.). *CAB Int. Cali, Colombia*, pp 332.
- Bellows, T. S., Perring, T. M., Gill, R. J. and Headrick, D. H., 1994, Description of a species of *Bemisia* (Homoptera: Aleyrodidae). *Ann. Entomol. Soc. America*, **87**: 195-206.

- Bellows, T. S., Thomas, Jr., Perring, M. I., Gill, R. J. and Headrick, D. H., 2015, Cryptic species composition and genetic diversity within *Bemisia tabaci* complex in soybean in India revealed by *mtCOI* DNA sequence. *J. Int. Agric.*, **14**(9): 1786-1795.
- Benor, S., Zhang, M., Wang, Z. and Zhang, H., 2008, Assessment of genetic variation in tomato (*Solanum lycopersicum* L.) inbred lines using SSR molecular markers. *J. Genet. Genomics*. **35**: 373-379.
- Berlinger, M. J., 1980, A yellow sticky trap for whiteflies: *Trialeurodes vaporariorum* and *Bemisia tabaci* (Aleyrodidae). *Entomol. Expt. Appl.*, **27**: 98-102.
- Berlinger, M. J., 1986, Host plant resistance to *Bemisia tabaci*. *Agric. Ecosyst. Environ.*, **17**: 69-82.
- Berry, S. D., Fondong, V. N., Rey, C., Rogan, D., Fauquet, C. M. and Brown, J. K., 2004, Molecular evidence for five distinct *Bemisia tabaci* (Homoptera: Aleyrodidae) geographical haplotypes associated with cassava plants in sub-Saharan Africa. *Ann. Entomol. Soc. America*, **97**: 852-859.
- Bethke, J. A., Paine, T. D. and Nuessly, G. S., 1991, Comparative biology, morphometrics and development of two populations of *Bemisia tabaci* (Homoptera: Aleyrodidae) on cotton and poinsettia. *Ann. Entomol. Soc. Am.* **84**: 407-411.
- Bharadia, A. M. and Patel, B. R., 2005, Succession of insect pests of brinjal in north Gujarat. *Pest Manag. Econ. Zool.*, **13**: 159-161.
- Bhardwaj, S. C. and Kushwaha, K. S., 1984, Whitefly, *Bemisia tabaci* (Genn.) infesting tomato in Rajasthan. *Bull. Entomol.*, **25**: 76-97.
- Binu, A. and Palaniswami, A. M., 2006, *Bemisia* feeding induces pathogenesis related proteins in Cassava (*Manihot esculenta* Crantz). *Indian J. Biochem. Biophys.*, **43**(3): 182-185.
- Bisaro, D. M., 1996, Geminivirus DNA replication. In: DNA replication in eukaryotic cell (Ed., DePamphilis, M.L.), cold spring harbor laboratory press, Cold Spring Harbor, pp 833-854.

- Bleeker, P. M., Diergaarde, P. J., Ament, K., Guerra, J., Weidner, M., Schütz, S., De Both, M. T. J., Haring, M. A. and Schuurink, R. C., 2009, The role of specific tomato volatiles in tomato-whitefly interaction. *Plant Physiol.*, **151**: 925-935.
- Boukhatem, N., Jdani, S., Mukovski, Y., Jacquemin, J. M. and Bouali, A., 2007, Identification of *Bemisia tabaci* (Gennadius) (Homoptera: Aleyrodidae) based on RAPD and design of two SCAR markers. *J. Bio. Res., (Thessalon)*, **8**: 167-176.
- Bouktila, D., El-Mnouchi-Skhiri, S., Mezghani-Khemakhem, M., Makni, H. and Makni, M., 2013, Genetic structure of the whitefly *Bemisia tabaci* (Homoptera: Aleyrodidae) in Tunisia, inferred from RAPD markers. *J. Entomol. Zool. Stu.*, **1**(5): 10-15.
- Boykin, L. M. and De Barro, P. D., 2014, A practical guide to identifying members of the *Bemisia tabaci* species complex: and other morphologically identical species. *Front. Ecol. Evol.*, **2**: 45.
- Boykin, L. M., 2013, *Bemisia tabaci* nomenclature: lessons learned. *Pest Manag. Sci.*, **70**: 1454-1459.
- Bradbury, P. J., Zhang, Z., Kroon, E. D., Casstevens, T. M., Ramdoss, Y. and Buckler, E. S., 2007, Genetics and population analysis TASSEL: software for association mapping of complex traits in diverse samples. *Bioinform. Applic. note*, **23**(19): 2633-2635.
- Bredemeijer, M., Cooke, J., Ganai, W., Peeters, R., Isaac, P. and Noordijk, Y., 2002, Construction and testing of a microsatellite database containing more than 500 tomato varieties. *Theor. Appl. Genet.*, **105**: 1019-1026.
- Briddon, R. W., Bull, S. E., Amin, I., Idris, A. M., Mansoor, S., Bedford, I. D., Dhawan, P. S., Rishi, N., Siwarch, S. S., Abdel-Salam, A. M., Brown, J. K., Zafar, Y. and Markham, P. G., 2003, Diversity of DNA B, a satellite molecule associated with some monopartite begomoviruses. *Virol.*, **312**: 106-121.

- Broekgaarden, C., Bucher, J., Bac-Molenaar, J., Keurentjes, J. J. B., Kruijer, W., Voorrips, R. E. and Vosman, B., 2015, Novel genes affecting the interaction between the cabbage whitefly and *Arabidopsis* uncovered by genome-wide association mapping. *PLoS ONE*, **10**(12): 1-14.
- Brown, J. K. and Bird, J., 1992, Whitefly-transmitted geminiviruses and associated disorders in the Americas and the Caribbean Basin. *Plant Dis.*, **76**: 220-225.
- Brown, J. K., 2007, The *Bemisia tabaci* complex: Genetic and phenotypic variability drives bignovirus spread and virus diversification. *Online. APSnet Features-0107*. pp 1-11.
- Brown, J. K., 2010, *Bemisia*: Bionomics and management of a global pest. (Stansly, P. A. and Naranjo, S. E. Eds.). *Dordrecht: Springer Netherlands*. **4**: 211-234.
- Brown, J. K., Costa, H. S. and Laemmen, F., 1992, First report of whitefly-associated squash silver disorder of *Cucurbita* and of white streaking disorder of *Brassica* species in Arizona and California. *Plant Dis.*, **76**: 426.
- Brown, J. K., Fauquet, C. M., Briddon, R. W., Zerbini, M., Moriones, E. and Navas-Castillo, J., 2012, Family geminiviridae. In: King, A. M. Q., Adams, M. J., Carstens, E. B. and Lefkowitz, E. J. (Ed), *Virus taxonomy: Classification and nomenclature of viruses-ninth report of the international committee on taxonomy of viruses. Elsevier Academic Press, USA*, pp. 351-373.
- Brown, J. K., Frohlich, D. R. and Rosell, R. C., 1995, The sweet potato or silver leaf whiteflies: Biotypes of *Bemisia tabaci* or a species complex? *Ann. Rev. Entomol.*, **40**: 511-534.
- Butler-Junior, G. D., Henneberry, T. J. and Wilson, F. D., 1986, *Bemisia tabaci* (Homoptera: Aleyrodidae) on cotton: adult activity and cultivar oviposition preference. *J. Econ. Entomol.*, **79**: 350-354.
- Byrne, F. J., Bedford, I. D., Devonshire, A. L. and Markham, P. G., 1995, Esterase variation and squash silver leaf induction in B-type *Bemisia tabaci* (Homoptera: Aleyrodidae). *Bull. Entomol. Res.*, **85**: 175-179.
- Byrne, N. D. and Bellows, T. S., 1991, Whitefly biology. *Ann. Rev. Entomol.*, **36**: 431-458.

- Capoor, S. P. and Ahmad, R. U., 1975, Yellow vein mosaic disease of field pumpkin and its relationship with the vector, *Bemisia tabaci*. *Indian Phytopath.*, **28**: 241-246.
- Cardoza, Y. J., McAuslane, H. J. and Webb, S. E., 1999, Mechanisms of resistance to whitefly-induced squash silverleaf disorder in *Cucurbita pepo* L. *J. Econ. Entomol.*, **92**: 700-707.
- Carreras-Carbonell, J., Macpherson, E. and Pascual, M., 2008, Utility of pairwise *mtDNA* genetic distances for predicting cross-species amplification and polymorphism success in fishes. *Conserv. Genet.*, **9**: 181-190.
- Castellani, E., Nour, A. M. and Mohammed, M. I., 1981, Tomato leaf curl in Somalia Larriciamento foliane del pomodoro in Somalia. *Annali della facolta do Scienze Agrarie della, Universita dequistudi Ti. Torino*, **12**: 145-161.
- Chague, V., Mercier, J. C., Genard, M., De Courcel, A. and Vedel, F., 1997, Identification of RAPD markers linked to a locus involved in quantitative resistance to TYLCV in tomato by bulked segregant analysis. *Theor. Appl. Genet.*, **95**: 671-677.
- Channarayappa, S. G., Muniyappa, V. and Frist, R. H., 1992, Resistance of *Lycopersicon* species to *Bemisia tabaci*, a tomato leaf curl virus vector. *Canadian J. Bot.*, **70**: 84-92.
- Charaabi, K., Guerfali, M. M., Belgacem, A. B., Saidi, M., Bel-Kadhi, M. S. and Makni, M., 2015, Species diversity and distribution patterns of *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) from various agricultural crops in Tunisia. *J. Entomol. Zool. Stud.*, **3**(4): 32-41
- Chaubey, R. and Andrew, R. J., 2015, Geometric morphometrics of puparia of *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) from western plateau and hill regions agroclimatic zone of India. *Indian J. Entomol.*, **77**(3): 283-289.
- Chaubey, R., Andrew, R. J., Naveen, N. C., Rajagopal, R., Ahmad, B. and Ramamurthy, V. V., 2015, Morphometric analysis of three putative species of *Bemisia tabaci* (Hemiptera: Aleyrodidae) species complex from india. *Ann. Entomol. Soc. Am.* 1-13.

- Chaudhary, L. B. and Prasad, B., 1968, Genetic variation and heritability of quantitative characters in Indian mustard (*Brassica juncea*). *Indian J. Agri. Sci.*, **38**: 820-825.
- Chen, Y., Ni, X. and Buntin, G. D., 2009, Physiological, nutritional, and biochemical bases of corn resistance to foliage-feeding fall armyworm. *J. Chem. Ecol.*, **35**: 297-306.
- Choudhary, P., Rai, G. K., Bagati, S., Jamwal, D., Bhadwal, D., Shanti, V. R. and Rai, P. K., 2018, Evaluation of genetic variability in tomato (*Solanum lycopersicum* L. Mill) genotypes using microsatellite markers. *Int. J. Curr. Microbiol. App. Sci.*, **7**(1): 2117-2124.
- Chowda-Reddy, R. V., Kirankumar, M., Seal, S. E., Muniyappa, V., Valand, G. B., Govindappa, M. R. and Colvin, J., 2012, *Bemisia tabaci* phylogenetic groups in India and the relative transmission efficacy of tomato leaf curl Bangalore virus by an indigenous and an exotic population. *J. Integrat. Agric.*, **11**(2): 235-248.
- Chu, C. C., Henneberry, T. J. and Cohen, A. C., 1995, *Bemisia argentifolii* (Homoptera: Aleyrodidae) on cotton: host preference and factors affecting oviposition and feeding site preference. *Ann. Entomol. Soc. America*, **94**: 354-360.
- Chu, D., Guo, D., Tao, Y., Jiang, D., Li, Y. and Zhang, Y., 2014, Evidence for rapid spatiotemporal changes in genetic structure of an alien whitefly during initial invasion. *Sci. Rep.*, **4**(4396): 1-6.
- Claridge, M. F., Dawah, H. A. and Wilson, M. R., 1997, Species in insect herbivores and parasitoids of sibling species, host races and biotypes, in: Claridge, M. F., Dawah, H. A. and Wilson, M. R. (Eds.), Species, the units of biodiversity. Chapman & Hall, London. pp 247-272.
- Cohen, S., Duffus, J. E. and Liu, H. T., 1992, A new *Bemisia tabaci* biotype in the South Western United States and its role in silver leaf of squash and transmission of lettuce yellows. *Phytopathol.*, **82**: 86-90.

- Comeault, A. A., Soria-Carrasco, V., Gompert, Z., Farkas, T. E., Buerkle, C. A., Parchman, T. L. and Nosil, P., 2014, Genome-wide association mapping of phenotypic traits subject to a range of intensities of natural selection in *Timema cristinae*. *Am. Nat.*, **183**(5): 1-19.
- Costa, H. S. and Brown, J. K., 1991, Variation in biological characteristics and esterase patterns among populations of *Bemisia tabaci* (Genn.) and the association of one population with silver leaf symptom induction. *Entomol. Exp. Appl.*, **61**: 211-219.
- Costa, H. S., Brown, J. K., Sivasubramaniam, S. and Bird, J., 1993, Regional distribution, insecticide resistance and reciprocal crosses between the A and B biotypes of *Bemisia tabaci*. *Insect Sci. Appl.*, **14**: 255-266.
- Crowder, D. W., Sitvarin, M. I. and Carriere, Y., 2010, Mate discrimination in invasive whitefly species. *J. Insect Behav.*, **23**: 364-380.
- Czosnek, H., 2008, Acquisition, circulation and transmission of begomoviruses by their whitefly vectors. *Viruses Environ.*, **14**: 1-16.
- Czosnek, H., Ghanim, M. and Ghanim, M., 2002, The circulative pathway of begomoviruses in the whitefly vector *Bemisia tabaci*-insights from studies with Tomato yellow leaf curl virus. *Ann. Appl. Biol.*, **140**: 215-231.
- Czosnek, H., Hariton-Shalev, A., Sobol, I., Gorovits, R. and Ghanim, M., 2017, The incredible journey of begomoviruses in their whitefly vector. *Viruses*, **9**(273): 1-19
- Dalmon, A., Halkett, F., Granier, M., Delatte, H. and Peterschmitt, M., 2005, Genetic structure of the invasive pest *Bemisia tabaci*: evidence of limited but persistent genetic differentiation in glasshouse populations. *Mol. Eco.*, **14**: 3695-3718
- Dalmon, A., Halkett, F., Granier, M., Delatte, H. and Peterschmitt, M., 2008, Genetic structure of the invasive pest *Bemisia tabaci*: evidence of limited but persistent genetic differentiation in glasshouse populations. *Heredity*, **100**: 316- 325.
- Dar, S. A., 2012, Screening of brinjal genotypes/ varieties against brinjal shoot and fruit borer. *M. Sc. Thesis*, Division of Entomology. SKUAST-K, Srinager, Kashmir. pp 43-46.

- Dar, S. A., Rather B. A., Wani, A. R. and Ganie, M. A., 2017, Chemical science review and letters. Resistance against insect pests by plant phenolics and their derivative compounds. *Chem. Sci. Rev. Lett.*, **6**(23): 1941-1949.
- Dar, S. A., Wani., A. R., Nehru, R. K., Mir, S. H. and Iqbal, M. J., 2014, Physio-chemical characteristics of brinjal genotypes imparting tolerance to brinjal shoot and fruit borer (*Leucinodes orbonalis*) under field conditions of Kashmir (India). *Eco. Env. Cons.*, **20**(4), 209-215.
- Das, R., Chowdhury, R., Singh, A. and Sarkar, S., 2017, Diversity of tomato leaf curl virus (Tolcv), *Bemisia tabaci* and its transmission. *Int. J. Curr. Microbiol. App. Sci.*, **6**(5): 78-87.
- David, B. V. and Ananthakrishnan, T. N., 1976, Host correlated variation in *Trialeurodes* and *Bemisia tabaci* (Gennadius) (Aleyrodidae: Homoptera: Insecta). *Curr. Sci.*, **45**: 223-225.
- De Barro, P. J., 2012, The *Bemisia tabaci* species complex: questions to guide future research. *J. Inte. Agric.*, **11**: 187-196.
- De Barro, P. J., Driver, F., Trueman, J. W. H. and Curran, J., 2000, Phylogenetic relationships of world populations of *Bemisia tabaci* (Gennadius) using ribosomal ITS1. *Mol. Phylogen. Evol.*, **16**: 29-36.
- De-Barro, P. J. and Driver, F., 1997, Use of RAPD-PCR to distinguish the B-biotype from other biotypes of *Bemisia tabaci* (Genn.) (Hemiptera: Aleyrodidae). *Australian J. Entomol.*, **36**: 149-152.
- De-Barro, P. J., Liu, S. S., Boykin, L. M. and Dinsdale, A. B., 2011, *Bemisia tabaci*: a statement of species status. *Ann. Rev. Entomol.*, **56**: 1-19.
- De-Barro, P. J., Scott, K. D., Graham, G. C., Lange, C. L. and Schutze, M. K., 2003, Isolation and characterization of microsatellite loci in *Bemisia tabaci*. *Mol. Eco. Notes*, **3**: 40-43

- De-Barro, P. J., Trueman, J. W. H. and Frohlich, D. R., 2005, *Bemisia argentifoliiis* a race of *B. tabaci* (Hemiptera: Aleyrodidae): The molecular genetic differentiation of *B. tabaci* populations around the world. *Bull. Entomol. Res.*, **95**: 193-203.
- Delatte, H., David, P., Granier, M., Lett, J. M., Goldbach, R., Peterschmitt, M. and Reynaud, B., 2006, Microsatellites reveal extensive geographical, ecological and genetic contacts between invasive and indigenous whitefly biotypes in an insular environment. *Genet. Res. Camb.*, **87**: 109-124.
- Delatte, H., Holota, H., Warren, B. H., Becker, N., Thierry, M. and Reynaud, B., 2011, Genetic diversity, geographical range and origin of *Bemisia tabaci* (Hemiptera: Aleyrodidae). *Bull. Entomol. Res.*, **101**: 487-497.
- Delatte, H., Reynaud, B., Granier, M., Thornary, L., Lett, J. M., Goldbach, R. and Peterschmitt, M., 2005, A new silver leaf inducing biotype Ms of *Bemisia tabaci* (Hemiptera: Aleyrodidae) indigenous to the islands of the south-west Indian Ocean. *Bull. Entomol. Res.*, **95**: 29-35.
- Diaz, F., Endersby, N. M. and Hoffmann, A. A., 2014, Genetic structure of the whitefly *Bemisia tabaci* populations in Colombia following a recent invasion. *Insect Sci.*, **22**: 483-494.
- Diaz, F., Endersby, N. M. and Hoffmann, A. A., 2015, Genetic structure of the whitefly, *Bemisia tabaci* populations in Colombia following a recent invasion. *Insect Sci.*, **10**: 1-12.
- Dickey, A. M., Osborne, L. S., Shatters, R. G., Hall, P. M. and Mckenzie, C. L., 2013, Population genetics of invasive *Bemisia tabaci* (Hemiptera: Aleyrodidae) cryptic species in the united states based on microsatellite markers. *J. Econ. Entomol.*, **106**(3): 1355-1364.
- Diehl, S. R. and Bush, G. L., 1984, An evolutionary and applied perspective of insect biotype. *Annu. Rev. Entomol.*, **29**: 471-504.

- Dinsdale, A., Cook, L., Riginos, C., Buckley, Y. M. and De Barro, P. J., 2010, Refined global analysis of *Bemisia tabaci* (Hemiptera: Sternorrhyncha: Aleyrodidae: Aleyrodidae) mitochondrial cytochrome oxidase 1 to identify species level genetic boundaries. *Ann. Entomol. Soc. America*, **101**: 196-208.
- Divya, T. C., Katageri, I. S., Jadhav, M. P., Adiger, S., Vamadevaiah, H. M. and Olekar, N. S., 2017, Biochemical constituents imparting resistance to sucking pest aphid in cotton (*Gossypium* spp.). *Int. J. Curr. Microbiol. App. Sci.*, **6**(12): 2749-2757.
- Duffey, S. S. and Stout, M. J., 1996, Antinutritive and toxic components of plant defense against insects. *Arc. Ins. Biochem. Physiol.*, **2**: 3-37.
- Earl, D., Von-Holdt, A. and Bridgett, M., 2012, STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conserv. Gen. Reso.*, **4**(2): 359-361.
- Edris, S., S., Abo-Aba, M. M., Algandaby, A. M., Ramadan, N. O., Gadalla, M. A., Al-Kordy, J. S. M., Sabir, F. M., Eldomyati, A. M., Alzhairy and Bahieldin, A., 2014, Molecular characterization of tomato cultivars grown in Saudi Arabia and differing in earliness of fruit development as revealed by AFLP and ISSR. *Life Sci. J.*, **11**: 602-612.
- Elbaz. M., Lahav, N. and Morin, S., 2010, Evidence for pre-zygotic reproductive barrier between the B and Q biotypes of *Bemisia tabaci* (Hemiptera: Aleyrodidae). *Bull. Entomol. Res.*, **100**: 581-590.
- Ellango, R., Asokan, R. and Mahmood, R., 2014, Host specific molecular variations in *Bemisia tabaci* (G.) as revealed by using mitochondrial and ribosomal marker. *The Bioscan*, **9**(2): 461-466.
- Ellango, R., Singh, S. T., Rana, V. S., Priya, N. G., Raina, H., Chaubey, R., Naveen, N. C., Mahmood, R., Ramamurthy, V. V., Asokan, R. and Rajagopal, R., 2015, Distribution of *Bemisia tabaci* genetic groups in India. *Environ. Entomol.*, 1-7.
- El-Sayed, A. M., Shalaby, F. F. and Abdel-Gawad, A. A., 1991, Ecological studies on *Bemisia tabaci* on different host plants. Fluctuation and population density of *Bemisia tabaci* on different host plants. *Egypt J. Agric. Res.*, **69**(1): 193-206.

- Elsey, K. D. and Farnham, M. W., 1994, Response of *Brassica oleracea* L. to *Bemisia tabaci* (Gennadius). *Hort. Sci.*, **29**: 814-817.
- Engelberth, J., Seidl-Adams, I., Schultz, J. C. and Tumlinson, J. H., 2007, Insect elicitors and exposure to green leafy volatiles differentially upregulate major octadecanoids and transcripts of 12 oxophytodienoic acid reductases in *Zea mays*. *J. Mol. Plant Micro. Inter.*, **10**: 707-716.
- Evanno, G., Regnaut, S. and Goudet, J., 2005, Detecting the number of clusters of individuals using the software structure: a simulation study. *Mol. Ecol.*, **14**: 2611-2620.
- Excoffier, L., Estoup, A. and Cornuet, J. M., 2005, Bayesian analysis of an admixture model with mutations and arbitrarily linked markers. *Genet.*, **169**: 1727-1738.
- Falush, D., Stephens, M. and Pritchard, J. K., 2003, Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. *Genet.*, **164**: 1567-1587.
- Fancelli, M., Vendramim, J. D., Lourencao, A. L. and Dias C. T. S., 2003, Atratividade e preferência para oviposição de *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) biótipo B em genótipos de tomateiro. *Neotrop. Entomol.*, **32**: 319-328.
- Fancelli, M., Vendramim, J. D., Lourenção, A. L. and Dias, C. T. S., 2005, Attractiveness and oviposition preference of *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) biotype B in tomato genotypes. *Neotrop. Entomol.*, **32**: 319-328.
- Fauquet, C. M., Mayo, M. A., Maniloff, J., Desselberger, U. and Ball, L. A., 2008, Virus taxonomy: VIII th report of the international committee on taxonomy of viruses. *Elsevier Academic Press, London*.
- Federer, W. T. and Raghav Rao, D., 1975. On augmented design. *Biometrics.*, **31**: 29-35.

- Firdaus, S., Heusden, Hidayati, A. W. N., Supena, E., Mumm, R., Vos, R. C. H., Visser, R. G. F. and Vosman, B., 2013, Identification and QTL mapping of whitefly resistance components in *Solanum galapagense*. *Theoretic. Appl. Genet.*, **126**: 1487-1501.
- Firdaus, S., Van Heusden, N. A. W., Hidayati, N., Supena, E. D. J., Visser, R. G. F. and Vosman, B., 2012, Resistance to *Bemisia tabaci* in tomato wild relatives. *Euphytica*, **187**:31-45.
- Fishpool, L. D. C. and Burban, C., 1994, *Bemisia tabaci*: the vector of African cassava mosaic virus. *Trop. Sci.*, **34**: 55-72.
- Fishpool, L. D. C., Fargette, D., Colvin, J., Thouvenel, J. C., Burban, C. and Fauquet, M., 1996, Sexual dimorphism of fourth-instar whitefly nymphs on cassava in the Cote d'Ivoire. *Trop. Sci.* **36**: 154-158.
- Fontes, F. H. M., Colombo, C. A. and Lourenção. A. L., 2012, Structure of genetic diversity of *Bemisia tabaci* (Genn.) (Hemiptera: Aleyrodidae) populations in Brazilian crops and locations. *Sci. Agric.*, **69**(1): 47-53.
- Freeman, T. P., Buckner, J. S., Nelson, D. R., Chu, C. C. and Henneberry, T. J., 2001, Stylet penetration by *Bemisia argentifolii* (Homoptera: Aleyrodidae) into host leaf tissue. *Ann. Entomol. Soc. America*, **94**: 761-768
- Gaurav, N. C., 2018, QTLomics and expression analysis of candidate genes of ToLCV resistance and selected fruit quality traits and marker assisted breeding in tomato (*Solanum lycopersicum* L.). *Ph. D. Thesis*, Univ. Hortic. Sci., Bagalkot.
- Gauthier, N., Dalleau-Clouet, C. and Bouvret, M. E., 2008, Twelve new polymorphic microsatellite loci and PCR multiplexing in the whitefly, *Bemisia tabaci*. *Mol. Eco. Res.*, **8**: 1004-1007.
- Gawel, N. J. and Bartlett, A. C., 1993, Characterisation of differences between whiteflies using RAPD-PCR. *Insect Mol. Biol.*, **2**: 33-38.

- Geethanjali, S., Kadirvel, P., Robert- de- la- Pena, Rao, E. S. and Wang, J. F., 2011, Development of tomato SSR markers from anchored BAC clones of chromosome 12 and their application for genetic diversity analysis and linkage mapping. *Euphytica*, **178**: 283-295.
- Gerling, D., Horowitz, A. R. and Baumgartner, J., 1986, Autoecology of *Bemisia tabaci*. In: *Proc. Sympo. Bemisia tabaci Ecology and Control: XVII Inter. Cong. Entomol.*, 19-23 August 1984, Hamburg. FRG. *Agric. Ecosyst. Environ. (Spl.)*, **17**: 15-20.
- Ghanim, M. and Czosnek, H., 2015, Replication of tomato yellow leaf curl virus in its whitefly vector, *Bemisia tabaci*. *J. Virol.*, **89**(19): 9791-9803.
- Ghanim, M., Morin, S., Zeidan, M. and Czosnek, H., 1998, Evidence for transovarial transmission of tomato yellow leaf curl virus by its vector, the whitefly *Bemisia tabaci*. *Virol.*, **240**: 295-303.
- Gill, R. J. and Brown, J. K., 2010, Systematics of *Bemisia* and *Bemisia* relatives: can molecular techniques solve the *Bemisia tabaci* complex conundrum-a taxonomist's viewpoint, in: Stansly, P. A. and Narahjo, S. E. (Eds.), *Bemisia: Bionomics and management of a global pest*. Springer, pp 5-29.
- Gill, R. J., 1990, *Bemisia* and *Bemisia* relatives: can molecular techniques solve the *Bemisia tabaci* complex conundrum-a taxonomist's viewpoint. *Bionom. Manag. Global Pest.*, **2**: 5-29.
- Giordano, L. B., Silva-Lobo, V. L., Santana, F. M., Fonseca, M. E. N. and Bio-Teux, L. S., 2005, Inheritance of resistance to the bipartite tomato chlorotic mottle begomovirus derived from *Lycopersicon esculentum* cv. 'Tyking'. *Euphytica*, **143**: 27-33.
- Glas, J. J., Schimmel, B. C., Alba, J. M., Escobar-Bravo, R., Schuurink, R. C. and Kant, M. R., 2012, Plant glandular trichomes as targets for breeding or engineering of resistance to herbivores. *Int. J. Mol. Sci.*, **13**: 77-103.
- Gocmen, H. and Devran, Z., 2002, Determination of genetic variation in populations of *Bemisia tabaci* in Antalya. *Turk. J. Agric. For.*, **26**: 211-216.

- Golan, K., Sempruch, C., Gorska-Drabik, E., Czerniewicz, P., Łagowska¹, B., Kot, I., Kmiec¹, K., Magierowicz, K. and Leszczynski, B., 2017, Accumulation of amino acids and phenolic compounds in biochemical plant responses to feeding of two different herbivorous arthropod pests. *Arthropod-Plant Interactions*, **11**: 675-682.
- Gottlieb, Y., Fein, E. Z., Daube, N. M., Kontsedalov, S., Skaljic, M., Brumin, M., Sobol, I., Czosnek, H., Vavre, Fleury, F. and Ghanimi, M., 2010, The transmission efficiency of Tomato yellow leaf curl virus by the whitefly *Bemisia tabaci* is correlated with the presence of a specific symbiotic bacterium species. *J. Virol.*, **84**(18): 9310-9317.
- Gotz, M., Popovski, S., Kollenberg, M., Gorovits, R., Brown, J. K., Cicero, J. M., Czosnek, H., Winter, S. and Ghanim. M., 2012, Implication of *Bemisia tabaci* heat shock protein 70 in Begomovirus-whitefly interactions. *J. Virol.*, **86**(24): 13241-13252.
- Govindaraju, D. R., 1989, Estimates of gene flow in forest trees. *Biol. J. Linn. Soc.*, **37**: 345-357.
- Govindu, H. C., 1964, A review on virus diseased of crop plants. Information pamphlet no. 2. Directorate of Agriculture, Bengaluru. 13pp.
- Green, S. K. and Kalloo, G., 1994. Leaf curl and yellowing viruses of pepper and tomato: an overview. Asian vegetable research and development center. *Tech. Bull.*, 21-51.
- Guershon, M. and Gerling, D., 2001, Effect of foliar tomentosity on phenotypic plasticity in *Bemisia tabaci* (Homoptera: Aleyrodidae). *J. Appl. Entomol.*, **125**: 449-453.
- Guo, D., Zhang, J. Y. and Liu, C. H., 2012, Genetic diversity in some grape varieties revealed by SCoT analyses. *Mol. Biol. Rep.*, **39**: 5307-5313.
- Guo, G., Gao, J., Wang, X., Guo, Y., Snyder, J. C. and Du, Y., 2013, Establishment of an in vitro method for evaluating whitefly resistance in tomato. *Breed. Sci.*, **63**: 239-245.

- Gurr, G. M. and McGrath, D., 2001, Effect of plant variety, plant age and photoperiod on glandular pubescence and host-plant resistance to potato moth (*Phthorimaea operculella*) in *Lycopersicon* spp. *Ann. Appl. Biol.*, **138**: 221-230.
- Gutbrodt, B., Mody, K. and Dorn, S., 2011, Drought changes plant chemistry and causes contrasting responses in lepidopteran herbivores. *Oikos*, **120**: 1732-1740.
- Hadjistylli, B. M., Schwartz, S. A., Brown, J. K. and Roderick, G. K., 2014, Isolation and characterization of nine microsatellite loci from *Bemisia tabaci* (Hemiptera: Aleyrodidae) Biotype. *J. Insect Sci.*, **14**(148): 1-3.
- Hadjistylli, M., Roderick, G. K. and Brown, J. K., 2016, Global population structure of a worldwide pest and virus vector: genetic diversity and population history of the *Bemisia tabaci* sibling species group. *PLoS ONE*, **11**(11): 1-32.
- Hagg, F. J., Zagrobelny, M. and Bak, S., 2013, Plant defense against insect herbivores. *Int. J. Mol. Sci.*, **14**:10242-10297.
- Hameed, S., Hameed, S., Sadia, M. and Malik, A., 2012, Genetic diversity analysis of *Bemisia tabaci* populations in Pakistan using RAPD marker. *Electronic J. Biotech.*, **15**(6): 1-9.
- Hamidi, H., Talebi, R. and Keshavarzi, F., 2014, Comparative efficiency of functional gene-based markers, start codon targeted polymorphism (SCoT) and conserved DNA derived polymorphism (CDDP) with ISSR markers for diagnostic fingerprinting in wheat (*Triticum aestivum* L.). *Cereal Res. Commun.*, **42**: 558-567.
- Hammer, O., Harper, D. A. T. and Ryan, P. D., 2001, PAST: paleontological statistics software package for education and data analysis. *Palaeontol. Electron.*, **4**(1): 9.
- Hanson, C. H., Robinson, H. R. and Comstock, R. S., 1956, Biometrical studies of yield in segregating population of Korean lespedeza. *Agron. J.*, **48**: 268-272.
- Hanson, P., Green, S. K. and Kuo, G., 2006, Ty-2, a gene on chromosomes 11 conditioning geminivirus resistance in tomato. *Rep. Tomato Genet. Coop.*, **56**: 17-18.

- Harish, E. R., Chellappan, M., Kumar, M. T., Ranjith, M. T. and Ambavane, A. R., 2016, Morphometric variations in cassava (*Manihot esculenta* Crantz) whitefly, *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) from different agro-ecological zones of Kerala, India. *J. Root Crops*, **42**(2): 90-102.
- Hasan, M. M., Bari, M. M. A. and Hossain, M. A., 2016, Genetic variability and traits association analysis of tomato (*Lycopersicon esculentum* L.) genotypes for yield and quality attributes. *Uni. J. Plant Sci.*, **4**(3): 23-34.
- Hasanuzzaman, A. T. M., Islam, M. N., Zhang, Y., Zhang, C. Y. and Liu, T. X., 2016, Leaf morphological characters can be a factor for intra- varietal preference of whitefly *Bemisia tabaci* (Hemiptera: Aleyrodidae) among egg plant varieties. *PLoS ONE*, **11**(4): 1-15.
- He, C., Poysa, V. and Yu, K., 2003, Development and characterization of simple sequence repeat (SSR) markers and their use in determining relationships among *Lycopersicon esculentum* cultivars. *Theor. Appl. Genet.*, **106**: 363-373.
- Heil, M. and Baldwin, I. T., 2002, Fitness costs of induced resistance: Emerging experimental support for a slippery concept. *Trends Plant Sci.*, **7**: 61-67.
- Heinz, K. M. and Zalom, F. G., 1995, Variation in trichome based resistance to *Bemisia argentifolii* (Homoptera: Aleyrodidae) oviposition on tomato. *J. Econ. Entomol.*, **88**: 1494-1502.
- Henareh, M., 2015, Genetic variation in superior tomato genotypes collected from North West of Iran. *Int J. Sci. Res. Env. Sci.*, **3**(6): 219-225.
- Henareh, M., A., Dursun, B., Mandoulakani, A. and Haliloğlu, K., 2016, Assessment of genetic diversity in tomato landraces using ISSR Markers. *Genetika*, **48**: 2535-2541.
- Hennink, S. and Zeven, A. C., 1991, The interpretation of Nei and Shannon-Weaver within population variation indices. *Euphytica*, **51**: 235-240.
- Hidayat, S. H. and Rahmayani, E., 2007, Transmission of tomato leaf curl begomovirus by two different species of whitefly (Hemiptera: Aleyrodidae). *Plant Pathol. J.*, **23**(2): 57-61.

- Hodges, G. S. and Evans, G. A., 2005, An identification guide to the whiteflies (Hemiptera: Aleyrodidae) of the southeastern united states. *Florida Entomol.*, **88**(4): 518-534.
- Hsieh, C. H., Chiang, Y. H. and Ko, C. C., 2011, Population genetic structure of the newly invasive Q biotype of *Bemisia tabaci* in Taiwan. *Entomol. Experiment. App.*, **138**: 263-271.
- Hsieh, C. H., Wang, C. H. and Ko, C. C., 2006, Analysis of *Bemisia tabaci* (Hemiptera: Aleyrodidae) species complex and distribution in Eastern Asia based on mitochondrial DNA markers. *Ann. Entomol. Soc. Am.* **99**(5): 768-775.
- Hu, J., De Barro, P. J., Zhao, J. H., Wang, Nardi, F. and Liu, S. S., 2011, An extensive field survey combined with a phylogenetic analysis reveals rapid and widespread invasion of two alien whiteflies in China. *PLoS One*, **6**: 160-161.
- Ibanez, S., Gallet, C. and Despres, L., 2012, Plant insecticidal toxins in ecological networks. *Toxins*, **4**: 228-243.
- Inbar, M. and Gerling, D., 2008, Plant-mediated interactions between whiteflies, herbivores, and natural enemies. *Ann. Rev. Entomol.*, **53**: 431-48.
- Islam, M. T. and Shunxiang, R., 2007, Development and reproduction of *Bemisia tabaci* on three tomato varieties. *J. Entomol.*, **4**: 231-236.
- Janssen, D., Simon, A., Crespo, O. and Ruiz, L., 2017, Genetic population structure of *Bemisia tabaci* in Spain associated with tomato leaf curl new delhi virus-short communication. *Plant Protect. Sci.*, **53**: 1-12.
- Jayasekera, S., Thomas, A., Kar, A. and Ramamurthy, V. V., 2010, Host correlated morphometric variations in the populations of *Bemisia tabaci* (Gennadius). *Oriental Insects*, **44**: 193-204.
- Jayashree, K., Pun, K. B. and Doraiswamy, S., 1999, Virus-vector relationship of yellow vein mosaic virus and whitefly (*Bemisia tabaci*) in pumpkin. *Indian Phytopath.*, **52**: 10-13.

- Ji, Y. and Scott, J. W., 2005, Identification of RAPD markers linked to *Lycopersicon chilense* derived Begomovirus resistant genes on chromosomes 6 of tomato. *Acta Hort.*, **695**: 407-416.
- Ji, Y., Scott, J. W., Hanson, P., Graham, E. and Maxwell, D. P., 2007, Sources of resistance, inheritance and location of genetic loci conferring resistance to members of the tomato-infecting begomoviruses. pp. 347-366.
- Jindal, V. and Dhaliwal, G. S., 2009, Bases of resistance in cotton to whitefly, *Bemisia tabaci* (Gennadius): Biochemical factors. *Indian J. Ecol.*, **36**(2): 166-169.
- Jing, L. I., Qing-bo, T., Run-e, B., Xiao-min, L. I., Jin-wei, J., Qing, Z. and Feng-ming, Y., 2013, Comparative morphology and morphometry of six biotypes of *Bemisia tabaci* (Hemiptera: Aleyrodidae) from China. *J. Int. Agric.*, **12**(5): 846-852.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E., 1955, Estimation of genetic and environmental variability in soyabean. *Agron. J.*, **47**: 477-483.
- Jyothi, G., 2015, Diversity of Tomato leaf curl virus (ToLCV) and role of endosymbionts in the transmission of ToLCV by *Bemisia tabaci*. *Ph. D. Thesis*. Univ. Agric. Sci. GKVK, Bengaluru. pp. 128-132.
- Kakimoto, K., Inoue, H., Yamaguchi, T., Ueda, S., Honda, K. I. and Yano, E., 2007, Host plant effect on development and reproduction of *Bemisia argentifolii* Bellows et Perring (*B. tabaci* [Gennadius] B-biotype) (Homoptera: Aleyrodidae). *App. Entomol. Zool.*, **42**: 63-70.
- Kaloshian, I. and Walling, L. L., 2005, Hemipterans as plant pathogens. *Ann. Rev. Phytopathol.*, **43**: 491-521.
- Kang, J., Shi, F., Jones, A. D., Marks, M. D. and Howe, G. A., 2010, Distortion of trichome morphology by the hairless mutation of tomato affects leaf surface chemistry. *J. Exp. Bot.*, **61**(4): 1053-1064.

- Kerchev, P. I., Fenton, B., Foyer, C. H. and Hancock, R. D., 2012, Plant responses to insect herbivory: interactions between photosynthesis, reactive oxygen species and hormonal signalling pathways. *Plant Cell Environ.*, **35**: 441-453.
- Khasdan, V., Levin, I., Rosner, A., Morin, S., Kontsedalov, S., Maslenin, L. and Horowitz, A. R., 2005, DNA markers for identifying biotypes B and Q of *Bemisia tabaci* (Hemiptera: Aleyrodidae) and studying population dynamics. *Bull. Entomol. Res.*, **95**: 605-613.
- Kheyr-Pour, A., Bendahmane, M., Matzeit, V., Accotto, G. P. M., Crespi, S. and Gronenborn, B., 1991, Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite geminivirus. *Nucleic Acids Res.*, **19**: 6763-6769.
- Kishaba, A. N., Castle, S., McCreight, J. D., and Desjardins, P. R., 1992, Resistance of white-flowered gourd to sweet potato whitefly. *Hort. Sci.*, **27**: 1217-1221.
- Klee, H. J. and Tieman, D. M., 2013, Genetic challenges of flavor improvement in tomato. *Trends Genet.*, **29**: 257-262.
- Klein-Lankhorst, R. M., Vermunt, A., Weide, R., Liharska, T. and Zabel, P., 1991, Isolation of molecular markers for tomato (*L. esculentum*) using random amplified polymorphic DNA (RAPD). *Theor. Appl. Genet.*, **83**: 108-114.
- Kloth, K. J., Thoen, M. P. M., Bouwmeester, H. J., Jongsma, M. A. and Dicke, M., 2012, Association mapping of plant resistance to insects. *Trends Plant Sci.*, **17**(5): 311-319.
- Koubala, B. B., Miafo, A. P. T., Bouba, B., Kamda, A. G. S. and Kansci, G., 2015, Evaluation of insecticide properties of ethanolic extract from *Balanites aegyptiaca*, *Melia azedarach* and *Ocimum gratissimum* leaves on *Callosobruchus maculatus* (Coleoptera: Bruchidae). *Asian J. Agric. Sci.*, **5**: 93-101.
- Kumar, S., Rowan, D., Hunt, M., Chagné, D., Whitworth, C. and Souleyre, E., 2015, Genome-wide scans reveal genetic architecture of apple flavour volatiles. *Mol. Breed.*, **35**: 118-134.

- Kumar, Y., Hallan, V. and Zaidi, A. A., 2008, Molecular characterization of a distinct begomovirus species infecting tomato in India. *Virus Genes*, **37**: 425-431.
- Kwon, Y. S., Park, S. G. and Yi, S. I., 2009, Assessment of genetic variation among commercial tomato (*Solanum Lycopersicum* L) varieties using SSR markers and morphological characteristics. *Genes and Genomics*, **31**: 1-10.
- Lacey, L. A., Kirk, A. A. and Hennessey, R. D., 1993, Foreign exploration for natural enemies of *Bemisia tabaci* and implementation in integrated control programs in the United States, *Third International Conference on Pests in Agriculture*, Montpellier, France. *Assoc.Nationale de Protection des Plantes, Paris, France*. pp 351-360.
- Lal, S. S. and Pillai, K. S., 1982, Ecological studies on whitefly, *Bemisia tabaci* (Genn.) infesting cassava in Kerala. *Ent.*, **7**(1): 101-102.
- Lattanzio, V., Lattanzio, V. M. T. and Cardinali, A., 2006, Role of polyphenols in the resistance mechanisms of plants against fungal pathogens and insects. In: Imperato F., ed. *Phytochemistry: advances in research*. Trivandrum, Kerala, India: Research Signpost. pp 23-67.
- Lee, W., Park, J., Lee, G. S., Lee, S. and Akimoto, S., 2013, Taxonomic status of the *Bemisia tabaci* complex (Hemiptera: Aleyrodidae) and reassessment of the number of its constituent species. *PLoS One*, **8**: 63-74.
- Li, F., Shi, X., Tang, X., Zhang, X., Zhang, D., Yan, F., Zhang, Y., Zhou, X. and Liu, Y., 2012, Transmission efficiency, preference and behavior of *Bemisia tabaci* MEAM1 and MED under the influence of tomato chlorosis virus. *Front. Plant Sci.*, **8**(2271): 1-9.
- Li, M., Hu, J., Xu, F. C. and Liu, S. S., 2010, Transmission of Tomato yellow leaf curl virus by two invasive biotypes and a Chinese indigenous biotype of the whitefly *Bemisia tabaci*. *Int. J. Pest Manag.*, **56**: 275-280.
- Li, S. J., Xue, X., Ahmed, M. Z., Ren, S. X., Du, Y. Z., Wu, J. H., Cuthbertson, A. G. S. and Qiu, B. L., 2011, Host plants and natural enemies of *Bemisia tabaci* (Hemiptera: Aleyrodidae) in China. *Insect Sci.*, **18**: 101-120.

- Lima, A. C. S. and Lara, F. M., 2004, Resistencia de genotipos de soja a mosca-branca *Bemisia tabaci* biotipo B (Hemiptera: Aleyrodidae). *Neotrop. Entomol.*, **33**: 71-75.
- Lima, L. H. C., Campos, L., Moretzsohn, M. C., Navia, D. and De-Oliveira, M. R. V., 2002a, Genetic diversity of *Bemisia tabaci* (Genn.) populations in Brazil revealed by RAPD markers. *Gen. Mol. Biol.*, **25**(2): 217-223.
- Lima, L. H. C., Navia, D., Inglis, P. W. and De-Oliveira, M. R. V., 2002b, Survey of *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) biotypes in Brazil using RAPD markers. *Gen. Mol. Bio.*, **23**(4): 781-785.
- Lisha, V. S., Antony, B., Palaniswami, M. S. and Henneberry T. J., 2003, *Bemisia tabaci* (Homoptera: Aleyrodidae) biotypes in India. Division of crop protection, ICAR-Central tuber crops research institute, Trivandrum, Kerala, India. *J. Econ. Entomol.*, **96**(2): 322-327.
- Liu, H. Y., Duffus, J. E. and Cohen, S., 1992, *Bemisia tabaci* population control by host manipulation and genetics. In: *Inter. Sympo. Plant Virus Epidemiology Valenzano, Italy*, pp 227-228.
- Liu, S. S., Colvin, J. and De Barro. P. J., 2012, Species concepts as applied to the whitefly *Bemisia tabaci* systematics: how many species are there?. *J. Integr. Agri.*, **11**: 176-186.
- Liu, S. S., De Barro, P. J., Xu, J., Luan, J. B., Zang, L. S., Ruan, Y. M. and Wan, F. H., 2007, Asymmetric mating interactions drive widespread invasion and displacement in a whitefly. *Sci.*, **318**: 1769-1772.
- Liu, T. X. and Stansly, P. A., 1995, Toxicity of biorational insecticides to *Bemisia argentifolii* (Homoptera: Aleyrodidae) on tomato leaves. *J. Eco. Entomol.*, **88**: 564-568.
- Lopez-Avilla, A., 1986, Taxonomy and biology. In: *Bemisia tabaci- A literature survey*. pp 3-11.

- Lucatti, A. F., Meijer-Dekens, F. R. G., Mumm, R., Visser, R. G. F., Vosman, B. and Heusden, S. V., 2014, Normal adult survival but reduced *Bemisia tabaci* oviposition rate on tomato lines carrying an introgression from *S. habrochaites*. *BMC Genetics*, **15**:142.
- Luckwill, L. C., 1943, The genus *Lycopersicon*.: An historical, biological and taxonomic survey of the wild and cultivated tomatoes. *Gen. Mol. Biol.*, **21**(4): 78-85.
- Luo, C., Jones, C. M., Devine, G., Zhang, F., Denholm, I. and Gorman, K., 2010, Insecticide resistance in *Bemisia tabaci* biotype Q (Hemiptera: Aleyrodidae) from China. *Crop Prot.*, **29**: 429-434.
- Lush, J. L., 1940, Intra-sire correlation and regression of offspring on dams as method of estimating heritability of characters. In: *Proc. American Soci. Ani. Prod.*, **33**: 293-301.
- Maluf, W. R., Inoue, I. F., Ferreira, R. P. D., Gomes, L. A. A., Castro, E. M. D. and Cardoso, M. G., 2007, Higher glandular trichome density in tomato leaflets and repellence to spider mites. *Pesq. Agropec. Bras., Brasília*, **42**(9): 1227-1235.
- Malumphy, C., Walsh, K., Suarez, M. B., Collins, D. W. and Boonham, N., 2009, Morphological and molecular identification of all developmental stages of four whitefly species (Hemiptera: Aleyrodidae) commonly intercepted in quarantine. *Zootaxa*, **21**(18): 1- 29.
- Mandali, R., Lakshmi, K. V. and Sujatha, M., 2016, Survey and biotype identification of whitefly, *Bemisia tabaci* transmitting tomato leaf curl virus in Andhra Pradesh, India. *J. Agric. Tech.*, **12**(7.1): 1687-1694.
- Mansour, A., Silva, J. T., Edris, S. and Younis, R. A. A., 2010, Comparative assessment of genetic diversity in tomato cultivating using IRAP, ISSR and RAPD molecular markers. *Genes Genom. Genom.*, **4**: 41-47.
- Manzano, M. R. and Van Lenteren, J. C., 2009, Life history parameters of *Trialeurodes vaporariorum* (Westwood) (Hemiptera: Aleyrodidae) at different environmental conditions on two bean cultivars. *Neotrop. Entomol.*, **38**: 452-458.

- Martin, J. H., 1987, An identification guide to common whitefly species of the world (Homoptera: Aleyrodidae). *Tropic. Pest Manage.*, **33**: 298-322.
- Maruthi, M. N., Alam, S. N., Kader, K. A., Rekha, A. R., Cork, A. and Colvin, J., 2005, Nucleotide sequencing, whitefly transmission, and screening tomato for resistance against two newly described begomoviruses in Bangladesh. *Phytopathol.*, **95**(12): 1472-1481.
- Maruthi, M. N., Navaneethan, S., Colvin, J. and Hillocks, R. J., 2004, Bionomics, morphometrics and molecular characterization of a cassava *Bemisia afer* (Priesner & Hosny) population. *Int. J. Tropic. Insect Sci.*, **24**(4): 323-329.
- Maruthi, M. N., Rekha, E. A. R., Mirza, E. S. H., Alam, E. S. N., and Colvin., E. J., 2007, PCR-based detection and partial genome sequencing indicate high genetic diversity in Bangladeshi begomoviruses and their whitefly vector, *Bemisia tabaci*. *Virus Genes*, **34**:373-385.
- Maskato, Y., Talal, S., Keasar and Gefen, E., 2014, Red foliage color reliably indicates low host quality and increased metabolic load for development of an herbivorous insect. *Arthropod Plant. Int.*, **8**: 285-292.
- Matsuda, F., Nakabayashi, R., Yang, Z., Okazaki, Y., Yonemaru, J. and Ebana, K., 2015, Metabolome-genome-wide association study dissects genetic architecture for generating natural variation in rice secondary metabolism. *Plant J.*, **81**: 13-23.
- Maudet, C., Luikart, G. and Taberlet, P., 2002, Genetic diversity and assignment tests among seven French cattle breeds based on microsatellite DNA analysis. *J. Ani. Sci.*, **80**: 942-50.
- McAuslane, H. J., 1996, Influence of leaf pubescence on ovipositional preference of *Bemisia argentifolii* (Homoptera: Aleyrodidae) on soybean. *Environ. Entomol.*, **25**: 834-841.

- McKenzie, C. L., Bethke, J. A., Byrne, F. J., Chamberlin, J. R., Dennehy, T. J., Dickey, A. M. Gilrein, D., Hall, P. M., Ludwig, S., Oetting, R. D., Osborne, L. S., Schmale, L. and Shatters, R. G., 2012, Distribution of *Bemisia tabaci* (Hemiptera: Aleyrodidae) biotypes in North America after the Q invasion. *J. Econ. Entomol.*, **105**(3): 753-766.
- McKenzie, C. L., Hodges, G., Lance, S., Osborne, Byrne, F. J. and Shatters, R. G., 2009, Distribution of *Bemisia tabaci* (Hemiptera: Aleyrodidae) biotypes in Florida-investigating the Q invasion. *J. Econ. Entomol.*, **102**(2): 670-676.
- Misra, C. S. and Lamba, S. K., 1929, The cotton whitefly (*Bemisia gossypiperda*). *Bull. Agri. Res. Institute, Pusa*, **196**: 1-7.
- Mohanty, A. K. and Basu, A. N., 1986, Effect of host plants and seasonal factors on intraspecific variations in pupal morphology of the whitefly vector, *Bemisia tabaci* (Gennadius) (Homoptera: Aleyrodidae). *J. Entomol. Res.*, **10**: 19-26.
- Morales, F. J. and Jones, P. G., 2004, The ecology and epidemiology of whitefly-transmitted viruses in Latin America. *Virus Res.*, **100**: 57-65.
- Morales, F. J., 2007, Tropical whitefly IPM project. *Adv. Virus Res.*, **69**: 249-311
- Mound, L. A. and Halsey, S. H., 1978, Whitefly of the world. In: *A Systematic Catalogue of the Aleyrodidae (Homoptera) with Host-plant and Natural Enemy Data*. John Wiley and Sons, Chichester, pp 456.
- Mound, L. A., 1963, Host-correlated variation in *Bemisia tabaci* (Gennadius) (Homoptera: Aleyrodidae). *Proceedings of the Royal Entomological Society of London*, **38**: 171-180.
- Mound, L. A., 1965, Effects of leaf hair on cotton whitefly populations in the Sudan Geriza. *The Empire Cotton Growing Review*. **42**: 33-40.
- Mound, L. A., 1962, Studies on the olfaction and colour sensitivity of *Bemisia tabaci* (Germ.) (Homoptera: Aleyrodidae). *Entomol. Exp. Appl.*, **5**: 99-104.

- Moya, A., Guirao, P., Cifuentes, D., Beitia, F. and Cenis, J. L., 2001, Genetic diversity of Iberian populations of *Bemisia tabaci* (Hemiptera: Aleyrodidae) based on Random Amplified Polymorphic DNA Polymerase Chain Reaction. *Mol. Ecol.*, **10**: 891-897.
- Mugerwa, H., Rey, M. E. C., Alicai, T., Ateka, E., Atuncha, H., Ndunguru, J. and Sseruwagi, P., 2012, Genetic diversity and geographic distribution of *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) genotypes associated with cassava in East Africa. *Eco. Evol.*, **2**(11): 2749-2762.
- Muigai, S. G., Schuster, D. J., Snyder, J. C., Scott, J. W., Bassett, M. J. and Mcauslane, H. J., 2002, Mechanisms of resistance in *Lycopersicon* germplasm to the whitefly *Bemisia argentifolii*. *Phytoparasitica*, **30**: 347-360.
- Muigai, S. G., Bassett, M. J., Schuster, D. J., Scott, J. W., 2003, Greenhouse and field screening of wild *Lycopersicon* germplasm for resistance to the whitefly, *Bemisia argentifolii*. *Phytoparasitica*, **31**: 27-33.
- Muniyappa, V. and Veeresh, G. K., 1984, Plant virus diseases transmitted by whiteflies in Karnataka. In: *Proc. Indian Acad. Sci. (Animal Sci.)*, **93**: 397-406.
- Muniyappa, V., 1980, Whiteflies. In: *Vectors of plant pathogens*. (Harris, K. F. and Maramorosch, K. Eds.). *Academic Press, New York*, pp 39-85,
- Muniyappa, V., Venkatesh, H. M., Ramappa, H. K., Kulkarni, R. S., Zeidan, M., Tarba, C. Y., Ghanim, M. and Czosnek, H., 2000, Tomato leaf curl virus from Bangalore (ToLCV-Ban4): sequence comparison with Indian ToLCV isolates, detection in plants and insects and vector relationships. *Arch. Virol.*, **145**: 1583-1598.
- Munoz, J. E., Londoño, X., Rugeles, P., Posso, A. M. and Vallejo, F. A., 2010, Diversidad y estructura genética de *Guadua angustifolia* en la ecorregión cafetera colombiana. *Recursos Naturales y Ambiente*, **61**: 45-52.
- Murray, H. G. and Thompson, W. F., 1980, Rapid isolation of high molecular weight DNA. *Nucleic Acids Res.*, **8**(19): 4321-4326.

- Mwila, N., Rubaihayo, P. R., Kyamanywa, S., Odong, T. L., Nuwamanya, E., Mwala, M., Agbahounga, S. and Badji, A., 2017, Biochemical factors associated with cassava resistance to whitefly infestation. *African Crop Sci. J.*, **25**(3): 365-385.
- Nakazato, T., Bogonovich, M. and Moyle, L. C., 2008, Environmental factors predict adaptive phenotypic differentiation within and between two wild Andean tomatoes. *Evol.*, **62**: 774-792.
- Navot, N., Plchersky, E., Zeidan, M., Zamir, D. and Czonsnek, H., 1991, Tomato yellow leaf curl virus: A whitefly transmitted geminivirus with a single genomic component. *Virol.*, **185**: 151-161.
- Nazareno, A. G. and Reis, M. S., 2011, The same but different: monomorphic microsatellite markers as a new tool for genetic analysis. *Am. J. Bot.* **98**: 265-267.
- Neal, J. W. Jr. and Bentz, J. A., 1999, Evidence for the stage inducing phenotypic plasticity in pupae of the polyphagous whiteflies *Trialeurodes vaporariorum* and *Bemisia argentifolii* (Homoptera: Aleyrodidae) and the raison d'être. *Ann. Entomol. Soc. America*, **92**: 774-787.
- Nei, M., 1973, Analysis of gene diversity in subdivided populations. *Proc. Nat. Acad. Sci. USA.*, **70**: 3321-3323.
- Nei, M., 1987, Molecular evolutionary genetics. *Columbia University Press, New York*. pp. 25-34.
- Neiva, I. P., Junior, V. C. A., Maluf, W. R., Oliveira, C. M. and Maciel, G. M., 2013, Role of allelochemicals and trichome density in the resistance of tomato to whitefly. *Ciênc. Agrotec., Lavras*, **37**(1): 61-67.
- Nuez, F., Prohens, J. and Blanca, J. M., 2004, Relationships, origin, and diversity of Galapagos tomatoes: implications for the conservation of natural populations. *American J. Bot.*, **91**: 86-99.
- Oliveira, M. R. V., Henneberry, T. J. and Anderson, P., 2001, History, current status, and collaborative research projects for *Bemisia tabaci*. *Crop Prot.*, **20**: 709-723.

- Oriani, G. M. A., Vendramim, J. D. and Brunherotto, R., 2005, Influence of trichomes on ovipositional preference of *Bemisia tabaci* (Genn.) biotype B (Hemiptera: Aleyrodidae) for bean genotypes. *Neotrop. Entomol.*, **34**: 97-103.
- Oriani, G. M. A., Vendramim, J. D. and Vasconcelos, C. J., 2011, Biology of *Bemisia tabaci* (Genn.) B biotype (Hemiptera: Aleyrodidae) on tomato genotypes. *Sci. Agric.*, **68**: 37-41.
- Ott, J., 2001, Analysis of human genetic linkage. *Revised edition*. Johns Hopkins University Press, Baltimore.
- Pandey, P., Mukhopadhyaya, S., Naqvi, A. R., Mukherjee, S. K., Shekhawat, G. S. and Choudhury, N. R., 2010, Molecular characterization of two distinct monopartite begomoviruses infecting tomato in India. *Viol. J.*, **7**(337): 1-10.
- Panase, V. C. and Sukhatme, P. V., 1967, Statistical methods for agricultural workers. *Indian Council of Agri. Res., New Delhi*. pp 12- 18.
- Patil, S., Fakrudin, B., Goud, K. B., Vijaykumar, Poornima, R., Babu, O., Shivaruddrappa, B. and Patil, B. V., 2012, Phenotypic plasticity in *Helicoverpa armigera* (Hübner) populations occurring on different host plants. *J. Exp. Zool.*, **15**(2): 473-476.
- Peakall, R. and Smouse P. E., 2006, GENALEX 6: genetic analysis in excel. Population genetic software for teaching and research. *Mol. Eco. Notes*, **6**: 288-295.
- Peralta, I. E., Spooner, D. M. and Knapp, S., 2008, Taxonomy of wild tomatoes and their relatives. *Systematic Bot. Monographs*, **84**:1-186.
- Perez-de-la-Vega, M. and García, P. G., 2000, Analisis de la variacion genetica en las poblaciones. In universidad politecnica de valencia and servicio de publicaciones (Eds.), Los marcadores genéticos en la mejora vegetal, pp. 409-440.
- Perring, T. M., Cooper, A. D., Rodriguez, R. J., Farrar, C. A. and Bellows, T. S., 1993, Identification of a whitefly species by genomic and behavioural studies. *Sci.*, **259**: 74-77.

- Perumal, Y. and Marimuthu, M., 2009, Host plant mediated population variations of cotton whitefly *Bemisia tabaci* Gennadius (Aleyrodidae: Homoptera) characterized with random DNA markers. *American J. Biochem. Biotechno.* **5**(1): 40-46.
- Perveen, S. S., Qaisrani, T. M. S., Amin, Perveen, R. and Naqvi, S. H. M., 2001, Biochemical basis of insect resistance in Cotton, *J. Bio. Sci.*, **116**: 496-500.
- Petro, L. O. and Redak, R. A., 2000, Host plant preference and performance of *Bemisia argentifolii* (Homoptera: Aleyrodidae) on poinsettia (*Euphorbia pulchirrima*) in relation to variety. *US Dept. Agric. Agric. Res. Serv.*, **15**: 12-25.
- Petro, L., Redak, R., Bethke, J. and Perring, T. M., 2002, Preference and performance of silver leaf whitefly on selected poinsettia varieties. *US Dept. Agric. Agric. Res. Serv.*, **12**: 11-18.
- Pollard, D. G., 1955, Feeding habits of the cotton whitefly, *Bemisia tabaci* (Genn.) (Homoptera: Aleyrodidae). *Ann. App. Biol.*, **43**: 664-671.
- Porras-Hurtado, L., Ruiz, Y., Santos, C., Phillips, C., Carracedo, A. and Lareu, M. V., 2013, An overview of STRUCTURE: applications, parameter settings and supporting software. *Front. Genet.*, **4**(98): 1-13.
- Portis, E., Cericola, F., Barchi, L., Toppino, L., Acciarri, N. and Pulcini, L., 2015, Association mapping for fruit, plant and leaf morphology traits in eggplant. *PLoS ONE*, **10**(8): 1-23.
- Prasanna, H. C., Kanakala, S., Archana, K., Jyothsna, P., Varma, R. K. and Malathi, V. G., 2014, Cryptic species composition and genetic diversity within *Bemisia tabaci* complex in Soybean in India revealed by *mtCOI* DNA sequence1. *J. Integrat. Agric.*, **11**: 1-17.
- Prasanna, H. C., Kanakala, S., Archana, K., Jyothsna, P., Varma, R. K. and Malathi, V. G., 2015, Cryptic species composition and genetic diversity within *Bemisia tabaci* complex in soybean in India revealed by *mtCOI* DNA sequence. *J. Integrat. Agric.*, **14**(9): 1786-1795.

- Pratap, D., Kashikar, A. R. and Mukherjee, S. K., 2011, Molecular characterization and infectivity of a tomato leaf curl New Delhi virus variant associated with newly emerging yellow mosaic disease of eggplant in India. *Viol. J.*, **8**: 305-309.
- Prathibha, B., 2015, Analysis of morphological and genetic relatedness among the populations of spiralling whitefly, *Aleurodicus dispersus* russell (Hemiptera: Aleyrodidae) occurring on different host plants and its management on guava. *M. Sc. (Hort.) Thesis*, Uni. Horti. Sci., Bagalkot. pp 35.
- Pritchard, J. K., Stephens, M. and Donnelly, P. J., 2000, Inference of population structure using multi locus genotype data. *Genet.*, **155**: 945-959.
- Pruthi, H. S. and Samuel, C. K., 1939, Entomological investigation on the leaf curl disease of tobacco in Northern India -III. The transmission of leaf curl by the whitefly, *Bemisia gossypipendra* to tobacco, sunhemp and a new alternate host of the leaf curl virus. *Indian J. Agric. Sci.*, **9**: 223-275.
- Qiu, B., Chen, Y., Liu, L., Peng, W., Li, X., Ahmed, M. Z., Mathur, V., Dud, Y. and Ren, S., 2009, Identification of three major *Bemisia tabaci* biotypes in China based on morphological and DNA polymorphisms. *Progress Nat. Sci.*, **19**: 713-718.
- Quaintance, A. L. and Baker, A. C., 1914, Classification of aleyrididae part II. US Department of Agriculture. Technical series. *Bull. Entomol.*, **27**: 95-109.
- Quintero, C., Rendon, F., Garcia, J., Cardona, C., Lopez-Avila, A. and Hernandez, P., 2001, Especies y biotipos de moscas blancas (Homoptera: Aleyrodidae) en cultivos semestrales de Colombia y Ecuador. *Revista Colombiana de Entomologia*, **27**(1-2): 27-31.
- Raghavendra, A. S., 2002, Histology, biochemical studies and management of tomato leaf curl. *M. Sc (Agri.) Thesis*, Uni. Agri. Sci., Dharwad, pp. 63.
- Rai, A. K., Vikram, A. and Pandav. A., 2016, Genetic variability studies in tomato (*Solanum lycopersicum* L.) for yield and quality traits. *Int. J. Agri. Environ Biotech.*, **9**(5): 739-744.

- Rajasri, M. and Vijayalakshmi, K., 2011, Molecular identification and artificial screening of tomato germplasm against tomato leaf curl virus in Andhra Pradesh, India. World congress on biotechnology, <http://www.omicsonline.org/biotechnology2011>.
- Rakha, M., Bouba, N., Ramasamy, S., Regnard. J. and Hanson. P., 2016, Evaluation of wild tomato accessions (*Solanum* spp.) for resistance to two-spotted spider mite (*Tetranychus urticae* Koch) based on trichome type and acylsugar content. *Genet. Res. Crop Evol.*, 1-14.
- Rakha, M., Hanson, P. and Ramasamy, S., 2017, Identification of resistance to *Bemisia tabaci* Genn. in closely related wild relatives of cultivated tomato based on trichome type analysis and choice and no-choice assays. *Genet. Resour. Crop Evol.*, **64**: 247-260.
- Raveendar, S., Chung, J. W., Lee, G. A., Lee, J. R., Lee, K. J., Shin, M. J., Cho Y. H. and Kyung-Ho, M., 2016, Genetic diversity and population structure of asian tomato. Accessions based on simple-sequence repeats. *Plant Breed. Biotech.* **4**(3): 306-314.
- Reddy, K. S., 1978, Studies on leaf curl virus disease of tomato. *Ph. D. Thesis*, Univ. Agri. Sci., Bengaluru, India, pp 134.
- Reddy, K. S., Yaraguntaiah, R. C. and Sastry, K. S., 1981, Strains of leaf curl virus in India. *Zeitschrift fur Pflanzenkrankheiten und Pflanzenkrankh*, **88**: 400-404.
- Rick, C. M., 1958, The role of natural hybridization in the derivation of cultivated tomatoes of western South America. *Econ. Bot.*, **12**: 346-367.
- Roberts, M. R. and Paul, N. D., 2006, Seduced by the dark side: Integrating molecular and ecological perspectives on the inflence of light on plant defence against pests and pathogens. *New Phytol.*, **170**: 677-699.
- Robinson, H. F., Comstock, R. E. and Harvey, P. H., 1949, Estimates of heritability and degree o f dominance in Com. *Agron. J.*, **41**: 353-359.

- Rodríguez-López, M. J., Garzo, E., Bonani, J. P., Fereres, A., Munoz, F. R. and Moriones, E., 2011, Whitefly resistance traits derived from the wild tomato *Solanum pimpinellifolium* affect the preference and feeding behavior of *Bemisia tabaci* and reduce the spread of tomato yellow leaf curl virus. *Phytopathol.*, **101**(10): 1191-1201.
- Roopa, H. K., Asokan, R., Rebijith, K. B., Hande, R. H., Mahmood, R. and Kumar, N. K. K., 2015, Prevalence of a new genetic group, MEAM-K of the whitefly *Bemisia tabaci* (Hemiptera: Aleyrodidae) in Karnataka, India, as evident from *mtCOI* Sequences. *Florida Entomol.*, **98**(4): 1062-1071.
- Rosell, R. C., Bedford, I. D., Frohlich, D. R., Gill, R. J., Brown, J. K. and Markham, P. G., 1997, Analysis of morphological variation in distinct populations of *Bemisia tabaci* (Homoptera: Aleyrodidae). *Ann. Entomol. Soc. Am.* **90**(5): 575-589.
- Ruggieri, V., Francese, G., Sacco, A., D'Alessandro, A., Rigano, M. M., Parisi, M., Milone, M., Cardi, T., Mennella, G. and Barone, A., 2014, An association mapping approach to identify favourable alleles for tomato fruit quality breeding. *BMC Plant. Bio.*, **14**(337): 1-15.
- Sajjanar, G. M. and Balikai, R. A., 2009, Molecular mapping and marker assisted selection for trichome mediated insect resistance in tomato. *Int. J. Agric. Sci.*, 327-333.
- Sambrook and Russel, D. W., 2001, Molecular cloning: A laboratory manual, cold spring harbor laboratory, cold spring harbor, New York, pp. 12-18.
- Sampedro, L., Moreira, X. and Zas, R., 2011, Costs of constitutive and herbivore-induced chemical defences in pine trees emerge only under low nutrient availability. *J. Ecol.*, **99**: 818-827.
- Sastry, K. S. and Singh, S. J., 1973, Assessment of losses in tomato by tomato leaf curl virus. *Indian. J. Mycol. Plant Pathol.*, **3**: 50-54
- Sauvage, C., Segura, V., Bauchet, G., Stevens, R., Thi Do, P., Nikoloski, Z., Fernie, A. R. and Causse, M., 2014, Genome-wide association in tomato reveals 44 candidate loci for fruit metabolic traits. *Plant Physiol.*, **165**: 1120-1132.

- Schauer, N., Semel, Y., Roessner, U., Gur, A., Balbo, I. and Carrari, F., 2008, Comprehensive metabolic profiling and phenotyping of interspecific introgression lines for tomato improvement. *Nat. Biotechnol.* **24**: 447-454.
- Schilmiller, A. L., Last, R. L. and Pichersky, E., 2008, Harnessing plant trichome biochemistry for the production of useful compounds. *Plant J.*, **54**: 702-711.
- Scholthof, K. B. G., Adkins, S., Czosnek, H., Palukaitis, P., Jacquot, E., Hohn, T., Hohn, B., Saunders, K., Candresse, T., Ahlquist, P., Hemenway, C. and Foster, G. D., 2011, Top 10 plant viruses in molecular plant pathology. *Mol. Plant Pathol.*, **12**(9): 938-954.
- Segbefia, M. M., Amoatey, H. M., Quartey, E. K., Ahiakpa, J. K., Appiah, A. S., Nunoo, J. and Kusi-Adjei, R., 2015, Detection of TYLCV in ten genotypes of tomato (*Solanum* spp L.) using serological and molecular techniques in a coastal savanna zone of Ghana. *J. Nat. Sci. Res.*, **5**(2): 17-24.
- Selvanarayanan, V. and Narayanasamy, P., 2006, Assessment of tomato germplasm for resistance to fruit borer *Helicoverpa armigera* (Hubner). *J. Veg. Sci.*, **12**: 71-79.
- Shah, G. S., Ashfaq, M., P., Hebert, D. N., Mirza, M. S., Khan, A. M., Mansoor, S. and Zafar, Y., 2013, DNA barcoding of *Bemisia tabaci* complex (Hemiptera: Aleyrodidae) reveals southerly expansion of the dominant whitefly species on cotton in Pakistan, *PLoS One*, **9**: 104-114.
- Shahlaei, A., Torabi, S. and Khosroshahli, M., 2014, Efficiency of SCoT and ISSR markers in assessment of tomato (*Lycopersicum esculentum* Mill.) genetic diversity. *Int. J. Biosci.*, **5**: 14-22.
- Shankarappa, K. S., Sriharsh, K. T., Aswathanarayana, D. S., Prameela, H. A. and Kulkarni, R. S., 2008, Development of tomato hybrids resistant to leaf curl virus disease in south India. *Euphytica.*, **164**: 531-539.
- Sharifova, S. S., Mehdiyeva, S. P. and Abbasov, M. A., 2017, Analysis of genetic diversity among different tomato genotypes using ISSR DNA marker. *Genetika*, **49**: 31-42.

- Shi, X., Tang, X., Zhang, X., Zhang, D., Li, F., Yan, F., Zhang, Y., Zhou, X. and Liu, Y., 2018, Transmission efficiency, preference and behavior of *Bemisia tabaci* MEAM1 and MED under the influence of tomato chlorosis virus. *Front. Plant Sci.*, **8**(2271): 1-9.
- Shibuya, T., Hirai, N., Sakamoto, Y. and Komuro, J., 2009, Effects of morphological characteristics of *Cucumis sativus* seedlings grown at different vapor pressure deficits on initial colonization of *Bemisia tabaci* (Hemiptera: Aleyrodidae). *J. Econ. Entomol.*, **102**: 2265-2267.
- Shivasubramanian, S. and Menon, M., 1973, Heterosis and inbreeding depression in Rice. *Madras Agri. J.*, **60**: 1139-1144.
- Simmons, A. T. and Gurr, G. M., 2005, Trichomes of *Lycopersicon* species and their hybrids: effects on pests and natural enemies. *Agric. For. Entomol.*, **7**: 265-276.
- Simon, B., Cenis, J. L. and Rua, D. L. P., 2007, Distribution patterns of the Q and B biotypes of *Bemisia tabaci* in the Mediterranean basin based on microsatellite variation. *Entomol. Experiment. Appl.*, **124**: 327-336.
- Simon, B., Cenis, J. L., Beitia, F., Khalid, S., Moreno, I. M., Fraile, A. and García-Arenal, F., 2003, Genetic structure of field populations of begomoviruses and of their vector *Bemisia tabaci* in Pakistan. *Phytopathol.*, **93**(11): 1422-1429.
- Singh, A. K., Chattopadhyay, B. and Chakraborty, S., 2012, Biology and interactions of two distinct monopartite begomoviruses and betasatellites associated with radish leaf curl disease in India. *Virol. J.*, **9**:43.
- Singh, B. K., Singh, A. K., Yadav, S. K., Vani, V. M., Kumar, H. and Kumar, R. B. V., 2014, Combining ability for yield and quality attributes in tomato (*Lycopersicon esculentum* Mill.). *Ann. Agri. Res.*, **19**(3): 479-482.
- Singh, D., Jaglan, R. S. and Singh, R., 2002, Leaf morphological characteristics of brinjal in relation to whitefly incidence. *Haryana J. Hort. Sci.*, **31**: 289-291.

- Singh, R. K., Rai, N., Singh, M., Singh, S. N. and Srivastava, K., 2014, Selection of tomato genotypes resistant to tomato leaf curl virus disease using biochemical and physiological markers. *J. Agri. Sci.*, **2**: 1-10.
- Singh, S. T., Priya, N. G., Kumar, J., Rana, V. S., Ellango, R., Joshi, A., Priyadarshini, G., Asokan, R. and Rajagopal, R., 2012, Diversity and phylogenetic analysis of endosymbiotic bacteria from field caught *Bemisia tabaci* from different locations of North India based on 16S rDNA library screening. *Inf. Genet. Evol.*, **12**: 411-419.
- Sippel, D. W., Bindra, O. S. and Khalifa, H., 1987, Resistance to whitefly (*Bemisia tabaci*) in cotton (*Gossypium hirsutum*) in the Sudan. *Crop Protec.*, **6**: 171-178.
- Smulders, M. J. M., Bredemeijer, G., Rus-Kortekaas, W., Arens, P. and Vosman, B., 1997, Use of short microsatellites from database sequences to generate polymorphisms among *Lycopersicon esculentum* cultivars and accessions of other *Lycopersicon* species. *Theor. Appl. Genet.*, **94**: 264-272.
- Snedecor, G. W., 1946, Statistical methods. IOWA State College, *American Press*. pp 12.
- Song, J., Chen, J., Chen, H. Y., Liu, Y. and Zhuang, T. M., 2006, Research of genetic diversity of tomato using SSR markers. *J. Shanghai Jiaotong Univ.*, **24**: 524–528.
- Soundararajan, R. P. and Baskaran, P., 2001, Mechanisms of resistance in brinjal (*Solanum melongena* L.) to whitefly *Bemisia tabaci* (Gennadius). *Madras Agric. J.*, **88**: 657-659.
- Srivastava, K. M., Mathur, A. K., Verma, H. N. and Varma, G. S., 1975, Complex infection of tomato (*Lycopersicon esculentum*) with cucumber mosaic and tomato leaf curl virus. *Curr. Sci.*, **44**: 716.
- Srivastava, K. P. and Butani, D. K., 2009, Pest management in vegetables. *Stadium press (India) private limited, New Delhi, India*, **1(2)**: 99-116.

- Ssekyewa, C., 2006, Incidence, distribution and characteristics of major tomato leaf curl and mosaic virus diseases in Uganda. *Ph.D. Thesis*. Faculty of Biosci. Engin., Ghent Uni., Ghent. Belgium.
- Sulistyo, A. and Inayati, A., 2016, Mechanisms of antixenosis, antibiosis, and tolerance of fourteen soybean genotypes in response to whiteflies (*Bemisia tabaci*). *Biodiversitas*, **17**(2): 447-453.
- Suresh, S., Chung, J. W., Cho, G. T., Sung, J. S., Park, J. H. and Gwag, J. G., 2014, Analysis of molecular genetic diversity and population structure in *Amaranthus* germplasm using SSR markers. *Plant Biosyst.*, **148**: 635-644.
- Taggar, G. K., Gill, R. S., Gupta, A. K. and Singh, S., 2014, Induced changes in the antioxidative compounds of *Vigna mungo* genotypes due to infestation by *Bemisia tabaci* (Gennadius). *J. Environ. Biol.*, **35**(6): 1037-1045.
- Taggar, K. G., Gill, R. S., Gupta, K. A. and Sandhu, J. S., 2012, Fluctuations in peroxidase and catalase activities in resistant and susceptible black gram (*Vigna mungo* L.) hepper genotypes elicited by *Bemisia tabaci* (Gennadius) feeding. *Plant Signaling Behav.*, **7**(10): 1321-1329.
- Tahiri, A., Halkett, F., Granier, M., Gueguen, G. and Peterschmitt, M., 2013, Evidence of gene flow between sympatric populations of the Middle East-Asia Minor 1 and Mediterranean putative species of *Bemisia tabaci*. *Ecol. Evol.*, **3**: 2619-2633.
- Tahiri, A., Sekkat, A., Bennani, A., Granier, M., Delvare, G. and Peterschmitt, M., 2006, Distribution of tomato-infecting begomoviruses and *Bemisia tabaci* biotypes in Morocco. *Ann. Appl. Biol.*, **149**:175-186.
- Tay, W. T., Evans, G. A., Boykin, L. M. and De Barro, P. J., 2012, Will the real *Bemisia tabaci* please stand up? *PLoS One*, **7**: 50550.
- Thomas, A., Chaubey, R., Naveen, N. C., Kar, A. and Ramamurthy, V. V., 2011, *Bemisia tabaci* (Hemiptera: Aleyrodidae) on *Leucaena leucocephala* (Fabaceae): a new host record from India and a comparative study with a population from cotton. *Int. J. Tropic. Insect Sci.*, **31**(4): 235-241.

- Thomas, A., Kar, A., Rebijith, K. B., Asokan, R. and Ramamurthy, V. V. 2014. *Bemisia tabaci* (Hemiptera: Aleyrodidae) species complex from cotton cultivars: A comparative study of population density, morphology, and molecular variations. *Ann. Entomol. Soc. Am.*, **107**(2): 389-398.
- Thompson, W. M. O., 2000, Development, morphometrics and other biological characteristics of the whitefly *Bemisia tabaci* (Gennadius) on cassava. *Insect Sci. Appl.*, **20**: 251-258.
- Tieman, D. M., Zeigler, M., Schmelz, E. A., Taylor, M. G., Bliss, P. and Kirst, M., 2006, Identification of loci affecting flavour volatile emissions in tomato fruits. *J. Exp. Bot.*, **57**: 887-896.
- Tomar, S., Malik, K., Ellango, R. and Singh, B., 2014, Analysis of whitefly, *Bemisia tabaci*: sequencing of the mitochondrial cytochrome oxidize I *mtCoI*. *Int. J. Gen. Eng. Biotech.*, **5**(2):185-190.
- Toscano, L. C., Boica, A. L. and Maruyama, W. I., 2002, Non preference of whitefly for oviposition in tomato genotypes. *Sci. Agric.*, **59**(4): 677-681.
- Treutter, D. 2006. Significance of flavonoids in plant resistance: a review. *Environ. Chem. Lett.*, **4**: 147-57.
- Tsagkarakou, A., Mouton, L., Kristoffersen, J. B., Dokianakis, E., Grispou, M. and Bourtzis, K., 2012, Population genetic structure and secondary endosymbionts of *Q Bemisia tabaci* (Hemiptera: Aleyrodidae) from Greece. *Bull. Entomol. Res.*, **102**: 353-365.
- Tsagkarakou, A., Tsigenopoulos, C. S., Gorman, K., Lagnel, J. and Bedford, I. D., 2007, Biotype status and genetic polymorphism of the whitefly *Bemisia tabaci* (Hemiptera: Aleyrodidae) in Greece: mitochondrial DNA and microsatellites. *Bull. Entomol. Res.*, **97**: 29-40.
- Tsai, J. H. and Wang, K., 1996, Development and reproduction of *Bemisia argentifolii* (Homoptera: Aleyrodidae) of five host plants. *Environ. Entomol.*, **25**: 810-816.

- Usman, A., Khan, I. A., Shah, M., Sohail, K. and Syed, F., J., 2015, Influence of various biochemical factors on the occurrence of *Helicoverpa armigera* (Hubner) in Tomato. *Entomol. Zool. Stud.*, **3**(3): 63-68.
- Valle, D. G. E., Lourencao, A. L., Zucchi, M. I., Pinheiro, J. B and Abreu, D. A. G., 2013, Population variability of *Bemisia tabaci* (Genn.) in different hosts. *Genet. Mol. Res.*, **12**(4): 4615-4624.
- Valle, G. E. and Lourencao, A. L., 2002, Resistencia de genotipos de soja a *Bemisia tabaci* (Genn.) biotipo B (Hemiptera: Aleyrodidae). *Neotrop. Entomol.*, **31**: 285-295.
- Valle, G. E., Lourencao, A. L., Zucchi, M. I. and Pinheiro, J. B., 2012, Low polymorphism revealed in new microsatellite markers for *Bemisia tabaci* (Hemiptera: Aleyrodidae). *Genet. Mol. Res.*, **11**(4): 3899-3903.
- Valle, G. E., Lourencao, A. L., Zucchi, M. I., Pinheiro, J. B. and Abreu, A. G., 2011, *mtDNA* variability in whitefly (*Bemisia tabaci*) populations in Brazil. *Genet. Mol. Res.*, **10**(3): 2155-2164.
- Valverde, R. A., Sim, J., Lotrakul, P., 2004, Whitefly transmission of sweet potato viruses. *Virus Res.*, **100**: 123-128.
- Varma, A. and Malathi, V. G., 2003, Emerging geminivirus problems-A serious threat to crop production. *Ann. App. Biol.*, **142**: 145-164.
- Varma, P. M., 1955, Ability of the whitefly to carry more than one virus simultaneously. *Curr. Sci.*, **24**: 317-318.
- Varsani, A., Castillo, J. N., Moriones, E., Zepeda, C. H., Idris, A., Brown J. K., Zerbini, F. M. and Martin, D. P., 2014, Establishment of three new genera in the family Geminiviridae: Becurtovirus, Eragrovirus and Turncurtovirus. *Arc. Virol.*, **159**: 2193-2203.
- Vasudeva, R. S. and Samraj, J., 1948, A leaf curl disease of tomato. *Phytopathol.*, **38**: 364-369.

- Visser, P. M., Brown, M. A., McCarthy, M. I. and Yang, J., 2012, Five years of GWAS discovery. *Am. J. Hum. Genet.*, **90**: 7-24.
- Walker, G. P., Perring, T. M. and Maxwell, J. R., 2010, Feeding and oviposition behavior of whiteflies (Homoptera: Aleyrodidae) interpreted from ac electronic feeding monitor waveforms. *Ann. Entomol. Soc. Am.*, **87**: 363-374.
- Wang, H. L., Yang, J., Boykin, L. M., Zhao, Q. Y., Wang, Y. J., Liu, S. S. and Wang, X. W., 2014, Developing conversed microsatellite markers and their implications in evolutionary analysis of the *Bemisia tabaci* complex. *Sci. Rep.*, **4**(6351): 1-10.
- Wang, H. L., Yang, J., Boykin, M., Zhao, Q. Y., Li, Q., Wang, X. W. and Liu, S. S., 2013, The first insight into the characteristics and expression profiles of the mitochondrial genome for the mediterranean species of the *Bemisia tabaci* species complex. *BMC Genomics*, **14**: 401.
- Wang, P., Ruan, Y. M. and Liu, S. S., 2010, Crossing experiments and behavioral observations reveal reproductive incompatibility among three putative species of the whitefly *Bemisia tabaci*. *Insect Sci.*, **17**: 508-516.
- War, A. R., Paulraj, M. G., Ahmad, T., Buhroo, A. A., Hussain, B., Ignacimuthu, S. and Sharma, H. C., 2012, Mechanisms of plant defense against insect herbivores. *Plant Signaling Behav.*, **7**: 1306-1320.
- Weigel, D., 2012, Natural variation in *Arabidopsis*: from molecular genetics to ecological genomics. *Plant Physiol.*, **158**: 2-22.
- Williams, W. G., Kennedy, G. G., Yamamoto, R. T., Tracker, J. D. and Bordner, J., 1980, 2-Tridecanone: a naturally occurring insecticide from the wild tomato, *Lycopersicon hirsutum* f. *glabratum*. *Sci.*, **207**: 888-889.
- Wright, S., 1978, Evolution and the genetics of populations, variability within and among natural populations. v. 4. Chicago: *University of Chicago Press*.

- Xiao-jun, G., Qiong, R., Fan, Z., Chen, L., Hong-yu, Z. and Xi-wu, G., 2012, Diversity and genetic differentiation of the whitefly *Bemisia tabaci* species complex in China based on *mtCOI* and cDNA-AFLP analysis. *J. Integ. Agric.*, **11**(2): 206-214.
- Xu, J., De Barro, P. J. and Liu, S. S., 2010, Reproductive incompatibility among genetic groups of *Bemisia tabaci* supports the proposition that the whitefly is a cryptic species complex. *Bull. Entomol. Res.*, **100**: 359-366.
- Xu, J., Lin, K. K. and Liu, S. S., 2011, Performance on different host plants of an alien and an indigenous *Bemisia tabaci* from China. *J. Appl. Entomol.*, **135**: 771- 779.
- Xu, J., Ranc, N., Munos, S., Rolland, S., Bouchet, J. P., Desplat, N., Le Paslier, M. C., Liang, Y., Brunel, D. and Causse, M., 2013, Phenotypic diversity and association mapping for fruit quality traits in cultivated tomato and related species. *Theor. Appl. Genet.*, **126**(3): 567-581.
- Yan, F. M., 1991, Morphological variations in whiteflies. *J. Beijing Agric. Coll.*, **6**: 68-71.
- Zaini, M. R. B., 2005, Biology, distribution and effect of selected insecticides against whitefly (*Trialeurodes vaporariorum* Westwood and *Bemisia tabaci* Gennadius) on brinjal (*Solanum melongena* L.). *M. Sc. Thesis*. Uni. Tek. MARA.
- Zamir, D., Michelson, I. E., Zakay, Y., Navot, N., Zeidan, M., Sarfatti, M., Eshed, Y., Harel, E., Pleban, T., Van, H., Kedar, N., Rabinowitch, H. D. and Czosnek, H., 1994, Mapping and introgression of a tomato yellow leaf curl virus tolerance gene, TY I. *Theor. Appl. Genet.*, **88**: 141-146.
- Zang, L. S., Chen, W. Q. and Liu, S. S., 2006, Comparison of performance on different host plants between the B biotype and a non-B biotype of *Bemisia tabaci* from Zhejiang, China. *Entomol. Exp. Appl.*, **121**: 221-227.
- Zeidan, M. and Czosnek, H., 1991, Acquisition of tomato yellow leaf curl virus by the whitefly *Bemisia tabaci*. *J. Gen. Virol.*, **72**: 2607-2614.

- Zeshan, M. A. Khan, M. A., Ali, S. and Arshad, M., 2016, Phenotypic evaluation of tomato germplasm for the source of resistance against tomato leaf curl virus disease. *J. Animal Plant Sci.*, **26**(1): 194-200.
- Zeshan, M. A., Khan, M. A., Ali, S. and Arshad, M., 2015, Correlation of conducive environmental conditions for the development of whitefly, *Bemisia tabaci* population in different tomato genotypes. *Pakistan J. Zool.*, **47**(6):15-51.
- Zhang, J., Zhao, J., Xu, Y., Liang, J., Chang, P., Yan, F., Li, M., Liang, Y. and Zou, Z., 2015, Genome-wide association mapping for tomato volatiles positively contributing to tomato flavor. *Front. Plant Sci.*, **6**(1042): 1-13
- Zhao, J., Xu, Y., Ding, Q., Huang, X., Zhang, Y., Zou, Z., Li, M., Cui, L. and Zhang, J., 2016, Association mapping of main tomato fruit sugars and organic acids. *Front. Plant Sci.*, **7**(1286): 1-11.
- Zhao, K., Tung, C. W., Eizenga, G. C., Wright, M. H., Ali, M. L., Price, A. H., Norton, G. J., Islam, M. R., Reynolds, A. and Mezey, J., 2011, Genome-wide association mapping reveals a rich genetic architecture of complex traits in *Oryza sativa*. *Nat. Commun.*, **2**: 467.

Appendix I. Details of locations selected for collection of *Bemisia tabaci* samples across agroclimatic zones of Karnataka and abbreviations used

Sl. No.	District	Abbreviations
1	Davanagere	DVN
2	Haveri	HVR or HR
3	Dharwad	DWD or DVD
4	Belagavi	BLV
5	Chikkaballapura	CKBR or CBR
6	Kolar	KLR or KL
7	Bengaluru rural	BR
8	Bagalkot	BGK
9	Chamarajanagara	CHA
10	Chikkamagaluru	CKM or CM
11	Shivamogga	SHI

**Appendix II. Details of various morphological characters recorded from
Bemisia tabaci puparia and abbreviations used**

Sl. No.	Variables	Characters
1	P L	Puparia length
2	P B	Puparia breadth
3	D V O A E	Distance of Vasiform orifice from anterior end
4	D T M S A E	Distance of transverse moulting suture from anterior end
5	L V O	Length of Vasiform orifice
6	B V O	Breadth of Vasiform orifice
7	L L	Length of lingula
8	L O	Length of operculum
9	B O	Breadth of operculum
10	L C F	Length of caudal furrow
11	L C S	Length of caudal setae
12	D C S	Distance between caudal setae

Appendix III. Details of various morphological characters recorded from *Bemisia tabaci* males and abbreviations used

Sl. No.	Variables	Characters
1	F W L	Fore wing length
2	F W W	Fore wing width
3	F W V L	Fore wing vein length
4	H W L	hind wing length
5	H W W	Hind wing width
6	F Fe L	Fore femur length
7	F Ti L	Fore tibial length
8	F Ta L	Fore tarsal length
9	H Fe L	Hind femur length
10	H Ti L	Hind tibial length
11	H Ta L	Hind tarsal length
12	L A	Length of antenna
13	L P	Length of proboscis
14	L C	Length of claspers
15	L Ab	Length of abdomen
16	L L Ab	Length of Last abdominal segment

**Appendix IV. Details of various morphological characters recorded from
Bemisia tabaci females and abbreviations used**

Sl. No.	Variables	Characters
1	F W L	Fore wing length
2	F W W	Fore wing width
3	F W V L	Fore wing vein length
4	H W L	hind wing length
5	H W W	Hind wing width
6	F Fe L	Fore femur length
7	F Ti L	Fore tibial length
8	F Ta L	Fore tarsal length
9	H Fe L	Hind femur length
10	H Ti L	Hind tibial length
11	H Ta L	Hind tarsal length
12	L A	Length of antenna
13	L P	Length of proboscis
14	L Ab	Length of abdomen

Appendix V. List of microsatellite primer pairs of *Bemisia tabaci*

Sl. No.	Locus	Forward Primer (5'–3')	Reverse Primer (5'–3')	T _m (°C)	H _o	H _E	References
1.	FbBEM11	TTCAATGATGCTTTCCTGAC	CAAATAAATACACCATTTACA	45.5	0.078	0.808	De-Barro <i>et al.</i> , 2003; Valle <i>et al.</i> , 2012; Hsieh <i>et al.</i> , 2011
2.	FbBEM14ii	AGAAGTCAGACAATATGTG	ATTAACCCCTCTCTCATCGC	46.75	0.178	0.938	
3.	FbBEM15	AGCAGCATCAACAGGCTC	CTAGATTCTGCTTGAAAGG	48.55	0.243	0.852	
4.	FbBEM22	GGCCCTAGTTAGAAGGTAGTA	CTAATCGGTCAAGAGATTTGG	51.45	0.158	0.723	
5.	FbBEM25	AAGTATCAACAAATTAATCGTG	TGAAGAATAAGAATAAAGAAGG	45.5	0.063	0.844	
6.	FbBEM31	AAGAACTAGCCAGGGACAAAC	GTCATTTCTGGATTCTCAGCA	51.45	0.065	0.820	
7.	FbBEM39	ACTCTAGGCTGTATGCATCCA	CGCATGACAAATCGTATCAAG	51.45	0.279	0.942	
8.	FbBEM40	TGGAGAATGTTATAAAGTGGA	GAAAGTGGAGAGTTTAGGTGA	48.5	0.194	0.739	
9.	FbBem15	AGCAGCATCAACAGGCTC	CTAGATTCTGCTTGAAAGG	48.55	0.235	0.253	
10.	FbBtIs1.17	GTGACCGAGTAAGGCCA	CACGTCCGCTCTCTATG	49.5	0.128	0.648	
11.	FbBtIs1.4	GAAATCCTCACACTGGC	CACTGATGTCAGACCTGG	48.7	0.242	0.889	
12.	FbBT-e49	GATCGAATCCAATCTCCCAC	GAGCTCTGCAATACTGCCAA	51.8	0.817	0.848	Tsagkarakou <i>et al.</i> , 2007; Valle <i>et al.</i> , 2012; Hsieh <i>et al.</i> , 2011
13.	FbBT-4	GAGATCATATCCCCATTGTTTC	ATCACGGGTCATAGATCACG	51.45	0.289	0.326	
14.	FbBT-b159	ACTCCATTTGGCTTATGTGC	ATTATCGTCTGAAAACCTGGTGG	50.4	0.568	0.599	Valle <i>et al.</i> , 2012; Hsieh <i>et al.</i> , 2011
15.	FbBem23	CGGAGCTTGCGCCTTAGTC	CGGCTTTATCATAGCTCTCGT	53.9	0.147	0.432	Valle <i>et al.</i> , 2012; DeBarro <i>et al.</i> (2003); Hsieh <i>et al.</i> , 2011
16.	FbBem37	TGACGACCTGAGGCTGAGAG	TGCAACGGCAACAGCAAGCAA	55.15	0.037	0.067	
17.	FbBT-83	GATGCCACAGGTTGTCTGG	GCTTGCCAGGCACTTTCTAG	53.5	0.606	0.68	Valle <i>et al.</i> , 2012; Tsagkarakou and Roditakis, 2003; Hsieh <i>et al.</i> , 2011

T_m- Primer Melting Temperature H_E, expected heterozygosity; H_o, observed heterozygosity.

Appendix VI. Meteorological data recorded during 2016 and 2017 covering the period of experimentation from agrometeorology unit University of Agricultural Sciences, GKVK, Bengaluru

Year/Month	Temperature (°C)		RH (RH)		Rainfall
	Max	Min	Max	Min	(mm)
Year-2016					
January	27.50	14.70	90.00	47.00	2.40
February	31.20	16.20	85.00	38.00	0.00
March	34.00	19.90	86.00	37.00	4.20
April	35.80	23.10	84.00	37.00	1.20
May	33.10	21.40	88.00	42.00	115.00
June	28.40	19.90	92.00	55.00	140.40
July	27.60	19.30	94.00	58.00	271.40
August	28.10	19.50	92.00	54.00	28.00
September	27.80	19.00	92.00	54.00	51.40
October	29.60	18.00	85.00	48.00	31.00
November	29.60	16.20	82.00	43.00	0.00
December	27.20	14.70	88.00	46.00	64.40
Year-2017					
January	27.30	14.50	88.90	39.50	0.00
February	30.60	14.90	84.00	33.00	0.00
March	33.00	19.50	82.00	39.00	9.80
April	35.10	21.90	83.00	36.00	1.60
May	32.70	20.70	85.00	42.00	246.60
June	28.60	20.10	89.00	54.00	65.40
July	28.80	19.80	89.00	56.00	33.40
August	28.20	20.20	91.00	58.00	199.80
September	27.70	19.60	90.00	59.00	275.60
October	28.10	19.00	91.00	56.00	264.00
November	26.90	18.50	90.00	60.00	11.40
December	26.30	14.90	89.00	58.00	8.80

Appendix VII. List of stock solutions used in study

Sl. No.	Chemicals/ Stock solutions	Concentration/Volume
1	Extraction buffer	:100 mM Tris HCl, pH 8.0 50 mM EDTA, pH 8.0 500 mM NaCl
2	20 % SDS	:20 g of Sodium Doedecyl Sulphate (sodium Lauryl Sulphate) 100 ml of dH ₂ O. Should not be autoclaved
3	5 M Potassium acetate	: 60.0 ml 5 M Potassium acetate 11.5 ml Glacial Acetic acid 28.5 ml H ₂ O
4	Isopropanol Ammonium Acetate Mixture	:Three volumes of 10 M Iso-propanol One volume of 10 M Ammonium acetate
5	T ₁₀ E ₁	: Tris 10 mM containing 1 mM EDTA
6	<i>RNase</i> (10 mg/ml)	: Dissolve <i>RNase</i> in water, place in a tube in boiling water bath for 10 minutes. Allow this to cool on a bench and store at -20 °C
7	Chloroform : isoamyl alcohol (24:1)	: Chloroform 240 ml Isoamyl alcohol 10 ml. Store in a dark at room temperature. Make up and dispense the solution in a fumed cupboard.
8	Ethanol (70 %)	: Absolute alcohol (70 ml) Distilled Water (30 ml)
9	NaCl 5 M	: Dissolve 292.2 g NaCl in 750 ml water. Make up to 1 litre with water, filter and autoclave.
10	Phenol /chloroform	: Mix equal volumes of the buffered phenol and chloroform : Isoamyl alcohol (24:1). Store at 4 °C
11	Sodium acetate (2.5 M, pH 5.2)	: Dissolve 340.2 g sodium acetate in 500 ml of water adjust pH to 5.2 with glacial acetic acid and make up the volume to 1 litre and autoclave.
12	Tris HCl (1 M, pH 8.0)	: Dissolve 121.1 g Tris in 800 ml of water. Adjust pH 8.0 with conc. HCl. Make up the volume to 1 L and autoclave
13	Ethidium bromide (10 mg/ml)	: Dissolve 100 mg ethidium bromide in 10 ml of distilled water wrap tube in aluminum foil and store at 4 °C. <i>Caution</i> : Ethidium bromide is extremely mutagenic
14	Loading dye (6X)	: 0.25% bromophenol blue : 40% (w/v) sucrose in water
15	Recipe for 1 % agarose gel (40 ml)	: 400 mg Agarose : 40 ml 1X TAE : 2 µl Ethidium bromide (10 mg/ml)
16	50X TAE composition	: 242 g Tris base 57.1 ml Glacial acetic acid : 100 ml 0.5 M EDTA (pH 8.0) Make up the volume to 1000 ml with double distilled water

Appendix VIII. List of primer pairs used in the genotyping the tomato association mapping panel

Sl. No.	Primer ID	Forward Primer (5'-3')	Reverse Primer (5'-3')
1.	AVRDC-TM719	TCGATTTGGAATGAGTTTTC	TGAAATAGATTTGTCAGGTGTT
2.	AVRDC-TM273	GGTGCTCATGGATAGCTTAC	CTATATAGGCGATAGCACCAC
3.	P6-25	GGTAGTGGAAATGATGCTGCTC	GCTCTGCCTATTGTCCCATATATAACC
4.	Mi23	TGGAAAAATGTTGAATTTCTTTTG	GCATACTATATGGCTTGTTTACCC
5.	AVRDC-TM947	TGCGTCTAGTTTTCTTTGTTT	CAAGCTGAAAGGAATTCAAC
6.	TES0344	GCCTTTTCCCACCTTATATTCCTCTC	ACACATACGACGTTCCGTCA
7.	Pb	TTGACGAGACCAATCGACG	CATCAAG ATCTGTAGAGAGC
8.	LEaat8	GAGTCAACAGCATAGTGGAGGAGG	CGTCGCAATTCTCAGGCATG
9.	T0800	GCCTCGAAAATTGCAGAAGA	GCGTGTCTTGCAATCACATT
10.	FBTGS0321	GTCCTTTTTGTAAAGGATGAACCG	CCCCTATGGATGTTGGATTG
11.	BF-CHO3	GCTAAGAACGCTGGACCTAATG	TGGGTGTGCCTTTCTGAATG
12.	BF-CHVR-12-542	TGCACGTGTGTCTCGTGTTA	AAACTCTCTAAATATTGTGCAAGCC
13.	BF-CHVR-01-182	GTTAGGTGGGCCAGGAATG	GATCTTCGTACCATGAAGCG
14.	BF-CHVR-10-3817	CACCCAAATCAGATCCGTCT	GTTTCTTGGACTIONGGTGGTGG
15.	BF-CHVR-08-2155	CCATAACCTACCTCCACCGA	GGGTAAAAGAAAGAGGGTTTGAA
16.	BF-CHVR-11-219	GCTCGCAATGGAAAAGACTC	CGTCTCTCGTGTTGTGAGA
17.	SSR241	TCAACAGCATAGTGGAGGAGG	TCCTCGGTAATTGATCCACC
18.	LEaat1	GATGGACACCCTTCAATTTATGGT	TCCAAGTATCAGGCACACCAGC
19.	FBTGS0244	CCAATTGCAAGTTAGCAAGC	GCAACATCAATAACCGCGTA
20.	LEaat7	CAACAGCATAGTGGAGGAGG	TACATTTCTCTCTCTCCCATGAG
21.	FBTGS0318	GTAGGTGGCATCACGTTTTTG	CTGCCACATCAGTGGTTTTG
22.	BF-CHVR-11-648	GGAGGACCTTTTAGACAAGACC	TTGCTAAATCCTCTCCAGCA
23.	BF-CHVR-12-616	GTCGCCAGCTAGCAAACTT	AAGGAGCGGAGAAAAGGGTA

Contd...

Sl. No.	Primer ID	Forward Primer (5'-3')	Reverse Primer (5'-3')
24.	BF-CHVR-05-290	TCCTTTTGAGATTTTGGTGACA	AAAAATGCGAAAATTTTAACAACA
25.	LEgata2	TTGGTAATTTATGTTTCGGGA	TTGAGCCAATTGATTAATAAGTT
26.	FBTGS0289	GGATTGCATCATGACTTTTGG	TCGATCCAACCAAGAAAAGAA
27.	BF-CHVR-03-3095	TCGTTACACCCGACCACTAA	TGACCCTATGCTATTATATGTGTCAAA
28.	SINAC1 (TAQ I)	TGCCTGGTTTCTGCTGTCA	TAAAGCTGAAGAAGGACTTACCCT
29.	TG178	GAGTCCCTAACGAATGGTCCTACT	GCAGACAAATGCTCAAAGGTCACACC
30.	BW4	TTGCAGAAGCAACCCTTGAC	TACATTCTCCCCATTCCATGC
31.	BF-CHVR-02-378	GGATTTGATCCCACAACCAA	CTGAAGAGGAGGAGGCTGTG
32.	FBTGS0209	TGCAAAAATCGAAAATCGAA	GGGAAAATTTTATGTTAAGCTCCA
33.	PM3	CCTGTGATGAGATTCCTCTTAG	ACCCTTTGTTGAGCGACTTTGCAGC
34.	BW3	TGAGGTGCAAATGGGGTAGTG	GCAATGAAGGCCTACAGATGAC
35.	LEaat3	CTTGAGGTGGAAATATGAACAC	AAGCAGGTGATGTTGATGAG
36.	LEat18	CGGCGTATTCAAACCTCTTGG	GCGGACCTTTGTTTTGGTAA
37.	SSR45	TGTATCCTGGTGGACCAATG	TCCAAGTATCAGGCACACCA
38.	TY-1/3	ACAGGAAAAATGGGTGATCC	CCTGCTCCTTGCAGATTCTA
39.	CD2	ACATGCATTGGTTTTGTATAC	CTTGGCAAAGCAACAAGAC
40.	T0302	TGGCTCATCCTGAAGCTGATAGCGC	AGTGTACATCCTTGCCATTGACT

Appendix IX. Mean values of different traits of tomato association mapping panel used in the study

Tamato accessions	Phenols (mg)	Tannins (g)	Terpinoid (mg)	Chlorophyll	Trichome density (mm ²)	Whitefly population in rabi season	Whitefly population in summer season
Ageta-32	5.186	8.146	914.091	46.72	601.17	1.73	32.60
Angoorlata	5.010	6.587	540.428	46.68	546.08	2.80	26.00
Arka Abha	7.435	8.431	514.674	46.96	569.00	2.33	33.93
Arka Alok	8.140	5.312	371.817	44.98	1080.60	1.33	30.40
Arka Meghalli	6.638	6.587	625.462	37.86	1274.20	1.33	20.27
Arka Vikas	8.257	4.582	507.386	49.1	763.75	1.00	33.73
Avinash-2-2-1	7.460	6.871	527.308	38.68	806.42	1.33	21.80
Azad T-2	7.938	5.064	613.800	38.3	990.58	1.47	27.20
Azad T-5	7.687	5.683	670.651	45.58	743.33	1.00	36.40
B-4-1	8.224	6.574	407.775	31.9	965.58	1.73	34.87
B-7-2	9.373	4.186	564.723	41.42	705.67	1.53	32.23
Bhillai	4.129	5.757	605.539	43.68	1053.80	1.80	41.40
BL-1208	4.255	3.851	521.477	38.96	796.33	1.00	37.53
BTH-9 M	3.290	3.864	456.851	46.98	900.42	2.00	28.73
C-1-4	3.147	3.616	534.111	43.34	453.75	1.07	21.27
C-3-2	11.471	12.045	442.760	45.58	704.75	2.53	20.53
C-4-1	11.169	8.047	454.422	46.08	224.58	2.73	36.40
C-8-1	9.801	7.168	568.610	48.06	384.42	1.27	34.87
C-9-2	7.636	8.938	557.434	47.12	609.67	0.27	26.67
C-10-2	2.619	4.582	591.934	54.28	886.83	1.60	27.60
C-11-1	10.581	6.797	614.286	46.88	1339.10	2.73	26.40
C-11-2	14.542	8.814	537.026	44.06	147.92	1.60	37.47
C-11-3	7.578	8.629	405.831	41.02	875.25	0.73	42.87
C-20-1	6.067	7.911	264.917	45.04	774.33	2.00	31.53
C-20-2	6.051	4.916	561.322	36.66	540.08	0.60	22.10
C-26-1	8.769	4.495	480.661	50.5	1039.50	1.67	26.87
CHRT-4	8.912	6.079	618.659	56.62	1230.70	2.13	35.27
CH-155	4.389	4.285	385.423	43.22	773.58	1.00	31.80
Co-3	4.909	4.545	628.377	39.66	530.25	1.33	28.40
CLN-2026	7.662	6.785	487.949	46.6	472.25	1.27	32.00
CLN-2116	5.547	6.153	619.145	52.3	427.50	1.47	27.10
CLN-1621	6.890	8.777	570.068	48.32	876.00	1.73	35.73
CLN-2366	4.330	3.356	556.948	43.6	657.08	0.87	32.60
D-1-1	5.748	5.782	659.961	44.48	468.42	0.33	33.60
D-2-2-1	6.017	3.554	401.944	41.82	1010.20	1.27	29.47
D-3-2	6.109	3.604	317.396	36.84	754.50	1.13	25.53
D-5-1	5.329	3.208	325.170	58.64	1144.80	1.67	26.60
DARL-66	1.889	3.641	537.998	43.46	499.33	1.53	32.33
Dhrubya	6.554	4.173	678.426	24.7	816.17	2.20	31.93
DT-10	3.726	5.139	258.601	46.26	1065.30	1.27	28.47
DVRT-1	12.310	7.243	742.080	60.48	708.08	2.20	37.27
DVRT-2	3.793	5.782	468.027	41.02	786.50	1.20	34.60
E-4-3	4.154	6.636	693.489	51.3	993.25	1.67	24.27
EC-2791	6.848	5.757	591.448	44.66	1250.70	2.00	35.07
EC-13904	6.671	4.668	438.873	40.38	893.58	1.87	25.53
EC-317-6-1	11.127	7.948	803.790	37.04	1092.80	1.07	23.80
EC-273966	11.605	4.124	623.032	37.76	937.00	1.93	33.33
EC-381263	5.899	5.881	788.241	42.94	1120.10	2.07	25.73
EC-381554	3.517	4.891	413.120	47.62	805.83	1.40	29.57
EC-501574	6.462	3.889	627.405	43.72	727.58	1.07	31.57

Contd...

EC-501575	7.015	3.839	351.409	43.42	1236.40	1.00	23.73
EC-501576	5.816	5.151	506.900	47.14	480.25	1.40	36.53
EC-501577	7.964	3.554	409.232	40.48	585.50	1.53	39.60
EC-501580	5.010	3.418	626.919	43.92	556.67	1.60	33.67
EC-501582	10.766	4.136	376.676	46.12	988.75	0.80	32.33
EC-501583	7.141	6.847	340.233	49.58	972.92	1.53	30.00
EC-519730	5.841	8.047	649.757	42.04	858.83	2.20	30.03
EC-520046	7.292	5.634	581.730	43.3	911.92	1.07	26.40
EC-520059	5.245	4.161	411.176	40.4	796.92	1.00	27.27
EC-520061	8.316	8.059	785.811	49.38	1370.10	1.93	44.20
EC-520071	6.906	8.134	617.687	44.58	461.75	1.80	37.13
EC-520074	7.855	4.619	595.335	45.52	977.89	1.00	31.40
EC-520075	5.690	7.837	380.564	38.3	918.58	2.00	31.00
EC -520078	5.648	4.483	289.699	39	412.00	1.33	37.13
EC -521039	6.848	5.473	638.581	40.56	874.92	1.00	32.80
EC -521056	6.411	4.396	266.375	39.66	761.50	2.07	27.53
EC -521078	5.841	4.668	387.366	47.32	1100.20	1.60	24.40
EC -526139	4.523	4.285	195.918	46.14	853.50	1.40	32.47
EC-528372	4.960	4.433	524.879	46.88	1066.10	2.00	27.07
EC-528374	4.842	5.361	404.859	51.6	1037.60	0.93	30.93
EC -529080	3.642	5.151	663.848	51.72	713.08	1.60	29.60
EC -529083	13.569	4.000	355.296	48.24	1155.70	1.40	31.40
EC-538138	4.171	6.228	412.634	35.14	837.50	1.73	26.40
EC -538155	5.899	4.483	660.447	52.68	351.92	0.80	23.07
EC-538380	6.176	4.359	458.309	49.24	728.42	0.87	26.60
EC-538404	7.192	6.822	838.290	52.9	815.67	1.40	35.07
EC-538405	5.111	3.196	498.639	51.8	547.33	1.47	29.67
EC-538408	9.088	6.636	652.672	41.68	848.42	2.07	31.53
EC-538419	5.463	6.537	361.613	43.08	1186.00	1.00	39.67
EC-538423	5.312	4.609	516.672	51.16	676.65	1.54	35.73
EC-538439	6.403	4.582	437.901	42.14	1140.40	1.33	27.40
EC-538440	6.067	4.879	363.557	42.78	750.67	1.80	30.73
EC-538441	7.922	4.767	547.716	38.54	1100.50	1.73	36.27
EC-538455	6.420	3.468	555.977	43.44	1057.70	2.53	25.33
EC-552141	7.544	5.002	468.513	46.82	596.67	1.73	36.60
EC-560340	10.078	4.074	478.231	36.34	597.33	1.60	34.27
EC-570028	7.309	5.918	624.004	50.34	784.00	1.47	32.80
EC-605694	4.935	11.822	428.669	45.92	557.25	1.67	37.40
EC-605695	5.044	4.903	472.400	39.32	568.92	1.93	31.53
EC-605696	5.287	8.344	374.247	44.58	597.58	1.40	32.27
EC-620362	6.814	5.238	632.264	45.16	489.00	1.53	27.47
EC-620366	7.569	4.619	541.399	42.48	996.08	2.27	23.53
EC-620370	8.140	6.710	589.990	58.76	818.08	2.07	34.93
EC-620373	6.428	6.574	474.830	48.48	756.50	1.60	38.27
EC-620374	10.858	6.772	441.302	40.2	929.25	1.33	34.07
EC-620375	6.277	4.124	640.525	46.36	559.33	1.40	34.07
EC-620383	9.658	12.304	533.139	52.96	444.17	1.13	29.47
EC-620386	7.712	5.361	679.883	38.46	501.92	1.67	32.00
EC-620398	6.009	5.869	534.597	49.28	628.33	2.33	32.80
EC-620401	7.024	5.448	605.539	53.8	1081.50	1.07	33.40
EC-620403	9.004	8.220	238.678	56.1	1049.40	1.47	25.40
EC-620406	10.078	9.210	474.344	53.88	952.92	1.60	33.07
EC-620409	7.603	5.114	222.157	38.16	1092.40	1.60	32.20
EC-620410	7.846	5.609	551.118	41.44	549.50	1.73	45.20
EC-620411	13.359	8.901	478.231	40.86	909.08	1.53	41.87

Contd...

EC-620413	4.733	5.349	382.021	42.74	606.83	1.73	43.67
EC-620419	5.623	4.854	587.561	44.8	697.33	1.07	39.33
EC-620421	6.285	7.886	341.691	54.52	699.75	0.87	28.80
EC-620438	4.742	3.604	507.386	34.32	843.25	2.07	36.87
EC-620444	7.578	6.748	460.739	36.6	894.75	1.07	32.40
EC-620446	5.589	5.275	493.294	41.8	690.17	1.87	33.67
EC-620455	7.745	3.913	804.762	43.16	778.00	1.40	32.33
EC-620456	5.128	6.265	589.018	39.2	628.75	1.40	27.13
EC-620464	8.543	9.879	751.312	51.34	698.17	1.47	41.20
EC-620469	9.273	10.200	568.124	31.7	540.08	0.47	44.67
EC-620470	6.185	8.814	340.233	39.26	981.42	1.67	41.27
EC-620474	5.153	8.257	355.782	44	763.42	1.73	41.13
EC-620476	7.779	4.050	521.477	42.78	838.17	1.40	33.07
EC-620480	5.388	6.475	392.711	30.82	221.75	1.33	32.40
EC-620486	4.465	4.124	430.126	37.72	929.25	1.73	34.20
EC-620500	6.831	5.436	618.659	43.44	1187.70	1.67	39.20
EC-620502	6.109	8.208	309.621	46.44	765.58	1.27	41.20
EC-620514	4.481	6.314	300.875	44.96	704.17	1.47	31.47
EC-620519	9.642	4.507	349.951	48.26	1199.80	1.87	46.07
EC -620530	10.179	8.864	489.407	46.84	1073.80	2.20	44.87
EC -620533	3.668	5.064	658.503	52.5	436.00	1.47	32.07
EC -620540	7.527	6.265	558.892	46.64	962.50	2.27	34.13
EC -620556	5.480	5.002	623.032	54.08	492.42	2.07	27.93
EC -620568	9.155	7.738	605.539	51.92	609.58	1.20	32.20
EC -620575	5.312	3.554	407.775	42.74	989.83	1.07	46.27
EC -620598	8.282	7.391	443.246	41.32	956.25	1.60	35.27
EC -625644	6.353	5.460	499.611	44.48	745.42	1.40	34.07
EC -625645	8.190	7.193	311.079	44.32	610.83	0.67	36.07
EC -625651	4.884	10.609	789.213	41.86	1131.40	1.87	39.20
EC -625652	4.540	5.658	624.004	48.08	1020.50	2.60	33.07
EC -625660	8.182	6.797	568.610	39.22	1053.60	1.47	46.13
EC-6202041	4.448	4.260	301.361	48.22	952.17	2.20	46.53
F-5020	4.238	5.881	414.577	50.72	372.58	1.80	33.10
F-6022	6.512	8.158	549.660	48.86	1060.50	2.13	45.33
F-6050-1	6.713	5.522	582.216	46.7	1177.30	0.80	46.07
F-6059	7.922	7.775	366.958	32.66	870.50	2.20	35.60
F-7012	8.350	8.307	544.801	47.84	731.08	1.40	35.47
F-7025	5.438	5.757	587.561	46.54	921.75	1.73	32.20
F-7028	5.916	4.693	795.044	42.34	973.08	2.13	37.27
F-6009	4.809	4.396	484.062	46.16	950.92	2.20	37.87
FEB.-02	1.805	7.787	471.429	47.64	802.17	1.20	41.20
FEB.-04	8.400	8.109	569.582	51	1497.00	1.53	28.20
FLA-7171	6.000	7.168	516.618	55.22	1007.80	1.87	31.20
FLA-7421	5.706	3.554	452.964	53.36	613.00	1.13	37.47
Flora-dade	13.770	8.567	664.820	46.38	795.58	1.40	35.07
G-4-5	7.049	4.099	515.160	48.94	1073.30	2.07	40.00
G-5-4	9.474	5.287	615.258	43.44	989.42	1.67	35.73
G-6-3	6.386	7.045	562.293	51.76	993.25	1.53	42.67
GT-1	6.269	3.889	495.238	47.44	698.33	1.20	43.60
GT-2	13.292	6.723	309.621	39.18	630.00	1.40	32.13
GT-3	4.951	4.173	668.707	43.04	619.75	1.40	33.67
H-24	3.030	3.715	566.667	45.38	413.08	1.87	24.07
H-88-78-2	9.264	5.498	565.209	48.9	1321.40	1.40	28.60
H-88-78-3	6.839	8.035	588.047	49.66	1065.80	1.47	41.20
H-88-78-4	4.985	4.767	489.893	52.02	346.25	1.13	32.67

Contd...

H-88-78-5	7.569	7.577	233.819	51.5	374.80	1.40	47.33
Hawai	5.572	6.240	547.230	45.16	942.17	2.27	31.13
Hisar Anmol	5.505	5.052	607.483	43.88	1348.90	1.00	28.10
Hisar Arun (Sel-7)	7.032	5.473	462.682	48.96	1303.20	2.20	31.53
Hisar Lalit	6.168	9.421	538.970	45.68	858.75	1.33	36.73
I-4-4	4.977	4.990	693.975	46.44	1161.60	1.73	39.40
IC-373378	6.713	4.978	751.312	50.96	906.75	1.80	34.93
IC-427766	5.799	5.547	335.374	48.14	943.67	1.67	45.20
IC-447708	3.961	6.475	276.579	57.38	1079.70	2.07	40.00
IC-469626	6.755	4.780	401.458	44.64	653.08	1.93	35.13
IIHR-01	7.452	5.250	385.909	39.2	727.83	2.07	41.67
IIHR-2202	6.235	6.092	619.145	53.46	1236.40	2.00	30.87
INDAM-2102	4.095	4.804	499.611	42.16	1058.40	1.53	41.27
INDAM-2103	4.641	4.483	471.429	35.88	812.17	1.33	31.33
INDAM-2103-1	6.655	7.899	580.272	45.12	1148.40	1.87	33.67
INDAM-2103-1-1	7.041	6.958	470.457	48.78	726.83	1.93	50.80
INDAM-2103-4	6.118	5.696	525.364	48.34	1139.80	1.60	32.80
INDAM-2103-6	5.253	3.975	509.329	40.98	1286.70	0.53	34.27
INDAM-2103-6-1	5.413	6.673	549.660	49.42	937.33	1.53	49.20
INDAM-2103-6-4	8.006	7.416	685.714	51.56	1352.70	2.00	33.10
Jawahar-99	7.208	6.822	540.914	42.8	1221.00	0.73	28.27
Kashi Hemant	7.695	7.800	518.076	58.74	1350.80	1.20	45.73
Kashi Sharad	2.652	3.604	604.082	37.36	1271.10	2.33	36.87
Kashi Vishesh	6.369	6.735	541.399	41.02	976.67	1.87	39.13
Kashi Amrit	4.087	5.250	533.139	34.4	1235.30	1.80	35.33
Kashi Anupam	7.729	5.955	710.982	51.72	1016.90	1.33	26.60
Kajla	3.995	4.272	433.042	35.42	749.08	1.27	41.27
Kalyanpur Type-1	5.086	3.183	706.122	47.96	488.00	1.67	30.13
Kashmiriya	4.666	3.208	623.032	47.52	733.83	0.80	40.47
LA-3772	4.255	6.525	555.005	47.88	805.50	1.40	32.33
LA-3957	8.224	5.114	640.525	50.26	1427.80	1.73	28.33
LA-3997	4.649	3.950	541.885	53.32	1137.80	1.07	32.33
M-1-4	3.894	4.161	697.376	41.34	845.42	2.47	32.53
M-3-2	8.920	4.916	509.815	41.36	1238.40	1.87	31.60
Mukthi	9.692	4.743	238.192	42.6	592.83	2.00	33.47
Money Maker	7.594	4.050	309.621	45.2	905.33	2.13	32.20
Monte Favet	6.596	7.874	702.235	43.28	510.50	1.53	34.07
N-2-2	5.144	4.941	747.425	46.56	1161.20	2.53	35.40
N-2-3	7.687	4.149	348.008	45.18	1098.60	0.80	32.33
Nandhi	7.510	4.050	483.090	47.6	998.58	0.87	36.13
NDT-1	8.794	3.926	582.702	48.04	943.58	1.27	35.60
NDT-8	7.259	3.950	304.762	40.48	775.75	0.87	43.53
NDT-4	3.265	3.084	900.000	39.26	730.50	1.53	40.33
NDTVR-60	5.891	7.453	459.767	46.82	1134.90	0.60	31.17
NDTVR-73	11.244	7.292	437.901	43.22	1103.50	1.60	28.73
NF37SB-8	7.267	3.851	314.966	45.7	799.08	1.27	32.33
Palam Pink	5.438	5.671	438.387	49.84	990.08	1.67	42.60
Pant T-3	5.195	4.520	143.440	38.44	762.25	1.67	34.87
Pant T-5	5.732	8.134	433.528	46.84	818.75	0.87	31.13
Parul	3.097	3.332	622.546	34.34	1061.70	1.13	29.60
Pb-Chhuhara	4.154	3.220	584.645	44.48	823.17	3.07	30.60
Pb.Upma	4.221	3.455	554.519	45.42	726.25	1.53	41.53
Persia Bed	5.472	4.161	404.859	47.26	648.83	2.00	24.33
PDT-3-1	7.913	6.760	596.793	56.32	608.33	3.53	28.20
PDVT-14	6.705	9.891	453.450	43.6	1064.90	1.33	33.13

Contd...

PKM-1	7.141	5.002	400.486	39.12	688.58	2.07	34.60
PS-1	6.940	5.040	405.345	35.56	454.08	2.07	34.40
Prestige	7.024	5.931	591.448	52.06	1137.60	1.80	30.40
Pusa Gaurav	4.532	4.458	620.603	47.7	1217.50	1.07	37.07
Pusa Ruby	5.614	4.309	513.217	49.66	671.50	0.93	31.07
Pusa-120	7.930	5.089	588.047	44.58	323.08	1.00	41.13
Punjab Barkha Bahar-2	3.575	3.084	641.497	56.56	1256.30	2.33	24.33
Pusa Hybrid-2	11.035	3.295	561.808	49.28	390.50	1.20	37.27
Roma	2.921	4.804	652.672	46.7	787.92	1.13	35.60
Sanjeevani	12.704	4.903	491.837	42.76	1189.80	1.60	40.60
Sankranti	3.122	4.520	229.446	44.9	905.50	1.67	36.73
Sel-18	2.870	2.824	408.746	52.42	883.50	1.67	36.33
Sioux	2.761	2.750	419.922	46.76	1094.00	1.60	33.40
Solan Gola	7.024	6.970	407.289	44.92	1185.60	1.07	32.87
Solan Vajr	7.049	3.257	501.069	45.02	692.83	1.80	35.67
Sun-Cherry	4.624	8.059	306.220	49.96	1090.20	1.60	25.47
Swarna Naveen	3.600	5.114	340.719	47.68	1105.70	2.13	39.00
Swarna Vaibhav	6.881	8.171	381.050	54.88	760.50	1.53	43.27
TLBR-6	5.002	5.572	553.547	48.16	1129.90	1.60	30.87
TLH-17	5.472	3.653	505.928	43.5	543.17	0.80	33.40
TLH-27	5.505	11.265	349.466	36.1	967.92	1.20	29.80
TLH-30	9.281	5.968	365.500	37.44	687.42	1.53	36.87
Tripura Local	8.131	6.426	417.007	59.38	935.50	1.20	31.60
Utkal Pragyan	7.930	7.292	696.404	52.26	1182.50	2.07	44.33
Utkal Raja	6.361	4.743	635.180	47.6	1348.40	2.27	34.60
VRT-32-1	5.547	4.817	507.872	47.1	995.25	1.47	40.80
VRT-101A	6.017	5.188	637.123	45.3	432.92	1.27	35.33
WIR-3957	6.839	3.666	720.700	46.22	1090.20	1.07	30.53
WIR-5032	6.562	7.156	511.759	41.98	1216.80	2.13	31.07
WIR-13706	5.564	3.455	413.605	60.76	1136.00	1.13	46.60
WIR-13708	6.797	7.020	266.375	45.26	907.50	2.07	53.47
97/384	8.224	4.322	543.343	50.04	818.92	0.93	31.27
97/753	5.983	6.413	679.883	53.32	1271.90	1.87	32.20
97/754 (Kewalo)	7.250	4.545	437.901	45.4	992.50	1.33	23.27
15 SB	7.662	6.030	428.183	51.34	1095.40	1.53	35.33
Rio Grande	6.655	4.854	202.235	48.56	1002.60	1.40	31.87
S.Lalima	8.425	4.743	300.389	50.98	691.67	1.73	40.80
Switzerland	11.714	6.550	480.661	47.34	797.08	2.13	36.27
Utkal Urvashi	5.698	5.609	826.628	50.42	561.00	1.40	31.60
WIR-13717	4.431	4.705	457.823	47.7	1164.90	1.60	35.13
Pallavi	7.603	5.361	559.378	42.88	705.00	3.13	32.40
Punjab Keshri	3.005	4.817	605.539	52.12	996.33	1.73	36.40
V. Pragyan	5.245	4.545	539.942	50.9	955.92	2.80	33.73
DMT1	3.886	3.171	511.273	47.78	598.08	2.07	28.20
DMT3	4.775	5.349	411.176	46.74	1142.50	1.87	35.00

Appendix X. *Bemisia tabaci* population (nymphs/ 3 leaves) at different days interval and per cent disease incidence in the tomato association mapping panel field evaluated during summer 2016-17 at COH, Bengaluru

Tomato accessions	No. of whitefly nymphs/ 3 leaves				PDI (%)
	30 DAT	45 DAT	60 DAT	Mean	
Ageta-32	41.20	33.00	23.60	32.60	58.33
Angoorlata	34.60	26.40	17.00	26.00	33.33
Arka Abha	42.00	35.80	24.00	33.93	25.00
Arka Alok	42.80	34.60	13.80	30.40	50.00
Arka Meghalli	28.60	20.20	12.00	20.27	41.67
Arka Vikas	40.80	32.60	27.80	33.73	66.67
Avinash-2-2-1	29.00	20.80	15.60	21.80	0.00
Azad T-2	31.20	27.20	23.20	27.20	0.00
Azad T-5	47.60	39.40	22.20	36.40	33.33
B-4-1	45.80	37.60	21.20	34.87	25.00
B-7-2	44.20	38.10	14.40	32.23	8.33
Bhillai	48.00	40.80	35.40	41.40	41.67
BL-1208	46.00	41.00	25.60	37.53	41.67
BTH-9 M	32.00	28.80	25.40	28.73	0.00
C-1-4	26.20	20.00	17.60	21.27	33.33
C-3-2	27.00	19.80	14.80	20.53	0.00
C-4-1	49.80	41.60	17.80	36.40	33.33
C-8-1	39.60	44.60	20.40	34.87	41.67
C-9-2	31.00	28.00	21.00	26.67	8.33
C-10-2	22.00	28.00	32.80	27.60	8.33
C-11-1	29.20	26.20	23.80	26.40	8.33
C-11-2	39.20	37.20	36.00	37.47	8.33
C-11-3	47.40	44.20	37.00	42.87	41.67
C-20-1	34.60	32.60	27.40	31.53	33.33
C-20-2	30.40	22.20	13.70	22.10	0.00
C-26-1	33.40	26.20	21.00	26.87	33.33
CHRT-4	39.20	35.00	31.60	35.27	25.00
CH-155	28.00	33.20	34.20	31.80	33.33
Co-3	25.20	27.40	32.60	28.40	33.33
CLN-2026	34.20	33.00	28.80	32.00	16.67
CLN-2116	29.60	27.10	24.60	27.10	8.33
CLN-1621	44.00	35.80	27.40	35.73	16.67
CLN-2366	40.40	31.20	26.20	32.60	50.00
D-1-1	39.20	34.40	27.20	33.60	58.33
D-2-2-1	34.80	31.60	22.00	29.47	0.00
D-3-2	31.00	25.80	19.80	25.53	0.00
D-5-1	32.00	25.80	22.00	26.60	0.00
DARL-66	37.20	33.00	26.80	32.33	16.67
Dhrubya	38.00	31.80	26.00	31.93	0.00
DT-10	24.20	32.40	28.80	28.47	0.00
DVRT-1	42.60	37.40	31.80	37.27	58.33
DVRT-2	39.60	34.40	29.80	34.60	41.67
E-4-3	32.00	23.80	17.00	24.27	0.00
EC-2791	36.40	39.60	29.20	35.07	16.67
EC-13904	36.40	28.20	12.00	25.53	8.33
EC-317-6-1	29.20	23.20	19.00	23.80	0.00
EC-273966	38.60	32.40	29.00	33.33	25.00
EC-381263	31.60	26.40	19.20	25.73	16.67
EC-381554	35.80	29.70	23.20	29.57	0.00
EC-501574	37.00	31.90	25.80	31.57	25.00
EC-501575	23.00	27.20	21.00	23.73	0.00

Contd...

EC-501576	42.00	37.80	29.80	36.53	16.67
EC-501577	48.40	40.20	30.20	39.60	33.33
EC-501580	43.80	35.60	21.60	33.67	8.33
EC-501582	39.60	33.40	24.00	32.33	16.67
EC-501583	35.20	29.00	25.80	30.00	33.33
EC-519730	28.80	33.00	28.30	30.03	8.33
EC-520046	30.60	26.40	22.20	26.40	0.00
EC-520059	29.20	24.00	28.60	27.27	0.00
EC-520061	47.20	45.00	40.40	44.20	58.33
EC-520071	42.20	34.00	35.20	37.13	16.67
EC-520074	33.20	28.00	33.00	31.40	50.00
EC-520075	37.40	32.20	23.40	31.00	58.33
EC-520078	39.60	36.80	35.00	37.13	33.33
EC-521039	29.00	34.20	35.20	32.80	16.67
EC-521056	32.80	26.60	23.20	27.53	41.67
EC-521078	31.00	24.80	17.40	24.40	16.67
EC-526139	37.00	31.80	28.60	32.47	33.33
EC-528372	32.00	26.80	22.40	27.07	25.00
EC-528374	35.80	31.60	25.40	30.93	50.00
EC-529080	35.00	24.80	29.00	29.60	0.00
EC-529083	31.40	35.60	27.20	31.40	33.33
EC-538138	30.20	26.00	23.00	26.40	16.67
EC-538155	28.60	26.40	14.20	23.07	33.33
EC-538380	32.40	26.20	21.20	26.60	0.00
EC-538404	39.40	34.20	31.60	35.07	8.33
EC-538405	34.60	30.40	24.00	29.67	0.00
EC-538408	32.00	36.20	26.40	31.53	16.67
EC-538419	43.00	37.20	38.80	39.67	33.33
EC-538423	43.00	34.80	29.40	35.73	33.33
EC-538439	33.00	27.80	21.40	27.40	0.00
EC-538440	35.40	30.20	26.60	30.73	16.67
EC-538441	43.40	35.20	30.20	36.27	0.00
EC-538455	31.60	25.40	19.00	25.33	0.00
EC-552141	41.40	37.20	31.20	36.60	0.00
EC-560340	38.20	34.00	30.60	34.27	33.33
EC-570028	38.20	34.00	26.20	32.80	66.67
EC-605694	43.20	39.40	29.60	37.40	8.33
EC-605695	37.40	32.20	25.00	31.53	0.00
EC-605696	39.00	32.80	25.00	32.27	0.00
EC-620362	29.40	22.20	30.80	27.47	0.00
EC-620366	28.60	23.40	18.60	23.53	0.00
EC-620370	39.60	35.40	29.80	34.93	0.00
EC-620373	41.00	37.80	36.00	38.27	8.33
EC-620374	33.20	37.40	31.60	34.07	41.67
EC-620375	40.00	35.80	26.40	34.07	16.67
EC-620383	34.60	29.40	24.40	29.47	16.67
EC-620386	41.20	33.00	21.80	32.00	25.00
EC-620398	37.60	32.40	28.40	32.80	58.33
EC-620401	28.60	36.80	34.80	33.40	25.00
EC-620403	31.40	25.20	19.60	25.40	0.00
EC-620406	37.10	31.10	31.00	33.07	66.67
EC-620409	31.80	29.60	35.20	32.20	58.33
EC-620410	37.40	45.60	52.60	45.20	41.67
EC-620411	48.60	44.40	32.60	41.87	33.33
EC-620413	50.00	43.80	37.20	43.67	33.33
EC-620419	29.20	39.40	49.40	39.33	50.00

Contd...

EC-620421	25.60	31.80	29.00	28.80	0.00
EC-620438	45.60	40.40	24.60	36.87	0.00
EC-620444	32.80	36.00	28.40	32.40	58.33
EC-620446	41.00	34.80	25.20	33.67	33.33
EC-620455	36.40	33.20	27.40	32.33	0.00
EC-620456	31.40	26.20	23.80	27.13	16.67
EC-620464	43.60	41.40	38.60	41.20	33.33
EC-620469	49.80	44.60	39.60	44.67	58.33
EC-620470	48.00	42.80	33.00	41.27	33.33
EC-620474	45.60	40.40	37.40	41.13	41.67
EC-620476	38.40	34.20	26.60	33.07	0.00
EC-620480	39.40	36.20	21.60	32.40	0.00
EC-620486	39.80	34.60	28.20	34.20	0.00
EC-620500	46.00	41.80	29.80	39.20	0.00
EC-620502	44.20	42.00	37.40	41.20	16.67
EC-620514	43.60	35.40	15.40	31.47	0.00
EC-620519	51.80	47.60	38.80	46.07	8.33
EC -620530	51.20	47.00	36.40	44.87	25.00
EC -620533	36.20	32.00	28.00	32.07	8.33
EC -620540	38.40	34.40	29.60	34.13	58.33
EC -620556	33.40	27.20	23.20	27.93	0.00
EC -620568	36.40	32.20	28.00	32.20	0.00
EC -620575	51.40	48.20	39.20	46.27	8.33
EC -620598	40.60	36.40	28.80	35.27	16.67
EC -625644	39.00	34.80	28.40	34.07	0.00
EC -625645	42.20	37.00	29.00	36.07	16.67
EC -625651	44.80	41.60	31.20	39.20	25.00
EC -625652	39.20	33.00	27.00	33.07	33.33
EC -625660	55.80	49.60	33.00	46.13	25.00
EC-6202041	46.60	51.80	41.20	46.53	16.67
F-5020	38.40	32.20	28.70	33.10	0.00
F-6022	53.00	47.80	35.20	45.33	16.67
F-6050-1	51.80	46.60	39.80	46.07	33.33
F-6059	39.00	34.80	33.00	35.60	0.00
F-7012	41.60	36.40	28.40	35.47	0.00
F-7025	37.80	32.60	26.20	32.20	16.67
F-7028	44.80	38.60	28.40	37.27	33.33
F-6009	49.60	40.40	23.60	37.87	0.00
FEB.-02	33.20	41.40	49.00	41.20	16.67
FEB.-04	29.80	24.60	30.20	28.20	0.00
FLA-7171	36.20	31.00	26.40	31.20	25.00
FLA-7421	46.00	40.80	25.60	37.47	0.00
Flora-dade	40.80	35.60	28.80	35.07	58.33
G-4-5	48.40	40.20	31.40	40.00	66.67
G-5-4	49.80	35.60	21.80	35.73	58.33
G-6-3	51.60	44.40	32.00	42.67	25.00
GT-1	49.00	42.80	39.00	43.60	41.67
GT-2	34.20	37.40	24.80	32.13	0.00
GT-3	36.00	30.80	34.20	33.67	41.67
H-24	19.80	28.00	24.40	24.07	0.00
H-88-78-2	27.20	25.00	33.60	28.60	8.33
H-88-78-3	48.40	40.20	35.00	41.20	50.00
H-88-78-4	34.60	30.40	33.00	32.67	33.33
H-88-78-5	41.20	49.40	51.40	47.33	66.67
Hawai	39.60	31.40	22.40	31.13	8.33
Hisar Anmol	28.00	21.80	34.40	28.10	0.00

Contd..

Hisar Arun (Sel-7)	31.20	35.40	28.00	31.53	41.67
Hisar Lalit	36.40	29.20	44.60	36.73	66.67
I-4-4	43.80	38.60	35.80	39.40	41.67
IC-373378	33.00	43.20	28.60	34.93	33.33
IC-427766	51.20	46.00	38.40	45.20	41.67
IC-447708	47.80	42.60	29.60	40.00	25.00
IC-469626	39.60	36.40	29.40	35.13	16.67
IIHR-01	47.60	42.40	35.00	41.67	33.33
IIHR-2202	35.60	29.40	27.60	30.87	25.00
INDAM-2102	49.00	42.80	32.00	41.27	16.67
INDAM-2103	38.40	33.20	22.40	31.33	41.67
INDAM-2103-1	40.40	33.20	27.40	33.67	8.33
INDAM-2103-1-1	38.60	51.80	62.00	50.80	33.33
INDAM-2103-4	31.80	25.60	41.00	32.80	0.00
INDAM-2103-6	37.00	32.80	33.00	34.27	0.00
INDAM-2103-6-1	55.00	48.80	43.80	49.20	41.67
INDAM-2103-6-4	39.80	31.60	27.90	33.10	41.67
Jawahar-99	32.60	28.40	23.80	28.27	16.67
Kashi Hemant	54.00	44.80	38.40	45.73	58.33
Kashi Sharad	37.40	41.60	31.60	36.87	25.00
Kashi Vishesh	43.60	35.40	38.40	39.13	50.00
Kashi Amrit	40.40	32.20	33.40	35.33	16.67
Kashi Anupam	28.80	19.60	31.40	26.60	0.00
Kajla	46.00	40.80	37.00	41.27	33.33
Kalyanpur Type-1	29.20	37.40	23.80	30.13	8.33
Kashmiriya	46.40	40.20	34.80	40.47	33.33
LA-3772	27.20	32.40	37.40	32.33	33.33
LA-3957	33.80	27.60	23.60	28.33	16.67
LA-3997	37.00	30.80	29.20	32.33	25.00
M-1-4	36.40	28.20	33.00	32.53	33.33
M-3-2	34.40	29.20	31.20	31.60	41.67
Mukthi	37.60	32.40	30.40	33.47	8.33
Money Maker	36.40	28.20	32.00	32.20	25.00
Monte Favet	41.60	33.40	27.20	34.07	8.33
N-2-2	43.60	35.40	27.20	35.40	16.67
N-2-3	32.20	27.00	37.80	32.33	58.33
Nandhi	45.60	37.40	25.40	36.13	8.33
NDT-1	31.00	37.20	38.60	35.60	16.67
NDT-8	62.20	50.00	18.40	43.53	25.00
NDT-4	43.80	37.60	39.60	40.33	41.67
NDTVR-60	33.00	27.80	32.70	31.17	33.33
NDTVR-73	33.60	25.40	27.20	28.73	0.00
NF37SB-8	25.60	33.80	37.60	32.33	0.00
Palam Pink	47.40	39.20	41.20	42.60	0.00
Pant T-3	40.80	35.60	28.20	34.87	50.00
Pant T-5	34.00	28.80	30.60	31.13	16.67
Parul	26.20	34.40	28.20	29.60	8.33
Pb-Chhuhara	39.60	30.40	21.80	30.60	8.33
Pb.Upma	46.40	41.20	37.00	41.53	16.67
Persia Bed	30.60	22.40	20.00	24.33	0.00
PDT-3-1	27.00	21.80	35.80	28.20	0.00
PDVT-14	41.80	34.60	23.00	33.13	0.00
PKM-1	30.80	42.00	31.00	34.60	16.67
PS-1	28.00	42.20	33.00	34.40	8.33
Prestige	35.80	29.60	25.80	30.40	16.67
Pusa Gaurav	40.40	36.20	34.60	37.07	33.33

Contd...

Pusa Ruby	39.40	31.20	22.60	31.07	0.00
Pusa-120	29.60	41.80	52.00	41.13	58.33
Punjab Barkha Bahar-2	31.40	23.20	18.40	24.33	0.00
Pusa Hybrid-2	42.40	39.20	30.20	37.27	8.33
Roma	37.60	33.40	35.80	35.60	41.67
Sanjeevani	40.80	44.00	37.00	40.60	33.33
Sankranti	31.40	37.60	41.20	36.73	33.33
Sel-18	34.00	38.20	36.80	36.33	66.67
Sioux	38.40	29.20	32.60	33.40	50.00
Solan Gola	39.20	33.00	26.40	32.87	0.00
Solan Vajr	32.60	36.80	37.60	35.67	41.67
Sun-Cherry	29.80	24.60	22.00	25.47	0.00
Swarna Naveen	36.60	42.80	37.60	39.00	25.00
Swarna Vaibhav	50.60	45.40	33.80	43.27	25.00
TLBR-6	36.40	31.20	25.00	30.87	8.33
TLH-17	28.60	32.80	38.80	33.40	16.67
TLH-27	29.60	33.80	26.00	29.80	25.00
TLH-30	34.60	40.80	35.20	36.87	58.67
Tripura Local	35.80	31.60	27.40	31.60	41.67
Utkal Pragyan	48.20	43.00	41.80	44.33	66.67
Utkal Raja	43.80	35.60	24.40	34.60	25.00
VRT-32-1	47.80	41.60	33.00	40.80	33.33
VRT-101A	39.80	35.60	30.60	35.33	25.00
WIR-3957	38.80	30.60	22.20	30.53	16.67
WIR-5032	36.40	31.20	25.60	31.07	0.00
WIR-13706	53.00	46.80	40.00	46.60	16.67
WIR-13708	59.20	53.00	48.20	53.47	41.67
97/384	36.80	29.60	27.40	31.27	50.00
97/753	36.60	31.40	28.60	32.20	16.67
97/754 (Kewalo)	30.60	21.40	17.80	23.27	0.00
15 SB	41.20	35.00	29.80	35.33	8.33
Rio Grande	37.80	31.60	26.20	31.87	16.67
S.Lalima	48.80	42.60	31.00	40.80	41.67
Switzerland	38.60	34.40	35.80	36.27	33.33
Utkal Urvashi	36.60	31.40	26.80	31.60	16.67
WIR-13717	43.60	37.40	24.40	35.13	25.00
Pallavi	37.20	32.00	28.00	32.40	0.00
Punjab Keshri	43.40	36.20	29.60	36.40	0.00
V. Pragyan	38.80	33.60	28.80	33.73	0.00
DMT1	34.40	28.20	22.00	28.20	0.00
DMT3	42.20	35.00	27.80	35.00	16.67
MIN	19.80	19.60	12.00	20.13	0.00
MAX	62.20	53.00	52.60	54.60	66.67
MEAN	38.27	34.31	29.20	34.35	22.50
Std dev	7.27	6.80	7.52	5.94	19.56

DAT- Days After Transplanting;

PDI- Per cent Disease Incidence

Appendix XI. Categorization of tomato association mapping panel for reaction individual accessions to the ToLCV incidence at 60 DAT under field conditions during summer 2016-17 at COH, Bengaluru

Sl. No.	Infection category	Accessions
1	Immune (I)	Avinash-2-2-1, Azad T-2, BTH-9 M, C-3-2, C-20-2, D-2-2-1, D-3-2, D-5-1, Dhrubya, DT-10, E-4-3, EC-317-6-1, EC-381554, EC-501575, EC-520046, EC-520059, EC -529080, EC-538380, EC-538405, EC-538439, EC-538441, EC-538455, EC-552141, EC-605695, EC-605696, EC-620362, EC-620366, EC-620370, EC-620403, EC-620421, EC-620438, EC-620455, EC-620476, EC-620480, EC-620486, EC-620500, EC-620514, EC -620556, EC -620568, EC -625644, F-5020, F-6059, F-7012, F-6009, FEB.-04, FLA-7421, GT-2, H-24, Hisar Anmol, INDAM-2103-4, INDAM-2103-6, Kashi Anupam, NDTV-73, NF37SB-8, Palam Pink, Persia Bed, PDT-3-1, PDVT-14, Pusa Ruby, Punjab Barkha Bahar-2, Solan Gola, Sun-Cherry, WIR-5032, 97/754 (Kewalo), Pallavi, Punjab Keshri, V. Pragyan, DMT1 (68) .
2	Moderately resistant (MR)	B-7-2, C-9-2, C-10-2, C-11-1, C-11-2, CLN-2116, EC-13904, EC-501580, EC-519730, EC-538404, EC-605694, EC-620373, EC-620519, EC -620533, EC -620575, EC -625645, H-88-78-2, Hawaii, INDAM-2103-1, Kalyanpur Type-1, Mukthi, Monte Favet, Nandhi, Parul, Pb-Chhuhara, PS-1, Pusa Hybrid-2, TLBR-6, 15 SB (29) .
3	Moderately susceptible (MS)	Arka Abha, B-4-1, CHRT-4, CLN-2026, CLN-1621, DARL-66, EC-2791, EC-273966, EC-381263, EC-501574, EC-501576, EC-501582, EC-520071, EC -521039, EC -521078, EC-528372, EC-538138, EC-538408, EC-538440, EC-620375, EC-620383, EC-620386, EC-620401, EC-620456, EC-620502, EC -620530, EC -620598, EC -625651, EC -625660, EC-6202041, F-6022, F-7025, FEB.-02, FLA-7171, G-5-4 G-6-3, IC-447708, IC-469626, IIHR-2202, INDAM-2102, Jawahar-99, Kashi Sharad, Kashi Amrit, LA-3957, LA-3997, Money Maker, N-2-2, NDT-1, NDT-8, Pant T-5, Pb.Upma, PKM-1, Prestige, Swarna Naveen, Swarna Vaibhav, TLH-17, TLH-27, Utkal Raja, VRT-101A, WIR-3957, WIR-13706, 97/753, Rio Grande, Utkal Urvashi, WIR-13717, DMT3 (66) .
4	Susceptible (S)	Angoorlata, Arka Alok, Arka Meghalli, Azad T-5, Bhillai, BL-1208, C-1-4, C-4-1, C-8-1, C-11-3, C-20-1, C-26-1, CH-155, Co-3, CLN-2366, DVRT-2, EC-501577, EC-501583, EC -520078, EC-521056, EC-526139, EC-528374, EC -529083, EC -538155, EC-538419, EC-538423, EC-560340, EC-620374, EC-620410, EC-620411, EC-620413, EC-620419, EC-620446, EC-620464, EC-620470, EC-620474, EC -625652, F-6050-1, F-7028, GT-1, GT-3, H-88-78-3, H-88-78-4, Hisar Arun (Sel-7), I-4-4, IC-373378, IC-427766, IIHR-01, INDAM-2103, INDAM-2103-1-1, INDAM-2103-6-1, INDAM-2103-6-4, Kashi Vishesh, Kajla Kashmiriya, LA-3772, M-1-4 M-3-2, NDT-4, NDTV-60, Pant T-3, Pusa Gaurav, Roma, Sanjeevani, Sankranti, Sioux, Solan Vajr, Tripura Local, VRT-32-1, WIR-13708, 97/384, S. Lalima, Switzerland (73) .
5	Highly susceptible (HS)	Ageta-32, Arka Vikas, D-1-1, DVRT-1, EC-520061, EC-520074, EC-520075, EC-570028, EC-620398, EC-620406, EC-620409, EC-620444, EC-620469, EC -620540, Flora-dade, G-4-5, H-88-78-5, Hisar Lalit, Kashi Hemant, N-2-3, Pusa-120, Sel-18, TLH-30, Utkal Pragyan (24) .

Appendix XII. Different types of trichomes identified in 260 tomato accessions and their effect on whitefly population analysed during field evaluation (*rabi* and summer seasons of 2016-17)

Tomato accessions	I	II	III	IV	V	VII
Ageta-32	+		+		+	+
Angoorlata			+		+	+
Arka Abha			+		+	
Arka Alok			+		+	+
Arka Meghalli	+	+	+	+	+	+
Arka Vikas			+		+	
Avinash-2-2-1			+		+	+
Azad T-2	+		+		+	+
Azad T-5			+	+	+	
B-4-1			+		+	+
B-7-2		+	+	+	+	+
Bhillai			+		+	
BL-1208			+		+	
BTH-9 M			+		+	+
C-1-4	+	+	+		+	+
C-3-2	+	+	+		+	+
C-4-1		+	+		+	+
C-8-1			+		+	+
C-9-2			+		+	+
C-10-2			+		+	+
C-11-1	+	+	+	+	+	+
C-11-2					+	+
C-11-3			+		+	
C-20-1			+		+	+
C-20-2	+	+		+	+	+
C-26-1	+		+		+	+
CHRT-4	+		+	+	+	+
CH-155			+		+	+
CO-3	+		+		+	+
CLN-2026			+		+	+
CLN-2116			+	+	+	+
CLN-1621			+		+	
CLN-2366			+		+	+
D-1-1			+		+	+
D-2-2-1	+		+		+	+
D-3-2	+		+		+	+
D-5-1			+	+	+	+
DARL-66			+		+	+
Dhrubya	+		+		+	+
DT-10	+	+	+		+	+
DVRT-1			+		+	+
DVRT-2			+		+	
E-4-3	+		+	+	+	
EC-2791	+		+		+	
EC-13904	+		+		+	+
EC-317-6-1			+	+	+	
EC-273966			+	+	+	
EC-381263	+		+	+	+	
EC-381554			+	+	+	+
EC-501574			+		+	+
EC-501575	+	+	+		+	+
EC-501576			+		+	+
EC-501577			+		+	+
EC-501580			+		+	+

Contd...

EC-501582			+		+	+
EC-501583			+	+	+	+
EC-519730	+		+		+	+
EC-520046		+	+		+	+
EC-520059	+		+	+	+	+
EC-520061			+		+	+
EC-520071			+		+	+
EC-520074			+		+	+
EC-520075			+		+	+
EC -520078			+		+	+
EC -521039			+		+	+
EC -521056			+		+	+
EC -521078	+	+	+		+	+
EC -526139			+		+	+
EC-528372	+	+	+		+	+
EC-528374	+		+	+	+	+
EC -529080	+		+		+	+
EC -529083			+		+	+
EC-538138			+		+	+
EC -538155			+		+	+
EC-538380	+	+	+		+	+
EC-538404	+		+		+	+
EC-538405		+	+		+	+
EC-538408	+		+	+	+	+
EC-538419			+		+	+
EC-538423			+		+	+
EC-538439	+		+		+	+
EC-538440			+		+	+
EC-538441			+		+	+
EC-538455			+	+	+	+
EC-552141	+		+		+	+
EC-560340			+		+	+
EC-570028	+		+		+	+
EC-605694			+		+	+
EC-605695			+		+	+
EC-605696			+		+	+
EC-620362	+		+	+	+	+
EC-620366			+	+	+	+
EC-620370			+		+	+
EC-620373			+		+	+
EC-620374			+		+	+
EC-620375			+		+	+
EC-620383	+		+		+	+
EC-620386			+		+	+
EC-620398			+		+	+
EC-620401	+		+		+	+
EC-620403	+	+	+		+	+
EC-620406			+		+	+
EC-620409	+		+	+	+	+
EC-620410			+		+	+
EC-620411			+		+	+
EC-620413			+		+	+
EC-620419			+		+	+
EC-620421			+	+	+	+
EC-620438			+		+	+
EC-620444	+		+		+	+
EC-620446	+		+		+	+
EC-620455			+		+	+
EC-620456	+	+	+		+	+

Contd...

EC-620464			+		+	+
EC-620469			+		+	+
EC-620470	+		+		+	
EC-620474			+		+	+
EC-620476			+		+	+
EC-620480			+		+	+
EC-620486	+		+	+	+	
EC-620500			+	+	+	+
EC-620502	+	+	+	+	+	+
EC-620514			+		+	+
EC-620519	+	+	+		+	+
EC -620530	+		+		+	+
EC -620533			+		+	+
EC -620540	+		+	+	+	+
EC -620556	+		+	+	+	+
EC -620568	+		+		+	+
EC -620575			+		+	+
EC -620598			+		+	+
EC -625644		+	+		+	+
EC -625645			+		+	+
EC -625651			+		+	+
EC -625652	+		+		+	+
EC -625660			+		+	+
EC-6202041			+		+	+
F-5020			+		+	+
F-6022			+		+	
F-6050-1	+		+		+	
F-6059			+		+	+
F-7012			+		+	+
F-7025			+		+	
F-7028	+		+		+	
F-6009			+		+	+
FEB.-02			+		+	
FEB.-04	+	+	+		+	+
FLA-7171	+		+		+	+
FLA-7421			+		+	+
Flora-dade			+		+	+
G-4-5	+		+		+	+
G-5-4			+		+	+
G-6-3			+		+	+
GT-1			+		+	+
GT-2	+		+		+	+
GT-3			+		+	+
H-88-78-1	+	+	+	+	+	+
H-88-78-2	+	+	+		+	+
H-88-78-3			+		+	+
H-88-78-4			+		+	+
H-88-78-5			+		+	+
Hawai	+		+	+	+	+
Hisar Anmol	+	+	+	+	+	+
Hisar Arun (Sel-7)	+	+	+		+	+
Hisar Lalit			+		+	+
I-4-4			+		+	+
IC-373378	+		+		+	+
IC-427766			+		+	+
IC-447708	+		+		+	+
IC-469626	+		+		+	+
IIHR-01			+		+	+
IIHR-2202	+	+	+		+	+

Contd...

INDAM-2102			+		+	+
INDAM-2103	+		+		+	+
INDAM-2103-1	+		+		+	+
INDAM-2103-1-1			+		+	+
INDAM-2103-4	+	+	+		+	+
INDAM-2103-6			+		+	+
INDAM-2103-6-1	+		+		+	
INDAM-2103-6-4		+	+		+	+
Jawahar-99	+	+	+		+	+
Kashi Hemant	+		+		+	+
Kashi Sharad	+	+	+		+	+
Kashi Vishesh	+		+		+	+
Kashi Amrit	+		+	+	+	+
Kashi Anu+am	+	+	+	+	+	+
Kajla			+		+	+
Kalyanpur Type-1	+	+	+		+	+
Kashmiriya			+		+	+
LA-3772			+		+	+
LA-3957		+	+	+	+	+
LA-3997	+		+		+	+
M-1-4	+		+		+	+
M-3-2			+		+	+
Mukthi			+		+	+
Money Maker	+		+		+	+
Monte Favet			+		+	+
N-2-2			+	+	+	+
N-2-3			+	+	+	+
Nandhi			+		+	+
NDT-1			+		+	+
NDT-8			+		+	
NDT-4			+		+	
NDTVR-60	+		+		+	+
NDTVR-73	+		+	+	+	
NF37SB-8			+		+	+
Palam Pink			+		+	+
Pant T-3			+		+	+
Pant T-5	+		+		+	+
Parul			+		+	+
Pb-Chhuhara			+	+	+	
Pb.U+ma			+		+	
Persia Bed	+		+	+	+	+
PDT-3-1	+	+	+		+	+
PDVT-14			+		+	+
PKM-1			+		+	+
PS-1			+		+	+
Prestige	+	+	+		+	+
Pusa Gaurav	+		+	+	+	+
Pusa Ruby	+		+		+	+
Pusa-120			+		+	+
Punjab Barkha Bahar-2	+	+	+	+	+	+
Pusa Hybrid-2	+		+		+	+
Roma	+		+	+	+	+
Sanjeevani	+		+		+	
Sankranti	+		+		+	
Sel-18			+		+	+
Sioux			+		+	+
Solan Gola	+		+	+	+	
Solan Vajr			+		+	+
Sun-Cherry	+		+	+	+	+

Contd...

Swarna Naveen			+		+	
Swarna Vaibhav			+		+	+
TLBR-6		+	+	+	+	+
TLH-17			+		+	+
TLH-27	+		+	+	+	+
TLH-30			+		+	+
Tripura Local	+	+	+		+	+
Utkal pragyan			+		+	+
Utkal Raja	+	+	+		+	+
VRT-32-1			+		+	+
VRT-101A		+	+		+	+
WIR-3957	+		+		+	+
WIR-5032		+	+		+	+
WIR-13706	+		+		+	+
WIR-13708			+		+	
97/384		+	+		+	+
97/753			+		+	+
97/754 (Kewalo)	+	+	+	+	+	+
15 SB			+		+	+
Rio Grande	+		+	+	+	+
S.Lalima			+		+	+
Switzerland			+	+	+	+
Utkal Urvashi			+		+	+
WIR-13717		+	+		+	+
Pallavi	+		+		+	+
Punjab Keshri			+		+	+
V. Pragyan			+		+	+
DMT1	+		+	+	+	+
DMT3			+		+	+

+ : Presence of trichome type

Appendix XIII. Effect of trichome type on *Bemisia tabaci* population in tomato accessions during *rabi* and summer season 2016-17 at COH, Bengaluru.

Sl. No.	Trichome type	Individuals	Whitefly population during Rabi season	Whitefly population during summer season		
				45 DAT	60 DAT	Mean
1	Type 1	Ageta-32, Arka Meghalli, Azad T-2, C-1-4, C-3-2, C-11-1, C-20-2, C-26-1, CHRT-4, CO-3, D-2-2-1, D-3-2, Dhrubya, DT-10, E-4-3, EC-2791, EC-13904, EC-381263, EC-501575, EC-519730, EC-520059, EC -521078, EC-528372, EC-528374, EC -529080, EC-538380, EC-538404, EC-538408, EC-538439, EC-552141, EC-570028, EC-620362, EC-620383, EC-620401, EC-620403, EC-620409, EC-620444, EC-620446, EC-620456, EC-620470, EC-620486, EC-620502, EC-620519, EC -620530, EC -620540, EC -620556, EC -620568, EC -625652, F-6050-1, F-7028, FEB.-04, FLA-7171, G-4-5, GT-2 H-88-78-1, H-88-78-2, Hawaii, Hisar Anmol, Hisar Arun (Sel-7), IC-373378, IC-447708, IC-469626, IIHR-2202, INDAM-2103, INDAM-2103-1, INDAM-2103-4, INDAM-2103-6-1, Jawahar-99, Kashi Hemant, Kashi Sharad, Kashi Vishesh, Kashi Amrit, Kashi Anupam, Kalyanpur Type-1, LA-3997, M-1-4, Money Maker, NDTVR-60, NDTVR-73, Pant T-5, Persia Bed, PDT-3-1, Prestige, Pusa Gaurav, Pusa Ruby, Punjab Barkha Bahar-2, Pusa Hybrid-2, Roma, Sanjeevani, Sankranti, Solan Gola, Sun-Cherry, TLH-27, Tripura Local, Utkal Raja, WIR-3957, WIR-13706, 97/754 (Kewalo), Rio Grande, Pallavi, DMT1 (101).	1.63	31.63	27.57	31.64
2	Type II	Arka Meghalli, B-7-2, C-1-4, C-3-2, C-4-1, C-11-1, C-20-2, DT-10, EC-501575, EC-520046, EC -521078, EC-528372, EC-538380, EC-538405, EC-620403, EC-620456, EC-620502, EC-620519, EC -625644, FEB.-04, H-88-78-1, H-88-78-2, Hisar Anmol, Hisar Arun (Sel-7), IIHR-2202, INDAM-2103-4, INDAM-2103-6-4, Jawahar-99, Kashi Sharad, Kashi Anupam, Kalyanpur Type-1, LA-3957, PDT-3-1, Prestige, Punjab Barkha Bahar-2, TLBR-6, Tripura Local, Utkal Raja, VRT-101A, WIR-5032, 97/384, 97/754 (Kewalo) WIR-13717 (43).	1.58	34.33	29.28	33.93
3	Type III	Ageta-32, Angoorlata, Arka Abha, Arka Alok, Arka Meghalli, Arka Vikas, Avinash-2-2-1, Azad T-2,, Azad T-5, B-4-1, B-7-2, Bhillai, BL-1208, BTH-9 M, C-1-4, C-3-2, C-4-1, C-8-1, C-9-2, C-10-2, C-11-1, C-11-3, C-20-1, C-26-1, CHRT-4, CH-155, CO-3, CLN-2026, CLN-2116, CLN-1621, CLN-2366, D-1-1, D-2-2-1, D-3-2, D-5-1, DARL-66, Dhrubya, DT-10, DVRT-1, DVRT-2, E-4-3, EC-2791, EC-13904, EC-317-6-1, EC-273966, EC-381263, EC-381554, EC-501574, EC-501575, EC-501576, EC-501577, EC-501580, EC-501582, EC-501583, EC-519730, EC-520046, EC-520059, EC-520061, EC-	1.58	34.36	29.31	33.96

		520071, EC-520074, EC-520075, EC -520078, EC -521039, EC -521056, EC -521078, EC -526139, EC-528372, EC-528374, EC -529080, EC -529083, EC-538138, EC -538155, EC-538380, EC-538404, EC-538405, EC-538408, EC-538419, EC-538423, EC-538439, EC-538440, EC-538441, EC-538455, EC-552141, EC-560340, EC-570028, EC-605694, EC-605695, EC-605696, EC-620362, EC-620366, EC-620370, EC-620373, EC-620374, EC-620375, EC-620383, EC-620386, EC-620398, EC-620401, EC-620403, EC-620406, EC-620409, EC-620410, EC-620411, EC-620413, EC-620419, EC-620421, EC-620438, EC-620444, EC-620446, EC-620455, EC-620456, EC-620464, EC-620469, EC-620470, EC-620474, EC-620476, EC-620480, EC-620486, EC-620500, EC-620502, EC-620514, EC-620519, EC -620530, EC -620533, EC -620540, EC -620556, EC -620568, EC -620575, EC -620598, EC -625644, EC -625645, EC -625651, EC -625652, EC -625660, EC-6202041, F-5020, F-6022, F-6050-1, F-6059, F-7012, F-7025, F-7028, F-6009, FEB.-02, FEB.-04, FLA-7171, FLA-7421, Flora-dade, G-4-5, G-5-4, G-6-3, GT-1, GT-2, GT-3, H-88-78-1, H-88-78-2, H-88-78-3, H-88-78-4, H-88-78-5, Hawaii, Hisar Anmol, Hisar Arun (Sel-7), Hisar Lalit, I-4-4, IC-373378, IC-427766, IC-447708, IC-469626, IIHR-01, IIHR-2202, INDAM-2102, INDAM-2103, INDAM-2103-1, INDAM-2103-1-1, INDAM-2103-4, INDAM-2103-6, INDAM-2103-6-1, INDAM-2103-6-4, Jawahar-99, Kashi Hemant, Kashi Sharad, Kashi Vishesh, Kashi Amrit, Kashi Anu+am, Kajla, Kalyanpur Type-1, Kashmiriya, LA-3772, LA-3957, LA-3997, M-1-4, M-3-2, Mukthi, Money Maker, Monte Favet, N-2-2, N-2-3, Nandhi, NDT-1, NDT-8, NDT-4, NDTVR-60, NDTVR-73, NF37SB-8, Palam Pink, Pant T-3, Pant T-5, Parul, Pb-Chhuhara, Pb.Upma, Persia Bed, PDT-3-1, PDVT-14, PKM-1, PS-1, Prestige, Pusa Gaurav, Pusa Ruby, Pusa-120, Punjab Barkha Bahar-2, Pusa Hybrid-2, Roma, Sanjeevani, Sankranti., Sel-18, Sioux, Solan Gola, Solan Vajr, Sun-Cherry, Swarna Naveen, Swarna Vaibhav, TLBR-6, TLH-17, TLH-27, TLH-30, Tripura Local, Utkal prgyan, Utkal Raja, VRT-32-1, VRT-101A, WIR-3957, WIR-5032, WIR-13706, WIR-13708, 97/384, 97/753, 97/754 (Kewalo), 15 SB, Rio Grande, S. Lalima, Switzerland, Utkal Urvashi, WIR-13717, Pallavi, Punjab Keshri, V. Pragyana, DMT1, DMT3 (258).				
4	Type IV	Arka Meghalli, Azad T-5, B-7-2, C-11-1, C-20-2, CHRT-4, CLN-2116, D-5-1, E-4-3, EC-317-6-1, EC-273966, EC-381263, EC-381554, EC-501583, EC-520059, EC-528374, EC-538408, EC-538455, EC-620362, EC-620366, EC-620409, EC-620421, EC-620486, EC-620500, EC-620502, EC -620540, EC -620556, H-88-78-1, Hawaii, Hisar Anmol, Kashi Amrit, Kashi Anupam, LA-3957, N-2-2, N-2-3, NDTVR-73, Pb-Chhuhara, Persia Bed, Pusa Gaurav, Punjab Barkha Bahar-2, Roma, Solan Gola, Solan Vajr, Sun-Cherry, TLBR-6, TLH-27, 97/754 (Kewalo), Rio Grande, Switzerland, DMT1 (50).	1.65	29.43	25.80	29.86
5	Type V	Ageta-32, Angoorlata, Arka Abha, Arka Alok, Arka Meghalli, Arka Vikas, Avinash-2-2-1, Azad T-2, Azad T-5, B-4-1, B-7-2, Bhillai, BL-1208, BTH-9, M C-1-4, C-3-2, C-4-1, C-8-1, C-9-2, C-10-2, C-11-1, C-11-2, C-11-3, C-20-1, C-20-2, C-26-1, CHRT-4, CH-155, CO-3, CLN-2026, CLN-2116, CLN-1621, CLN-2366, D-1-1, D-2-2-1, D-3-2, D-5-1, DARL-66, Dhruvya, DT-10, DVRT-1, DVRT-2, E-4-3, EC-2791, EC-13904, EC-317-6-1, EC-273966, EC-381263, EC-381554, EC-501574, EC-501575,	1.58	33.83	29.04	33.49

		EC-501576, EC-501577, EC-501580, EC-501582, EC-501583, EC-519730, EC-520046, EC-520059, EC-520061, EC-520071, EC-520074, EC-520075, EC -520078, EC -521039, EC -521056, EC -521078, EC -526139, EC-528372, EC-528374, EC -529080, EC -529083, EC-538138, EC-538155, EC-538380, EC-538404, EC-538405, EC-538408, EC-538419, EC-538423, EC-538439, EC-538440, EC-538441, EC-538455, EC-552141, EC-560340 EC-570028, EC-605694, EC-605695, EC-605696, EC-620362, EC-620366, EC-620370, EC-620373, EC-620374, EC-620375, EC-620383, EC-620386, EC-620398, EC-620401, EC-620403, EC-620406, EC-620409, EC-620410, EC-620411, EC-620413, EC-620419, EC-620421, EC-620438, EC-620444, EC-620446, EC-620455, EC-620456, EC-620464, EC-620469, EC-620470, EC-620474, EC-620476, EC-620480, EC-620486, EC-620500, EC-620502, EC-620514, EC-620519, EC -620530, EC -620533, EC -620540, EC -620556, EC -620568, EC -620575, EC -620598, EC -625644, EC -625645, EC -625651, EC -625652, EC -625660, EC-6202041, F-5020, F-6022 , F-6050-1, F-6059, F-7012, F-7025, F-7028, F-6009, FEB.-02, FEB.-04, FLA-7171, FLA-7421, Flora-dade, G-4-5, G-5-4, G-6-3, GT-1, GT-2, GT-3, H-88-78-1, H-88-78-2, H-88-78-3, H-88-78-4, H-88-78-5, Hawaii, Hisar Anmol, Hisar Arun (Sel-7), Hisar Lalit, I-4-4, IC-373378, IC-427766, IC-447708, IC-469626, IIHR-01, IIHR-2202, INDAM-2102, INDAM-2103, INDAM-2103-1, INDAM-2103-1-1, INDAM-2103-4 , INDAM-2103-6, INDAM-2103-6-1, INDAM-2103-6-4, Jawahar-99, Kashi Hemant, Kashi Sharad, Kashi Vishesh, Kashi Amrit, Kashi Anupam, Kajla, Kalyanpur Type-1, Kashmiriya, LA-3772, LA-3957, LA-3997, M-1-4, M-3-2, Mukthi, Money Maker, Monte Favet, N-2-2, N-2-3, Nandhi, NDT-1, NDT-8, NDT-4, NDTV-60, NDTV-73, NF37SB-8, Palam Pink, Pant T-3, Pant T-5, Parul, Pb-Chhuhara, Pb.Upma, Persia Bed, PDT-3-1, PDVT-14, PKM-1, PS-1, Prestige, Pusa Gaurav, Pusa Ruby, Pusa-120, Punjab Barkha Bahar-2, Pusa Hybrid-2, Roma, Sanjeevani, Sankranti, Sel-18, Sioux, Solan Gola, Solan Vajr, Sun-Cherry, Swarna Naveen, Swarna Vaibhav, TLBR-6, TLH-17, TLH-27, TLH-30, Tripura Local, Utkal pragyan, Utkal Raja, VRT-32-1, VRT-101A, WIR-3957, WIR-5032, WIR-13706, WIR-13708, 97/384, 97/753, 97/754 (Kewalo), 15 SB, Rio Grande, S.Lalima, Switzerland, Utkal Urvashi , WIR-13717, Pallavi, Punjab Keshri, V. Pragyan, DMT1, DMT3 (260).				
6	Type VII	Ageta-32, Angoorlata, Arka Alok, Arka Meghalli, Avinash-2-2-1, Azad T-2, B-4-1, B-7-2, BTH-9 M, C-1-4, C-3-2, C-4-1, C-8-1, C-9-2, C-10-2, C-11-1, C-11-2, C-20-1, C-20-2, C-26-1 CHRT-4, CH-155, CO-3, CLN-2026, CLN-2116, CLN-2366, D-1-1, D-2-2-1, D-3-2, D-5-1, DARL-66, Dhruvya, DT-10, DVRT-1, EC-13904, EC-381554, EC-501574, EC-501575, EC-501576, EC-501577, EC-501580, EC-501582, EC-501583, EC-519730, EC-520046, EC-520059, EC-520061, EC-520071, EC-520074, EC-520075, EC -520078, EC -521039, EC -521056, EC -521078, EC -526139, EC-528372, EC-528374, EC -529080, EC -529083, EC-538138, EC -538155, EC-538380, EC-538404, EC-538405, EC-538408, EC-538419, EC-538423, EC-538439, EC-538440, EC-538441, EC-538455, EC-552141, EC-560340, EC-570028, EC-605694, EC-605695, EC-605696, EC-620362, EC-620366, EC-620370, EC-620373, EC-620374, EC-620375, EC-620383, EC-620386, EC-620398, EC-620401, EC-620403, EC-620406,	1.64	29.36	25.19	29.37

EC-620409, EC-620410, EC-620411, EC-620413, EC-620419, EC-620421, EC-620438, EC-620444, EC-620446, EC-620455, EC-620456, EC-620464, EC-620469, EC-620474, EC-620476, EC-620480, EC-620500, EC-620502, EC-620514, EC-620519, EC -620530, EC -620533, EC -620540, EC -620556, EC -620568, EC -620575, EC -620598, EC -625644, EC -625645, EC -625651, EC -625652, EC -625660, EC-6202041, F-5020, F-6059, F-7012, F-6009, FEB.-04, FLA-7171, FLA-7421, Flora-dade, G-4-5, G-5-4, G-6-3, GT-1, GT-2, GT-3, H-88-78-1, H-88-78-2, H-88-78-3, H-88-78-4, H-88-78-5, Hawai, Hisar Anmol, Hisar Arun (Sel-7), Hisar Lalit, I-4-4, IC-373378, IC-427766, IC-447708, IC-469626, IIHR-01, IIHR-2202, INDAM-2102, INDAM-2103, INDAM-2103-1, INDAM-2103-1-1, INDAM-2103-4, INDAM-2103-6, INDAM-2103-6-4, Jawahar-99, Kashi Hemant, Kashi Sharad, Kashi Vishesh, Kashi Amrit, Kashi Anupam, Kajla, Kalyanpur Type-1, Kashmiriya, LA-3772, LA-3957, LA-3997, M-1-4, M-3-2, Mukthi, Money Maker, Monte Favet, N-2-2, N-2-3, Nandhi, NDT-1, NDTVR-60, NF37SB-8, Palam Pink, Pant T-3, Pant T-5, Parul, Persia Bed, PDT-3-1, PDVT-14, PKM-1, PS-1, Prestige, Pusa Gaurav, Pusa Ruby, Pusa-120, Punjab Barkha Bahar-2, Pusa Hybrid-2, Roma, Sel-18, Sioux, Solan Vajr, Sun-Cherry, Swarna Vaibhav, TLBR-6, TLH-17, TLH-27, TLH-30, Tripura Local, Utkal pragyan, Utkal Raja, VRT-32-1, VRT-101A, WIR-3957, WIR-5032, WIR-13706, 97/384, 97/753, 97/754 (Kewalo), 15 SB, Rio Grande, S. Lalima, Switzerland, Utkal Urvashi, WIR-13717, Pallavi, Punjab Keshri, V. Pragyan, DMT1, DMT3 (229).

SEm				
CD @ 5 %	NS	0.31	0.36	0.25
		0.98	1.15	0.80

DAT: Days After Treatment,

NS: Non Significant

Appendix XIV. Tomato association mapping panel arranged in different groups for diversity analysis

Sl. No.	Group	Tomato accessions
1	Group 1	Ageta_32, Angoorlata, Arka_Abha, Arka_Alok, Arka_Meghalli, Arka_Vikas, Avinash_2_2_1, Azad_T_2, Azad_T_5, Bhillai, DHVRubya, Hisar_Anmol, Hisar_Arun_(Sel_7), Hisar_Lalit, IIHVR_01, IIHVR_2202, INDAM_2102, INDAM_2103, INDAM_2103_1, INDAM_2103_1_1, INDAM_2103_4, INDAM_2103_6, INDAM_2103_6_1, INDAM_2103_6_4, Jawahar_99, Kashi_Hemant, Kashi_Sharad, Kashi_Vishesh, Kashi_Amrit, Kashi_Anupam, Kajla, Kalyanpur_Type_1, Kashmiriya, Nandhi, Palam_Pink, Pant_T_3, pant_T_5, Parul, Pb_Chuhara, Pb_Upma, Persia_Bed, PKM_1, Prestige, Pusa_Gaurav, Pusa_Ruby, Pusa_120, Punjab_BB_2, Pusa_Hybrid_2, Roma, Sanjeevani, Sankranti, Sel_18, Sioux, Solan_Gola, Solan_Vajr, Sun_Cherry, Swarna_Naveen, Swarna_Vaibhav, Tripura_Local, Utkal_Pragyan, Utkal_Raja, S_Lalima, Switzerland, Utkal_Urvashi, Pallavi, Punjab_KesHVRi, V_Pragyan, DMT1, DMT3, Mukthi, Co_3.
2	Group 2	EC_2791, EC_13904, EC_317_6_1, EC_273966, EC_381263, EC_381554, EC_501574, EC_501575, EC_501576, EC_501577, EC_501580, EC_501582, EC_501583, EC_519730, EC_520046, EC_520059, EC_520061, EC_520071, EC_520074, EC_520075, EC_520078, EC_521039, EC_521056, EC_521078, EC_526139, EC_528372, EC_528374, EC_529080, EC_529083, EC_538138, EC_538155, EC_538380, EC_538404, EC_538405, EC_538408, EC_538419, EC_538423, EC_538439, EC_538440, EC_538441, EC_538455, EC_552141, EC_560340, EC_570028, EC_605694, EC_605695, EC_605696, EC_620362, EC_620366, EC_620370, EC_620373, EC_620374, EC_620375, EC_620383, EC_620386, EC_620398, EC_620401, EC_620403, EC_620406, EC_620409, EC_620410, EC_620411, EC_620413, EC_620419, EC_620421, EC_620438, EC_620444, EC_620446, EC_620455, EC_620456, EC_620464, EC_620469, EC_620470, EC_620474, EC_620476, EC_620480, EC_620486, EC_620500, EC_620502, EC_620514, EC_620519, EC_620530, EC_620533, EC_620540, EC_620556, EC_620568, EC_620575, EC_620598, EC_625644, EC_625645, EC_625651, EC_625652, EC_625660, EC_6202041.
3	Group 3	Flora_dade, Hawaii, Money_Maker, Monte_Favet, Rio_Grande.
4	Group 4	B_4_1, B_7_2, BL_1208, BTH_9M, C_1_4, C_3_2, C_4_1, C_8_1, C_9_2, C_10_2, C_11_1, C_11_2, C_11_3, C_20_1, C_20_2, C_26_1, CHVRT_4, CH_155, D_1_1, D_2_2_1, D_3_2, D_5_1, DARL_66, DT_10, DVRT_1, DVRT_2, E_4_3, F_5020, F_6022, F_6050_1, F_6059, F_7012, F_7025, F_7028, F_6009, FEB_02, FEB_04, FLA_7171, FLA_7421, G_4_5, G_5_4, G_6_3, GT_1, GT_2, GT_3, H_88_78_1, H_88_78_2, H_88_78_3, H_88_78_4, H_88_78_5, I_4_4, IC_373378, IC_427766, IC_447708, IC_469626, LA_3772, LA_3957, LA_3997, M_1_4, M_3_2, N_2_2, N_2_3, NDT_1, NDT_8, NDT_4, NDTVR_60, NDTVR_73, NF37SB_8, PDT_3_1, PDVT_14, PS_1, TLBR_6, TLH_17, TLH_27, TLH_30, VRT_32_1, VRT_01A, WIR_3957, WIR_5032, WIR_13706, WIR_13708, 97/384, 97/753, 97/754_(Kewalo), 15_SB, WIR_13717.
5	Group 5	CLN_2026, CLN_2116, CLN_162, CLN_2366.

**STUDIES ON GENETIC DIVERSITY OF WHITEFLY, *Bemisia tabaci*
(GENN.) (HEMIPTERA: ALEYRODIDAE) AND MOLECULAR ANALYSIS
FOR ITS RESISTANT TRAITS IN TOMATO**

SACHIN, U. S.

2019

**Dr. VENKATESHALU
Major Advisor**

ABSTRACT

The present study was conducted at College of Horticulture, Bagalkote and Bengaluru, University of Horticultural Sciences, Bagalkote during 2016-17 to 2019. The morphometric analysis for different characters of adult male, female and puparia revealed the existence of unique population from Chikkaballapura district and has recorded significantly higher values for majority of the characters studied which was evident in cluster analysis. The genetic diversity and population structure of *B. tabaci* recorded significant genetic diversity among eleven populations of *B. tabaci*. The Analyses of Molecular Variance (AMOVA) across all the populations exhibited 49.79 per cent variation among the populations and 50.21 per cent within population with a mean fixation index of 0.498. The clustering analysis from both morphometrics and molecular analysis revealed almost similar type of results. The population genetic structure analyses of *B. tabaci* populations indicated the presence of fourteen genetic clusters (K=14) which spread across all the sampled populations from eleven districts of Karnataka, forming genetically mixed populations. Among the population studied, 30.90 per cent of the individuals were detected with monopartite virus particles, 1.82 per cent with bipartite and 10.36 per cent of the individuals detected with both mono and bipartite virus particles which were amplified at 270 bp and 477 bp regions, respectively.

Field evaluation of 260 tomato minicore accessions was done during rabi and summer seasons of 2016-17. The trichome density and trichome type played an important role in whitefly resistance on tomato combined with phenol and terpinoid content which were exhibited significant and negative correlation with whitefly population at 45 DAT. The molecular analysis of 260 tomato minicore accessions indicated the presence of significant genetic diversity among five clusters population. Population genetic structure analyses of tomato accessions indicated the presence of seven genetic clusters (K=7) which spread across all the populations, forming high level of genetically mixed population. Association analysis between biochemical, biophysical traits and SSR markers revealed that, phenols were associated with three markers, tannins with nine markers, two markers with terpinoid, chlorophyll with seven markers and trichomes were associated with three markers.

©½ ÉÉt UÁVÀ CĒĀāĀ²PÀ áĚ«zĀVÉ āĀVĀĀ méEĀāĀĪmÉZā ° CzĀgĀ ḡgÉĒZĀPÀ
UĀĀ t®PĀ t UĀ½UĀV D t PĀ «±ĒμūÉĀĪĀ PĀĀ jvĀZĀ CzĀĪĀĀĒĀāĒĒĀĀ, vÉĒĀ l UĀj PĀ āĀ°Ā«zĀĪ®ĀĪ,
“ĀUĀ®PÉĒĀmé āĀVĀĀ “ĒAUĀVĀEjĒā ° 2016-17 jAzĀ 2019 āĠÉÚÉ ĒqÉ,ĀĴĀĴĀVĀ. ©½ ÉÉt UÁVÀ
¥Ēē UĀAqĀĀ āĀVĀĀ °Ét Ā ÉÉt UÁVĀĀ “Ā°Ā CAUĀ gĀZĒÉUĀVĀ PĀ,Ġgī «±ĒμūÉĀĪĀ CzĀĪĀĀĒĀCzĀ
a p S¼ĀĀĠgĀ fĒĒĀĀ ° «©ĒĀ ©½ ÉÉt UÁVĀ ,ĀSĒĒĀĀ zĀSĴĀĴĀVĀ. ¥Ēē UĀAqĀĀ, °Ét Ā
āĀVĀĀ PéĒĀ±ĀĀ,ĒĀĀ PĀ,Ġgī «±ĒμūÉĀĪĀ °ĀĀĀ EzĒĀ jwĀĀĀ ¥Āēw ¥Āēδ¹zĀĀ. ©½ ÉÉt UÁVĀ
CĒĀāĀ²PÀ áĚ«zĀVÉ āĀVĀĀ UĀĀ¥ĀUĀVĀ gĀZĒÉĀĀ CzĀĪĀĀĒĀzĀ°, °ĒÉĒĒĀzĀĀ ©½ ÉÉt UÁVĀ
UĀĀ!Ēā ° UĀĀĒĒĀ°Āđ CĒĀāĀ²PÀ áĚ«zĀVÉĀĀ zĀRĴĀĴĀVĀ. Ct PĀ āĀVĀ,ĀZĀ «±ĒμūÉ
āĀĪrzĀUĀ UĀĀ¥ĀUĀVĀ ĒqĀĀĒÉ, ±ĒĀ. 49.79 gμĀĀ āĀVĀ,ĀĀĒĀ ¥Āēδ¹āĒ āĀVĀĀ UĀĀ¥ĀUĀVĀE VĀUÉ
±ĒĀ. 50.21 gμĀĀ āĀVĀ,ĀĀĀ 0.498 ¹jĀPĀgĀ t ,ĀEZĀĀPĀZÉĒĀCÚÉ zĀRĴĀĴĀVĀ. “ĒwPĀ ®PĀ t UĀVĀĀ
(¥Ēē+ PéĒĀ±ĀĀ,Ē) āĀVĀĀ D t PĀ PĀ,jĀUī CzĀĪĀĀĒĀzĀ° Š°ĀVÉĀPĀ MAZĒĀ jĀwĀĀĀ ¥ā°vĀĀ±ĀĀ
Š»gĀUĀUÉĒArzĒ. ©½ ÉÉt zĀ DEĀāĀ²PĀ gĀZĒÉĀĀ «±ĒμūÉĀĪĀ ° °ĀĒĒĀ®Ā DEĀāĀ²PĀ
,ĀĀĒĒ°ĀUĀVĀ (Pé=14) G¥Ā¹wĀĀĀ PĀAqĀĀ ŠAzĀĀ «Ā²ē CĒĀāĀ²PĀVÉĀĀĒĀĀ °ÉĒĀCzĒ CzĀĪĀĀĒĀ
āĀĪrzĀ ©½ ÉÉt UÁVĀ ,ĀSĒĒĀĀ°, ¥ĀēVĀ 30.90 gμĀĀ āÉĒĒĒĒĒmĒēōmī āĒĠgĀ,i PĀ t UĀVĀĀ,
¥Āē±ĀVĀ 10.36 gμĀĀ ©½ ÉÉt UÁVĀ° āÉĒĒĒĒĒmĒēōmī āĀVĀĀ JgĀqĀĀ āĒĠĀĴĀ PĀ t UĀVĀĀ
PĀAqĀĀ ŠĀCvĀĀ. ,ĀĀāĀĠgĀĀ 260 méEāĀĪmÉE «Ā®PÉĒĠgī zĀRĴĀWUĀVĀĒÉĒĒĒĒĒUÉĒĀQĀ ZĀ½UĀ®ZĀ
CzĀĪĀĀĒĀzĀ° ©½ÉÉt UÁVĀ ,ĀSĒĒĀĀ wĠĠĀ PĀrĒĒĀ EzĀĀĪ (1.5/VqĀ), “ĒĀ¹UÉ PĀ®ZĀ° CĀPĀ
¥ĀēĀ t zĀ° PĀAqĀĀ ŠAvĀĀ. méĒĒĒĒĒĀĪ ,ĀZĀē āĀVĀĀ ««zĀ āĀĪZĀjĀĀĀ ©½ ÉÉt UÁVĀ
ḡgÉĒZĀPĀVÉĀĀ° Š°ĀāĀĀĀRī ¥ĀVĀēĀĀ ā»¹zĒ, °ĀUĀE !ĒĴĴĀ āĀVĀĀ !,!đĒēqī ¥ĀēĀ t āĀ
©½ÉÉt UÁVĀ ēĒĀĒÉ UĀĀĒĒĀ°Āđ ¥ĀēĀ t zĀ° l ĀuĀVĀPĀ ¥ā°vĀĀ±ĀĒĒĀĀ ĒĀn 45 ĄĒUĀVĀ ĒĀVĀgĀ
PĀAqĀĀ ŠĀCvĀĀ. 260 méEāĀĪmÉE «Ā®PÉĒĠgī zĀRĴĀWUĀVĀ Ct PĀ «±ĒμūÉĀĪĀ UĀĀĒĒĀ°Āđ
¥ĀēĀ t zĀ° CĒĀāĀ²PĀ áĚ«zĀVÉĀĀ EgĀĀ«PĒĀĀĒĀĀ ,ĀĒā¹āĒ. UĀĀ¥ĀUĀVĀ CĒĀāĀ²PĀ gĀZĒÉĀĀ
CzĀĪĀĀĒĀzĀ° K¼ĀĀ CĒĀāĀ²PĀ PĀ,ĠgĀUĀVĀ EgĀĀ«PĒĀĀĀ JĴĀ UĀĀ¥ĀUĀVĀ° PĀAqĀĀ ŠAvĀĀ.
fĀĠgĀ,ĀĀĀāPĀUĀVĀĀ, ēĒē«PĀ“ĒwPĀ UĀĀ t®PĀ t UĀVĀĀ āĀVĀĀ J,i J,i Dgī āĀĀPĀđgīUĀVĀ
ēÉĒVĒUĀj Pé, «±ĒμūÉ CzĀĪĀĀĒĀĀĀ ««zĀ fĀĠgĀ,ĀĀĀāPĀ āĀVĀĀ “ĒwPĀ ®PĀ t UĀVĀEĒĀCÚÉ
āĀĀPĀđgīUĀVĀ ēÉĒVĒUĀj PéĀĀĒĀĀ Š»gĀUĀ¥Ār¹zĒ.