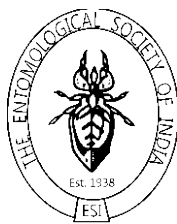


ESI Event 2025 to Commemorate the Birth Centenary of Prof. T. N. Ananthakrishnan



National Dialogue on
**Insects in Agriculture,
Health and Environment**

15-16 December 2025

Bengaluru, India



Prof. T. N. Ananthakrishnan Foundation

Entomological Society of India

Society for Biocontrol Advancement

Central Silk Board

ICAR-National Bureau of Agricultural Insect Resources

BOOK OF ABSTRACTS

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National Dialogue on Insects in Agriculture, Health and Environment

15–16 December 2025

Bengaluru, India

EDITORS

Rajgopal N N

Ramya R S

Rachana R R

Sagar D

Gundappa B

Shashank P R

Suresh M Nebapure

Rajna S

Bhagyashree S N

Shivanna B

Sachin S Suroshe

Sushil S N



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Front Cover (left to right): Dorsal habitus of *Franklinothrips vespiformis*, a predatory thrips (R.R. Rachana); *Goniozus apoderophagus*, an ectoparasitoid of *Apoderus tranquebaricus* (Ankita Gupta); Dorsal habitus of *Tritaeiopteran obscurum*, a fruit fly (K.J. David)



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FOREWORD

It is my honour and privilege to pen this foreword for the Abstract Book and the Proceedings brought out on the occasion of the ESI Event 2025 on the National Dialogue on Insects in Health, Agriculture and Environment. This is no doubt, an event deeply meaningful as it commemorates the centenary of Prof. T. N. Ananthakrishnan, one of India's towering figures in entomology. His pioneering scholarship, mentorship, and vision have shaped generations of scientists and continue to inspire new inquiries into the world of insects.

Founded in 1991 and later formalized as a Trust, the Prof. T. N. Ananthakrishnan Foundation remains a lasting tribute to his influence. A defining pillar of this legacy is the biennial Prof. T. N. Ananthakrishnan Awards, which recognize exceptional researchers in India and abroad, carrying forward his commitment to encouraging scientific leadership and discovery.

This National Dialogue, therefore, is more than just a commemorative event. It is an intellectual ecosystem where Prof. Ananthakrishnan's legacy takes living form. Unlike conventional conferences, it has been envisaged as a thinking arena for open discussion, critical reflection, and collaborative ideation on pressing issues in insect science. By bringing together academic leaders, policymakers, industry partners, students, and innovators, the Dialogue aims to co-create solutions that will influence research pathways, public policy, and sustainable agricultural practices in the years ahead. This is a befitting tribute to Prof. T.N. Ananthakrishnan who was known for conducting serious discussion meetings on all the frontier aspects of entomology, as long as he was alive.

It is especially fitting that the ICAR–National Bureau of Agricultural Insect Resources (NBAIR) hosts this event, as its national mandate in insect biodiversity, biological control, and the sustainable use of beneficial insects closely aligns with Prof. Ananthakrishnan's contributions. NBAIR's leadership in advancing insect-based technologies for agriculture and ecological security underscores its suitability as the venue for such reflections and forward-looking discussions. Likewise, the ethos of the Society for Biocontrol Advancement (SBA), a co-organizing partner, resonates with Prof. Ananthakrishnan's advocacy for environmentally conscious approaches. By bringing together these institutions with the Entomological Society of India and the TNA Foundation, this Dialogue becomes a meeting point of legacy, leadership, and learning, reflecting both the breadth of today's entomological thought and the interdisciplinary curiosity he championed.

As we celebrate one hundred years since his birth, may this Dialogue inspire the collaborative culture he envisioned. I warmly welcome all participants and wish you meaningful discussions, academic enrichment, and collaborative friendships that endure beyond this event.

“Let this gathering not merely remember a legacy, but renew the responsibility to build upon it.”

Dr. V. V. Ramamurthy
President, Entomological Society of India, New Delhi &
Trustee, Prof. T. N. Ananthakrishnan Foundation, Chennai

PREFACE

I am pleased to present the Abstract Book of the *National Dialogue on Insects in Agriculture, Health and Environment*, commemorating the birth centenary of Prof. T. N. Ananthakrishnan, an iconic figure in Indian entomology. This volume not only captures the scientific vibrancy of the Dialogue but also reflects the lasting impact of Prof. Ananthakrishnan's pioneering work in insect ecology, systematics, and biodiversity research. His insightful scholarship, meticulous field studies, and dedication to mentoring young scientists continue to shape the evolution of entomological research in India and beyond.

This event, jointly organised by ICAR–National Bureau of Agricultural Insect Resources, Bengaluru; Entomological Society of India, New Delhi; The Prof. T. N. Ananthakrishnan Foundation, Chennai; University of Agricultural Sciences, Bengaluru; and the Society for Biocontrol Advancement (SBA), will be held on 15–16 December 2025. Seven additional organisations are associated with this Dialogue as proud Co-organisers.

Insects play a central yet often underrecognized role in maintaining the delicate balance among ecosystems, food security, and human health. As pollinators, decomposers, natural enemies, and sources of medicinal value, they underpin ecological resilience. At the same time, the challenges posed by pest outbreaks, vector-borne diseases, invasive species, and climate-driven changes call for innovative, interdisciplinary approaches.

The abstracts in this volume showcase a broad spectrum of contemporary research and perspectives on the diverse roles of insects in ecological stability, agricultural sustainability, and advancements in Indian Thysanoptera studies. In an era marked by climate variability, habitat degradation, emerging pathogens, and globalised food systems, the insights offered by researchers gain particular relevance. Their contributions highlight the pressing need for integrated strategies that unite scientific rigour with sustainable, community-focused solutions.

As we observe the birth centenary of Prof. Ananthakrishnan, this publication stands as a tribute to his remarkable legacy and as an inspiration to further explore the intricate and indispensable world of insects. We hope the ideas and innovations captured in these pages will encourage deeper inquiry, meaningful collaborations, and a renewed commitment to sustainable development.

The programme features four plenary lectures and thematic sessions with lead presentations, encouraging exchange of knowledge across generations of researchers. A brainstorming session on the status, challenges, and future directions of conventional insect taxonomy in India is also an important component of the Dialogue.

I extend my sincere best wishes to the organising team, co-organisers, and delegates for their invaluable contributions to this landmark event. Welcome to Bengaluru—may this Dialogue inspire collective efforts toward sustainable agriculture and a healthier planet

Dr Satya Nand Sushil
Director, ICAR-NBAIR &
President, Society for Biocontrol Advancement,
Bengaluru



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PROF. T. N. ANANTHAKRISHNAN FOUNDATION – AN OVERVIEW

About the TNA Foundation

As a mark of reverence and affection some of his old scholars and colleagues and well-wishers decided to establish a Foundation viz., Professor T. N. Ananthakrishnan Foundation. The deed of Endowment was executed on 18th November 1991 by Dr. N. Muraleedharan, who was then with UPASI Tea Research Institute, Valparai. The Board of Trustees of the foundation were Mrs. Menaka Ananthakrishnan, Dr. B. Vasantharaj David, Dr. M. C. Muralirangan, Dr. N. Muraleedharan and Dr. A. Raman and the endowment amount deposited was Rs.75,000/-. Later this amount was further strengthened by the contributions from Kannan Nagarajan, B V David, VV Ramamurthy, and many others who contributed / contributing continuously.

One of the objectives was to institute Prof. T. N. Ananthakrishnan Award for significant contributions in the field of entomology and the award made once in two years.

The first award was presented in 1996 for the biennium 1994-95 to Dr. Raghavendra Gadagkar, Indian Institute of Science, Bengaluru.

1998 - Dr. Dharam Pal Abrol, Univ. of Agricultural Sciences & Technology, Jammu for 1996-97

2000 - Dr. J. S. Bentur, Directorate of Rice Research, Hyderabad for 1998-99

2002 - Dr. H. C. Sharma, ICRISAT, Hyderabad for 2000-01

2004 - 80th Birthday celebrations. No award was given.

2006 - Dr. Chandish R Ballal, Sr. Scientist, Project Directorate of Biological Control, Bengaluru for 2004-05

2008 - Dr. Shajahan Johny, Visiting Scientist, Canadian Forest Service, Ontario for 2006-07

2010 - Dr. Anil Kumar Dubey, IARI, New Delhi for 2008-09

2012 - Dr. Omkar, Dept. of Zoology, Univ. of Lucknow for 2010-11

2014 - Dr. N. Bakthavatsalam, Principal Scientist, National Bureau of Ag. Imp. Insects, Bengaluru and Dr. S. Manickavasagam, Prof. of Entomology, Faculty of Agriculture, Annamalai University, Chidambaram, for 2012-13

2016 - Dr. R. Asokan, Principal Scientist, IIHR, Bengaluru and Dr. T. Venkatesan, Principal Scientist, NBAIR, Bengaluru for 2014-15

About the Prof. T. N. Ananthakrishnan Foundation Trust and The Professor T. N. Ananthakrishnan Awards

The Prof. T. N. Ananthakrishnan Foundation was registered as a Trust on 6th December 2017. It is undertaking the activities of the Foundation, mainly the Professor T N Ananthakrishnan Awards and Memorial Lecture

Professor T.N. Ananthkrishnan Awards 2018

Prof. T. N. Ananthkrishnan Senior Scientist Award

Dr. S. Mohan Kumar of TNAU and Dr. Kesavan Subaharan of NBAIR, Bengaluru

Prof. T. N. Ananthkrishnan Special Senior Scientist Award

Dr. M. K. Dhillon of IARI, New Delhi

Prof. T. N. Ananthkrishnan Young Scientist Award

Dr. Jagadish Patil of NBAIR, Bengaluru and Dr. Geetanjali Mishra of Zoology Department, Lucknow University

The second prize awarded to Dr. Somnath Roy of Tocklai Tea Research Institute, Jorhat

From the biennium 2018-2019 the awardees were given cash award: First place Rs.25000/-, Second place Rs. 15000/- and Third place Rs.10000/- for both the categories viz., Senior Scientist and Young Scientist awards.

2020

Senior Scientist Awards

First position: Dr. P. D. Kamala Jayanthi, IIHR, Bengaluru

Second position: Dr. Ankita Gupta, NBAIR, Bengaluru

Third position: Dr. A. Joseph Rajkumar, CPCRI, Kayankulam

Young Scientist Awards

First position: Dr. B. S. Gotyal, CRIJ, Barrackpore

Second position: Dr. K. Selvaraj, NBAIR, Bengaluru

Third position: Dr. Babasaheb B. Fand, CICR, Nagpur

2022

Senior Scientist Awards

First position: Dr. T. Boopathi, ICAR-IIOR, Hyderabad

Second position: Dr. K. J. David, ICAR-NBAIR, Bengaluru

Third position: Dr. Krushnamegh J Kunte, NCBS, Tata Institute of Fundamental Research, Bengaluru; Dr. Rakesh Kumar Gupta, Faculty of Agriculture, SKUAST. J, Chatha, J & K.

Young Scientist Awards

First position: Dr. Sagar, D., ICAR-IARI, New Delhi

Second position: Dr. N. R. Prasannakumar, ICAR-IIHR, Bengaluru

Third position: Dr. A. Mohanasundaram, ICAR-NRCB, Trichy; Dr. R. Maruthadurai, ICAR-CCARI, Goa

2024

TNAF invited nominations for TN Ananthkrishnan Senior Scientist Awards, Young Scientist Awards, and Best PhD Thesis Awards for the biennium 2022- 2023. As per the executive council decision that the awards will carry the sponsor's names, the Young Scientist Award and Best PhD Thesis Awards were rechristened as Prof T N Ananthkrishnan Kannan Nagarajan Awards. The shortlisting of these included- For Senior Scientist Awards 12 nominations; Young Scientist Awards 16 nominations; and Best PhD Thesis – 15 nominations. The TNAF thank all the nominees for their interest in the awards, and congratulate the various awardees and look forward to continued participation of others for the biennium 2024– 2025. The nominations were referred to three anonymous eminent entomologists and the evaluations done by the system based on documents submitted were confirmed. Dr. S. Varatharajan, former Dean, Life Sciences, Manipur, and Dr. Alok Sen, former Principal Scientist, CSIR- NCL, Poona and Dr K Raman, TNAF further checked these for the evaluation criteria. The marks offered by them were consolidated and the ranking was done. Accordingly, under each category the following were ranked:

THE PROFESSOR T.N. ANANTHAKRISHNAN AWARD FOR SENIOR SCIENTIST

FIRST- Dr. Shravan M Haldhar, Principal Scientist, ICAR-NCIPM, New Delhi, Immediate Past Address- Dr. Shravan M Haldhar, Head, Department of Entomology, College of Agriculture, CAU, Imphal

SECOND- Dr. Kalleshwara Swamy CM, Postdoctoral Researcher, Okinawa Institute of Science and Technology (OIST), Okinawa 904-049, Japan; Associate Professor of Entomology, College of Agriculture University of Agricultural and Horticultural Sciences (UAHS) Shivamogga 577204 Karnataka

THIRD- Dr. B. S. Gotyal, Senior Scientist (Agrl. Entomology), ICAR-National Bureau of Agricultural Insect Resources Bengaluru 560024, Karnataka

THE PROFESSOR T.N. ANANTHAKRISHNAN- KANNAN NAGARAJAN AWARD FOR YOUNG SCIENTIST

FIRST- Dr. Shashank P. R., Senior Scientist, National Pusa Collection (NPC), Division of Entomology, ICAR-Indian Agricultural Research Institute, Pusa Campus, New Delhi 110 012

SECOND- Dr. Guru Pirasanna Pandi, G., Scientist (Entomology), Crop Protection Division, National Rice Research Institute, Bidyadarpur, Cuttack, Odisha 753006

THIRD- Dr. Shivaji Hausrao Thube, Scientist, Entomology, ICAR-Central Institute for Cotton Research, Nagpur 440010

THE PROFESSOR T.N. ANANTHAKRISHNAN- KANNAN NAGARAJAN AWARD FOR BEST PHD THESIS

FIRST- Dr. M. Vasanth Research Associate (KINFRA), Southern Regional Centre, Zoological Survey of India, Chennai- 600028.

SECOND- Dr. Safeena Majeed, A. A., Dept. of Agril. Entomology, University of Agricultural Sciences, GKVK, Bengaluru-560065 Karnataka

THIRD - Dr. Ashok, K., Post Doctoral Research Associate, Tata Institute for Genetics and Society, Bengaluru, Karnataka, India; Dr. Karthick, C. M., s/o Mallaiah, R. Matthihalli P.O. Tiptur Taluk, Tumkur District 572201; Dr. Shrawan Kumar Sahani, Department of Entomology, Bihar Agricultural University, Sabour, Bhagalpur- 813210 Bihar

The Professor T.N. Ananthkrishnan Awards 2024-25

TNAF invited nominations for TN Ananthkrishnan Senior Scientist Awards, Young Scientist Awards, and Best PhD Thesis Awards for the biennium 2024- 2025. As per the executive council decision that the awards will carry the sponsor's names, the Young Scientist Award and Best PhD Thesis Awards were rechristened as Prof T N Ananthkrishnan Kannan Nagarajan Awards. The shortlisting of these included- For Senior Scientist Awards 12 nominations; Young Scientist Awards 17 nominations; and Best PhD Thesis – 10 nominations. The TNAF thank all the nominees for their interest in the awards, and congratulate the various awardees and look forward to continued participation of others for the biennium 2026-2027. The nominations were referred to three anonymous eminent entomologists and the evaluations done by the system based on documents submitted were confirmed. TNAF further checked these for the evaluation criteria and these were communicated to the anonymous jury of three members. The marks offered by them were consolidated and the ranking was done. Accordingly, under each category the following were ranked:

The Professor T.N. Ananthkrishnan Award for Senior Scientist

First- Dr. Amalendu Ghosh, Senior Scientist (Entomology), ICAR- Indian Agricultural Research Institute (IARI), New Delhi

Second- Dr. Navneet Singh, Scientist E, ICAR- Zoological Survey of India, Kolkata

Third- Dr. K. Selvaraj, Senior Scientist (Entomology), ICAR- National Bureau of Agricultural Insect Resources, Bangalore; Dr. Sevgan Subramanian, Principal Scientist and Head, International Centre of Insect Physiology and Ecology (ICIPE), Kenya; Dr. Imroze Khan., Associate Professor (Biology), Ashoka University, Haryana

The Professor T.N. Ananthkrishnan- Kannan Nagarajan Award for Young Scientist

First- Dr. Basana Gowda G, Senior Scientist (Agri. Entomology), ICAR- Central Rice Research Institute, Cuttack

Second- Dr. Keerthi MC, Scientist (Sr. Scale), ICAR- Indian Institute of Horticultural RESEARCH, Bangalore

Third- Dr. Suresh M Nebapure, Senior Scientist (Entomology), ICAR- Indian Agricultural research institute, New delhi

The Professor T.N. Ananthkrishnan- Kannan Nagarajan Award for Best PhD Thesis

First- Dr. Sanjay Kumar Pradhan, The University of Agricultural Sciences, GKVK Bangalore & Western Sydney University, Australia

Second- Dr. Santhosh Naik G, ICAR- Indian Agricultural Research Institute, New Delhi

Third- Dr S Pavithran, Tamil Nadu Agricultural University, Coimbatore; Dr Abhishek V, Keladi Shivappa Nayaka University of Agricultural & Horticultural Sciences, Shivamogga, Karnataka; Dr Balaji B N, The University of Agricultural Sciences, GKVK, Bangalore

Prof. T. N. Ananthkrishnan Memorial Lecture

The Prof. TN Ananthkrishnan Memorial Lecture series in commemoration of Prof. TN Ananthkrishnan was started in 2017 by the Prof. T N Ananthkrishnan Foundation (TNAF). The first of this series was scheduled by the TNAF for the 15th of December 2016. But due to unfortunate cyclone it was postponed and held in February 2017. The first memorial lecture was delivered by none other than Prof. M S Swaminathan. This was followed by the second and third memorial lectures – delivered by Dr. J S Bentur, formerly from the ICAR- IIRR, Hyderabad in 2018 and Dr. N. Muraleedharan, formerly from the UPASI, Tamil Nadu in 2020. The fourth memorial lecture was delivered by Dr. Dhriti Banerjee, ZSI, Kolkata in August 2022. Prof. Janarthanan Sundaram, University of Madras, Madras delivered the most recent 5th memorial lecture on 4th October 2024 at the Department of Zoology, University of Madras, Guindy Campus, Chennai.

This year 2025, being the centenary year of Prof. T N Ananthkrishnan, the above lecture is being christened as the Prof. T N Ananthkrishnan Centenary Lecture series. It will form the 6th and will be a series with two each of centenary, and distinguished alumni lectures. These are being delivered on the 15th December, in the ESI Event 2025 to commemorate the birth centenary of Prof. T.N. Ananthkrishnan viz., National Dialogue on Insects in Agriculture, Health and Environment. The venue is the ICAR- National Bureau of Agricultural Insect Resources (NBAIR), Yelahanka Campus, Bangalore, and held between 15 and 16 December, 2025. This event is organized by the Entomological Society of India, New Delhi; TNAF, Chennai; NBAIR, Bangalore; University of Agricultural Sciences, Bangalore; and the Society of Biocontrol Advancement, Bangalore; and Central Silk Board, Bangalore. The details are as follows- T. N. Ananthkrishnan Birth Centenary Lecture I on “You are how much you eat: Caste and nutrition in the Indian paper wasp, *Ropalidia marginata*” by Dr. Raghavendra Gadagkar, IISc, Bangalore; T. N. Ananthkrishnan Birth Centenary Lecture II on “Signal transduction and omics in plant defense mechanisms under insect attack” by Dr. Madhavan Soundararajan, University of Nebraska-Lincoln, USA; T.N. Ananthkrishnan Distinguished Alumnus Lecture I on “Aedes transmitted Arboviruses – The global threat” by Dr. Raman Velayudhan, World Health Organization, Switzerland; and the T. N. Ananthkrishnan Distinguished Alumnus Lecture II on “Conception and implementation of classical weed biological control programs using insects-The Queensland experience by Dr. Dhileepan Kunjithapatham, Biosecurity Queensland, Queensland, Australia The Entomological Society of India, Society for Biocontrol Advancement, Central Silk Board, Zoological Survey of India and few from among the associates/ students of the Prof. T.N. Ananthkrishnan, and his family (son Ramdas Iyer) are supporting this event. At this juncture TNAF would like to thank our trustee Mr. Kannan Nagarajan who owns the Southern Flora supplying fresh cut flowers throughout India, for continuously contributing a heavy sum towards young scientists/ PhD thesis awards from the biennium 2022-2023 to the present. Other significant contributors are Dr. B. V. David, Dr. V. V. Ramamurthy, Dr. John Peter and Dr. Partho Dhang. These have come forward to support the TNAF in its difficult times of financial crunch, as always.

TNAF is obliged and indebted to them and thanks them profusely for this sustained support and devotion to late Prof. T.N. Ananthkrishnan. This support is timely, valuable, and sustains the TNAF and its activities, and the TNAF Trust is indebted to all, and the donations are gratefully acknowledged.

On behalf of the trustees, the TNAF gratefully acknowledges Dr. S. N. Sushil, Director, ICAR- NBAIR for his wholehearted support and guidance, and for organising the event as the Organising Secretary. NBAIR scientists along with faculty of the UAS, GKVK, Bangalore led by Dr. Shivanna B, have done exemplary work in conducting the event and are striving to make it a success and befitting the centenary of the late Prof. T. N. Ananthakrishnan. The TNAF is indebted to Dr. Anantanarayanan Raman, Commonwealth Scientific and Industrial Research Organisation, Australia, who has worked for more than a year to not only bring together a galaxy of renowned scientists for delivering the centenary eve lectures but also in bringing out a special centenary commemorative publication as a special issue of the Indian Journal of Entomology on this occasion. The support from Dr. Raghavendra Gadagkar, Dr. S Madhavan, Dr. R. Velayuthan and Dr. K. Dhileepan will ever be remembered.

Dr. V.V. Ramamurthy
Trustee, TNAF

Dr. B.V. David
Chairman, TNAF

Plenary Session

**YOU ARE HOW MUCH YOU EAT: CASTE AND NUTRITION IN THE INDIAN
PAPER WASP *ROPALIDIA MARGINATA***

RAGHAVENDRA GADAGKAR

Centre for Ecological Sciences, Indian Institute of Science, Bengaluru,
Karnataka 560012, India

Email: ragh@iisc.ac.in (corresponding author)

In eusocial insects such as ants, bees and wasps, only one or a small number of individuals in the colony reproduce. The remaining function as sterile workers that labour for the colony's welfare. A knowledge of the mechanisms that might bring about such caste differentiation into fertile reproductives and sterile workers is essential for understanding the evolution of eusociality. Caste differentiation in highly eusocial species such as ants and honey bees is pre-imaginal, meaning that differentiation occurs through a process of developmental regulation when the individuals are still in their larval stage. In primitively eusocial species such as many wasps and bees, caste differentiation is believed to be post-imaginal, meaning that differentiation takes place through a process of behavioural regulation after the individuals have become adults. Using the primitively eusocial Indian paper wasp *Ropalidia marginata*, we have shown that although social regulation in the adult stage is important, there is nevertheless a pre-imaginal caste bias. Wasps that are relatively well-fed as larvae develop into adults that feed more even as adults and have a high probability of becoming queens and a high probability of changing from worker to queen roles. Conversely, wasps that are relatively poorly fed as larvae develop into adults that feed less even as adults and have a high probability of becoming workers and a low potential to revert from worker to queen roles. Using this knowledge, we have recently succeeded in controlling adult nutrition to make selected wasps more selfish, i.e., more likely to revert from worker to queen roles either by replacing the queens of their colonies or by leaving their natal colonies to start their own new colonies.



**SIGNAL TRANSDUCTION AND OMICS IN PLANT DEFENSE MECHANISMS
UNDER INSECT ATTACK**

MADHAVAN SOUNDARARAJAN

Department of Biochemistry, University of Nebraska-Lincoln, Nebraska 68588, USA

Email: msoundararajan1@unl.edu (corresponding author)

Upon insect infestation plants display altered metabolic events at the cellular, tissue and organismal levels. It becomes necessary to understand the ways by which plants perceive signals under insect attack. This presentation is mainly focused on plant signal transduction with some insight into basic omics methodologies, such as genomics, transcriptomics, proteomics and metabolomics, and to an extent on phenotyping strategies to understand changes in plant behavior during insect attack. This presentation is neither exhaustive nor comprehensive but to emphasize an integrated approach using proteomics, metabolomics and high throughput phenotyping (HTP) technology to further the understanding of the complex genetic, metabolic and molecular responses of plants infested by insects.

AEDES TRANSMITTED ARBOVIRUSES – THE GLOBAL THREAT

RAMAN VELAYUDHAN

World Health Organization, Geneva, Switzerland

Email: VelayudhanR@who.int (corresponding author)

The global threat of *Aedes*-borne arboviruses is a significant and growing public health concern. These viruses are transmitted by mosquitoes of the *Aedes* genus, particularly *Aedes aegypti* and *Aedes albopictus*. They are responsible for several serious viral infections, including dengue, Zika, chikungunya, and yellow fever. The growing incidence of dengue, with its geographical expansion and a notable shift from urban to rural areas in recent years, is a matter of grave concern. Rapid urbanisation, characterised by population growth, increased travel, and inadequate urban planning, has created favourable conditions for *Aedes* mosquito breeding, leading to higher transmission rates. This has been observed since the late 1990s. Urban settings provide abundant breeding sites, such as discarded containers, construction sites, used tyres and poorly managed waste, which support mosquito proliferation and dengue transmission. In 2018, approximately 55% of the global population lived in urban areas, and projections suggest that by 2050, this figure will rise to 68%. Climate change is anticipated to exacerbate the global burden of dengue and other arboviruses. Rising temperatures, altered precipitation patterns, and increased humidity create conducive environments for *Aedes* mosquito breeding and the transmission of dengue. Geographical expansion of *Aedes* mosquitoes into previously unaffected regions further escalates the risk of dengue outbreaks. Additionally, altered climate conditions can influence the virus's replication rates within mosquitoes and affect the virus-mosquito-host interactions, potentially leading to higher transmission rates and increased disease severity. Controlling *Aedes* species is a complex task, necessitating the application of standardised control measures, quality assurance activities, monitoring protocols, community-based interventions, and routine and emergency vector control plans to reduce the risk of an epidemic.



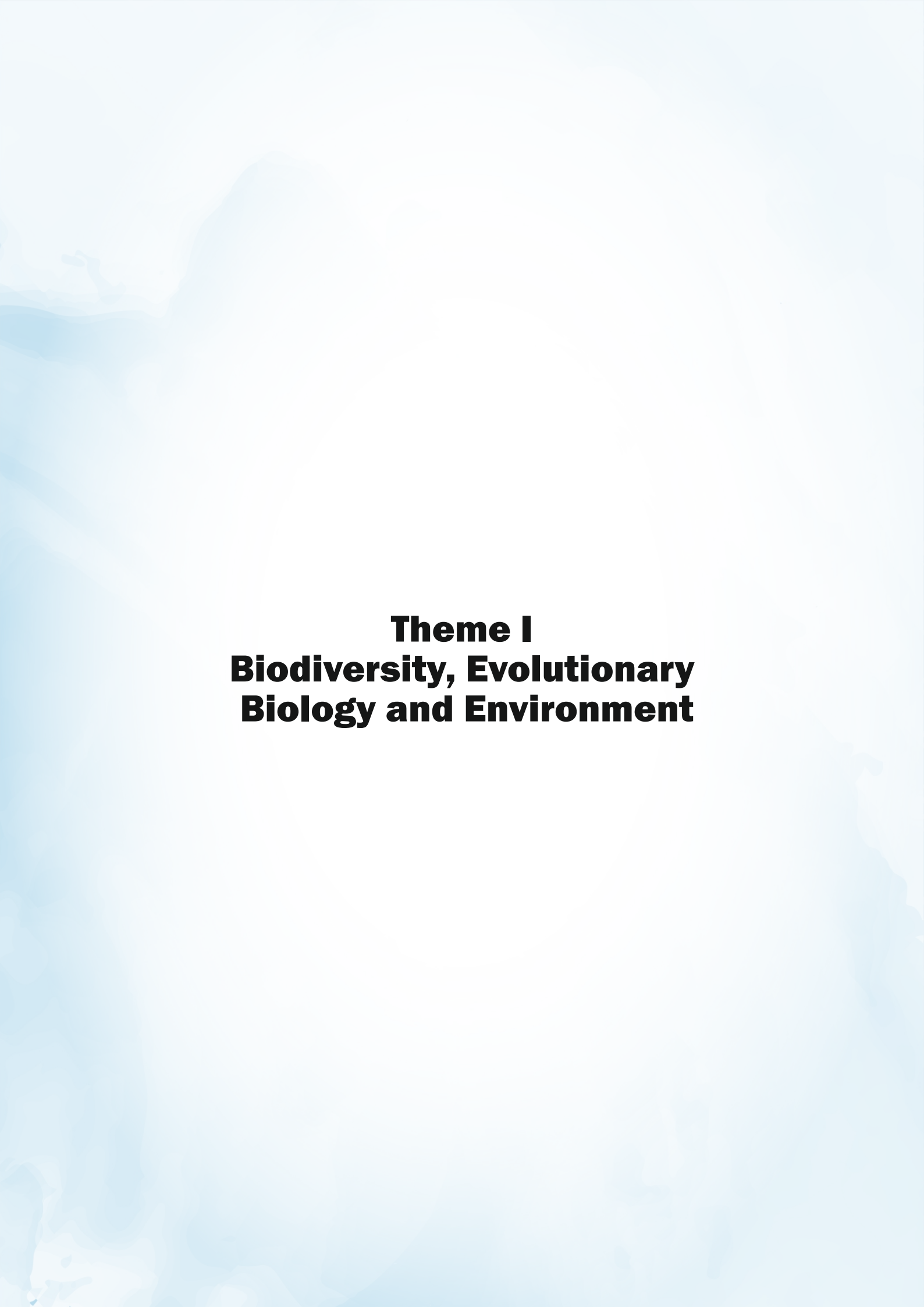
**CONCEPTION AND IMPLEMENTATION OF CLASSICAL WEED BIOLOGICAL
CONTROL PROGRAMS USING INSECTS – THE QUEENSLAND EXPERIENCE**

KUNJITHAPATHAM DHILEEPAN*, DIANNE B J TAYLOR AND BOYANG SHI

Biosecurity Queensland, Department of Primary Industries, Ecosciences Precinct,
Dutton Park, Queensland, Australia

*Email: k.dhileepan@qld.gov.au (corresponding author)

Classical weed biological control are long-term programs spanning over many decades. Target weeds are prioritised based on the current and potential impact, and biological control feasibility. The program essentially involves native range surveys, host specificity testing and agent release and monitoring. The methodology evolved over the years, incorporating genetic and climatic modelling tools to prioritise native range to source biological control agents, and plant response to herbivory, field host range and potential impact as filters to prioritise agents for host specificity testing. Modern host specificity testing based on centrifugal phylogenetic method involve no-choice tests, followed by choice and multi-generational demographic trials, if non-target attack occurs in no-choice tests. Approval to release the agent is based on the non-target risk assessment derived from host specificity tests. Agents released in climatically favourable areas, over a three-to-five-year period and the time taken for establishment range from a few months to more than a decade. To fast-track dispersal, agents are field collected and redistributed to wider geographic range. Evaluation of the impact and economic benefits is the least studied aspect of biological control programs. Successful agents in Queensland have been introduced into other countries around the world.



Theme I
Biodiversity, Evolutionary
Biology and Environment

**AN ANALYSIS ON THE DIVERSITY AND HOST PLANTS OF INDIAN
ALEYRODIDS (HEMIPTERA: ALEYRODIDAE)**

SUNDARARAJ R^{1*}, SELVARAJ K² AND KAVYA YADAV G A²

¹Institute of Wood Science & Technology, Bengaluru, Karnataka 560003, India

²ICAR-National Bureau of Agricultural Insect Resources, Bengaluru, Karnataka 560024, India

*Email: rsundariwst@gmail.com (corresponding author)

Aleyrodids (Hemiptera: Insecta), commonly known as whiteflies or mealywing bugs, belong to the superfamily Aleyrodoidea within the family Aleyrodidae (Hemiptera: Insecta), comprising three subfamilies: Aleyrodinae, Aleurodicinae, and Udamoselinae. They are mostly confined to the tropics and subtropics and typically inhabit the surfaces of leaves and leaf sheaths of plants, although a few species are found on petioles and stems. Aleyrodids are typically pests of angiosperms; most species inhabit dicotyledonous plants, and a few have been reported to infest ferns and are considered one of the world's major agricultural pest groups, causing crop losses. They cause damage to their host plants both directly and indirectly. Direct damage results from their feeding, which extracts plant sap and stunts plant growth, particularly in young plants. Indirect damage is caused by excretion of the large amounts of sticky honeydew during feeding. Honeydew covers plants and supports the growth of sooty mold, which reduces the plant's photosynthesis. In addition, they also act as vectors and transmit many viral diseases in plants. In aleyrodids, adults exhibit only minor morphological differences, which are of little value in species-level identification. Therefore, the fourth nymphal instar, or the puparium of the aleyrodid, is primarily chosen for the diagnostic distinction of species and higher taxa, as it displays distinct diagnostic features. Thus, aleyrodid taxonomists are considering mainly the puparium for the taxonomy of this group, which makes this group distinct from other insect groups. An analysis on the diversity of Indian aleyrodids revealed that only the subfamilies Aleurodicinae and Aleyrodinae are represented from India, in which the Aleurodicinae is represented by three genera with eight species, while the Aleyrodinae is represented by 492 species under 79 genera. Their host range is mainly on dicot plants compared to monocot plants, as well as one species each on gymnosperms and pteridophytes. Among aleyrodids, the cosmopolitan whitefly, *Bemisia tabaci* (Gennadius) is recognized for having the widest host range within the Aleyrodinae, whereas the invasive whitefly, *Aleurodicus dispersus* Russell has the widest host range within the Aleurodicinae. This communication highlights these observations and discusses future prospects of aleyrodid taxonomy in India.



SPECIES DIVERSIFICATION IN AN ECOSYSTEM– A CASE STUDY OF WHITE GRUBS
(COLEOPTERA: SCARABAEIDAE) IN SUGARCANE ECOSYSTEM ACROSS INDIA

KOLLA SREEDEVI^{1*}, SAKSHI TYAGI², JAYASHREE S¹ AND SUSHIL S N¹

¹ICAR-National Bureau of Agricultural Insect Resources, Bengaluru,
Karnataka 560025, India

²ICAR-Indian Agricultural Research Institute, Pusa, New Delhi 110012, India

*Email: kolla.sreedevi@gmail.com (corresponding author)

Sugarcane is one of the important commercial crops grown in an area of 5.6 mha with 82 tonnes/ha productivity in India, which is the second largest producer of sugar in the world. The largest sugarcane producing state is Uttar Pradesh (205 m tonnes) followed by Maharashtra (106 m tonnes) and Karnataka (53 m tonnes). These three states alone contribute nearly 80% (45%, 23% and 10% from U.P., Maharashtra, Karnataka, respectively) to the total country production (Directorate of Sugarcane Development, 2024). The major biotic stress of the crop are white grubs, which incur 40 to 80% yield loss depending upon season and region. Of late, white grubs are becoming serious pests of sugarcane resulting in huge economic loss, which warrants immediate attention. The white grubs belong to the subfamilies Melolonthinae, Sericinae, Rutelinae and partly Dynastinae of family Scarabaeidae under Coleoptera. The predominant genera of white grubs causing damage to the crop are *Holotrichia* and *Anomala*. The surveys carried out for last ten years from 2014 to 2024 in Uttar Pradesh, Maharashtra, Karnataka, Tamil Nadu, Andhra Pradesh, Assam (Majuli Island) and Kerala revealed 32 species under 14 genera infesting sugarcane crop. The diversity of white grubs in sugarcane crop is high with few species occurring all over India and a few limited to specific regions. The most predominant white grub species recorded across India include *Holotrichia serrata*, *H. consanguinea*, *H. nagpurensis*, *H. fissa*, *Lepidiota mansueta* of Melolonthinae, *Anomala bengalensis*, *A. dimidiata* of Rutelinae, *Maladera insanabilis*, *M. rufocuprea* of Sericinae and *Phyllognathus dionysius*, *Heteronychus* sp of Dynastinae. A few species like *Holotrichia consanguinea*, *Lepidiota mansueta*, *Maladera insanabilis*, *Anomala dimidiata* are specific to North India and occur in particular regions/states while *Holotrichia fissa*, *Maladera rufocuprea*, *Brahmina mysorensis* occur in Central to South India. Species like *Holotrichia serrata*, *Anomala bengalensis*, *Phyllognathus dionysius* occur across the country. The species abundance and richness of the white grubs occurring in sugarcane crop in states, Uttar Pradesh, Maharashtra, Karnataka, Andhra Pradesh and Tamil Nadu along with their dynamics and distribution are discussed.

**BIODIVERSITY RICHNESS AND TAXONOMIC PROGRESS IN INDIA:
INSIGHTS FROM CASE STUDIES ON LEPIDOPTERA**

NAVNEET SINGH

Zoological Survey of India, New Alipore, Kolkata, West Bengal 700053, India

Email: nsgill007@gmail.com (corresponding author)

India is the seventh largest country, accounting for only about 2.4% of the Earth's total land area. Despite this, it is one of the 17 mega diverse countries of the World, harbouring approximately 105,000 animal species (around 8% of the global faunal diversity) and is home to four major biodiversity hotspots: the Himalaya; North-eastern region as part of Indo-Burma Hotspot; the Western Ghats as part of the Western Ghats-Sri Lanka Global Hotspot, and the Nicobar Islands, which are part of the Sundaland Hotspot. Regardless, it is estimated that the species currently known from India represent only about 12 % of the actual faunal diversity. This implies that we remain astonishingly unaware of nearly 770,000 species coexisting with us in India, along with the crucial roles they play in our ecosystems. The core scientific disciplines responsible for bridging this enormous knowledge gap, through discovering, naming, describing and classifying the biodiversity in a hierarchical system, is taxonomy. Yet, taxonomy is clearly not a priority in the current scientific scenario. Over the past decade, taxonomists have described nearly 5,000 species from India, averaging around 500 species per year. At this pace, it could take us an unimaginable 15 centuries to achieve a comprehensive understanding of our faunal diversity. What's even more concerning is that the world is entering its sixth mass extinction event, with species extinction rates estimated to be as high as 11 to 690 per week. Can we even begin to imagine how many species will vanish, along with the invaluable knowledge they hold about their roles in the biosphere, evolutionary history, and adaptations for survival? Probably not.

Taxonomic progress of different Lepidoptera taxa in India, along with gap areas and possible ways forward, will be discussed in detail.



**EVOLUTIONARY ECOLOGICAL DYNAMICS OF INSECT IMMUNITY: PERSPECTIVES
FROM INNATE IMMUNE MEMORY TO EVOLUTION UNDER MULTIPLE INFECTION**

IMROZE KHAN

Trivedi School of Biosciences, Ashoka University, Sonapat,
Haryana 131029, India

Email: imroze.khan@ashoka.edu.in (corresponding author)

Most organisms have a highly complex immune system, but our understanding of how this complexity and diversity evolved in natural populations has been surprisingly limited. Recently, however, the frequent emergence of deadly pathogens has turned this curiosity into a pressing issue. For example, strong immunity can protect hosts from invaders but may also cause significant damage to their own DNA, cells, and vital organs. So, how do immune responses balance these costs and still evolve effectively against lethal pathogens? Additionally, how do ecological drivers, such as pathogen prevalence and exposure rate, influence these processes? What are the underlying mechanisms? In my talk, I will share how my lab at Ashoka University aims to answer these questions by studying the rapid divergence and evolution of immune systems in model insects like fruit flies and flour beetles, both at the organismal and molecular levels, to reveal the evolution of design features of various aspects of immune system, ranging from evolution of immune memory in insects to optimisation of immune responses against multiple infection. To this end, we are using diverse methods, including theoretical modelling, population biology, experimental evolution, and genetic and genomic approaches, to unravel the complexities of evolving immune responses.

INTEGRATIVE TAXONOMY: A TOOL TO UNRAVEL INVASIVE WHITEFLIES AND THEIR
NATURAL ENEMIES

SELVARAJ K^{1*}, KAVYA YADAV G A¹, VASUNDHARA J¹, SUMALATHA B V¹ AND RAMESH KUMAR A²

¹ICAR- National Bureau of Agricultural Insect Resources, Bengaluru 560024, India

²Hymenoptera Section, Zoological Survey of India, Kolkata 700053, India

*Email: selvaentomo@gmail.com (corresponding author)

In India, invasive whiteflies (Hemiptera: Aleyrodidae) have become a major concern due to their rapid spread, high reproductive potential, and reduce crop yields both directly and indirectly. Integrative taxonomy has played a crucial role in identifying and managing whiteflies and their natural enemies. In last three decade (1995-2025), ten invasive whiteflies invaded India viz., spiraling whitefly, *Aleurodicus dispersus* Russell during 1995, solanum whitefly, *Aleurotrachelus trachoides* (Back) during 2015, rugose spiraling whitefly (RSW), *Aleurodicus rugioperculatus* Martin during 2016, legume feeding whitefly, *Tetraleurodes acaciae* (Quaintance), Bondars nesting whitefly, *Paraleyrodes bondari* Peracchi and neotropical nesting whitefly, *Paraleyrodes minei* Iaccarino during 2018, palm infesting whitefly, *Aleurotrachelus atratus* Hempel, woolly whitefly, *Aleurothrixus floccosus* (Maskell) during 2019, respectively, annona whitefly, *Aleurotrachelus anonae* (Corbett) during 2024 and nesting whitefly, *Paraleyrodes pseudonaranjiae* Martin during 2024. These invasive species are native to the Neotropical region, mostly from Central America and the Caribbean. Extensive surveys revealed that these species are spreading rapidly in the large geographical region, expanding their host range and co-existence with other invasive and native whiteflies also observed and reported. The most insidious spread of these species in India is likely mediated by humans through the movement of infested seedlings and plant materials. As part of integrative taxonomy both morphological and molecular characterisation of all the invasives has been carried out. Several biological control agents have also been recorded to parasitize and predator on invasive whiteflies. An exotic parasitosis viz., *Encarsia guadeloupae* Viggiani and *Encarsia dispersa* Polaszek on *A. rugioperculatus* and *A. dispersus*; *Encarsia cubensis* Gahan (Hymenoptera: Aphelinidae) parasitize on *A. atratus*, *A. trachoides* and *A. floccosus*. Aphelinid parasitoids, *Encarsia* sp. and *Eretmocerus* sp. (Hymenoptera: Aphelinidae) on *A. anonae*; *Eretmocerus* spp. on *A. floccosus*, *A. atratus* and *A. trachoides* and *Signiphora* sp. (Hymenoptera: Signiphoridae) on *T. acaciae* were also recorded. Generalist predators viz., *Apertochrysa astur* (Banks) (Neuroptera: Chrysopidae); *Acletoxenus indicus* Malloch (Diptera: Drosophilidae); *Jauravia pallidula* (Motschulsky), *Cheilomenes sexmaculata* (Fabricius), *Scymnus latemaculatus* Motschulsky (Coleoptera: Coccinellidae) and *Cybocephalus indicus* Tian & Ramani (Coleoptera: Cybocephalidae), were reported to predate on invasive whiteflies. This integrated research has significantly enhanced our understanding of invasive whiteflies in India, shedding light on their diversity, invasion pathways, and ecological interactions. Early detection of invasive species and its natural enemies could minimize the economic losses and pest control in the country.



TAXONOMIC STUDIES ON SUPERFAMILY TORTRICOIDEA (LEPIDOPTERA)

SANTHOSH NAIK G* AND SHASHANK P R

National Pusa Collection, Division of Entomology, ICAR-Indian Agricultural Research Institute, New Delhi 110012, India

*Email: santhoshckm55@gmail.com (corresponding author)

The Superfamily Tortricoidea, comprising the single family Tortricidae (leafroller moths), is a highly speciose group within the microlepidoptera, ranking second only to Gelechioidea. This family includes approximately 1,151 genera and nearly 11,365 recognized species globally. Tortricidae is organized into three subfamilies: Chlidanotinae, Olethreutinae, and Tortricinae. Adults are morphologically distinguished by a combination of features, including a roof-like resting posture of the wings and specific scale patterns on the frons and vertex; species delimitation traditionally relies on the morphology of the male and female genitalia. Economically, this family is significant due to its status as a pest of horticultural, agricultural, and forest plants. The current study focuses addressing a critical gap in the understanding of their taxonomy and diversity. Extensive fieldwork across 37 localities in five states and one union territory, supplemented by the examination of over 2,000 museum specimens from 13 additional regions, led to a comprehensive documentation of the family. The study confirmed 53 species across 37 genera belonging to seven tribes under the subfamilies Olethreutinae and Tortricinae. Significantly, the study resulted in the description of thirteen species new to science and recorded five genera for the first time from India. Additionally, fifteen species were added as new national records. Also, DNA barcodes (mtCOI marker) were generated for 31 species, 27 of which were submitted for the first time from India, with 14 representing novel global entries to GenBank. Phylogenetic analysis using these markers revealed critical evolutionary relationships and provided insights into the taxonomic relationship within the family. Molecular confirmation also helped resolve cases of sexual dimorphism within the group. Furthermore, environmental modelling based on 2,123 species records shed light on the biogeographic distribution patterns of the family. The analysis identified two species richness centres (Northeastern and western Himalayan region) and three endemism centres (Northeastern, Western Himalayan and Western Ghat) for Tortricidae in India. Climatic variables showed a clear correlation with species distribution. Mean annual precipitation and floral diversity showed a positive correlation with species richness, whereas mean annual temperature showed a negative correlation for Tortricidae. The integration of morphological taxonomy with molecular tools and biogeographic analysis will help in accurate species delimitation, distributional range and reveal the true diversity of Tortricidae.

TAXONOMIC STUDIES ON FRUIT FLIES OF TRIBE DACINI (DIPTERA:
TEPHRITIDAE: DACINAE) IN INDIA

ABHISHEK V^{1*}, PRADEEP S¹, DAVID K J², KALLESHWARASWAMY C M¹,
SRIDHARA S³ AND SATISH K M⁴

¹Department of Entomology, College of Agriculture, Keladi Shivappa Nayaka University of
Agricultural and Horticultural Sciences, Shivamogga 577204, Karnataka, India

²ICAR-National Bureau of Agricultural Insect Resources, Bengaluru 560024, Karnataka,
India

³Department of Agronomy, College of Agriculture, Keladi Shivappa Nayaka University of
Agricultural and Horticultural Sciences, Shivamogga 577204, Karnataka, India

⁴Department of Biotechnology, College of Agriculture, Keladi Shivappa Nayaka University
of Agricultural and Horticultural Sciences, Shivamogga 577204, Karnataka, India

*Email: abhiento97@gmail.com (corresponding author)

Roving surveys undertaken during 2022-24 across India including Western Ghats, northeast India, Andaman Islands and examination of fruit flies deposited at National Insect Museum, ICAR-NBAIR, Bengaluru, UASB GKV and Natural History Museum, London led to the identification of 85 species of fruit flies belonging to 3 genera namely *Bactrocera* Macquart, *Dacus* Fabricius and *Zeugodacus* Hendel in 15 subgenera of tribe Dacini belonging to nine species complexes viz., *dorsalis*, *nigrotibialis*, *trilineatus*, *scutellaris*, *tau* and *watersi* species complexes of which three complexes viz., *bipustulata*, *rubigina* and *crabroniformis* are newly proposed from the current study. Six new species were described during the course of the study viz., *Bactrocera kyrdemkulai* Abhishek and David, *Dacus nagarathnae* Abhishek, David and Hancock and *Zeugodacus nasivittatus* David and Abhishek from Meghalaya; *Bactrocera ettinabhujia* Abhishek and David and *Dacus venkateshi* Abhishek and David from Karnataka; *Zeugodacus sinuvittatus* David and Abhishek from Himachal Pradesh. Two putative new species belonging to *Bactrocera* and *Dacus* from Andaman Islands attracted to Zingerone were also collected. An updated checklist of fruit flies of tribe Dacini from India was prepared which include 110 species with six new records viz., *Bactrocera abbreviata* (Hardy), *Bactrocera gombakensis* Drew and Hancock, *Bactrocera ochroma* Drew and Romig, *Bactrocera profunda* Tsuruta and White, *Bactrocera wuzhishana* Li and Wang and *Dacus vijaysegarani* Drew and Hancock. Male and female postabdominal structures were studied including the external morphology and morphometrics along with an updated key to all the members of species complexes recorded from India. The specific region of mitochondrial cytochrome oxidase I (mtCOI) gene of 36 fruit fly species DNA was amplified and the accession numbers were obtained by submitting the sequences to the NCBI's GenBank. Phylogenetic analysis using morphological and molecular characters using maximum likelihood method based on mtCOI revealed that *Bactrocera* and *Dacus* are monophyletic, whereas *Zeugodacus* was polyphyletic. Besides, host plant data and lure responses of all the collected species were also recorded.



**HYMENOPTERAN PARASITOID ASSEMBLAGE SHOWCASING ENRICHED
FAUNAL DIVERSITY IN CAJANUS CAJAN (L.) HUTH FIELDS ADOPTING
NATURAL FARMING**

ANKITA GUPTA*, KOLLA SREEDEVI, JUDITH COROLIN CORREYA AND GOWRI M

ICAR-National Bureau of Agricultural Insect Resources, Bengaluru,
Karnataka 560024, India

*Email: drankitagupta7@gmail.com (corresponding author)

During the surveys undertaken in 2024-2025 in the pigeon pea fields with natural farming practices, rich faunal diversity of parasitoids of Order Hymenoptera was observed. The fields were selected in Yelahanka, Bengaluru (Karnataka) and RARS, Tirupathi (Andhra Pradesh). Six predominant species were observed in the fields viz., *Bassus relativus* (Bhat and Gupta) (Braconidae); *Cotesia ruficrus* (Haliday) (Braconidae); *Phanerotoma hendecasisella* Cameron (Braconidae); *Trathala flavoorbitalis* (Cameron) (Ichneumonidae); *Mantibaria* sp. (Scelionidae) and *Parapanteles* sp. (Braconidae) emerged from gregarious cocoons attached to the pigeon pea leaves. In the present study interestingly, 22 specimens of the rare scelionid genus *Mantibaria* Kirby, 1900, were first time reared from a mantid ootheca attached to the pigeon pea stem in Andhra Pradesh, all earlier Indian specimens were collected using sweep net in Karnataka. Till date, barely four valid species of *Mantibaria* have been recorded worldwide: *M. seefelderiana* (De Stefani, 1891) from Africa, western Mediterranean regions in Europe and Indo-Malayan regions; *M. mantis* (Dodd, 1913) from Australia and India (Karnataka); *M. kerouaci* Veenakumari and Rajmohana, 2012 solely from India (Karnataka) and *M. solygiea* Risbec, 1950 from Afrotropical region (Senegal), although Masner (1976), Mineo (1980), Galloway and Austin (1984) and Oliveira and Schoeninnger (2017) opiated that distinct differences to separate *M. mantis*, *M. seefelderiana* (= *M. anomala*) and *M. solygiea* are not available, hypothesizing that these three species actually comprise only one species that is widely distributed in the Old World. Due to the taxonomic conundrum associated with *Mantibaria* it is presently not possible to confirm the species; however, through this discovery, the richness of parasitoid fauna in natural fields is clearly evident. Perhaps such parasitoid assemblages represent a healthy crop in an ecofriendly environment and thus presses the need for adopting natural farming practices. This study is undertaken as one of the core activities of biodiversity documentation under the CRP on Agrobiodiversity Project (Insect Biodiversity Component) progressing at ICAR-National Bureau of Agricultural Insect Resources, Bengaluru, India.

**ESTABLISHING DNA BARCODE REFERENCE LIBRARIES FOR INDIAN
INSECTS: FOCUSING ON SPECIALIZED GROUPS**

SHASHANK P R

National Pusa Collection, Division of Entomology, ICAR-Indian Agricultural
Research Institute, New Delhi 110012, India

Email: spathour@gmail.com (corresponding author)

Insect species contribute the majority of animal biodiversity on earth, yet accurately measuring or evaluating their species diversity remains largely incomplete. Several recent studies have provided substantial evidence demonstrating the accelerated rate at which insect populations are declining. There is a need to accurately document and quantify insect fauna diversity to achieve a comprehensive understanding of terrestrial ecosystems. Modern technology significantly accelerates species identification, surpassing traditional methods in speed and accuracy. The molecular approach using DNA barcoding, when combined with traditional morphological identification, must be prioritized and expedited. The present study provides a comprehensive overview of the current status of DNA barcoding for insect species in India and highlights critical gaps that require urgent attention. Analysis indicates that specimens with DNA barcodes account for less than 3.73% of the total known and described insect taxa in India. Within this limited dataset, the orders Lepidoptera and Hemiptera are the most extensively represented, followed by Diptera and Coleoptera. The Barcode of Life Data System (BOLD) currently contains barcode sequences for approximately 2,300 Indian insect species, a figure that remains disproportionately low relative to India's vast insect diversity, which includes over 63,000 described species. Currently, similar initiatives focusing on the leaf roller micromoth family Tortricidae (Lepidoptera) in India are advancing, aimed at establishing a comprehensive DNA barcoding reference library for this specialized group. Till now, around 100 species of tortricid have been barcoded using taxonomically validated specimens. Around them, >80% are novel barcodes. There is a pressing need to implement similar DNA barcoding initiatives across other insect groups in India. To accelerate the discovery and documentation of diverse insect groups, a collaborative approach that integrates traditional taxonomic expertise with molecular biology is essential. This interdisciplinary synergy is crucial for achieving comprehensive DNA barcoding coverage of all known insect taxa in India, thereby supporting future applied research and the conservation of India's rich biodiversity.



BIODIVERSITY AND BIOGEOGRAPHIC PATTERNS OF HIMALAYAN
BUMBLEBEES: IMPLICATIONS FOR ECOSYSTEM FUNCTIONING

RIFAT HUSSAIN RAINA

Desert Regional Centre, Zoological Survey of India (ZSI), Jodhpur,
Rajasthan 342 006, India

Email: rifat72001@rediffmail.com (corresponding author)

This study examines the taxonomy, distributional patterns and pollination networks of Himalayan bumblebees, highlighting their ecological significance and contributions to ecosystem functioning. The Himalayan region extending from the subtropical foothills to alpine habitats exceeding 5,000m amsl., supports one of the richest assemblages of bumblebees (*Bombus* spp.) in the world. Of the 288 species known globally, 62 occur across the greater Himalayan region, representing nearly 20% of global bumblebee fauna. The Indian Himalayan Region (IHR) harbours 59 species. In comparison, 77 species have been reported from northern China. Many bumblebee species recorded from China, Nepal, Bhutan, Tibet, Myanmar, Pakistan and Bangladesh are likely to occur in the IHR as well, particularly in border landscapes that share similar habitats, floristic elements, and biogeographic continuity. Targeted surveys in these transboundary zones may reveal additional species for India. This exceptional richness reflects the region's steep elevational gradients, diverse microclimates, complex topography, and long evolutionary history, all of which shape highly structured biogeographic and ecological patterns.

Himalayan bumblebees exhibit a suite of morphological and behavioural adaptations including dense insulating pile, enlarged wings, and advanced thermoregulatory abilities that enable successful foraging and colony activity under cold, hypoxic, and climatically unpredictable high-altitude conditions. Distinct elevational structuring characterizes their distribution: generalist species dominate lower and mid-elevation habitats, whereas specialized and often narrowly distributed taxa are associated with subalpine and alpine zones. Seasonal altitudinal migrations, synchronized with sequential flowering across elevation gradients, allow many species to exploit ephemeral floral resources during short phenological windows. Additionally, resource partitioning, manifested through differences in floral preferences, foraging periods, tongue length and microhabitat selection facilitates coexistence and contributes to the high species richness across the Himalayan landscape.

These biogeographic patterns underpin critical ecosystem functions. Bumblebees are keystone pollinators for a wide range of Himalayan montane and alpine flora, including *Rhododendron*, *Primula*, *Delphinium* and *Gentiana* as well as agricultural and horticultural crops such as buckwheat, apple and off-season vegetables. Their ability to forage effectively under low temperatures and variable weather ensures reliable pollination during the brief growing seasons characteristic of high-altitude environments.

In doing so, they maintain plant reproductive success, support genetic connectivity and contribute to the stability of fragile mountain ecosystems.

However, these pollinator plant interactions are increasingly threatened by rapid climate warming, habitat fragmentation, land-use change, pesticide exposure and phenological mismatches between bees and their floral hosts. Upward elevational shifts, shrinking alpine habitats and intensified interspecific competition pose particular risks to cold-adapted and range-restricted species. These challenges highlight the urgent need for enhanced understanding of bumblebee diversity, distribution and ecological roles across the Himalaya.

Integrating comprehensive taxonomic research, long-term ecological monitoring, climate–species interaction modelling and community-based conservation initiatives will be essential to safeguard Himalayan bumblebees and the ecosystem services they provide. As environmental pressures intensify the biodiversity and biogeographic dynamics of Himalayan bumblebees serve both as indicators of ecological vulnerability and as foundations for ecosystem resilience in one of the world's most sensitive mountain regions.



**PATTERNS, PROCESSES AND ECOSYSTEM-LEVEL DISTRIBUTION OF INDIAN
BEETLES: A NATIONAL SYNTHESIS OF DIVERSITY AND BIOGEOGRAPHY**

DEVANSHU GUPTA

Zoological Survey of India, M-Block, New Aliore, Kolkata, West Bengal 700053, India

Email: devanshuguptagb4102@gmail.com (corresponding author)

India's beetle fauna represents one of the most diverse components of the country's biodiversity, yet its consolidated assessment has remained fragmented for decades. Based on an extensive review of published literature and a newly compiled national dataset, we present the first comprehensive enumeration of Indian Coleoptera. The analysis documents over 21,000 valid species across 114 families, constituting one-third of India's insect diversity and nearly 22% of its total fauna. Beetles display strong ecosystem-level associations, with 766 species restricted to freshwater habitats, 340 to mangroves, 359 to agroecosystems, and nearly 8,862 species inhabiting soil ecosystems, highlighting their critical functional roles in nutrient cycling, pollination, decomposition, pest suppression, and environmental health.

The distribution of beetles across India is highly heterogeneous and shaped by ecological gradients, habitat complexity, and historical biogeographic processes. Diversity peaks along latitudinal and altitudinal gradients in the moist tropical and montane forests of the Himalayas and Northeast India, with the Himalayan biogeographic zone alone supporting 10,533 species from 107 families, accounting for almost half of the country's beetle fauna. Other rich zones include the Northeast (3,521 species), Deccan Peninsula (3,474), Ganges Plains (3,318), and the Western Ghats (1,967), all influenced by high habitat heterogeneity and climatic stability. In contrast, the Desert and Trans-Himalaya show lower but ecologically unique assemblages shaped by aridity, isolation, and microhabitat specialization. Significant patterns of endemism and micro-endemism occur in the Western Ghats, Eastern and Central Himalayas, Andaman–Nicobar Islands, and isolated hill ranges, where many species are restricted to single valleys, shola forests, montane wetlands, or cave systems. Historical sampling biases are also evident, with older colonial-era research stations (Darjeeling–Sikkim, Nilgiris, Shillong, Pune, and Kolkata) being relatively well-documented, while vast landscapes in central, western, and trans-Himalayan regions remain poorly surveyed.

Province-level analyses further reveal stark contrasts, with the Central Himalayas (5,081 species) being the richest, followed by the Western Himalayas (4,075), Northwestern Himalayas (2,903), and Upper Ganges (2,638). Under-sampled provinces such as the Tibetan Plateau, Ladakh Mountains, Western Drylands, and Nicobar Islands require focused exploration to uncover their true diversity. A critical concern is that many species remain known only from their type localities, and several taxa are represented by single locality records, indicating the urgent need for revisiting historical sites and conducting

systematic biodiversity surveys. The challenge is compounded for species described prior to India's independence, as their type specimens lie in foreign museums, complicating taxonomic clarity. Addressing these gaps demands comprehensive taxonomic revisions, integrative species delimitation approaches, enhanced access to type material, and long-term, region-specific sampling.

This national-level synthesis provides a crucial foundation for biodiversity monitoring, ecological research, and conservation planning. Strengthening coleopteran taxonomy and distributional knowledge is essential for informed decision-making in agriculture, environmental health, ecosystem management, and climate-resilient conservation strategies.



**HIDDEN HEALTH WORKERS OF SOIL: THE ROLE OF TROGIDAE IN CARCASS
DECOMPOSITION AND ENVIRONMENTAL HYGIENE FOR SUSTAINABLE ECOSYSTEMS**

APARNA SURESHCHANDRA KALAWATE

Zoological Survey of India, Western Regional Centre, Vidhya Nagar, Sector 29, P.C.N.T.
(PO), Rawet Road, Akurdi, Pune, Maharashtra 411044, India

Email: aparna_ent@yahoo.co.in (corresponding author)

Soil ecosystems support diverse biological communities that contribute to essential ecological processes such as nutrient cycling, decomposition, and environmental sanitation. Within these systems, several faunal groups remain understudied despite their functional relevance. Among them, Trogidae (carcass beetles) are key yet overlooked contributors to decomposition dynamics, particularly during the final phase of carrion breakdown. These beetles specialize in consuming dried animal remains including keratinous tissues such as skin, feathers, and bones, acting as nature's final cleaning agents responsible for the last stage of carcass recycling.

Globally, the family Trogidae is relatively small but widespread, comprising approximately 300–340 described species distributed across multiple continents. In India, trogid beetle diversity is still emerging as recent discoveries, distributional updates, and species records continue to expand the national checklist. The extant species from India including recent discoveries and new record stands at 16 species. These findings suggest that Indian trogid fauna is underexplored, and remote or ecologically unique landscapes likely hold additional undocumented species. The ongoing revision of this group highlights the importance of linking biodiversity documentation with ecological understanding to reveal the true functional value of these beetles.

The present paper includes information on the diversity, ecological role, and environmental contributions of trogid beetles in selected landscapes across India. It is based on the field surveys were conducted across a range of habitats including protected forests, dry grasslands, agricultural zones, and peri-urban environments and literature. Sampling efforts utilized pitfall traps, carcass-baited traps, and opportunistic examination of natural decomposing remains.

Their feeding activity enables the mineralization of keratin-rich materials, returning essential nutrients such as nitrogen, phosphorus, calcium, and trace minerals to the soil. In doing so, trogids play a role in pathogen reduction, natural sanitation, and organic waste breakdown, contributing to overall soil health and ecological balance.

Beyond their direct ecological role, trogid beetles provide ecosystem services that align with global sustainability frameworks. Their natural contribution to biological waste removal supports Sustainable Development Goal (SDG) 12: Responsible Consumption and Production, while their role in soil fertility and biodiversity resilience aligns with SDG 15: Life on Land. Additionally, by reducing the persistence of decomposing biomass and preventing environmental contamination, they indirectly support SDG 6: Clean Water and Sanitation and SDG 13: Climate Action.

Despite their important contributions, trogid beetles remain largely absent from biodiversity monitoring programs, forensic entomology applications, and environmental policy discussions. Increasing research attention toward this family can enhance our understanding of decomposition ecology, improve soil biodiversity documentation, and support conservation priorities.

In conclusion, Trogidae serve as hidden health workers of soil ecosystems, providing essential yet underrecognized services in carcass decomposition, natural sanitation, nutrient recycling, and sustainable ecosystem functioning. A deeper understanding of their diversity and ecological role is essential for advancing soil biodiversity science and supporting long-term environmental sustainability.



**THE BIOGEOGRAPHIC SIGNIFICANCE OF HOST SPECIFICITY IN TRACKING OF
DIVERGENT GONDWANAN AND ORIENTAL LINEAGES OF PARASITIC
HYMENOPTERA IN INDIA**

BINOY C

Marine Aquarium & Regional Centre, Zoological Survey of India, Digha, West Bengal
721428, India

Email: binoybijoy619@gmail.com (corresponding author)

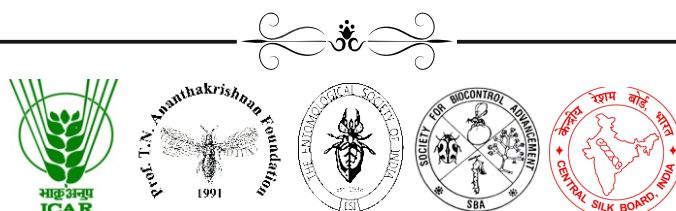
The Indian subcontinent presents a historically singular biogeographic domain, shaped by its long isolation as a drifting Gondwanan fragment during the Cretaceous (c. 130–100 Ma) and its tectonic collision with Asia in the Eocene (c. 55–35 Ma). This geological trajectory has produced a deeply stratified and spatially heterogeneous biodiversity, offering an ideal system for testing macroevolutionary hypotheses. Parasitic Hymenoptera is hyperdiverse, ecologically dominant, and tightly bound to their hosts, which provide an especially sensitive model for uncovering the evolutionary consequences of India's tectonic and climatic past. Major lineages under Chalcidoidea, Ichneumonoidea, Platygastroidea, Cynipoidea, Ceraphronoidea, Evanioidea, Diaprioidea, and Proctotrupeoidea collectively form the regulatory foundation of terrestrial ecosystems, their life cycles obligately tied to single-host systems. This extreme specialization makes their host associations uniquely informative: each host record reflects habitat specificity, potential niche shifts, and the coevolutionary pressures that shape lineage stability, diversification, and geographic expansion. Recent field surveys have also uncovered elements traditionally associated with the New World within India's Hymenopteran fauna, highlighting the subcontinent as a bridge between biogeographic realms and suggesting previously unrecognized dispersal or vicariant events.

Building on this foundation, emphasis is directed at host-association research as a central tool in understanding parasitoid ecology and as an emerging pillar in taxonomy. Detailed host records, all the way from gall inducers, endophytic beetles, phytophagous caterpillars, litter-dependent dipterans, to concealed feeders, provide critical insight into microhabitat specialization, developmental timing, and host-driven ecological partitioning. These data reveal how parasitoids respond to fine-scale environmental gradients, track host availability, and partition niches across complex landscapes such as mangroves, dry forests, and arid scrublands. Novel host associations from intensive field surveys demonstrate that host ecology directly informs species boundaries, providing reproducible, biologically meaningful criteria for taxonomic delimitation. Additionally, some newly described taxa show affinities to lineages from Madagascar and South America, emphasizing India's role as a nexus of ancient Gondwanan and transoceanic lineages.

Parasitoid biology and host interactions are therefore central to species identification and classification: extreme host specificity, tightly synchronized life cycles, and sensitivity to microclimatic variation generate biological signatures that complement morphological traits. Populations exploiting distinct hosts or host guilds often exhibit subtle but consistent morphological or behavioural differentiation, highlighting cryptic diversity. In this sense, host association studies serve as a practical, empirically grounded method for resolving taxonomic ambiguities in hyperdiverse groups where morphology alone may be insufficient.

While evolutionary and phylogenomic patterns remain informative, they are interpreted here in support of ecological and biological data. Molecular evidence broadly confirms two trends: deep-rooted Gondwanan lineages with restricted host ranges and ecological fidelity persist in stable refugia like the Western Ghats, while younger Oriental clades display broader host spectra and ecological flexibility, reflecting post-collision habitat expansion. These patterns underscore the necessity of integrating ecological, host-association, and biological knowledge into modern taxonomic frameworks.

By foregrounding host ecology and parasitoid biology, this study provides a robust framework for delimiting species, understanding lineage dynamics, and interpreting biogeographic distributions. Host-association studies emerge not only as a window into ecological functioning but also as a crucial, evidence-based tool in taxonomy, enabling more precise, biologically informed classification. This ecology- and host-driven perspective is essential for conserving functional diversity and maintaining the integrity of India's biodiversity hotspots, where ancient relicts and rapidly radiating taxa coexist. The discovery of elements previously thought restricted to other biogeographic realms reinforces India's significance as a repository of global Hymenopteran diversity and emphasizes the importance of cross-realm comparative studies.



**BIODIVERSITY AND ECOLOGY OF MAYFLY (INSECTA: EPHEMEROPTERA)
IN ARUNACHAL PRADESH, INDIA**

KUBENDRAN T

Miscellaneous Insect Order Section, Zoological Survey of India, Prani Vigyan Bhawan,
535, M-Block, New Alipore, Kolkata 700053, India

Email: tkbaetis@gmail.com (corresponding author)

Arunachal Pradesh, located in the Eastern Himalaya, harbours exceptionally rich Ephemeroptera (mayfly) diversity driven by steep altitudinal gradients, varied freshwater habitats and long-term landscape stability. Recent surveys and taxonomic work document the Indian Himalayan Ephemeroptera fauna as comprising dozens of genera and many regionally endemic species, with Arunachal among the richest states for mayfly diversity. Previously only 47 species are recorded from this region. Presently our expeditions increase the species to 64 from the same geography. The collections were made through hand picking and kick-net and light trap methods. Mayflies in this region exhibit evolutionary features typical of the order while also showing pronounced local differentiation: larval adaptations to fast-flowing, oxygen-rich streams, and clades restricted to particular elevational bands point to allopatric and ecological speciation across river drainages and mountain barriers. Recent taxonomic descriptions from Arunachal Pradesh (*Platybaetis arunachalensis*, *Vietnamella* sp. *Notacanthurus pange*, *Megabranchiella* sp. etc.) highlight both previously undocumented lineage diversity and the region's role as a centre for on-going mayfly diversification. Ecologically, mayfly larvae are key components of stream food webs and reliable bio-indicators of water quality-their presence and community composition reflect substrate, flow and chemical conditions of pristine headwaters. Arunachal's intact forest-stream mosaics therefore support high mayfly richness but are vulnerable to hydrological alteration, land-use change, pollution and climate-driven shifts in flow and temperature. Conservation of upland catchments, coupled with systematic sampling and integrative taxonomy, is essential to document diversity, resolve evolutionary relationships, and monitor freshwater health in this biodiversity hotspot.

CURRENT STATUS OF VESPID WASPS (HYMENOPTERA: VESPIDAE) OF INDIA

GIRISH KUMAR P

Western Ghat Regional Centre, Zoological Survey of India, Kozhikode,
Kerala 673006, India

Email: kpgiris@gmail.com (corresponding author)

The family Vespidae is one of the large families within the superfamily Vespoidea of the order Hymenoptera consisting of 292 valid species from India. It is a widely distributed cosmopolitan family consisting of six subfamilies: Euparagiinae, Eumeninae, Masarinae, Stenogastrinae, Polistinae, and Vespinae. The members are mostly predatory in nature and are commonly known as potter wasps (Eumeninae), pollen wasps (Masarinae), hover wasps (Stenogastrinae), paper wasps (Polistinae), and yellow jackets and hornets (Vespinae). Due to their predatory behavior, they play an important role in controlling pests in agroecosystems and are one of nature's best architects owing to their skill in making a variety of nests. Among the six subfamilies, except Euparagiinae all are present in India. Among them, Eumeninae and Masarinae are solitary, Stenogastrinae is primitively social, and Polistinae and Vespinae are eusocial. Eumeninae and Masarinae make a variety of nests ranging from simple burrows, use of pre-existing cavities to build beautiful mud or clay nests. Social vespids lead a social life in colonies. Each colony consists of at least one queen (fertile female), drones (males) and workers (sterile females).

Eumeninae is the largest subfamily within the family Vespidae. It is one of the poorly studied subfamily, particularly in comparison with the better known Vespinae. However, recent studies have provided a more comprehensive knowledge of the size of the fauna and its systematics. A total 196 valid species with many additional subspecies under 47 genera in 3 tribes are currently recognized from India. Of them 60 species are endemic to India. The taxonomic understanding of the many genera are still pretty poor. The members of the subfamily Masarinae provision their larvae with pollen and nectar rather than hunting prey like most other vespids. This subfamily is reported from India by a single endemic species. The members of the subfamily Stenogastrinae unique for their nesting habits. They make delicate paper-like nests that hang from a single stalk. It is one of the poorly studied subfamily with only 6 species under 3 genera are currently recognized from India. The subfamily Polistinae is comparatively a well-studied subfamily from India. A total 62 species with many additional subspecies under 4 genera in 2 tribes are currently recognized from India of which the genera *Polistes* Latreille, 1802 and *Ropalidia* Guérin-Méneville, 1831 are having large number of species, 28 and 27 respectively. In this subfamily 14 species are endemic to India only. The taxonomic understanding of genera such as *Belanogaster* de Saussure, 1853 and *Parapolybia* de Saussure, 1853 are pretty poor. The subfamily Vespinae is also a well-studied subfamily from India. A total 26 species with many additional subspecies under 4 genera are currently recognized from India of which the genus *Vespa* Linnaeus, 1758 is having maximum number of species i.e., 14.



IMPACT OF CLIMATE CHANGE ON THE DISTRIBUTION OF HILL STREAM
ODONATA (INSECATATA) OF THE WESTERN GHATS: A CASE STUDY ON
EUPHAEA FRASERI (LAIDLAW, 1920)

GIJA ANNA ABRAHAM, SUBRAMANIAN K A* AND BABU R

Zoological Survey of India, Southern Regional Centre, Chennai, Tamil Nadu 600028, India

*Email: subbuka.zsi@gmail.com (corresponding author)

Ongoing climate change has been a major factor in changing geographic distribution and range of species. The expected decline in geographic range caused by climate change is more pronounced in freshwater biodiversity than in marine and terrestrial biodiversity, increasing the risk of species extinction. The dragonflies and damselflies (Insecta: Odonata) are primarily aquatic and also serve as excellent model organisms for studying the effects of climate change due to their high diversity, various developmental stages and phenological responses to climatic change. Species distribution modelling using current occurrence data and bioclimatic and other environmental variables is an effective method for understanding the potential impact of climate change on species distribution. In the present study, we used an ensemble model approach to examine the current and future habitat suitability of an endemic damselfly *Euphaea fraseri* (Laidlaw, 1920) (Insecta: Odonata: Zygoptera: Euphaeidae) restricted to the hill streams of the Western Ghats. The Species Distribution Modelling (SDM) was carried under two shared Socio-Economic Pathways (SSP 126 and SSP 585) for the years 2041-2060, 2061-2080, and 2081-2100. A total of 287 species occurrence data and 9 environmental variables were used to predict the current and future distribution. Model performance was evaluated using True Skill Statistic (TSS), and Area Under Curve (AUC). Among the models tested, machine learning algorithms such as Random Forest (RF) and MaxEnt achieved the highest accuracy, with area under the curve (AUC) values of 0.91. The modelling results indicated that the mean diurnal temperature range [mean of monthly (max. temp. – min. temp.)] and annual precipitation were the most influential environmental parameters influencing the current distribution. The results of the current distribution show that *Euphaea fraseri* was found to be currently distributed in 83922.57km² whereas it was expected to expand its range to 97517.12 km² under SSP 585 for the year 2090, indicating the expansion of its range. There is a significant range expansion of about 16.2% for *Euphaea fraseri* under future climate scenarios SSP 585 for the year 2090, indicating that the projected future increase in rainfall under SSP 126 and SSP 585 potentially favour the range expansion of the species in the region. However, the current study is based only on the distribution records of the adults. The climate related changes in the hydrology of hill streams may also influence larval habitats and future species distribution modelling studies need to incorporate larval habitat variables to comprehensively understand the impact of climate change on hill stream damselflies.

SPIDERS (ARACHNIDA: ARANEAE) AS NATURAL ENEMIES OF TEA PESTS
IN THE TEA ECOSYSTEM OF MEGHALAYA

T1-A-10

SOUVIK SEN

Zoological Survey of India, Prani Vigyan Bhawan, M-Block, New Alipore, Kolkata,
West Bengal 700053, India

Email: sensouvik07@gmail.com (corresponding author)

Tea, *Camellia sinensis* (L.) O. Kuntze is an intensively managed, perennial monoculture crop which is widely cultivated across India, especially in South and North East India. In Meghalaya, one of India's seven northeastern states, tea cultivation is rising due to its distinct biogeographic location within the Indo-Burma biodiversity hotspot, along with its cool, moist, and high-altitude climatic conditions. Tea ecosystems provide a stable and favourable environment that harbours a wide range of phytophagous insect and mite pests. Spiders (Arachnida: Araneae), one of the most diverse and ecologically important group of predaceous terrestrial arthropods, play a pivotal role as natural enemies in the suppression of such notorious pests. However, adequate knowledge regarding the role of spiders as natural enemies of tea pests across tea ecosystems of Meghalaya is largely lacking. Previous studies primarily focused on documenting the overall diversity of spiders across various habitat types in the hilly regions of Meghalaya. To bridge this gap, a comprehensive study was conducted across tea plantations in Meghalaya from April 2022 to March 2024. Spider diversity was recorded for three distinct seasons, pre-monsoon (March to May), monsoon (June to August), and post monsoon (September to November). The study documented a total of 52 species of spiders. Recorded spiders were classified under six different guild types (orb-weavers, space-weavers, sheet-weavers, stalkers, ambusher and runners). The most dominant family was revealed to be Salticidae Blackwall, 1841 (14 species), followed by Araneidae Clerck, 1757 (12 species), Oxyopidae Thorell, 1869 (08 species), Lycosidae Sundevall, 1833 (08 species). Spiders exhibited greater abundance during the wet season compared to the dry season. The most encountered tea pests were *Helopeltis theivora* Waterhouse, 1886 (Hemiptera: Miridae), *Toxoptera aurantii* (Boyer de Fonscolombe, 1841) (Hemiptera: Aphididae) and *Oligonychus coffeae* (Nietner, 1861) (Acari: Tetranychidae). Marked stratification strategies were recorded among orb-weavers, utilized for capturing diverse prey types. The study also documented 10 new records to the state. The findings of this study indicate that Meghalaya's tea ecosystems support a diverse array of spiders, which can potentially contribute to ecologically sustainable pest management strategies. Key determinants of spider diversity within these tea plantations include habitat structure, prey availability, pesticide application, cultivation process and microclimatic conditions. The study also emphasizes the importance of conservation of spiders as natural enemies which can further lead to a reduction in the use of broad-spectrum chemical pesticides. Establishment of such a comprehensive baseline taxonomic inventory will facilitate the understanding of predator-prey dynamics of a complex ecosystem. This will ultimately result in a more resilient and environmentally sustainable tea production system in the state.



SILENT EXTORTIONER: MONOCOT-FEEDING WHITEFLIES OF THE
EASTERN GHATS OF INDIA

KAVYA YADAV G A^{1*}, VASUNDHARA J¹, SELVARAJ K^{1*} AND SUNDARARAJ R²

¹ICAR-National Bureau of Agricultural Insect Resources, Bengaluru,
Karnataka 560024, India

²Institute of Wood Science & Technology, Bengaluru, Karnataka 560003, India

*Email: g.a.kavya@gmail.com; selvaentomo@gmail.com (corresponding authors)

Whiteflies (Hemiptera: Aleyrodidae) are economically significant phloem-feeding insect pests, predominantly associated with dicotyledonous hosts. However, in the Indian ecosystem, several species have increasingly expanded their host range to important monocotyledonous plants during the study period (2024-2025). This shift presents emerging challenges for crop production and protection. Both the subfamilies i.e., Aleurodicinae and Aleyrodinae are found associated with monocotyledonous hosts, particularly members of the families Arecaceae and Poaceae. Major monocot-infesting whiteflies species were identified morphologically using taxonomic keys, and the species documented in Eastern ghats region of India include *Aleurodicus rugioferulatus* Martin on coconut, banana, date palm, oil palm, ornamental palms and maize; *Aleurodicus dispersus* Russell on coconut, banana, date palm, oil palm, and ornamental palms; *Paraleyrodes bondari* Peracchi on coconut, banana, cardamom, sugarcane, date palm, oil palm, ornamental palms, bamboo and *Cynodon*; *Paraleyrodes minei* Iaccarino on coconut, cardamom and ornamental palms; and *Aleurotrachelus atratus* Hempel on coconut, date palm, oil palm and ornamental palms. Additional species such as *Neomaskellia andropogonis* Corbett on lemongrass, *Aleurolobus barodensis* (Maskell) on sugarcane and wild sugarcane, *Aleurocanthus longispinus* Quaintance & Baker on bamboo, *Bemisia formosana* Takahashi on rice, and *Vasadavidius indicus* (David and Subramaniam) on *Cynodon*. This survey highlights the emerging significance of whiteflies on coconut, rice, and grasses in India and underscores the need for strengthened surveillance to understand their expanding host associations and ecological impact in developing integrated pest management strategies tailored to monocot crops.

**DIVERSITY OF THRIPS SPECIES ACROSS VEGETABLE ECOYSTEM FROM
KARNATAKA**

DURGA G^{1*}, KALLESHWARASWAMY C M¹ AND RACHANA R R²

¹Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga,
Karnataka 577412, India

²ICAR-National Bureau of Agricultural Insect Resources, Bengaluru, Karnataka 560024, India

*Email: durga.g.chowdary@gmail.com (corresponding author)

Thrips are among the most economically significant pests on vegetables due to their high polyphagy, rapid reproduction, and ability to transmit tospoviruses. Given their high polyphagy in vegetable crop ecosystems, the potential for thrips to occur on alternate hosts is substantial and cannot be overlooked. Consequently, surveys from 2020-2023 across Karnataka, revealed that they were expanded host plant ranges which include weeds and surrounding crops, as thrips readily infest diverse plant families. A total of 31 thrips species under 21 genera, belonging to three subfamilies and two families were reported to predominantly infest families such as Anacardiaceae, Apiaceae, Asteraceae, Cucurbitaceae, Euphorbiaceae, Fabaceae, Liliaceae, Malvaceae, Punicaceae, Rosaceae, Solanaceae. Among these, the family Thripidae was the most dominant, comprising 29 species under 19 genera, while Phlaeothripidae was represented by only two species under two genera. Within Thripidae, the subfamily Thripinae accounted for the majority with 23 species, followed by Panchaetothripinae with six species under six genera. The genus *Thrips* Linnaeus was the most diverse with nine species, reported from more than 50 host plants, followed by *Scirtothrips* Shull from 11 hosts, *Frankliniella* Karny from six hosts, and *Megalurothrips* Bagnall from four hosts. In Panchaetothripinae, each of the genera *Caliothrips* Daniel, *Heliiothrips* Haliday, *Retithrips* Marchal, *Rhipiphorotherips* Hood and *Selenothrips* Karny, was represented by two species. This study highlights significant thrips diversity across vegetable ecosystems and underscores the need for continuous monitoring to manage them effectively.



Theme II
Insect Toxicology, Physiology,
Genetics, Molecular Entomology
and Biotechnology

MULTIREGIONAL ASSESSMENT OF INSECTICIDE RESISTANCE AND DETOXIFICATION
MECHANISMS IN MAJOR INDIAN PEST SPECIES

MURUGAN M*, SENGUTTUVAN K, ALAGAR M, MUTHU LAKSHMI BAVITHRA
C AND PRAKASH K

Department of Agricultural Entomology, TNAU, Coimbatore, Tamil Nadu, India

*Email: muruganmarimuthu@tnau.ac.in (corresponding author)

Insecticides remain fundamental to modern agriculture, yet their intensive and repetitive use has accelerated the development of resistance in many economically important pests. This review synthesizes recent findings on insecticide resistance mechanisms and field-level resistance trends in major crop pests across India. Insecticide resistance primarily arises through enhanced metabolic detoxification and target-site modifications, supported by additional mechanisms such as behavioral avoidance, reduced penetration, and fitness-related changes. Recent studies on *Leucinodes orbonalis* have reported low to high resistance to spinosyns and diamides, associated with elevated CYP, GST, and CarE activity, and the presence of key RyR mutations such as I4775M. In *Tuta absoluta*, high resistance to flubendiamide and correlated cross-resistance patterns were linked to substantial increases in detoxification enzyme activity. Field populations of *Maruca vitrata* exhibited high resistance to several insecticides, while *Plutella xylostella* demonstrated strong diamide resistance along with the G4946E RyR mutation, unlike *Spodoptera litura*. Moderate resistance to neonicotinoids and pyrethroids was recorded in *Bemisia tabaci*, with continued susceptibility to cyantraniliprole. Additional studies on *Spodoptera frugiperda* and *Tribolium castaneum* highlight the roles of detoxification and antioxidant enzymes in mediating resistance. The widespread and increasing levels of resistance across crops and regions emphasize the urgent need for robust Insecticide Resistance Management (IRM) strategies. Integrating chemical rotation, optimized application practices, biological control, and continuous resistance monitoring is essential to sustain effective pest management and safeguard agricultural productivity.



APPLICATIONS AND CONSTRAINTS FOR CRISPR/CAS BASED GENOME
EDITING IN INSECT PEST MANAGEMENT & ALLIED RESEARCH IN INDIA

ASOKAN R

Principal Scientist (Rtd.), ICAR-Indian Institute of Horticultural Research Bengaluru,
Karnataka 560089, India

Email: asokanihr@gmail.com (corresponding author)

Advent of CRISPR/Cas based eukaryotic genome editing during the early 2013 paved way for introducing programmable, site-specific mutations, mainly aimed at achieving loss-of-function of the target gene/s. The unprecedented ease has stimulated research in various domains that include agriculture for crop improvement, developing newer approaches in insect pest management etc. In this regard Cas9 protein was the first one to have been discovered and employed for an RNA directed DNA cleavage for obtaining locus-specific random mutations primarily to establish the gene function. Later several other Cas proteins belonging to Class 1, Class 2 and different types under these came to be used in insect genome editing. To cite a few other prominent members are used in insect genome editing are Cas12a, CasX, Cas14, Cas13a etc. Further research led to the discovery newer Cas proteins and their natural variants that require a different Protospacer Adjacent Motif (PAM) extending the scope of efficient insect genome editing. Additionally precise insect genome editing has become possible with the development of Base editing and Prime editing to introduce RNA directed specific mutation/s. The power of genome editing can be harnessed in realizing chemical-free, areawide pest management by editing insect genome in order to develop precision guided sterile insect technique (pgSIT) which is driven through a suitable gene drive method. In addition, editing crops is also a lucrative option by targeting insect responsive host gene/s. In this regard, India has recently permitted field-release of genome edited crops developed at site directed nuclease 1 (SDN 1) and site directed nuclease 2 (SDN 2) levels. This will facilitate field deployment of genome edited, insect resistant crops in near future in India. Currently there are no guidelines are available for insect genome editing research excepting for handling transgenic insects essentially developed through *piggyBac* transposon. Lack of annotated genomic information for many pest species is also a serious limitation in order to reduce off-target and non-target effects. Never the less, various CRISPR proteins such as Cas9, Cas12a and Cas13a are being employed in insect taxonomy, development of diagnostic kits for insect transmitted viruses etc. There is lot of scope in employing genome editing for improving biocontrol agents and also ecosystem service providers for various traits such as resistance to insecticides and other biotic and abiotic stresses.

FROM TRANSMISSION TO MOLECULAR INTERACTIONS: DECODING VIRUS-
VECTOR RELATIONSHIPS FOR SUSTAINABLE PEST MANAGEMENT

AMALENDU GHOSH

Insect Vector Laboratory, Advanced Centre for Plant Virology, ICAR-Indian Agricultural
Research Institute, New Delhi 110012, India

Email: amal4ento@gmail.com (corresponding author)

Insect vectors transmit nearly 90% of plant viruses, causing significant economic losses in agriculture. *Thrips palmi* serves as a predominant vector of tospoviruses in the Indian subcontinent, facilitating the spread of viruses such as groundnut bud necrosis virus (GBNV) and watermelon bud necrosis virus (WBNV). Tospovirus infection alters thrips biology, longevity, and sex ratio, favouring the virus transmission. Adults can only become viruliferous if virus acquisition occurs in early instar larvae. The virus is acquired during the early larval stage, progressing from the midgut to the salivary glands. Our research revealed that anatomical connections between the midgut and salivary glands persist in adults, indicating that midgut susceptibility is stage-specific rather than anatomical discontinuity serving as a transmission barrier. The establishment of *T. palmi* primary cell culture has enabled in-depth molecular investigations. The key genes of *T. palmi* associated with tospovirus transmission have been identified. Functional analyses indicate silencing *UHRF1BP1* and *PFAS* reduces viral titers in thrips and induces developmental deformities. Targeting *Btk29A*, *COL3A1*, and *V-ATPase-B* through RNAi significantly impairs thrips fitness and alters tospovirus acquisition by *T. palmi*. Silencing *E3-UBR7* significantly inhibits the tospovirus replication in thrips and reduces the vectoring efficiency. Topical dsRNA targeting *V-ATPase-B* protects thrips, and slow-release dsRNA bioformulations further enhance efficacy under field conditions. These findings enhance our understanding of thrips-tospovirus interactions and provide a foundation for RNAi- and gene-editing-based strategies, offering a sustainable alternative to chemical pesticides for thrips and virus management in agriculture.



PERSISTENT COVERT INFECTIONS AND NOVEL RNA VIRUSES IN THE
MELON FLY, *ZEUGODACUS CUCURBITAE*

SANJAY KUMAR PRADHAN^{1,2,3*}, JENNIFER L MORROW¹, SHIVANNA
BYNAKAL², ASOKAN RAMASAMY³ AND MARKUS RIEGLER^{1*}

¹Hawkesbury Institute for the Environment, Western Sydney University, Locked Bag 1797,
Penrith, NSW 2751, Australia

²Department of Agricultural Entomology, University of Agricultural Sciences,
Bengaluru 560065, India

³ICAR-Indian Institute of Horticultural Research, Hesaraghatta Lake (PO),
Bengaluru 560089, India

*Email: spradhan314@uky.edu; m.riegler@westernsydney.edu.au (corresponding authors)

RNA viruses are increasingly recognised as integral components of insect biology, influencing host physiology, ecology and evolution. While some cause overt pathogenic effects, many persist asymptotically, yet can still affect host fitness and thereby shape population dynamics. The melon fly, *Zeugodacus cucurbitae* (Diptera: Tephritidae), is one of the most destructive agricultural pests across the world, infesting cucurbits and several other crops of economic significance. Originally of Indomalayan origin, the species has spread widely across Asia, Africa and the Pacific, where it poses major challenges to crop production, quarantine and biosecurity. Despite its pest status, little is known about the viral communities associated with *Z. cucurbitae*, especially in native-range populations from the Indian subcontinent. To address this gap, we analysed RNA-Seq transcriptome data from both field-collected and laboratory-reared *Z. cucurbitae* populations from Bangalore, India. The analysis revealed ten putative RNA virus genomes from diverse families: two sigmaviruses (*Rhabdoviridae*), one chimbavirus (*Leviviridae*), one cripavirus (*Dicistroviridae*), one noda-like virus (*Nodaviridae*), one nora virus (*Noraviridae*), one orbivirus (*Sedoreoviridae*), one partiti-like virus (*Partitiviridae*), one sobemovirus (*Solemoviridae*) and one toti-like virus (*Totiviridae*). Screening of the available host genome from a Hawaiian laboratory population showed no integration of these viruses, supporting their occurrence as active infections. Notably, all ten viruses were present in the Bangalore field population, but only seven were found in the Bangalore laboratory population, suggesting that the latter may represent persistent covert infections capable of long-term maintenance under laboratory conditions. Further validation using RT-PCR using RNA-dependent RNA polymerase gene primers confirmed the presence of nine viruses in individual flies sampled from four out of five Indian regions (National Capital Territory of Delhi, Punjab, Bihar, Karnataka, Kerala). Variant diversity was generally low, although some viruses exhibited heterogeneity among individuals, reflecting natural infection dynamics.

Broader comparative screening of 39 available transcriptomes from *Z. cucurbitae* laboratory colonies in East Asia (Guangdong, Hainan, Taiwan) and the Pacific (Hawaii) identified seven of the viruses detected in India, along with two additional genomes belonging to a picorna-like virus and a negev-like virus. Strikingly, the Hawaiian population, representing the invasive range, carried only a single virus, pointing to a possible reduction of virome diversity during colonisation. The present study constitutes the first comprehensive virome analysis of *Z. cucurbitae*, revealing remarkable RNA virus richness in Indian populations and evidence of persistent covert infections in laboratory colonies. The contrast between native and invasive populations underscores the potential role of ecological and demographic factors in shaping viral diversity. By documenting these novel viral associations, the study provides a critical baseline for future investigations into virus–host interactions, their epidemiological implications, and their possible exploitation in the biological control of tephritid pests.



SILENT SABOTEURS: THE HIDDEN POWER OF APHID SALIVA IN PEST-PLANT
INTERACTIONS

PAVITHRAN S¹²

¹Department of Agricultural Entomology, Tamil Nadu Agricultural University, Coimbatore,
Tamil Nadu 641003, India

²Central Silk Board, Bangalore, India

Email: sspavithranmsd@gmail.com (corresponding author)

Aphids, commonly referred to as plant lice, are phloem-feeding insects that pose serious challenges to crop cultivation and global food security. Among them, the cowpea aphid *Aphis craccivora* and the cotton aphid *Aphis gossypii* are economically significant pests in tropical regions, causing extensive damage through direct feeding and transmission of plant viruses. Both species possess paired salivary glands, each comprising a bilobed principal gland and a spherical accessory gland connected by an 18–23 μm duct. The principal gland is deeply innervated, while the accessory gland lacks innervation. In adult *A. craccivora*, the salivary glands measure 189–236.33 μm , with earlier instars showing reduced gland lengths. In *A. gossypii*, adult gland lengths range from 127–139 μm , progressively increasing from 97 μm in the L1 instar to 127 μm in L4. The salivary sheath architecture in both species resembles a pearl-necklace structure, with individual bead-like units measuring 65.49–103 μm . Proteomic analysis identified 171 proteins in the watery saliva of *A. craccivora*, of which 35 possessed N-terminal signal peptides, indicating secretion. The salivary proteome also revealed proteins of *Buchnera aphidicola*, including isoleucine-tRNA ligase, DNA gyrase subunit A, homoserine kinase, and SecA. Known aphid effector proteins Mp1 and Mp58 were also detected. In total, 151 salivary gland proteins were profiled, with 43 classified as secreted. In *A. gossypii*, 112 saliva proteins and 214 salivary gland proteins were identified, with 23 and 18, respectively, predicted as secretory. Sixteen proteins overlapped between saliva and salivary gland datasets. Saliva collected from artificial-diet feeding showed fewer cytoskeletal and structural proteins than excised salivary glands, likely reflecting diet-based physiological differences. Transcriptomic sequencing generated 1,08,275 transcripts for *A. craccivora* and 1,23,008 transcripts for *A. gossypii*, with BUSCO completeness scores of 99.4% and 99.1%, respectively.

Theme II
Insect Toxicology, Physiology, Genetics, Molecular Entomology and Biotechnology

Trans Decoder identified 1,08,275 predicted proteins in *A. craccivora* and 57,988 complete protein sequences in *A. gossypii*. Signal peptide prediction and localization analyses identified 2,159 putative secreted proteins in *A. craccivora* and 2,933 in *A. gossypii*, many functioning in plant defense modulation, detoxification, and host specialization. Orthology analysis of *A. gossypii* revealed 183 clusters shared with other aphids, including 61 conserved effector homologs. Cross-species comparison with hemipterans identified 88 orthologous clusters, with the greatest overlap between *A. gossypii* and *Bemisia tabaci*. Computational modeling of protein–plant interactions using D-Script predicted 27 secreted proteins of *A. craccivora* and two of *A. gossypii* to interact with host NBS-LRR resistance proteins, suggesting roles in manipulating plant immunity. All transcriptome and proteome datasets were deposited in NCBI and ProteomeXchange (PRJNA1006194, PRJNA1014193; PXD044614, PXD045238), providing comprehensive genomic resources to facilitate future studies on aphid–plant interactions.



EVOLVING PATTERNS OF INSECTICIDE RESISTANCE IN INDIA:
TRENDS, CHALLENGES AND RESEARCH PRIORITIES

RAJNA S

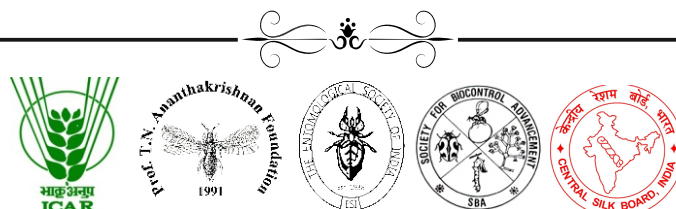
Division of Entomology, ICAR-Indian Agricultural Research Institute, New Delhi 110012, India

Email: rajnasalim@gmail.com (corresponding author)

Insecticide resistance has emerged as one of the most serious threats to sustainable crop protection in India, where intensive, input-responsive production systems rely heavily on chemical control. Synthesizing recent evidence on major field and horticultural pests shows a consistent increase in both the number of resistant species and the spectrum of active ingredients to which they are no longer susceptible. Key pests in India such as the gram pod borer (*Helicoverpa armigera*), diamond back moth (*Plutella xylostella*), fall army worm (*Spodoptera frugiperda*), tobacco cut worm, (*S. litura*), brown planthopper (*Nilaparvata lugens*), whitefly (*Bemisia tabaci*), *Aphis* spp. etc have evolved resistance to multiple insecticide groups, including organophosphates, carbamates, pyrethroids, neonicotinoids, diamides, phenylpyrazoles and insect growth regulators, often with cross-resistance across chemistries that share molecular targets or detoxification pathways. Metabolic resistance mediated by overexpressed cytochrome P450 monooxygenases, esterases and glutathione-S-transferases, and target-site mutations in acetylcholinesterase, voltage-gated sodium channels, nicotinic acetylcholine receptors and GABA receptors, are the dominant resistance mechanisms. Repeated use of single modes of action, calendar spraying, sub-lethal field doses, off-label mixtures and poor integration with non-chemical tactics, together with ecological drivers like polyphagy, continuous host availability under irrigated systems and extended pest occurrence in changing weather etc. have accelerated the selection and spread of resistant populations in India and across world. Currently, there are several critical gaps for resistance management and future research in India. Information on the spatial and temporal distribution of resistance remains patchy, with systematic monitoring confined to a limited set of crops, pests and active ingredients. Region-wise mapping of resistance status for key insect-insecticide combinations, using standardized bioassay protocols, is urgently needed to guide location-specific recommendations, refine economic thresholds and tackle control failures. Cross-resistance relationships among older chemistries and newer active ingredients are poorly characterized under Indian condition. Coordinated bioassay and molecular studies across representative field populations, covering major insecticide groups used in rice, cotton, maize, vegetables etc should be prioritized. Development, validation and deployment of simple, robust, field-compatible diagnostic kits based on discriminating concentrations, metabolic enzyme markers or key target-site mutations would enable real-time decisions by researchers, extension personnel and industry.

**Theme II
Insect Toxicology, Physiology, Genetics, Molecular Entomology and Biotechnology**

Establishing a national open-access database, harmonized with the global Arthropod Pesticide Resistance Database can facilitate resistance mapping and evidence-based policy on insecticide registration and label claims. Increasing insecticide resistance in major crop pests across India shows an urgent need for regular monitoring, mapping, and better resistance-management practices to protect crops and ensure long-term effective pest control.



GENOMIC WORKFLOW FOR WHITEFLIES AND THEIR NATURAL ENEMIES
SYSTEMATICS

VASUNDHARA J^{1*}, KAVYA YADAV G A¹, SELVARAJ K^{1*}, RAMESH KUMAR A²
AND VENKATESAN T¹

¹ICAR-National Bureau of Agricultural Insect Resources, Bengaluru, Karnataka 560024, India
²Zoological Survey of India (HQ), Kolkata, West Bengal 700053, India

*Email: vasundharajagan1710@gmail.com; selvaentomo@gmail.com (corresponding authors)

Taxonomic research on whiteflies (Hemiptera: Aleyrodidae) has traditionally relied on puparial morphology, a stage that provides several diagnostic features. In parallel, their natural enemies particularly aphelinid parasitoids and predatory taxa (Diptera and Coccinellids) are identified through adult morphological characters (antennae, wing venation, and genitalia) of slide-mounted specimens. Following morphological confirmation, specimens were subjected to molecular identification through genomic DNA extraction using the DNeasy Blood and Tissue Kit (Qiagen, Germany) and standardised for individual specimens to obtain high-quality DNA. Target gene regions were amplified using specific primers for whitefly (mtCOI) and parasitoids (COI, ITS2, 28S-D2/D3 primers) under optimized polymerase chain reaction (PCR) conditions for each primers. The resulting amplicons were purified and sequenced bidirectionally. Sequence chromatograms were edited, assembled, and validated to generate high-confidence consensus sequences. These processed sequences, along with detailed specimen metadata, were annotated and submitted in National Center for Biotechnology Information (NCBI) database. A total of 65 gene sequences representing both whiteflies and their natural enemies were submitted to NCBI from specimens collected during extensive surveys conducted from 2024–2025 across multiple locations in India. These curated sequences of whiteflies and natural enemies from different location provide a valuable molecular resource that will support future studies on genetic diversity, population structure, species delimitation, and phylogeography. This workflow also enhances the reliability of whitefly taxonomy and contributes to improving global access to authenticated molecular data supporting future taxonomic, ecological, and pest management research.

RELATIVE TOXICITY OF NEUROTOXIC INSECTICIDES TO THE
STINGLESS BEE *TETRAGONULA* NR. *PAGDENI* (SCHWARZ, 1939)

DIVYA K K¹ AND KESAVAN SUBAHARAN^{2*}

¹IARI-Bengaluru hub, ICAR-NBAIR, Bengaluru, Karnataka 560024, India

²Division of Germplasm Conservation and Utilization, ICAR-NBAIR, Bengaluru,
Karnataka 560024, India

*Email: subaharan_70@yahoo.com (corresponding author)

Stingless bees are important native pollinators that contribute significantly to crop production and the functioning of natural ecosystems, yet their sensitivity to synthetic insecticides remains far less understood than that of honey bees and other managed pollinators. This study assessed the comparative toxicity of major neurotoxic insecticide groups commonly applied in muskmelon cultivation, where the indigenous stingless bee *Tetragonula* nr. *pagdeni* plays a key role in enhancing yield. To evaluate the effects of these insecticides on foraging bees across different exposure routes, standardized topical, residual contact, and acute oral laboratory bioassays were conducted using certified reference materials.

Three commonly used insecticides representing distinct IRAC modes of action were tested: the neonicotinoid imidacloprid (Group 4A; nAChR competitive modulator), the pyrethroid deltamethrin (Group 3A; voltage-gated sodium channel modulator), and the diamide flubendiamide (Group 28; ryanodine receptor modulator). In topical applications, imidacloprid exhibited the highest toxicity, with an LD₅₀ of 0.867 ng/bee making it 5.44 times more toxic than deltamethrin and 9.17 times more toxic than flubendiamide clearly demonstrating strong neonicotinoid sensitivity in adult foragers. Residual contact tests reinforced these results, as imidacloprid again caused elevated mortality at relatively low concentrations. Flubendiamide, by contrast, showed extremely low contact toxicity, with LC₅₀ values above 200,000 ppm, categorizing it as “practically non-toxic” under EFSA environmental risk guidelines.

Acute oral exposure produced a similar pattern: imidacloprid induced high mortality even at low doses (0.062 ng/μL), whereas flubendiamide had the highest LC₅₀ value (61.73 ng/μL), making it the least harmful under ingestion pathways. Consistently across all exposure routes-topical, contact, and oral-imidacloprid emerged as the most toxic insecticide to *T. nr. pagdeni*, followed by deltamethrin and flubendiamide, highlighting the pronounced susceptibility of stingless bees to neurotoxic compounds.

Overall, the findings underscore the ecological risks associated with neurotoxic insecticide use in Indian agriculture and stress the need for pollinator-conscious pest management approaches, including careful pesticide choice, reduced exposure, and adoption of bee-friendly farming practices.



Theme III
Urban Entomology, Public Health
and Post-Harvest Entomology,
Utility of Medicinal Plants and their
Metabolites

TRENDS IN URBAN ENTOMOLOGY

PARTHO DHANG

Partho Dhang Consulting Inc., Makati City, Philippines

Email: partho@urbanentomology.com (corresponding author)

Humans have chosen to live in urban centers, and by 2050 an estimated 70% of human population will reside in cities. These cities present a concentrated resource for food and shelter and thus have become an ideal refuge for a group of insects called urban insects. Such insects namely German cockroach, *Blattella germanica*; Yellow fever mosquito, *Aedes aegypti*; Common bed bug, *Cimex lectularious*, and Cloth moth, *Tineola bisselliella* are so unique that they are not found anywhere except in the proximity of humans.

Encounter of urban insects with humans are mostly reported with alarm and distress, and an intent to control becomes desirable. Use of insecticide has remained the dominant method for insect control, providing immediate respite, however turning the act to be a long-term failure. In fact, increasing reliance on chemicals to manage urban insects has diverted the subject away from realms of natural science to a mere industry formalized act, requiring minimal knowledge and skill to accomplice the task.

Multiple factors including persistent site failure, insecticide resistance, health of unsuspecting population and complexity of urban niches have revived the study of urban entomology as a new discipline, separate from agricultural entomology. In the last 30 years this field have gained in sophistication in not only understanding the unique behavior of urban insects but also their adaptation to changes human constantly bring into living habitats.

The result of the last 30-year development are technologies which have become dominant method of choice of insect control. These technologies are not only replacing insecticide spray but also the companies which manufactured them. Structural termite is now eliminated using baiting techniques; skip ovipositing mosquitoes are managed by contaminating lures; German cockroach is controlled by self-spreading baits and indoor houseflies are trapped by the use of ultraviolet lights. As a consequence, companies which developed these biorational methods are now global leaders, shadowing the traditional manufacturers.

This talk is aimed at highlighting the growing importance of entomology as a way to invent new methods and technologies in the field of urban entomology.



**BUTTERFLIES AND MOTHS IN THE URBAN ECOSYSTEMS: THE SYNERGIES
FOR SUSTAINABILITY**

MAYANGLAMBAM OJIT KUMAR SINGH

Ramjas College, University Enclave, Delhi 110007, India

Email: ojitsingh@ramjas.du.ac.in (corresponding author)

The interspecies relationships and their entanglements are contemporary matter of discussion among many scholars ranging from the conservationists, ecological restoration ecologists, evolutionary biologists, political ecologists, historians to the policy makers. Many of the seasonal wetlands, marshes of the river Yamuna region in Delhi have been shrunk and destroyed and replaced by human settlements such as housing colonies, built spaces for development activities to accommodate the rising human population and their demands. Urbanization has intensified ecological pressures on biodiversity, making effective bioindicators essential for understanding environmental health. Butterflies and Moths (Lepidopterans) are ecologically significant organisms due to their sensitivity to microhabitat alterations and pollution gradients. The present work is an attempt in establishing the unique significance of insects and butterflies and moths in particular in a degraded wetland once fed by Yamuna River which is getting restored. The contesting landscape of the Dheerpur Wetland Park and the surrounding areas in the midst of the city today has trapped and sustained many diverse species of plants and animals because of the restoration work. Adult butterflies of more than 15 species out of the total nearly 76 species recorded in the recent butterfly count in the whole city are seen in the Dheerpur Wetland Park. Proper surveillance and documentation of the insect diversity in restoration ecosystem projects and endeavours will surely be one of the cheapest and the surest ways of proper documentation and understanding the changes that are being accompanied in the process of restoring the ecosystem. Field observations using light trapping methods across varied habitat zones indicate noticeable differences in Lepidopteran richness and abundance corresponding to pollution intensity and vegetation structure. Observed phenomena suggests that anthropogenic factors such as artificial lighting, reduced vegetation heterogeneity, and pollutant accumulation may significantly influence Lepidopteran diversity and community composition. Sustaining habitats and life forms is a matter of synergy, the synergy among the components of the habitats.

EXPLORING ALTERNATIVES FOR STORAGE INSECT PESTS MANAGEMENT

SURESH M NEBAPURE

Division of Entomology, ICAR-Indian Agricultural Research Institute, New Delhi 110012, India

Email: nebapuresuresh@gmail.com (corresponding author)

Storage insect pests cause significant post-harvest losses in food grains and seeds, posing a persistent challenge to food security and economic stability. In India, with a grain storage capacity of around 870 lakh metric tons, insect-related damage accounts for losses worth approximately Rs. 1300 crore annually. Currently, phosphine remains the primary fumigant, while deltamethrin and malathion are the only approved surface insecticides. However, prolonged reliance on these chemicals has resulted in reduced susceptibility among pest populations, underscoring the urgent need to identify effective alternatives for integrated pest management (IPM) in bulk grain storage. Our studies are aimed to evaluate the contact toxicity of modern insecticides such as spinosad, spinetoram, chlorfenapyr, and lambda-cyhalothrin against major storage pests: red flour beetle *Tribolium castaneum*, the almond moth *Cadra cautella*, saw-toothed grain beetle *Oryzaephilus surinamensis*, and rice weevil *Sitophilus oryzae*. Bioassays were conducted on different surface substrates such as glass, jute and tile surfaces. The larvae and adults of *C. cautella* exhibited highest susceptibility to spinetoram, with LC₅₀ values of 15.90 and 10.82 mg/m², respectively. *O. surinamensis* was most susceptible to lambda-cyhalothrin, with LC₅₀ values of 1.24 mg/m² for larvae and 0.13 mg/m² for adults. Adults of *S. oryzae* were most susceptible to spinetoram, showing an LC₅₀ of 129.0 mg/m². In addition to contact toxicity assays, progeny suppression studies were conducted for *S. oryzae* by treating jute bag surfaces with LC₉₉ values to assess residual impact on subsequent generations. These findings demonstrate that spinetoram and lambda-cyhalothrin possess substantial potential as effective alternatives to traditionally used insecticides for managing stored-product pests. Their high efficacy across diverse storage surfaces suggests their suitability for incorporation into sustainable pest management programs. Furthermore, enzyme profiling revealed variations in the activity of key detoxifying enzymes—esterases, glutathione-S-transferases, and cytochrome P450 monooxygenases—highlighting their role in species-specific susceptibility and resistance development. Collectively, these results contribute to the advancement of safer, more resilient pest management strategies, minimizing post-harvest grain losses and enhancing food security in India.



ELECTRONIC NOSE TECHNOLOGY: A SMART TOOL FOR EARLY DETECTION
AND MANAGEMENT OF STORAGE PESTS

SIRI CHANDANA M* AND MADHUMATHI T

Department of Entomology, Acharya N. G. Ranga Agricultural University, Bapatla,
Andhra Pradesh 522101, India

*Email: msirichandana222@gmail.com (corresponding author)

Stored grain pests cause significant post-harvest losses worldwide by damaging food quality, reducing market value, and contaminating produce. Conventional detection methods such as visual inspection, sieving, or CO₂ measurement are often labor-intensive, time-consuming and fail to identify early infestations. The Electronic Nose (E-nose) has emerged as a promising, rapid and non-destructive tool for early detection and monitoring of storage pests. This technology mimics the human olfactory system and uses an array of gas sensors to detect volatile organic compounds (VOCs) emitted from infested grains, pests or their metabolic by-products. Each type of infestation produces a unique VOC pattern or “odor fingerprint,” which can be analyzed using pattern recognition algorithms such as Principal Component Analysis (PCA), Linear Discriminant Analysis (LDA) and Artificial Neural Networks (ANN). Studies have demonstrated the ability of E-nose systems to distinguish between uninfested and infested grains, identify different pest species such as *Sitophilus oryzae*, *Tribolium castaneum* and *Callosobruchus maculatus* and even detect varying infestation levels. Moreover, E-nose devices can operate in real-time, allowing for continuous monitoring of storage environments without disrupting grain handling. Thus, the E-nose represents a sustainable and innovative approach in integrated pest management (IPM) by enabling early warning, minimizing chemical pesticide use and ensuring food safety and quality in stored commodities.

**OVIPOSITION DETERRENCE BY ESSENTIAL OILS AGAINST *HELICOVERPA
ARMIGERA* (HÜBNER)**

WILSON BROWNY M¹ AND KESAVAN SUBAHARAN^{2*}

¹IARI-Bengaluru hub, ICAR-NBAIR, Bengaluru, Karnataka 560024, India

²Division of Germplasm Conservation and Utilization, ICAR-NBAIR, Bengaluru,
Karnataka 560024, India

*Email: subaharan_70@yahoo.com (corresponding author)

The gram pod borer, *Helicoverpa armigera* (Hübner), is a major polyphagous pest known for developing resistance to multiple insecticide groups as well as transgenic crops such as Bt cotton. Intensive and repeated use of chemical insecticides has resulted in resistance build-up, pest resurgence, and environmental contamination, underscoring the importance of safer, eco-friendly pest management strategies. Plant-derived products, particularly essential oils, are gaining prominence due to their diverse modes of action and low toxicity to non-target vertebrates.

In this context, the present study aimed to evaluate the oviposition-repellent properties of ten essential oils against *H. armigera*. Electroantennography (EAG) assays showed that gravid females exhibited significantly stronger antennal responses to cinnamon, betel leaf, clove bud, and basil oils compared to the others. Oils inducing higher antennal activity were further tested using Y-tube olfactometer assays to assess behavioural responses. Cinnamon and betel leaf oils produced marked repellence in gravid females.

To substantiate these findings, cage experiments using tomato plants were carried out to determine oviposition deterrence under choice conditions. Both essential oils reduced oviposition, with cinnamon oil showing a notably higher deterrence effect, reflected in an oviposition deterrence index (IDO) of 60.75%. None of the tested oils caused phytotoxicity to tomato plants. Overall, the study demonstrates the strong oviposition-repellent activity of cinnamon oil, indicating its potential as an environmentally benign component in the management strategy for *H. armigera*.



ANTIMICROBIAL ACTIVITY OF BLACK SOLDIER FLY EXTRACTS

MAHESH S YANDIGERI*, SAMPADA N, PAVITHRA S AND GUNDAPPA

ICAR-National Bureau of Agricultural Insect Resources, Bengaluru, Karnataka 560024,
India

*Email: micromahesh@gmail.com (corresponding author)

Antimicrobial resistance (AMR) is an increasingly serious global health concern, threatening the effectiveness of existing antibiotics leading to treatment failures in infectious diseases. As a result, there is an urgent need to identify and develop new, natural sources of antimicrobial agents. Insects particularly due to their strong innate systems, have been recently gained attention as promising candidates in this search. The Black Soldier Fly is one such insect known for its ability to produce bioactive compounds in response to microbial exposure. This study aimed to evaluate the *in vitro* antimicrobial activity of extracts obtained from *H. illucens* larvae. A group of larvae was challenged with bacterial pathogens to stimulate an immune response while the other group remained unchallenged to serve as control. Bio active compounds were extracted using acidified methanol and further purified with column chromatography. The antimicrobial activity of both crude and purified extracts was tested against selected bacterial and fungal strains using the agar disc diffusion method. The results demonstrated extracts from pathogen-challenged larvae exhibited significantly greater antimicrobial activity than those from unchallenged larvae. The strongest antimicrobial effect was observed when extracts from larvae challenged with *Staphylococcus aureus* were tested against *Citrobacter koseri*, resulting in a zone of inhibition measuring 168.85mm². This was followed by extracts from *Escherichia coli*-challenged larvae tested against *Bacillus altitudinis*, which produced a zone of inhibition of 142.47 mm². These results indicate that pathogen exposure enhances the production of antimicrobial compounds in the larvae and that these compounds possess a broad spectrum of activity against both gram positive and gram-negative bacteria. Further analysis of the purified fractions using UV-Vis spectrophotometry revealed maximum absorbance peaks associated with peptide activity. Fraction 13 from *Bacillus thuringiensis*-challenged group showed the highest absorbance (3.81) at 260nm. Similarly fraction 9 from *S. aureus*-challenged larvae showed a peak of 3.75 at 230nm and fraction 7 from *E. coli* showed a peak of 3.70 at 230nm. These findings demonstrated a strong correlation between the optical absorbance of the fractions and their antimicrobial activity. To further confirm the presence of antimicrobial peptides SDS-PAGE was performed. The analysis revealed the protein bands of approximately 11KDa in all active fractions, suggesting the presence of low molecular weight antimicrobial peptides commonly produced by insects in response to infection.

Theme IV
Productive and Beneficial
Insects - Bees, Silkworm,
Lac Insects, Insects as Food

POLLINATION BIOLOGY IN THE ANTHROPOCENE

RENEE M BORGES

Centre for Ecological Sciences, Indian Institute of Science, Bangalore,
Karnataka 560012, India

*Email: renee@iisc.ac.in (corresponding author)

The Anthropocene is a time period defined as beginning in 1950. As its name suggests, it is a time period in which humans have had an undue and unprecedented influence on Earth. Most of this influence has been negative in terms of greenhouse gas emissions, pollutants, habitat fragmentation, global warming and climate change. Humans have had to face unprecedented heat waves, floods, cold spells and other disturbances in global and local weather phenomena. How has the Anthropocene affected pollination services? This talk will outline the problems of pollination within the Anthropocene. Pollination is an important ecosystem service that impacts food and nutritional security for humans and non-human animals. The talk will describe experiments that have been conducted to measure the extent of perturbation of pollination under warming, tropospheric ozone and NO_x pollution, and also alerts researchers to the burgeoning issue of artificial light at night that leads to light pollution. This talk emphasises the huge gap in our knowledge on pollination biology in India and outlines a research agenda that is required for India and Asia to make significant knowledge contributions about pollination biology within the Anthropocene.



**EXPLORING THE UNTAPPED POTENTIAL OF SOLITARY BEES IN INDIA:
CHALLENGES AND OPPORTUNITIES**

AMALA UDAYAKUMAR* AND VENU H S

ICAR-National Bureau of Agricultural Insect Resources, Bengaluru, Karnataka 560024, India

*Email: amala.uday@gmail.com (corresponding author)

Solitary bees represent over 90% of India's 700+ reported bee species and hold significant, yet largely untapped, potential species, primarily in securing crop pollination and enhancing agricultural biodiversity. These bees often thrive in diverse ecosystems, including urban and semi-natural landscapes. Their specific solitary nesting habits (in soil, wood cavities, mud) and diverse floral needs make them harder to study, unlike social bees in hives. The diversity of solitary bee species in India is not yet fully documented, which is a challenge for large-scale management strategies. These bees employ several specialised mechanisms for pollination, often linked to unique morphological features and behaviours that make them highly efficient at transferring pollen. Studies on complex floral morphologies and their associated floral handling behaviour by specialised solitary bees ensure high precision of pollen transfer to integrate these crucial wild pollinators for effective cross-pollination. Major challenges for solitary bee research in India include habitat loss (agriculture/urbanization), pesticide overuse, limited trained researchers, biodiversity loss (food scarcity/nesting sites), and difficulty in studying small, elusive species, hindering effective conservation and understanding of their vital pollination role, despite highly diverse populations. Promoting solitary bee research in India requires a multi-faceted approach involving targeted research, public engagement, and policy development. "Domiciliation" through artificial nesting structures is a practical way to support solitary bee populations, especially in urban and agricultural areas where natural nesting sites are declining. Incentivising sustainable practices to adopt ecologically friendly agricultural practices, such as creating green corridors and leaving uncultivated patches of land with wild flowers adjacent to crops, is the need of the hour to conserve the solitary bee population. There is a need to develop locally appropriate conservation plans based on the findings from regional biodiversity assessments and threat analyses. Understanding the specific plant-pollinator interactions will help in the targeted conservation and habitat management strategies to support healthy solitary bee populations and enhance crop yields in India. Providing optimal nesting conditions, well-designed trap nests can help support native solitary bee populations, especially in areas where natural nesting sites are scarce due to urbanisation or altered land use. Focused research is needed to understand the specific pollination ecology of various solitary bee species in different protected cultivation systems in India, to develop more effective pollination strategies. Understanding these "silent pollinators" is essential for effective conservation, revealing knowledge gaps in their response to environmental stressors and highlighting their role in ecosystem resilience and food security, often outperforming honeybees in specific contexts.

Theme V
IPM, Biological Control, Sustainable
Agriculture, Biosafety, Insecticides,
Quarantine, Policy and Regulations

**ADVANCING PLANT PROTECTION: TECHNOLOGICAL INTERVENTIONS
FOR QUALITY INPUTS AND SUSTAINABLE AGRICULTURE**

T5-LS-01

SINGH J P

Plant Protection Advisor, Directorate of Plant Protection, Quarantine & Storage, NH-IV,
Faridabad, Ministry of Agriculture & Farmers Welfare, Government of India

Email: ppa@nic.in (corresponding author)

Plant protection strategies and activities play a critical role in sustainable agriculture, ensuring quality inputs and minimizing crop losses due to pests. Modern interventions encompass integrated pest management (IPM), plant quarantine, pesticide regulation, locust monitoring and control, and training/capacity building. Together, these measures safeguard productivity, trade, and ecological balance.

Recent advancements have improved precision and transparency in pest surveillance and quarantine systems. The National Pest Surveillance System (NPSS) mobile app, launched in 2024, leverages AI and ML to provide instant solutions for pest attacks, crop diseases, and damages, issuing real-time advisories to farmers. NPSS app is available in 9 languages. Bio-pesticide testing laboratories have been established at regional CIPMC centers to ensure quality bio-inputs for farmers. Drone technology was deployed during the 2019–2020 desert locust upsurge in India. FAO-designed GPS devices such as *eLocust3* and the *eLocust3m Pro* mobile app enabled real-time surveillance. GPS-guided machinery, ultra-low volume (ULV) sprayers, and CDA atomizer units mounted on Mi-17 helicopters allowed precise pesticide application in Rajasthan and Gujarat. PQMS mobile app and e-Phyto certification introduced GPS-based, real-time inspection of export/import commodities, enhancing transparency and trust among member countries. Since 1 March 2023, PQMS has been integrated with IPPC's e-Phyto hub, linking 64 countries for export and 29 countries for import. Third-party inspection under NSPM-23 has accredited 43 Phytosanitary Service Agencies (PSSA) and 72 Phytosanitary Service Providers (PSSP) for export inspection. Packhouse system inspection and registration of processing units with DPPQ&S/APEDA has enabled exports to multiple destinations.

Efficiency in plant protection has further improved through Promotion of Integrated Pest Management (IPM) technologies to reduce environmental impact and enhance production quality, including the use of bio-pesticides, microbial inoculants, and beneficial insects. Revision of Pest Risk Assessment (PRA) and the Plant Quarantine Order in alignment with international standards and current phytosanitary requirements. Post-entry Quarantine certification incorporated as an online module under the PQMS portal. Online certification of NSPM-12 and NSPM-22 accreditation systems through the PQMS web portal. Integration of PQMS with ICEGATE SWIFT 2.0 (Single Window Interface for Facilitating Trade) to streamline clearance of imported commodities and reduce the



need to approach multiple agencies. Registration of packhouses and processing units under the PQMS web portal (currently under development), enabling a single-point interface for diverse stakeholders. Planned incorporation of phytosanitary treatment providers such as Vapor Heat Treatment (VHT), Hot Water Immersion Treatment (HWT), and Irradiation Treatment into the PQMS portal for simplified certification processes. Regular stakeholder engagement through meetings and training programmes with immigration officers, customs officials, agents, and exporters/importers to ensure timely grievance redressal and dissemination of real-time updates on export/import regulations.

Sustainability remains central to these efforts, with Promotion of a balanced approach combining judicious chemical pesticide use with IPM practices to deliver environmentally friendly produce and enhance ecosystem sustainability. Successful implementation of classical biological control programmes by DPPQ&S in collaboration with ICAR-NBAIR, targeting introduced pests in India. Establishment of a credible export/import certification system using digital tools and technologies to ensure safe international trade of agricultural commodities.

The true strength of these innovations lies in their integration. By combining precision agriculture, biological controls, advanced formulations, and digital tools, farmers can adopt comprehensive, sustainable crop protection strategies tailored to their specific agro-ecological conditions. This ensures quality inputs, resilient production systems, and long-term agricultural sustainability.

**INTEGRATED AND SUSTAINABLE MANAGEMENT OF
THRIPS: CURRENT SCENARIO AND PROSPECTS**

SUBRAMANIAN SEVGAN

International Centre of Insect Physiology and Ecology, Kasarani, Nairobi, Kenya

Email: ssubramania@icipe.org (corresponding author)

Economic losses due to thrips are particularly significant in high-value fruits, vegetables and ornamentals, such as tomato, onions, beans, chillies, banana, citrus, orchids, roses and others. Thrips are among the smallest insects, that are highly diverse in their host preference, reproductive behaviour and biology, ecological preferences, capacity to vector tospoviruses and ability to resist interventions, constraining their sustainable management. Challenges associated with thrips management goes beyond the farm. Their small size, declining taxonomic expertise and expanding markets makes them a phytosanitary risk difficult to monitor and manage. Management of thrips by farmers is currently largely based on use of insecticides, most often indiscriminate in nature. However, innovations in improved thrips monitoring tools; development and promotion of alternatives to pesticides, such as resilient habitats, biopesticides and natural enemies, breeding for resistant crops are emerging as key tools for integrated and sustainable management of thrips. Efficacy of these sustainable tools for management of thrips could be further improved with better understanding of thrips bioecology and its integration in thrips management, for instance, development of novel thrips attractants and “lure and infect/kill” strategies. However, key bottlenecks for scaling sustainable thrips management include lack of awareness on the innovations among farmers, weak supply chains for the Integrated Pest Management (IPM) interventions and weak supportive policies and market incentives for adoption which needs to be urgently addressed to reduce dependence on pesticides for thrips management.



SUSTAINABLE BIOLOGICAL CONTROL: LINKING SCIENCE, INNOVATION AND INDUSTRY

BASANA GOWDA G

ICAR-National Research Centre on Pomegranate, Kegaon, Solapur, Maharashtra 413255, India

Email: basanagowda4099@gmail.com (corresponding author)

Biological control is a cornerstone of sustainable crop protection, providing eco-friendly solutions to reduce reliance on synthetic pesticides while preserving ecological balance. The mass production of bioagents is crucial for their effective commercialization and widespread adoption. Traditionally, the mass production of biocontrol agents relied on host-dependent, small-scale, and labour-intensive methods, often resulting in inconsistent quality of parasitoids. Although these approaches played a crucial role in demonstrating feasibility, they were limited by inconsistent quality, short shelf life, low scalability, restricted farmer access, and high cost of production. Recent advances in science and innovation have transformed biological control into a more reliable and industry-compatible technology. Low-cost production processes, artificial diets, strain improvement, and automation have enabled large-scale production of biocontrol agents. A critical factor in biological control success is the quality and suitability of host or prey used for mass multiplication of parasitoids and predators, as suboptimal hosts can yield weak or behaviorally compromised bioagents. External factors such as pesticide exposure, release timing, and climatic conditions further influence field performance, meaning failures often arise from gaps in implementation rather than the concept itself. Limited availability of quality bioagents remains a major constraint. Linking science, innovation, and industry is therefore essential to move biological control from experimental success to commercial reliability. Establishing robust production protocols, quality standards, and entrepreneurship-driven decentralized production models involving local youth and agripreneurs can ensure consistent regional supply and adoption.

**INVASION OF FALL ARMYWORM, *SPODOPTERA FRUGIPERDA* (J.E. SMITH) IN INDIA:
BIOLOGY, HOST RANGE EXPANSION, NATURAL ENEMIES AND SUSTAINABLE
PEST MANAGEMENT**

KEERTHI M C

ICAR-Indian Institute of Horticultural Research Bengaluru, Karnataka 560089, India

Email: keerthimanikya@gmail.com (corresponding author)

The fall armyworm, *Spodoptera frugiperda* (J.E. Smith) (Noctuidae: Lepidoptera), invaded India in 2018 and quickly became a major threat to maize and several food and fodder crops. In the present study, an attempt was made to study integrated basic biology, ecology and sustainable pest management of *S. frugiperda* in India. A chickpea-based diet was standardised to support continuous laboratory rearing of *S. frugiperda*, and the results showed that the meridic diet enhanced reproductive performance compared to maize. This breakthrough enabled mass rearing and rigorous bioassays. To understand the invasion, we have screened 52 varieties of 25 fodder crops, documenting damage across cereals and fodder, including Nandi grass and Anjan grass. Further attempt was made to quantify oviposition preferences among the fodder crops and nutritional indices on multiple sorghum genotypes was studied under laboratory conditions. Through extensive surveys, we have documented a wide diversity of natural enemies, including parasitoids *Chelonus* nr. *blackburni* and *C. formosanus* and predator *Eocanthecona furcellata*. Seasonal monitoring revealed pest peaks and correlations with weather, enabling targeted interventions. The bio-efficacy of selected essential oils and biopesticides was studied under laboratory conditions. The results showed that the Citronella and annona oils caused 100 % larval mortality, and *Metarhizium rileyi* performed comparably to neem formulations in field trials. The influence of intercropping of selected vegetables on the incidence of *S. frugiperda* was evaluated under field conditions, and the results showed that the cob damage was significantly higher in control plots (6.33) and lablab intercropped field (5.00), and the lowest cob damage was observed in the lady's finger intercropping system (0.30). The maize + lady's finger recorded the highest grain yield (6.17 quintal/ha), whereas the control plot recorded the lowest grain yield (5.13 quintal/ha). Farmer-friendly integrated pest management modules combining pheromone traps, botanicals, biological agents and economic-threshold-based insecticide applications were developed and demonstrated across multiple seasons. These modules reduced infestation, increased yields by up to 25 % and delivered favourable benefit-cost ratios. The modules were validated with farmers and improved adoption across diverse agro-climatic zones. Farmer surveys in southern and north-eastern India revealed preferences and knowledge gaps, guiding extension efforts. Collectively, this work has deepened scientific understanding of *S. frugiperda* ecology in India, expanded the inventory of natural enemies and delivered practical, eco-friendly management strategies. It provides a model for farmer-centric pest management and shows how sustainable science can protect livelihoods and ecosystems while supporting national ambitions for a resilient agriculture.



**INCIDENCE PATTERN, DAMAGE ASSESSMENT AND MANAGEMENT OF
YELLOW STEM BORER, *SCIRPOPHAGA INCERTULAS* (WALKER)
(LEPIDOPTERA: CRAMBIDAE) IN RICE**

BALAJI B N

Central Silk Board, Bengaluru, Karnataka 560068, India

Email: balajibvn123@gmail.com (corresponding author)

This doctoral research presents a comprehensive and impactful scientific investigation into one of the most persistent and yield-limiting insect pests of rice. Through a multi-dimensional approach combining pest ecology, plant resistance mechanisms, climate interactions, and sustainable management tactics, the work offers significant advancements that directly contribute to resilient rice production systems. The study generated fine-scale temporal insights into the seasonal incidence patterns of the yellow stem borer (YSB), *Scirpophaga incertulas* across different transplanting windows, identifying October 15th, October 1st and March 15th as critical periods of heightened infestation. Through correlation analyses, the research established strong linkages between key meteorological parameters, minimum temperature, relative humidity, rainfall, sunshine hours and major damage symptoms (dead hearts and white ears). These findings provide an empirical foundation for weather-based pest forecasting models, a crucial step toward climate-resilient rice pest management. The research also quantified the extent of damage caused at different crop stages, demonstrating significant reductions in plant height, leaf sheath and blade length, internode length, panicle length, test weight, and grain yield under increasing infestation levels. Even though certain levels of vegetative damage were partially compensated through increased tillering, the reproductive stage damage resulted in irreversible yield losses. This quantification of damage across multiple crop stages provides valuable information for refining Economic Threshold Levels and optimizing intervention timing. Another major contribution of the work was the screening of 273 rice genotypes, including local landraces and popular cultivars. This screening had insights into morphological and biochemical traits underlying host plant resistance. Traits such as increased plant height, longer flag and second leaves, longer panicle and spike length and higher trichome density were found to be strongly associated with reduced infestation. Conversely, broader leaves, larger stem diameter, high reducing sugar content and higher crude protein levels were identified as susceptibility factors. Additionally, the study elucidated the role of nutrient profiles, revealing negative associations of phosphorus, potassium, calcium and silicon with YSB incidence, thus indicating their potential role in strengthening structural resistance. Equally impactful was the evaluation of new and conventional granular and foliar insecticides, where spinetoram 0.8 GR and flubendiamide 39.35 SC demonstrated superior efficacy in reducing pest incidence, enhancing grain yield, and providing the highest benefit-cost ratios. These results offer actionable recommendations for sustainable insecticide rotation and improved integrated

pest management strategies. Overall, this research stands out for its scientific rigor, originality, and practical relevance, providing a clear pathway for developing YSB resistant varieties, optimizing climate-adaptive pest management and reducing pesticide dependence. By linking ecological, physiological, biochemical, and economic dimensions, the work significantly advances current understanding and contributes to sustainable rice production.



INTEGRATION OF SYCANUS COLLARIS FABRICIUS (HEMIPTERA: REDUVIIDAE) AS A
POTENTIAL BIOLOGICAL CONTROL AGENT FOR HELOPELTIS THEIVORA WATERHOUSE
MANAGEMENT IN TEA ECOSYSTEM

THATTANTE PARAMBIL RABEESH^{1*}, KAMMATTERIKUNNU ASHIF², NAGARAJ SANTHANA
BHARATHI¹, ANNET BABU¹ AND AZARIAH BABU³

¹Entomology Division, UPASI TRF Tea Research Institute, Nirar Dam BPO, Valparai,
Coimbatore, Tamil Nadu 642127, India

²Parisons Estates, Manathavady, Wayanad, Kerala, India

³UPASI Tea Research Foundation, Glenview, Coonoor, The Nilgiris,
Tamil Nadu 643101, India

*Email: rabeeshp@gmail.com (corresponding author)

The tea mosquito bug *Helopeltis theivora* Waterhouse is a major sap-sucking pest of tea (*Camellia sinensis* (L.) O. Kuntze) in South India, causing severe damage to tender shoots and young leaves leading to substantial yield losses. To strengthen sustainable tea cultivation and minimize chemical pesticide use, regulated mass release of natural predators offers a promising strategy. Although several predatory arthropods such as spiders, praying mantids, robber flies, and dragonflies occur naturally in tea plantations, reduviids constitute one of the most important and easily manageable predator groups. *Sycanus collaris* can be efficiently mass-reared under laboratory conditions using the rice moth *Corcyra cephalonica* as an alternative host, by providing its larvae as prey. Laboratory bioassays, *S. collaris* adults were carried out by providing different developmental stages of *H. theivora*, and it was found consuming an average of 4.2 ± 0.3 and 4.5 ± 0.9 fourth and fifth instar nymphs, respectively, and 6.1 ± 0.4 adults per day. The predator exhibited a marked preference for adult prey, likely due to larger prey size. The desirable biological traits and high predatory efficiency of *S. collaris* highlighted its suitability for laboratory mass-rearing and possible inclusion in integrated pest management (IPM) programs in tea plantations. These findings confirm the potential of reduviid predators as an effective biological control agent against *H. theivora*, thereby contributing to ecologically sustainable pest suppression in tea ecosystem.

BIOLOGY AND LIFE TABLE TRAITS OF *CHRYSOPERLA ZASTROWI SILLEMI* ESSEN-PETERSEN (NEUROPTERA: CHRYSOPIDAE) ON RED SPIDER MITE, *OLIGONYCHUS COFFEA* NIETNER (ACARI: TETRANYCHIDAE), A MAJOR PEST OF TEA CROP

NAGARAJ SANTHANA BHARATHI^{1*}, KRISHNASWAMY SUJATHA², THATTANTE
PARAMBIL RABEESH¹ AND AZARIAH BABU³

¹Entomology Division, UPASI TRF Tea Research Institute, Nirar Dam BPO,
Valparai, Coimbatore, Tamil Nadu 642127, India

²Post Graduate and Research Department of Zoology, Government Arts College, Coimbatore,
Tamil Nadu 641018, India

³UPASI Tea Research Foundation, Glenview, Coonoor, The Nilgiris,
Tamil Nadu 643101, India

*Email: santhanabharathin@gmail.com (corresponding author)

A comprehensive study was conducted on the biology and life table of *Chrysoperla zastrowi sillemi* Esben-Petersen feeding on *Oligonychus coffeae* Nietner at three different temperatures: 20 °C, 25 °C and 30 °C with a relative humidity of 75 ± 5% and a 16 L: 8 D photoperiod. The study revealed that *C. z. sillemi* undergoes six life stages: eggs, first instar, second instar, third instar larva, pupa and adult. Various biological parameters, including the incubation period, larval duration, pupal duration, adult longevity, and female longevity, were significantly affected by temperature, with durations decreasing as temperature increased. The female-to-male ratio was 1:0.81, 1:0.89 and 1:0.85 at 20 °C, 25 °C and 30 °C, respectively. Life table parameters such as gross reproduction rate, net reproductive rate and finite rate of increase in numbers per day of *C. z. sillemi* were highest at 25 °C. The intrinsic rate of increase was 0.11, 0.13, and 0.13 females per female per day at 20 °C, 25 °C, and 30 °C, respectively. Weekly multiplication rate and per-day doubling time of *C. z. sillemi* were greater at lower temperatures (20 °C) and increased as the temperature rose. The study concluded that *C. z. sillemi* completed its predatory stage on *O. coffeae*, and its developmental, reproductive characteristics and life table parameters were notably higher at 25 °C compared to the other temperature regimes.



**EVALUATION OF ADATHODA 10% LEAF EXTRACT SOAP AGAINST THE MAJOR
SUCKING PESTS OF TOMATO**

SATYA BHANU G^{1*} AND ELAIYABHARATHI T²

¹Department of Agricultural Entomology, Acharya N. G. Ranga Agricultural University,
Bapatla, Andhra Pradesh 522101, India

²Department of Medicinal and Aromatic Crops, Tamil Nadu Agricultural University,
Coimbatore, Tamil Nadu 641003, India

*Email: giddisatya1999@gmail.com (corresponding author)

Whiteflies (*Bemisia tabaci*), thrips (*Thrips tabaci*), aphids (*Aphis crassivora*), and serpentine leaf miners (*Liriomyza sativae*) are the major sucking pest of tomatoes and lab lab beans that have increasingly threatened crop health and caused significant economic losses in recent years due to climate change. They act as vectors for transmitting the virus, thereby reducing crop quality and productivity. For the management of sucking pests, farmers rely on insecticidal control methods which can lead to resurgence and residue problems in the ecosystem. Considering the ill effects of insecticides, a botanical alternative was looked for. Bio efficacy field experiments demonstrated Adathoda 10% soap effectiveness against sucking pests conducted at two sites in Coimbatore District demonstrated a substantial reduction in whiteflies by 68.5 and 69.78%, thrips by 72.96 and 71.66%, aphids by 58.02 and 62.82%, and serpentine leaf miners by 55.82 and 69.56%. Adathoda 10% leaf extract soap caused no phytotoxicity in tomato and lablab plants, and it has no negative impact on insect natural enemies with their populations remaining similar to the untreated control, indicating its safety to natural enemies. The preparation of this formulation is commercially viable and economically feasible, with all the ingredients used for the formulation development are biodegradable and eco-friendly. These findings indicate that Adathoda 10% leaf extract soap is a highly effective and eco-friendly alternative to chemical insecticides, especially for managing sucking pest complexes in horticultural crops.



PREDATORY MITES IN THRIPS MANAGEMENT: A PRESSING PRIORITY

PRAKYA SREERAMA KUMAR

ICAR–National Bureau of Agricultural Insect Resources, Bengaluru,
Karnataka 560024, India

Email: psreeramakumar@yahoo.co.in (corresponding author)

Thrips constitute one of the most economically significant pest groups in horticultural and protected cultivation systems, inflicting direct damage through feeding and serving as vectors of numerous plant viruses. Globally, predatory mites have been established as integral components of integrated pest management (IPM) frameworks. Nevertheless, in the Indian context, predatory mites are conspicuously absent from current pest management programmes, despite extensive evidence of their efficacy in suppressing thrips populations in other regions.

This paper critically examines the ecological functions of predatory mites, the determinants of their effectiveness and the systemic reasons underlying their non-adoption in India. Drawing upon recent scientific literature and international case studies, it is argued that the absence of predatory mites in Indian IPM represents a substantive lacuna in sustainable thrips management. Addressing this pressing priority through the introduction of predatory mite-based strategies, supported by advances in mass-rearing techniques, habitat manipulation and targeted extension services, could substantially enhance the resilience of pest management systems while reducing dependence on chemical interventions.





**Indian Thysanoptera: After
T. N. Ananthakrishnan**

INDIAN THYSANOPTERA: FROM 1980 TO DATE

RACHANA R R^{1*}, SUJITH K M² AND RAMAIYER VARATHARAJAN³

¹ICAR-National Bureau of Agricultural Insect Resources, Bengaluru,
Karnataka 560024, India

²Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences,
Shivamogga, Karnataka 577204, India

³Department of Zoology, Manipur University, Imphal, Manipur 795003, India

*Email: vavarachana@gmail.com (corresponding author)

Taracad Narayanan Ananthkrishnan (T. N. Ananthkrishnan) and Samir Sen (both of the Zoological Survey of India, Calcutta) published the comprehensive monograph *Taxonomy of Indian Thysanoptera* in 1980. Post this publication, 815 species in 322 genera are presently known of which 112 species belonging to 16 genera are described new to science. In addition, 89 species belonging to 11 genera have been indicated as new records for India. A detailed list of 201 species of Thysanoptera is supplied in this article for both Terebrantia and Tubulifera, along with a note on invasive species and molecular taxonomy of Thysanoptera. Coincidentally the 100th birth anniversary of T. N. Ananthkrishnan synchronises with 100 years of Thysanoptera research in India.



POLLINATING THYSANOPTERA

ANNA JOSE¹, SAMRAJ J M², RACHANA R R³ and NEENU AUGUSTINE^{2*}

¹Department of Agricultural Entomology, University of Agricultural Sciences, Bengaluru, Karnataka 560065, India

²VIT School of Agricultural Innovations and Advanced Learning (VAIAL), Vellore Institute of Technology, Tamil Nadu 632014, India

³Division of Germplasm Collection & Characterization, ICAR- NBAIR, Bengaluru, Karnataka 560024, India

*Email: neenu.augustine@vit.ac.in (corresponding author)

The Thysanoptera are small insects that also play a useful role as pollinators. Their role in pollination has been largely overlooked due to their pest reputation, small size, subtle pollination behavior, and limited research. However, they contribute significantly to pollination through obligate thripophily, supplementary pollination, and ambophily. An analysis of existing literature on pollination by Thysanoptera was done with respect to different zoogeographic realms. Evidence from both extant plant species and fossil records proves the Thysanoptera-plant interaction dating back to the Cretaceous period, suggesting a strong co-evolutionary relationship. The common morphological features in flowers that facilitate pollination by Thysanoptera, as well as morphological and behavioral adaptations of Thysanoptera that facilitate pollen transfer, have been reviewed in this paper. Understanding the role of Thysanoptera as pollinators is essential for biodiversity conservation, especially in the context of global pollinator decline.



THYSANOPTERA AND TOSPOVIRIDAE

AMALENDU GHOSH

Insect Vector Laboratory, Advanced Centre for Plant Virology, ICAR-Indian Agricultural
Research Institute, New Delhi 110012, India

Email: amal4ento@gmail.com (corresponding author)

Insect vectors transmit c. 90% of plant viruses, thus posing a significant threat to global agricultural productivity. Among them, certain Thysanoptera are exclusive vectors of tospoviruses (*Tospoviridae: Elliovirales*), with their transmission dynamics intricately linked to their bionomics. Tospovirus infection alters the biology and behaviour of the Thysanoptera in ways that facilitate the spread of the tospoviruses. Critically, the acquisition of the tospovirus occurs only during the larval stages of the involved taxa of Thysanoptera, after which the virus infection disseminates from the midgut to the salivary glands, enabling the adults to transmit the virus. Our research has elucidated the stage-specific transmission biology of the Thysanoptera vectors, highlighting anatomical and cellular factors that regulate the propagation of the tospoviruses. Notably, the connections between the anterior midgut and primary salivary glands facilitate the movement of the virus, and the susceptibility level of the midgut epithelial cells during larval stages is essential for successful infection. To further elucidate the molecular interactions, we established a primary cell culture system for *Thrips palmi*. Transcriptomic analyses enabled us to determine key genes associated with viral transmission. Silencing of *UHRF1-binding protein 1 (UHRF1BP1)* and *Phospho ribosyl formyl-glycinamide synthase (PFAS)* genes led to a significant reduction in viral titres and induced developmental deformities. Moreover, the RNA interference (RNAi)-mediated silencing of the *tyrosine kinase Btk29A (Btk29A)*, *collagen α -1 (III) chain-like (COL3A1)*, and *vacuolar-type ATPase subunit B (V-ATPase-B)* genes impaired the fitness of the thrips and altered their tospovirus transmission efficiency. Topical application of double-stranded RNA (dsRNA) targeting *V-ATPase-B* conferred protection with sustained efficacy achieved through slow-release formulations in field conditions. These findings advance our understanding of the interactions between the Thysanoptera and Tospoviridae and demonstrate the potential of RNAi-based strategies as environment friendly alternatives to chemical pesticides in the agro-ecosystems.



BIOCONTROL OF THYSANOPTERA: LEVERAGING NATURAL ENEMIES

CHANDISH R BALLAL

Former Director, ICAR-National Bureau of Agricultural Insect Resources and Former
Project Coordinator, AICRP on Biological Control, Bengaluru, Karnataka
560024, India

Email: ballalchandish@gmail.com (corresponding author)

Frankliniella schultzei Trybom, *Scirtothrips dorsalis* Hood, *Thrips palmi* Karny, *T. tabaci* Lindmann and the recent invasive *T. parvispinus* (Karny) (Thysanoptera: Thripidae) are important species infesting field and polyhouse crops in India. Any effort to manage their populations through application of chemicals poses innumerable challenges, including the development of resistance to majority of the popular insecticides. Additional challenges are their piercing and sucking mode of feeding of plant sap and cryptic habitats. When we are looking for a long term, sustainable, and environmentally safe option for their management, biological control singularly emerges as an ideal and favourable alternative. In India, thus far, research focus has been on the identification of Thysanoptera and their management using chemical insecticides. In the area of biocontrol, detailed documentation on the indigenous predatory Anthocoridae (Hemiptera) targeting the Thysanoptera, mass-production protocols for rearing some of the predatory Anthocoridae, few records of locally available parasitoids (mostly Hymenoptera) and data on field evaluation of entomopathogenic microbials are available. In this article an attempt is made to consolidate all information on the indigenous biocontrol agents of Indian Thysanoptera. In addition, the feasible biocontrol options for the major thysanopteran harmful species in different parts of the globe and the significant factors which lead to either the success or the failure of biocontrol initiatives against the Thysanoptera are detailed.

INFOCHEMICALS FOR THE MANAGEMENT OF THYSANOPTERA

NANADAGOPAL BAKTHAVATSALAM^{1*}, KESAVAN SUBAHARAN¹, ANJENAPPA
RAGHAVENDRA¹ AND SEVGAN SUBRAMANIAM²

¹ICAR- National Bureau of Agricultural Insect Resources,
Bengaluru, Karnataka 560024, India

²Environmental Health Theme, International Centre for Insect
Physiology and Ecology (ICIPE), Nairobi, Kenya

Email: bakthavatsalamn2023@gmail.com (corresponding author)

Infochemicals, classified as pheromone, kairomone, allomone, synomone and apneumone, play significant role in insect communication. Unlike Lepidoptera, Thysanoptera utilize male produced aggregation pheromone for their communication. Neryl (S)-2-methylbutanoate, (R) lavandulyl acetate, (+) R-lavandulyl 3 methyl-butenoate, dodecyl acetate and tetradecyl acetate are the compounds identified as aggregation pheromones for several species. Pheromone lures placed in blue or yellow or white sticky traps are effective in capturing adults of *Frankliniella*, *Thrips*, *Megalurothrips* and *Odonotohrips*. Decyl acetate and dodecyl acetate along with other volatile chemicals have been identified as alarm pheromones for many Thysanoptera. Push-Pull technology using alarm pheromone and aggregation pheromone or kairomones with repellent activity and pheromone or kairomone with attractant activity has shown promise in the management of Thysanoptera. Kairomones, mostly plant volatiles attract or repel or exite the Thysanoptera. Most common kairomones are *P*-anisaldehyde and methyl isonicotinate which are multispecies attractants and commercial formulations such as “Lurem TR” are used as an IPM tool in the management of Thysanoptera. Volatiles determined from either cultivars resistant to attack by Thysanoptera or non-host plants, e.g., methyl salicylate and α -pinene are considered potential repellents. Herbivore-induced plant volatiles (HIPV) or pathogen induced plant volatiles (PIPV) attract certain Terebrantia. Prospects of using these volatiles either as attractants or repellents for the nuisance species of Thysanoptera are outlined.



THYSANOPTERA ASSOCIATED WITH FOREST TREES IN INDIA

**SRIJITA GANGULY*, SENTHILKUMAR NATCHIAPPAN AND JOHN PRASANTH
JACOB**

Institute of Forest Genetics and Tree Breeding, Coimbatore, Tamil Nadu 641002, India

*Email: ganguly.srijita9@gmail.com (corresponding author)

A total of 83 prioritized tree species across the country has been evaluated based on literature survey. The Thysanoptera associated with forest trees are compiled and discussed in relation to their distribution, habit, seasonality, and management. In this inventory, as many as 182 species of Thysanoptera have been listed in an alphabetic sequence along with the names of associated trees. This article forms not only an updated database but equips the researchers to fill gaps in Thysanoptera research in Indian forestry, which should help the management of harmful insects or the protection of beneficial species through their varied functional dynamics.

THYSANOPTERA ASSOCIATED WITH PLANTATION CROPS

AZARIAH BABU^{*1}, RABEESH THATTANTEPARAMBIL¹, ANNET BABU¹,
BHABESH DEKA² AND NAGARAJ SANTHANA BHARATHI¹

¹Division of Entomology, UPASI TRF Tea Research Institute, Valparai,
Tamil Nadu 642127, India

²Department of Entomology, Faculty of Agricultural Sciences, Rajiv Gandhi University,
Arunachal Pradesh 791112, India

*Email: azariah.babu@gmail.com (corresponding author)

The Thysanoptera include slender, relatively small insects with fringed wings, and asymmetrical mouthparts. These are an important group in plantation forestry, because they damage a wide variety of plantation crops globally. These organisms have adapted themselves to diverse habitats and food sources over Millenia, and a vast majority of them are polyphagous, exhibiting a short life cycle of 40-60 d, and reproduce both sexually and parthenogenetically. A number of them, such as *Scirtothrips dorsalis* Hood, *S. bispinosus* (Bagnall), *Sciothrips cardamomi* (Ramakrishna), *Selenothrips rubrocinctus* (Giard), *Panchaetothrips indicus* Bagnall, *Heliethrips haemorrhoidalis* (Bouche), *Thrips palmi* Karny, and *Dendrothrips minowai* Priesner (Terebrantia: Thripidae) and *Liothrips karnyi* (Bagnall) (Tubulifera: Phlaeothripidae) associates with diverse plantation crops such as *Camellia* (Camelliaceae), *Coffea* spp. (Rubiaceae), *Elatteria cardamomum* Maton (Zingiberaceae), *Hevea brasiliensis* Mull. Arg. (Euphorbiaceae), and spices such as *Piper nigrum* L. (Piperaceae), and *Curcuma longa* L. (Zingiberaceae). The infestation on the above listed crop plants by several Thripidae and Phlaeothripidae lead to substantial yield losses. Possible measures to suppress the populations of these nuisance organisms are discussed in this article in conjunction with the integrated pest management (IPM).



DNA BARCODING OF INDIAN THYSANOPTERA

**ABHISHEK GHOSH, ANINDITA DATTA, SOUMI DEY, SHRUTI KUMARI, SANDIP
MANDAL, KAOMUD TYAGI* AND VIKAS KUMAR***

Centre for DNA Taxonomy, Molecular Systematics Division, Zoological Survey of India,
Kolkata 700053, India

*Email: kumud.tyagi5@gmail.com, vikaszsi77@gmail.com (corresponding authors)

Worldwide 6,400 species of the Thysanoptera are presently valid. About 800 species are known from India. Scientific exploration of this group has grown markedly because of their growing understanding of their role as nuisance organisms, pollinators, predators, ectoparasites, and vectors of plant-disease agents. Identification of cryptic species has constrained the effectiveness of management efforts of nuisance organisms due to challenges associated with morphology-based species determinations. DNA barcoding has been useful in resolving taxonomic conflicts. Standard molecular markers such as cytochrome oxidase I (predominantly used), tubulin α -1, histone-3, 18S-ribosomal DNA, and 28S-ribosomal DNA are presently used to generate DNA- barcode sequence data, facilitating definitions of taxa and providing clear evolutionary insights. Currently, India ranks 6th among the mega-diverse nations having generated 1806 barcodes for the Thysanoptera using mitochondrial cytochrome oxidase I (~650 bp) submitted to the Barcode of Life Data Systems (BOLD). Among the 1806 barcodes, 74.36% have been achieved by the Zoological Survey of India (ZSI), whereas the remainder (25.64%) have been generated by other Indian institutions. Approximately 86% of all the DNA barcodes for the Indian Thysanoptera pertain to the Terebrantia. Of the 448 recorded Indian taxa of the Thysanoptera, only 49 of the Tubulifera have been barcoded, representing c. 14% of the total barcodes created in India. Currently, 176 out of 816 documented species from India have been barcoded. The contribution of the barcode generation centers and their respective taxa wise barcode counts are examined in detail. The present paper evaluates and analyzed the advancements made thus far, potential obstacles, and future prospects of DNA barcoding of Indian Thysanoptera. This paper also outlines the role played by prominent Indian institutions for their contribution to the molecular systematics of the Thysanoptera.



BEHAVIOURAL DYNAMICS OF THE THYSANOPTERA

RAMAIYER VARATHARAJAN AND CHINGTHANGKHOMBA SINGH H*

Department of Zoology, Manipur University, Imphal 795 003, India

*Email: chingthangkhomba@gmail.com (corresponding author)

Thysanoptera constitute a unique group of insects with fringed wings, protrusible bladder at the end of all tarsi, asymmetrical mouthparts with only functional left mandible for piercing and sucking mode of feeding, sexual and parthenogenic modes of reproduction, with variable feeding habits such as pollen and nectar, plant sap, fungal spore, and soft-bodied insects. They exhibit alary polymorphism and intra-specific variation within a population. This article highlights the feeding and breeding behaviors of Thysanoptera along with a note on predatory Thysanoptera.



**THYSANOPTERA ASSOCIATED WITH THE BAMBUISOIDEAE (POACEAE)
OF THE NORTH-EASTERN INDIA**

JOHNSON Th.², SHYAM MAISNAM^{2*}, BALA Kh.¹ AND RAMAIYER VARATHARAJAN¹

¹Department of Zoology, Manipur University, Imphal, Manipur 795003, India

²Department of Zoology, North-Eastern Hill University, Shillong, Meghalaya 793022, India

*Email: shammaisnam@gmail.com (corresponding author)

A total of 34 species belonging to the Phlaeothripidae, Thripidae, and Merothripidae have been recorded from different species of the Bambusoideae (Poaceae) growing in the north-eastern (NE) India (21°57'–29°30' N; 89°46' E– 97°30' E). In terms of their composition, the Phlaeothripinae with 24 species dominated the collection, followed by five species of the Idolothripinae and four of the Thripinae, besides one litter inhabiting taxon, *Merothrips indicus* Bhatti and Ananthakrishnan (Merothripidae). A dichotomous key to determine 31 genera of the Thysanoptera (Terebrantia and Tubulifera) associated with Bambusoideae is provided. Details of microhabitats of the Thysanoptera on the wildy occurring Bambusoideae are included along with their altitudinal distribution in NE India. Nearly 68% of the Bambusoideae-associated Thysanoptera preferred the altitude ranging from 700 to 1400 m asl. In addition, 10 species associated with the Bambusoideae from NE India are reported here for the first time.

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