



Second International Conference on **BIOLOGICAL CONTROL:** Biocontrol Contributions to One Health

25–28 February 2025
Bengaluru, India



BOOK OF ABSTRACTS



Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources



BOOK OF ABSTRACTS

Second International Conference on Biological Control: Biocontrol Contributions to One Health

25–28 February 2025

Bengaluru, India

Editors

Prakya Sreerama Kumar

R.R. Rachana

R.S. Ramya

M. Sampathkumar

D. Sagar

A. Kandan

R. Gandhi Gracy

Deepa Bhagat

Kolla Sreedevi

G. Sivakumar

Kesavan Subaharan

Sunil Joshi

T. Venkatesan

Satya Nand Sushil

Organisers



Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources



Book of Abstracts – Second International Conference on Biological Control: Biocontrol Contributions to One Health

Citation:

Sreerama Kumar, P., Rachana, R.R., Ramya, R.S., Sampathkumar, M., Sagar, D., Kandan, A., Gandhi Gracy, R., Bhagat, D., Sreedevi, K., Sivakumar, G., Subaharan, K., Joshi, S., Venkatesan, T. and Sushil, S.N. (2025). *Book of Abstracts – Second International Conference on Biological Control: Biocontrol Contributions to One Health*. Society for Biocontrol Advancement & ICAR–National Bureau of Agricultural Insect Resources, 25–28 February 2025, Bengaluru, India, xxxii + 303 pp.

Published by:

Society for Biocontrol Advancement & ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

Typeset by:

Krishi International Publisher | A Unit of Krishi Junction
#126, 1st Floor, 5th Cross, 2nd Stage,
Brindavan Extension, Mysuru, India

Printed by:

CNU Graphic Printers
#35/1, South End Road, Malleshwaram
Bengaluru, India

ISBN:



About 2icbc2025 logo

The 2icbc2025 logo, skillfully crafted by **Dr Prakya Sreerama Kumar** using AI and Canva, showcases the theme of the conference through symbolic elements. The ladybird symbolises biocontrol, while the leaves, water, insects and fungal spores collectively illustrate the One Health concept, which is the central theme of the event.

Front cover (top to bottom): Drone use for biological control in coconut (Dr K. Selvaraj); female broad mite, *Polyphagotarsonemus latus*, infected with *Hirsutella thompsonii* (Dr Prakya Sreerama Kumar); *Anagyrus lopezi* parasitising the cassava mealybug, *Phenacoccus manihoti* (Dr M. Sampathkumar)

Back cover: ICAR–NBAIR images (Dr Prakya Sreerama Kumar)

CONTENTS

Preface	V
Messages.....	vii–xvii
Advisory Panel & Committees	xix
Organising Committee.....	xx
Co-Organisers / Knowledge Partners	xx
Plenary Speakers.....	xxi–xxii
Lead Speakers.....	xxiii–xxix
Programme Schedule	xxxi–xxxii
Plenary Session I	1–5
Plenary Session II	7–10
Session I	11–13
Session II	15–55
Session III	57–61
Session IV	63–85
Session V	87–129
Session VI	131–154
Session VII	155–183
Session VIII	185–236
Session IX	237–242
Session X	243–275
Session XI	277–287
Author Index.....	289–299
Conference Sponsors	301–303

PREFACE

On behalf of the Organising Committee and the Editors, we are delighted to present the *Book of Abstracts* pertaining to the Second International Conference on Biological Control: Biocontrol Contributions to One Health (2icbc2025).

This significant event, jointly organised by the Society for Biocontrol Advancement (SBA) and the ICAR–National Bureau of Agricultural Insect Resources (ICAR–NBAIR), is scheduled for 25–28 February 2025 in Bengaluru, India. Eight international and national organisations are proudly associated with this conference as Co-Organisers/ Knowledge Partners.

SBA has been at the forefront of promoting biocontrol through conferences and meetings and via its publication, the *Journal of Biological Control*. For over a half-century, ICAR–NBAIR has championed biological control as a sustainable and economical alternative to chemical pesticides, achieving significant successes. The bureau continues to lead research in insect taxonomy, germplasm conservation and pest management innovation, and boasts a rich repository of natural enemies and entomopathogens.

Just like our previous international conference, 2icbc2025 also seeks to offer a comprehensive platform for sharing innovative ideas, pioneering research and practical strategies to promote biological control as a key component of sustainable agriculture. It promises to serve as a pivotal platform for advancing biocontrol research and highlighting its crucial contributions to the One Health framework. It will address challenges in biocontrol, including formulation development, bioagent quality, field performance prediction and farmer adoption, underscoring the need for stronger public–private partnerships and policy advocacy.

The programme includes five plenary speeches and thematic sessions featuring lead, oral and poster presentations, fostering active engagement across generations of researchers. An Interface Meeting and a Panel Discussion are part of the agenda. Additionally, the conference will host two concurrent Satellite Symposia highlighting significant advancements in pest management research. Eminent scientists from five continents have confirmed their participation in this event, bestowing it with a truly global perspective.

We extend our hearty best wishes to our organising team, co-organisers/ knowledge partners, sponsors and delegates for their contributions to this transformative event. Welcome to Bengaluru — let this conference inspire our collective efforts towards sustainable agriculture and a healthier planet.

Dr Prakya Sreerama Kumar
Chief Organising Secretary

Dr Satya Nand Sushil
President



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25–28 February 2025, Bengaluru, India



सत्यमेव जयते

डॉ. हिमांशु पाठक

DR. HIMANSHU PATHAK

सचिव (डेयर) एवं महानिदेशक (आईसीएआर)

Secretary (DARE) &
Director General (ICAR)

भारत सरकार
कृषि अनुसंधान और शिक्षा विभाग एवं
भारतीय कृषि अनुसंधान परिषद
कृषि एवं किसान कल्याण मंत्रालय, कृषि भवन, नई दिल्ली-110 001

**GOVERNMENT OF INDIA
DEPARTMENT OF AGRICULTURAL RESEARCH AND EDUCATION (DARE)
AND**

**INDIAN COUNCIL OF AGRICULTURAL RESEARCH (ICAR)
MINISTRY OF AGRICULTURE AND FARMERS WELFARE
Krishi Bhavan, New Delhi 110 001**

Tel: 23382629 / 23386711 Fax: 91-11-23384773

E-mail: dg.icar@nic.in

MESSAGE

I am happy to know that the Society for Biocontrol Advancement and the ICAR–National Bureau of Agricultural Insect Resources (ICAR–NBAIR) are organizing the Second International Conference on Biological Control: Biocontrol Contributions to One Health during February 25- 28, 2025. The conference will serve as a platform for researchers, students and industry professionals worldwide to deliberate on sustainable pest management strategies. The challenges posed by insect pests and diseases to global agriculture are both persistent and evolving. In a world where food security remains a pressing concern, the adoption of sustainable, environmentally friendly plant protection technologies has become imperative. Biological control represents a cornerstone of these efforts, offering solutions that minimize reliance on chemical pesticides and support the goals of sustainable agriculture. ICAR–NBAIR, as a leading research institute, has made remarkable strides in developing and disseminating biocontrol technologies. From a robust repository of natural enemies and entomopathogens to innovations in pest management compatible with biological control, the bureau has significantly contributed to advancing the field.

This conference will highlight the role of biological control in addressing the global agricultural challenges, including its contributions to the broader framework of One Health. I hope that the discussions and collaborations fostered during this event will further refine the strategies, bridge research gaps and encourage the integration of biological control into mainstream agricultural practices.

I wish the International conference a grand success.

(Himanshu Pathak)

**Dated the 19th February, 2025
New Delhi**



भारतीय कृषि अनुसंधान परिषद

डॉ. राजेंद्र प्रसाद रोड, कृषि भवन, नई दिल्ली-10001

Indian Council of Agricultural Research

Dr. Rajendra Prasad Road, Krishi Bhavan, New Delhi-110001

फोन कार्यालय/Tel (Off.): 011 23382545, 23046560; Fax: 011 23097003, E-mail: ddgcs.icar@nic.in

डॉ. देवेन्द्र कुमार यादव

Dated: 18.02.2025

उप महानिदेशक (फसल विज्ञान)

Dr. Devendra Kumar Yadava

Deputy Director General (Crop Science)

MESSAGE

Addressing the emerging and re-emerging crop pests, invasive species, insecticide resistance and pesticide residues in agricultural commodities is the need of the hour which requires innovative and sustainable pest management strategies. As a cost-effective and safe alternative to chemical pesticides, biological control offers eco-friendly solutions to these issues, supporting the comprehensive objectives of the 'One Health' approach. This approach recognises the interconnections between environmental, animal and human health. By adopting natural enemies, biopesticides and other biotechnological advancements; biological control has the potential to increase agricultural productivity without compromising environmental health.

The ICAR–National Bureau of Agricultural Insect Resources (ICAR–NBAIR) has developed numerous technologies for the mass production and field application of biocontrol agents. The NBAIR in collaboration with the ICAR–All India Coordinated Research Project on Biological Control of Crop Pests, identifies potential biocontrol agents, promotes biocontrol strategies among various stakeholders, monitors invasive pests and unexpected outbreaks and provides sustainable solutions for pest problems in diverse crops. However, certain research gaps, such as the enhancement of storage, virulence, mass production protocols and the survival and competitiveness of bioagents, need to be addressed on priority. This can only be achieved through networking, collaborations and public–private partnerships.

In this context, I am happy to learn that the Society for Biocontrol Advancement and ICAR–NBAIR are jointly organising the 2nd International Conference on Biological Control: Biocontrol Contributions to One Health (2icbc2025) during 25–28 February 2025. I am confident that this conference will provide a unique platform for researchers, students, policymakers and industry leaders from around the world to exchange knowledge, experiences and explore collaborations in research for advancing the area of biological control. Together, we can harness its full potential to address the complex challenges we face.

I congratulate the organisers and wish the conference a great success. I look forward to the fruitful exchanges and collaborations that will emerge out of deliberations during this conference.

(D.K. YADAVA)

डॉ. पूनम जसरोटिया
सहायक महानिदेशक
(पादप संरक्षण एवं जैव सुरक्षा)

Dr. Poonam Jasrotia
Assistant Director General
(Plant Protection and Biosafety)



भारतीय कृषि अनुसंधान परिषद
कृषि एवं किसान कल्याण मंत्रालय, भारत सरकार
क.सं. 215, कृषि भवन, नई दिल्ली, भारत

Indian Council of Agricultural Research
Ministry of Agriculture & Farmers Welfare, Govt. of India
R.No. 215, Krishi Bhawan, New Delhi 110001, India

☎: 91-11-23384414; ☎: 91-11-23046550
✉: adgpp.icar@nic.in; poonam.jasrotia@icar.org.in

Date: 11.02.2025

MESSAGE

It gives me an immense pleasure that the Society for Biocontrol Advancement, in collaboration with ICAR–NBAIR, is organizing the Second International Conference on Biological Control (2icbc2025) from February 25–28, 2025, in Bengaluru.

In recent years, the resurgence of pests, rising insecticide resistance, and the frequent arrival of invasive species have increasingly threatened food security and the environment. As we seek effective and eco-friendly solutions, biological control has emerged as a leading approach. Various standalone biocontrol agents and products are available for managing insect pests. In established integrated pest management (IPM) systems, incorporating one or more biocontrol agents can enhance biointensive IPM strategies.

ICAR–NBAIR is a leading institute specializing in insect taxonomy and developing pest management strategies through biocontrol and compatible technologies. To combat invasive pests, farmers often resort to indiscriminate chemical insecticide use, which negatively impacts the ecosystem. ICAR–NBAIR's successful biocontrol programs, such as those targeting the papaya mealybug, sugarcane woolly aphid, and eucalyptus gall wasp, have gained widespread farmer confidence. Insights from these successes have strengthened the country's ability to tackle emerging invasive pests like the tomato pinworm, fall armyworm, cassava mealybug, and Southeast Asian thrips. Despite these advancements, challenges remain in ensuring the availability of high-quality biocontrol agents, effective formulations, and timely deployment strategies. I hope that this conference will tackle key challenges in crop pest biocontrol and explore new research opportunities. I appreciate the efforts of the 2icbc2025 organizers in uniting researchers, students, and entrepreneurs to share knowledge and showcase biocontrol technologies.

I extend my heartfelt greetings and commendations to everyone involved in organizing this conference, and I wish the event great success.

(Poonam Jasrotia)



Asia-Pacific Association of Agricultural Research Institutions

Bangkok, Thailand

Dr. Ravi Khetarpal
Executive Director

I am delighted that the Society for Biocontrol Advancement, in collaboration with ICAR–NBAIR, is organizing the Second International Conference on Biological Control: Biocontrol Contributions to One Health (2ICBC2025) from 25–28 February 2025 in Bengaluru.

I also appreciate APAARI's role as a Co-Organizer of this significant event. Regrettably, due to conflicting commitments, I will be unable to attend in person.

At a time when pest resurgence, insecticide resistance, and invasive species pose escalating threats to global food security and environmental sustainability, biocontrol emerges as a critical eco-friendly solution. Stand-alone biocontrol agents and biointensive IPM strategies are proving to be increasingly viable and sustainable alternatives to chemical pesticides. ICAR–NBAIR's pioneering programs against invasive pests such as the papaya mealybug, sugarcane woolly aphid, and eucalyptus gall wasp exemplify its leadership in building national capacity to address emerging biosecurity challenges. APAARI's recent collaborations with Asia-Pacific countries, including initiatives under STDF and USDA projects to promote biopesticides, further underscore the region's commitment to advancing biocontrol.

I am confident this conference will catalyze meaningful dialogue on implementing crop pest biocontrol strategies and identifying innovative research pathways. I commend the organizers of 2ICBC2025 for creating a platform to unite international scientists, students, and industry stakeholders to share knowledge and showcase cutting-edge biocontrol technologies.

A special congratulations to Dr. S N Sushil for spearheading this pivotal event, which promises to significantly bolster biopesticide adoption both regionally and globally.

My heartfelt wishes for a productive and impactful conference. May it inspire collaborative strides toward a sustainable future.

Best regards,

Ravi Khetarpal (Ph.D.)
Executive Director, APAARI

Dr Ulrich Kuhlmann
Tel: +41 (32) 4214882
Email: u.kuhlmann@cabi.org

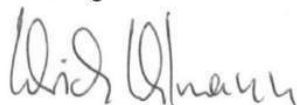
It is a pleasure to be a part of the Second International Conference on Biological Control, hosted in Bengaluru, India, by the Society for Biocontrol Advancement in collaboration with the ICAR–National Bureau of Agricultural Insect Resources (ICAR–NBAIR). The conference theme is Biocontrol Contributions to One Health, and promises to serve as an essential platform for researchers, students, and industry professionals to explore sustainable Integrated Pest Management (IPM) practices and their benefits to the environment and human health.

We all are aware that persistent and evolving challenges posed by insect pests to global agriculture require the development and implementation of sustainable, eco-friendly plant protection technologies. Biological control plays a pivotal role in these efforts by reducing our reliance on chemical pesticides and advancing our efforts in sustainable agriculture.

This conference highlights the critical role of biological control in addressing global agricultural challenges and its broader contributions to the One Health approach. As a leading research institute, ICAR–NBAIR has achieved significant advancements in biocontrol technologies, aligning its initiatives with the United Nations Sustainable Development Goal 2. On a global scale, CABI is at the forefront of promoting biological control initiatives and emphasizing pesticide risk reduction through its various programmes and projects. The CABI BioProtection Portal is a prime example of this: the world's largest free resource for biological plant protection product information which, through collaboration with governments and private sector companies, enables stakeholders to identify registered products in 48 countries around the world and learn more about biocontrol and specific products.

I am confident that the discussions and collaborations fostered during this event will refine strategies, bridge research gaps, and promote the integration of biological control into mainstream agricultural practices. My best wishes go to the organisers and all participants for a successful and impactful conference. May this gathering inspire innovation, forge new partnerships, and pave the way for a more sustainable future in agriculture.

Kind regards



Dr Ulrich Kuhlmann
CABI, Executive Director, Global Operations

Incorporating [SciDev.Net](#), CABI's independent news network

CABI is a not-for-profit organization

CABI improves people's lives worldwide by providing information and applying scientific expertise to solve problems in agriculture and the environment.

CABI, the trading name of CAB International, is an international organization recognized by the UK Government under Statutory Instrument 1982 No. 1071

CABI
Rue des Grillons 1, CH-2800 Delémont
Switzerland
T: +41 (0) 32 421 4870
E: europa-ch@cabi.org



February 2025

Dear Organizing Committee and attendees of 2icbc2025,

Congratulations on the Second International Conference on Biological Control: Biocontrol Contributions to One Health (2icbc2025) being hosted by the Society for Biocontrol Advancement (SBA) and the ICAR–National Bureau of Agricultural Insect Resources (ICAR–NBAIR).

The SBA and ICAR-NBAIR are important collaborators for IOBC's Asia and Pacific Regional Section in sharing a common mission to promoting the science and applications of biological control in pursuit of sustainable agricultural, environmental and social outcomes.

Wishing you all a successful conference and look forward to learning about the innovative science that is showcased at this meeting. We encourage all attendees and colleagues to review and connect with the range of IOBC working groups on biocontrol to amplify the reach and impacts of our discipline.

kind regards,

Dr Toni Withers

President – IOBC Asia and the Pacific Regional Section (APRS)

<https://www.aprs.iobc.info/>

Dr Raghu Sathyamurthy

President – IOBC Global

<https://www.iobc-global.org/>



Advisory Panel & Committees

ADVISORY PANEL

Chief Patron

Dr Himanshu Pathak
Secretary, DARE & DG, ICAR, New Delhi

Patrons

Dr Tilak Raj Sharma
Former DDG (CS), ICAR, New Delhi

Dr Devendra Kumar Yadava
DDG (CS), ICAR, New Delhi

Co-Patron

Dr Poonam Jasrotia
ADG (PP&B), ICAR, New Delhi

INTERNATIONAL ADVISORY COMMITTEE

Dr Patrick De Clercq, Ghent University, Belgium
Dr Kunjithapatham Dhileepan, DAF, Queensland, Australia
Dr Zhihong Hu, Wuhan Institute of Virology, China
Dr Johannes A. Jehle, Julius Kühn Institute, Germany
Dr Ravindra Chandra Joshi, PhilRice, Philippines
Dr Ravi K. Khetarpal, APAARI, Thailand
Dr Ulrich Kuhlmann, CABI, Switzerland
Dr Boddupalli Maruthi Prasanna, CIMMYT, Kenya
Dr Quirico Migheli, University of Sassari, Italy

Dr Rangaswamy Muniappan, Virginia Tech, USA
Dr Subba Reddy Palli, University of Kentucky, USA
Dr Raghu Sathyamurthy, CSIRO, Australia
Dr Anantanarayanan Raman, CSIRO, Australia
Dr Jean-Louis Schwartz, University of Montreal, Canada
Dr Marion K. Seier, CABI, United Kingdom
Dr Rajan Sharma, ICRISAT, India
Dr Ramasamy Srinivasan, AVRDC, Taiwan
Dr Sevgan Subramanian, ICIPE, Kenya

NATIONAL ADVISORY COMMITTEE

Dr D.J. Bagyaraj, Former Emeritus Professor, UAS, Bengaluru
Dr Chandish R. Ballal, Former Director, ICAR-NBAIR, Bengaluru
Dr P.K. Chakrabarty, Former ADG (PP&B), ICAR, New Delhi
Dr R.S. Chandel, Vice-Chancellor, Dr YSPUHF, Nauni
Dr Subash Chander, Former Director, ICAR-NRIIPM, New Delhi
Dr Malvika Chaudhary, CABI, Bengaluru
Dr B.V. Vasantharaj David, Vasantharaj David Foundation, Chennai
Dr S.C. Dubey, Vice-Chancellor, BAU, Ranchi
Dr P.K. Ghosh, Former Director, ICAR-NIBSM, Raipur
Dr A.K. Karnatak, Vice-Chancellor, MPUA&T, Udaipur
Dr N.K. Krishna Kumar, Former DDG (HS), ICAR, New Delhi
Dr Bikash Mandal, ADG (IR), ICAR, New Delhi
Dr T.M. Manjunath, Former Director (Research), Monsanto, Bengaluru
Dr A.N. Mukhopadhyay, Former Vice-Chancellor, AAU, Jorhat

Dr Z.P. Patel, Vice-Chancellor, NAU, Navsari
Dr B.V. Patil, Former Vice-Chancellor, UAS, Raichur
Dr S.N. Puri, Former Vice-Chancellor, CAU, Imphal
Dr T.P. Rajendran, Former ADG (PP&B), ICAR, New Delhi
Dr V.V. Ramamurthy, President, ESI, New Delhi
Dr K.V. Sankaran, Former Director, KFRI, Peechi
Dr B. Sarath Babu, President, PPAI, Hyderabad
Dr H.C. Sharma, Former Vice-Chancellor, Dr YSPUHF, Nauni
Dr J.P. Singh, Plant Protection Advisor, GoI, New Delhi
Dr S. Sithanatham, Sun Agro Private Limited, Chennai
Dr A.K. Srivastava, Director, ICAR-NBAIM, Mau
Dr M. Swamiappan, Former Registrar, TNAU, Coimbatore
Dr Abraham Verghese, Former Director, ICAR-NBAIR, Bengaluru
Dr C.A. Viraktamath, Former Professor, UAS, Bengaluru



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25-28 February 2025, Bengaluru, India



Organising Committee

PRESIDENT

Dr Satya Nand Sushil, ICAR-NBAIR

CHIEF ORGANISING SECRETARY

Dr Prakya Sreerama Kumar, ICAR-NBAIR

CONVENORS

Dr T. Venkatesan, ICAR-NBAIR

Dr Sunil Joshi, ICAR-NBAIR

Dr K. Subaharan, ICAR-NBAIR

ORGANISING SECRETARIES

Dr K. Sreedevi, ICAR-NBAIR

Dr A. Kandan, ICAR-NBAIR

Dr Deepa Bhagat, ICAR-NBAIR

Dr D. Sagar, ICAR-NBAIR

CO-CONVENORS

Dr A. N. Shylesha, ICAR-NBAIR

Dr M. Pratheepa, ICAR-NBAIR

Dr G. Sivakumar, ICAR-NBAIR

Dr M. Mohan, ICAR-NBAIR

Dr Mahesh Yandigeri, ICAR-NBAIR

Dr R. Gandhi Gracy, ICAR-NBAIR

CO-ORGANISING SECRETARIES

Dr B.S. Gotyal, ICAR-NBAIR

Dr G. Mahendiran, ICAR-NBAIR

Dr Ankita Gupta, ICAR-NBAIR

Dr Jagadeesh Patil, ICAR-NBAIR

Dr K.J. David, ICAR-NBAIR

Dr S. Salini, ICAR-NBAIR

Dr M. Sampathkumar, ICAR-NBAIR

Dr K. Selvaraj, ICAR-NBAIR

Dr U. Amala, ICAR-NBAIR

Dr Gundappa, ICAR-NBAIR

Dr Richa Varshney, ICAR-NBAIR

Dr R.R. Rachana, ICAR-NBAIR

Dr Omprakash Navik, ICAR-NBAIR

Dr C. Manjunatha, ICAR-NBAIR

Dr R.S. Ramya, ICAR-NBAIR

Dr T. Prabhulinga, ICAR-NBAIR

Dr B.S. Manjunatha, ICAR-NBAIR

Mr K.T. Shivakumara, ICAR-NBAIR

Dr N.N. Rajgopal, ICAR-NBAIR

Dr K. Suresh, Member, EC, SBA

Dr Sharad M. Galande, Member, EC, SBA

Co-Organisers / Knowledge Partners

International

Asia-Pacific Association of Agricultural Research Institutions (APAARI)

CABI BioProtection

International Association for the Plant Protection Sciences (IAPPS)

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)

International Organisation for Biological Control – Asia and the Pacific Regional Section (IOBC-APRS)

National

Directorate of Plant Protection, Quarantine and Storage (DPPQS)

Entomological Society of India (ESI)

Plant Protection Association of India (PPAI)



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25–28 February 2025, Bengaluru, India



Plenary Speakers



Dr Johannes A. Jehle

Dr Johannes A. Jehle leads the Institute for Biological Control at the Federal Research Centre for Cultivated Plants (Julius Kuehn-Institut) in Dossenheim, Germany. The institute focusses on developing methods and strategies for the biological control of plant pests and diseases within organic and integrated production systems. Dr Jehle's scientific work aims to enhance the use of insect viruses and microorganisms as biocontrol agents for pest insects. He obtained his Ph.D. from the University of Braunschweig and completed a postdoctoral fellowship at Wageningen University in the Netherlands. Dr Jehle has worked for both state and federal research institutes in Germany. In 2012, he was awarded an adjunct professorship at the Technical University of Darmstadt. With over 125 peer-reviewed publications and book chapters to his name, Dr Jehle has made significant contributions to his field. He served as President of the Society for Invertebrate Pathology from 2016 to 2018, and has been Vice-President of the IOBC-WPRS since 2021.

Dr Subba Reddy Palli

Dr Subba Reddy Palli received his doctorate from the University of Western Ontario and postdoctoral training at the University of Washington. Upon graduation, he worked as a Research Scientist at the Canadian Forest Service's Great Lakes Forestry Centre and later at Rohm and Hass Company as Senior Research Scientist and Group Leader. Dr Palli played a key role in the development of Ecdysone Receptor-based Gene Switch technology that is being tested in clinical trials for the regulation of anticancer genes in humans and the production of bioplastics in plants. Dr Palli is the Chairman of the Department of Entomology at the University of Kentucky. He is serving as the founding Director of One Health Center, being established at the University of Kentucky. He has received several prestigious awards, including a University Research Professorship, Thomas Poe Cooper Research Award, Bobby Pass Excellence in Grantsmanship Award, High Impact Research/Extension Award and Wethington Award. Dr Palli's research focusses on hormonal regulation of gene expression in insects. He has published more than 250 peer-reviewed journal articles and book chapters, wrote a book and co-edited two books. He holds 30 patents.



Dr Raghu Sathyamurthy

Dr Raghu Sathyamurthy is the Research Director for Biosecurity at CSIRO in Australia and is the current President of IOBC-Global. He has worked as an academic, researcher and research manager for over two decades, with a focus on environmental management in the context of developing sustainable biological solutions for invasive plants and insects across the Asia Pacific. Through his leadership role at CSIRO, Dr Sathyamurthy supports the coordination of complex national and international R&D to achieve outcomes and impacts in agricultural and environmental biosecurity. In his IOBC-Global role, he aims to strengthen the translation of the discipline of biological control through collaborations and partnerships, and through harmonisation of global policy and governance frameworks.



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25–28 February 2025, Bengaluru, India



Plenary Speakers



Dr Shiroma Sathyapala

Dr Shiroma Sathyapala, Forestry Officer at the Food and Agriculture Organization (FAO) of the United Nations, has led the Forest Health and Protection Programme in Rome, Italy, since 2014. She oversees global efforts to safeguard forest health by addressing threats from insect pests, diseases and other harmful biotic agents, while also facilitating the Forest Invasive Species Network across multiple regions covering more than 100 countries. The programme assists countries on prevention, integrated pest management (IPM), as well as assistance, which includes projects that deliver both emergency response and long-term prevention strategies. In addition, she is leading the biosecurity pillar of the FAO One Health programme.

Dr Andy Sheppard

Dr Andy Sheppard, Chief Research Scientist at CSIRO in Australia, is renowned internationally for his expertise in population ecology, biosecurity and invasive species management. He has spearheaded significant international research projects in USA, France and South Africa. He currently serves as the Co-Executive Director of the Catalysing Australia's Biosecurity Initiative, a joint venture between the Department of Agriculture, Fisheries & Forestry and CSIRO. This \$50–\$100 million mission was launched in early 2024. He serves as the Director of CSIRO's European Laboratory in Montpellier, France, and is the Deputy Chair of Australia's Threatened Species Scientific Committee. Additionally, he represents Australia in the OECD Cooperative Research Programme, and is the IUCN Species Survival Commission Australian Focal Point. He is an elected fellow of the Australian Academy of Technology & Engineering, and the Académie d'Agriculture de France, where he also received the Ordre du Mérite agricole.



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25–28 February 2025, Bengaluru, India



Lead Speakers



Dr R. Asokan

Dr R. Asokan, Principal Scientist at the ICAR-Indian Institute of Horticultural Research, Bengaluru, is a distinguished entomologist specialising in insect molecular science and pest management. With over three decades of research experience, he has made significant contributions to CRISPR/Cas-based genome editing, RNA interference and DNA barcoding. Dr Asokan has authored numerous peer-reviewed publications and holds a granted patent on RNAi and CRISPR technology. His pioneering work has earned him prestigious accolades, including the Fulbright-Nehru Academic and Research Excellence Award. A frequent speaker at international scientific fora, he has received multiple travel grants to present his research worldwide. As a mentor and research leader, he continues to advance innovative genetic approaches for sustainable insect pest control, shaping the future of agricultural biotechnology for pest control.

Dr Rohini Balakrishnan

Dr Rohini Balakrishnan is a senior Professor at the Centre for Ecological Sciences, Indian Institute of Science, Bengaluru. She is a bioacoustician and behavioural ecologist who studies animal acoustic communication at the interface of sensory, behavioural and community ecology. She has pioneered bioacoustics research in India and also collaborates with electrical and mechanical engineers in interdisciplinary projects at the interface of biology and engineering. Her current interests are focussed on the use of animal sounds and soundscapes for monitoring biodiversity and ecosystem health.



Dr Malvika Chaudhary

Dr Malvika Chaudhary, Global Team Leader for Digital Product Usage at CABI, is a distinguished scientist in international development and biocontrol. With over two decades of experience, she has contributed to research, production and quality control, and now focusses on international development to drive the global adoption of BioProtection products through digital interventions. She has authored more than 40 peer-reviewed papers, book chapters and technical manuals in this field. Dr Chaudhary's unwavering commitment to translating biocontrol technology from laboratory to field has earned her numerous accolades for her outstanding contributions. Passionate about making biocontrol science a practical reality, she continues to champion the use of digital tools for decision-making and digital learning across 27 countries through CABI's flagship programme, PlantwisePlus.



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25–28 February 2025, Bengaluru, India



Lead Speakers



Dr Surendra Dara

Dr Surendra Dara is a Professor and Extension Entomologist at Oregon State University, United States of America. He has over 25 years of experience in integrated pest management (IPM) and microbial control developing sustainable agricultural solutions for several high-value specialty crops in California and other places. He is an internationally recognised expert in IPM and biologicals. Dr Dara has authored over 400 scientific and extension articles, including three co-edited books, 25 book chapters and more than 50 peer-reviewed journal articles. He has extensive international outreach experience, training farmers in several countries. He has editorial responsibility for multiple journals, and holds offices in the Entomological Society of America and the Society for Invertebrate Pathology. Dr Dara has received multiple awards for his research and extension work. He has recently been recognised as the Fellow of Royal Entomological Society.

Dr Nilanjan Dey

Dr Nilanjan Dey is an Assistant Professor at the Department of Chemistry, Birla Institute of Technology and Science Pilani, Hyderabad, India. He obtained his Ph.D. in 2017 from the Indian Institute of Science, Bengaluru, under the supervision of Professor Santanu Bhattacharya. The main research focus of Dr Nilanjan's laboratory is to develop optical sensors for monitoring food quality and detection of agriculturally relevant analytes, such as harmful pesticides, herbicides, etc.



Dr Merid Negash Getahun

Dr Merid Negash Getahun is a Senior Research Scientist and interim Head of Behavioural and Chemical Ecology Unit at the International Centre of Insect Physiology and Ecology (*icipe*), Nairobi, Kenya. His research interests focus on the neuroethology of insects significant to veterinary, medical and agricultural fields, aiming to develop olfaction-based insect-vector and pest control technologies to enhance health and food security. With over ten years of research experience, Dr Getahun studies the interactions between vectors, livestock and pathogens. His work is critical to understanding how vectors make decisions, how livestock utilise secondary metabolites to defend themselves against pathogens, and how pathogens modulate both host physiology and vector behaviour to ensure their own survival. He aims to use infection-induced/modified secondary metabolites to formulate vector control (attractants and repellents) and to develop simple, user-friendly diagnostic tools for livestock diseases, as well as naturally inspired drugs. He is a dedicated mentor to future scientists in chemical ecology at various levels.



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25–28 February 2025, Bengaluru, India



Lead Speakers



Dr Markandeya Gorantla

Dr Markandeya Gorantla is a pioneering scientist and entrepreneur dedicated to revolutionising sustainable agriculture through innovative pest management solutions. As the Chairman and Managing Director of ATGC Biotech Private Limited, he has led groundbreaking research in pheromone-based pest control, significantly reducing reliance on chemical pesticides. With a Ph.D. in plant biotechnology from the University of Hyderabad, Dr Gorantla has an impressive academic and research background, including a Rockefeller Fellowship in drought tolerance. He holds 26 patents and has developed platform technologies targeting over 50 pest species worldwide. His 'insect mating disruption' approach has been instrumental in advancing ecofriendly pest control methods. Dr Gorantla has collaborated with DBT, USDA, US Forestry, USISTEF, USAID, and global industry leaders, playing a key role in international efforts to combat pest infestations sustainably. Recognised with multiple awards, he has contributed to shaping the Indo-US Bioeconomy partnership as a committee member of the US National Academy of Sciences, Engineering and Medicine (NASEM). His mission is to drive sustainable agriculture across 100 million hectares globally, empowering farmers with cost-effective and accessible solutions.

Dr Pagadala Damodaram Kamala Jayanthi

Dr Pagadala Damodaram Kamala Jayanthi, National Professor at the ICAR-Indian Institute of Horticultural Research, Bengaluru, is a distinguished scientist specialising in insect-plant interactions, semiochemicals and integrated pest management (IPM). She has extensive postdoctoral experience at Rothamsted Research, Penn State University and Kansas State University, secured through competitive fellowships, including the Rothamsted International Fellowship, Fulbright-Nehru Professional and Academic Excellence Fellowship and BOYSCAST Fellowship. With over two decades of research experience, Dr Jayanthi has authored more than 200 peer-reviewed papers and holds multiple technologies and patents. She has received numerous accolades, including the prestigious Young Scientist Award from the Indian Science Congress, the Lal Bahadur Shastri Young Scientist Award from ICAR, the Dr Punjabrao Deshmukh Outstanding Woman Scientist Award from ICAR, the 5th Dr Krishna Mohan Singh Memorial Award from IARI and the Professor T.N. Ananthakrishnan Foundation Senior Scientist Award, among others. She is a fellow of several esteemed scientific academies, including the National Academy of Agricultural Sciences



Dr Nagalingam Kumaran

Dr Nagalingam Kumaran (Senior Research Scientist/Team Leader, CSIRO, Australia) is dedicated to advancing the understanding of plant-insect interactions to develop more effective pest management strategies. With a keen focus on ecological and genomic methodologies, Dr Kumaran investigates intricate pest dynamics, aiming to develop innovative management solutions. Managing a dynamic team, Dr Kumaran leads the development of biocontrol and genetic control techniques to tackle invasive pests. Through leading-edge research projects, Dr Kumaran translates novel technologies into practical tools for on-the-ground deployment, facilitating their adoption and implementation by end-users. Dr Kumaran serves on the editorial boards of several international journals and reviews research proposals for leading funding bodies. He has published over 30 articles in peer-reviewed journals in ecology, entomology and genetics. As a trusted advisor, Dr Kumaran provides expert guidance to various Commonwealth and State departments in Australia on topics ranging from innovations for biodiversity outcomes and understanding RNA potential to biocontrol prospects, fire ant eradication and invasive species management.



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25-28 February 2025, Bengaluru, India



Lead Speakers

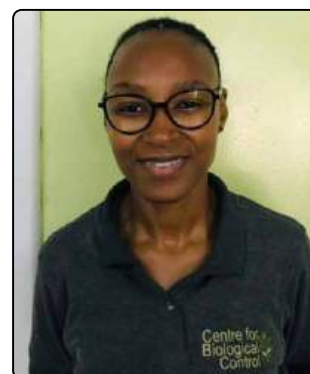


Dr Rangaswamy (Muni) Muniappan

Dr Rangaswamy (Muni) Muniappan served as the Director of the IPM Innovation Lab, Virginia Tech, Blacksburg, USA, from 2006 until 2025. He is a specialist in tropical economic entomology, biological control of insect pests and weeds, and integrated pest management (IPM). Dr Muniappan has devoted his life's work to improving conditions of farmers in the developing world. He has made considerable contributions to the development of crop-specific IPM techniques, fostering partnerships with private sector organisations, encouraging scaling up through the dissemination of information, and promoting partnerships as a means of capacity building. Dr Muniappan has also served in management positions for international scientific bodies and conducted international workshops in Africa, Asia, Europe, USA, Central America and Australia. Dr Muniappan has published four books. While managing the IPM Innovation Lab, Dr Muniappan has made time to mentor dozens of young scientists in developing countries, and to continue his own research – making discoveries about invasive pests and publishing his findings.

Ms Samella Ngxande-Koza

Ms Samella Ngxande-Koza is the Mass-Rearing Facility Manager for waterweeds at Rhodes University's Centre for Biological Control (CBC) in South Africa. She earned a B.Sc. in Honours from the University of Fort Hare before moving to Rhodes University to complete her M.Sc. In 2016, she began her internship at CBC as a research technician. In 2021, she started managing the mass-rearing facility. Her role is to ensure the facility's functionality by overseeing the team that breeds various biocontrol agents for waterweeds. The main focus includes waterweeds such as water hyacinth, water lettuce, kariba weed, parrot's feather and Brazilian waterweed. She leads a team of nine employees, six of which are people living with disabilities. She is also involved in community engagement projects, which aim to educate and recruit more students to participate in the biological control of invasive species.



Dr Sagar Pandit

Dr Sagar Pandit, Head of the Agricultural Biotechnology and Chemical Ecology (ABCE) Research Laboratory at the Indian Institute of Science Education and Research (IISER) Pune, India, is a distinguished scientist in the field of plant–environment interactions, biocontrol and reforestation chemical ecology. He has authored several research publications and patents. He was a group leader of Tritrophic Interactions and Lepidopteran Reverse Genetics groups in the Max Planck Institute for Chemical Ecology. He headed a Max-Planck Partner Group on Multitrophic Interactions at IISER Pune. His ABCE laboratory continues to bring groundbreaking discoveries on plant interactions, translating these into innovative agrobiotech applications.



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25–28 February 2025, Bengaluru, India



Lead Speakers



Dr Anantanarayanan Raman

Dr Anantanarayanan Raman (Professor of Ecological Agriculture & Sustainable Land Management, Charles Sturt University, Orange, NSW, Australia; and Senior Scientist, Commonwealth Scientific & Industrial Research Organisation [CSIRO], Floreat Park Campus, Western Australia) specialises in the field of arthropod–plant interactions, focussing on the biology, bionomics, ecology and economic relevance of gall-inducing arthropods. With over 40 years of research experience, he has published more than 300 peer-reviewed articles, including many in the class entomological journals of the world and about a dozen research volumes, including the *Biological Control of Tropical Weeds using Arthropods* published by the Cambridge University Press, Cambridge, UK, along with Rangaswamy Muniappan and Gadi V.P. Reddy.

Dr K.V. Sankaran

Dr K.V. Sankaran is an invasive species specialist. He served the Kerala Forest Research Institute, Peechi, India, as a scientist for 25 years and later as Director until 2012. Post retirement he worked with the FAO of the UN as a consultant on invasive alien species (IAS) until 2021. Dr Sankaran successfully completed 27 research programmes on various forestry aspects and led eight international collaborative research programmes with CSIRO, CABI, FAO and CIFOR. He was the first Coordinator of the Asia-Pacific Forest Invasive Species Network (APFISN), a cooperative alliance of 33 member countries of the Asia-Pacific Forestry Commission. He was Deputy Chair, Working Party 7.03.12, IUFRO; Co-Chair, Expert Committee on IAS, National Biodiversity Authority, Government of India; and Lead Editor of the GRIIS database (India). He was one of the Coordinating Lead Authors of the thematic assessment of IAS by the IPBES. Dr Sankaran has published over 120 research papers and authored/edited several books.



Dr Shantanu P. Shukla

Dr Shantanu P. Shukla is an Assistant Professor at the Department of Developmental Biology and Genetics, Indian Institute of Science, Bengaluru. He is also the Head, International Max Planck Partner Group, and a current Ramalingaswami Fellow. Dr Shukla is a former Fulbright Fellow. His research interests lie in the field of insect symbioses and host–microbiome interactions. His research group uses a multi-disciplinary approach involving microbiology, molecular biology, biochemistry and bioinformatics to understand the role of microbes in host adaptation and physiology. He has published papers in leading journals on the molecular and ecological interactions between insects and their bacterial and fungal symbionts, and their impact on insect roles in nutrient recycling, predation and as pests.



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25–28 February 2025, Bengaluru, India



Lead Speakers



Dr Ramasamy Srinivasan

Dr Ramasamy Srinivasan is an accomplished agricultural entomologist and the Flagship Program Leader for Safe and Sustainable Value Chains at the World Vegetable Center, Tainan, Taiwan, where he also serves on the Research Management Team. He holds a Ph.D. in agricultural entomology from Tamil Nadu Agricultural University, India, and the Asian Vegetable Research and Development Center, Taiwan. Dr Srinivasan specialises in host-plant resistance, biological control, chemical ecology, molecular entomology and integrated pest management (IPM). In his career, he has secured over \$31 million in funding for research and development projects and has facilitated collaborations across more than 30 countries on six continents with diverse partners. He has trained and mentored over 75 students, postdoctoral fellows and researchers from 15 countries, and has authored more than 225 publications, including a notable 2021 review on *Maruca vitrata* in the *Annual Review of Entomology*. Dr Srinivasan's outstanding contributions have been recognised with numerous awards, such as the International Plant Protection Award of Distinction (2011), the ISHS Medal (2018), the VEGINET-SEAVEG Award (2019), the Fellowship of the Royal Entomological Society (2021), and the Lifetime Achievement in International Agriculture Research Award from the Asian PGPR Society (2024).

Dr Sevgan Subramanian

Dr Sevgan Subramanian is a Principal Scientist at the International Centre of Insect Physiology and Ecology (icipe), Nairobi, Kenya, where he heads the Environmental Health Theme. With a Ph.D. in agricultural entomology from Tamil Nadu Agricultural University, India, he has close to 20 years of research experience in Africa. His work focusses on integrated pest management (IPM), biopesticides, thrips and tospovirus management, climate change adaptation, and edible insects. He has published over 150 peer-reviewed articles, digital identification keys for thrips and book chapters. Dr Subramanian has led significant projects, such as the thrips IPM programme in East Africa, the EntoNUTRI project on edible insect research, CHIESA programme on climate change impacts in East Africa, and has led the fall armyworm IPM efforts at icipe. He is dedicated to building African capacity in IPM and climate change research, mentoring numerous graduate students and researchers. Outside of his professional work, he is passionate about documenting East Africa's arthropod and bird biodiversity.



Dr N. Rama Gopala Varma

Dr N. Rama Gopala Varma, currently working as Principal Scientist (Entomology) & Nodal Officer (Drones), Institute of Rice Research, Professor Jayashankar Telangana Agricultural University, Hyderabad, India, has vast experience in rice research, particularly related to plant protection aspects like semiochemicals, host plant resistance, development of weather-based forecasting models and integrated pest management. He identified several novel insecticide molecules and compatible pesticides for managing vivid rice pests effectively and developed scale for screening against panicle mite. He has handled ten projects and is involved in three agri-startup projects, namely Marut Dronetech, Delta Things and Farm Needs and two externally funded projects. He has played a pivotal role in generating vital information on standard operating procedures for pesticide applications using drones for seven major crops.



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25–28 February 2025, Bengaluru, India



Lead Speakers



Dr Satya Nand Sushil

Dr Satya Nand Sushil is the serving Director of the Bengaluru-based ICAR–National Bureau of Agricultural Insect Resources (ICAR–NBAIR), a premier Indian institution dedicated to insect science. He is also holding the position of Project Coordinator of All-India Coordinated Research Project on Biological Control of Crop Pests. Earlier, he has served as the Plant Protection Advisor to the Government of India, and played a significant role in policy reforms pertaining to plant protection in India. He has chaired and been a member of significant national committees, and has led the Indian delegation in various international fora. Over the years, he has developed, commercialised and patented numerous ecofriendly technologies for insect pest management. He has published more than 400 research publications in the form of research papers, books, technical bulletins, etc. His exceptional contributions to the field of entomology have earned him numerous awards and recognitions, including WIPO Gold Medal, Societal Innovation Award, ICAR Team Award, Global Biopesticides Excellency Award and several fellowships, including Fellowship of the National Academy of Agricultural Sciences (FNAAS, New Delhi). As the Director of ICAR–NBAIR, Dr Sushil envisions making the institute the nodal point for serving the national and global needs, focussing on identification services, ecosystem services and ecofriendly management of invasive and native insect species.

Dr Thiruvengadam Venkatesan

Dr Thiruvengadam Venkatesan, Head & Principal Scientist, Division of Genomic Resources at ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India, is an outstanding scientist in the field of biological control. With over three decades of research experience, he has authored more than 150 peer-reviewed research papers and commercialised biocontrol-based technologies, including stress-tolerant biocontrol agents. He has earned numerous accolades including Fellow of National Academy of Agricultural Sciences (FNAAS, New Delhi) and Fellow of Royal Entomological Society (FRES, London). He has presented invited papers at international conferences, and was a panellist at the Third International Congress of Biological Control, San Jose, Costa Rica, in 2024. His current focus is on RNAi technology against economically important insect pests and conducting a series of brainstorming and satellite symposia on insect genomics and its prospects in pest management in order to explore the development of commercial formulations of dsRNA-based spray-induced gene silencing, and the development of genomic platforms to advance global research in insect molecular biology. He has mentored many Ph.D., M.Sc. and PDFs. He is currently serving as the Vice-President of Society for Biocontrol Advancement.



Second International Conference on Biological Control: Biocontrol Contributions to One Health
25–28 February 2025, Bengaluru, India



Second International Conference on Biological Control: Biocontrol Contributions to One Health (2icbc2025)

Programme Schedule

Dates: 25–28 February 2025

Venue: Radisson Blu Atria Bengaluru, India

Day 1 | 25 February 2025 | Tuesday | Chancery

14:00–14:30 **Registration and Welcome Drink**

14:30–15:30 **Opening Ceremony**

15:30–15:45 **High Tea**

15:45–17:15 **Plenary Session I**

17:15–17:30 **Session Break**

17:30–19:00 **SESSION I**
Biocontrol Entrepreneurship: Industries, Start-Ups and Incubation Centres

19:30–20:30 **Cultural Programme**

20:30 onwards **Gala Dinner**

Day 2 | 26 February 2025 | Wednesday

Time	Chancery	Chamber 2	Council	Conclave (Digital Poster Sessions)	
				Section A	Section B
09:30–11:15	SESSION II Biodiversity, Biosecurity and Biosystematics of Crop Pests and Natural Enemies	SESSION III Satellite Symposium on Insect Multi-Omics: Molecular Insight Meets Pest Management Solutions	Industry–Regulators–Academia Interface Meeting	SESSION V Biocontrol-Compatible Technologies, Conservation Strategies and Pollinators	SESSION VI Ecological Chemistry in Biological Control: Pheromone Synthesis, Sensors and Nanotechnology
11:15–11:30	Tea Break				
11:30–13:00	Session II (Cont.)	SESSION IV Invasive Alien Pests, Diseases and Weeds: Biocontrol Interventions	Panel Discussion: Potential of Biological Control to Gradually Replace Chemical Control — Myth or Reality?	SESSION VII Climate-Resilient Biocontrol Technologies	SESSION X Integration of Microbials and Microbials in Organic Farming
13:00–14:00	Lunch Break				
14:00–15:30	SESSION V Biocontrol-Compatible Technologies, Conservation Strategies and Pollinators	SESSION VI Ecological Chemistry in Biological Control: Pheromone Synthesis, Sensors and Nanotechnology	Networking Space	SESSION VIII Genomics in Biological Control of Crop Pests and Diseases	SESSION II Biodiversity, Biosecurity and Biosystematics of Crop Pests and Natural Enemies
15:30–15:45	Tea Break				
15:45–17:30	Session V (Cont.)	SESSION VII Climate-Resilient Biocontrol Technologies	Networking Space	SESSION XI Information and Communication Technology in Biological Control: Artificial Intelligence, Internet of Things, Mobile Apps, Drones and Robotics	SESSION IV Invasive Alien Pests, Diseases and Weeds: Biocontrol Interventions
18:00–19:00	Annual General Meeting of SBA				
19:30 onwards	Dinner				



Second International Conference on Biological Control: Biocontrol Contributions to One Health (2icbc2025)

Programme Schedule

Dates: 25–28 February 2025

Venue: Radisson Blu Atria Bengaluru, India

Day 3 27 February 2025 Thursday		
	Chancery	Chamber 2
09:30–11:15	SESSION VIII Genomics in Biological Control of Crop Pests and Diseases	SESSION IX Satellite Symposium on Chemoecological Innovations in Modern Pest Management
11:15–11:30	Tea Break	
11:30–13:00	Session VIII (Cont.)	SESSION X Integration of Macrobiotics and Microbiotics in Organic Farming
13:00–14:00	Lunch Break	
14:00–15:00	Plenary Session II	SESSION XI Information and Communication Technology in Biological Control: Artificial Intelligence, Internet of Things, Mobile Apps, Drones and Robotics
15:30–17:00	Valedictory Session	
17:00–17:30	High Tea	

Day 4 28 February 2025 Friday	
Post-Conference Excursions (Delegates must pre-register for one of the following excursions)	
08:00–18:30	<ol style="list-style-type: none"> ICAR–NBAIR, Bengaluru Bengaluru (Lal Bagh, Vidhana Soudha, Visvesvaraya Museum and ISKCON Temple) Mysuru (Palace and Zoo)



Plenary Session I



**Biological control in Europe — a path forward to reduce the usage of
chemical pesticides**

Johannes A. Jehle

Institute for Biological Control, Julius Kühn Institute, Dossenheim, Germany

Correspondence: johannes.jehle@julius-kuehn.de

Integrated plant protection follows the concept of combining plant breeding, cultivation measures, as well as physical, biological and chemical methods for efficient and environmentally friendly pest control. The European efforts to reduce the use of chemical pesticides are embedded in the farm-to-fork strategy. Biological control plays an increasingly important role in integrated and organic plant production. Biocontrol agents recruit a broad spectrum of organisms and biological substances: naturally occurring bacteria, fungi and viruses, predatory and parasitic insects, predatory mites and insect-pathogenic nematodes. Plant extracts can also be used to produce healthy plants and to avoid environmental damage. Most of them qualify as low-risk substances within the European framework of pesticide assessment. The presentation will review the current status of biological control in Europe from scientific, regulatory and market perspectives.

Keywords: biological control; biopesticides; farm-to-fork strategy; low-risk substances





Advances needed to sustain the next chapter(s) of biological control

Sathyamurthy Raghu^{1,2}

¹*International Organisation for Biological Control – Global*

²*Commonwealth Scientific and Industrial Research Organisation, Brisbane, Australia*

Correspondence: s.raghu@csiro.au

The intersecting impacts of climate change, increased trade and travel, changing land use patterns, and significant international efforts to reduce the use of chemicals in agricultural and environmental interventions, necessitate sophisticated approaches to mitigating biosecurity risks. Biological control has been a valuable asset in the management of such risks (invasive pests [vertebrate and invertebrate], weeds and diseases) for over a century. While this historical legacy is assured (even if sometimes questioned), sustaining the discipline over the next century will require ongoing efforts to modernise all aspects of the discipline. In this talk, I will highlight some emerging trends and approaches, including One Health, spanning the spectrum of activities in biological control (i.e. target selection, agent selection, risk assessment, post release evaluation, integrated management, regulatory engagement, international conventions governing access and benefit sharing). Some of this will challenge the modus operandi in the discipline, but meeting this challenge will be essential to strengthen and advance the future of the discipline and share its benefits globally.

Keywords: biocontrol; Nagoya Protocol; One Biosecurity; One Health; sustainable biological solutions; translation





**Biological control is considered high risk by most governments around
the world — why is this and how can it be addressed?**

Andy Sheppard^{1*} and K.V. Sankaran²

¹*Commonwealth Scientific and Industrial Research Organisation, Canberra, Australia*

²*Kerala Forest Research Institute, Peechi, India*

**Correspondence: andy.sheppard@csiro.au*

Despite more than 100 years of successful use and effective management of many exotic pests and invasive alien species, classical biological control (cbc) is still considered high risk by most governments around the world. These are often landlocked countries, where the use of biological control is not common practice and there is little or a lack of policy approaches to regulate its use. Over non-target effects of cbc agents also dissuade these countries in adopting biological control as a management tool. This situation is despite the acceptance and promotion of cbc as an effective management approach of widespread invasive alien species by the International Plant Protection Convention, the Convention on Biological Diversity and the Food and Agriculture Organisation. Why is this? In the recent report by the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) on Invasive Alien Species, the authors covered biological control as a management approach globally in some detail. Countries with no history of science-based and regulated use of cbc generally see this approach as encompassing the early and completely unregulated use; for example, the release of cats and mongoose onto islands and cane toads around the world to control pests. Examples such as this underrate cbc as a valuable tool in the eyes of the public, despite many studies on the lack of unexpected non-target impacts of biocontrol agent releases. Indeed, the release of beneficial biological control agents is generally much more highly regulated than the unregulated introduction of live organisms, despite documented lower risks. Most governments seem unable to distinguish between such early opportunistic unregulated use and today's highly and regulated application of cbc using internationally accepted risk analysis and public consultation. This has tarnished the whole modern discipline of cbc. India is a good example of this 'regulator risk aversion' despite a strong historic and effective use of cbc across the subcontinent. This talk analyses the relevant evidence from the IPBES assessment and proposes ways forward to address the current huge lack of global trust in what the science evidence shows is a safe and effective invasive alien species management approach. We also discuss recent advances in biological control and future regulatory challenges.

Keywords: classical biological control; exotic pests; invasive alien species; risk analysis



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Plenary Session II



**Arthropod vector surveillance and management are cornerstones of
global One Health**

Subba Reddy Palli

*Department of Entomology, Martin-Gatton College of Food, Agriculture and Environment, University of
Kentucky, Lexington, USA*

Correspondence: rpalli@uky.edu

One Health is an integrated, unifying approach that aims to sustainably balance and optimise the health of people, animals and ecosystems. It recognises that the health of humans, domestic and wild animals, plants, and the wider environment (including ecosystems) are closely linked and interdependent solutions (WHO, 2023). Recent changes in climate and land use due to agriculture intensification, urbanisation, and international travel and trade have increased the threat of infectious diseases to humans, animals and the environment. Roughly 75% of emerging infectious diseases originate from animals and/or are transmitted by animals. Human, animal and plant diseases caused by pathogens transmitted by arthropod vectors (e.g., mosquitoes and ticks) are on the rise and have recently emerged as high-priority areas of research all over the world. Recent efforts on surveillance, speciation and management of arthropod vectors and the detection of pathogens they transmit will be presented. Understanding the biology of vectors is key to their management and prevention of pathogen transmission. Recent research in my laboratory on the biology and management of the yellow fever mosquito, *Aedes aegypti*, will also be presented.

Keywords: genome editing; Lyme disease; mosquito; RNAi; tick



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Global perspectives on biological control in forestry and One Health

Shiroma Sathyapala

Food and Agriculture Organization of the United Nations, Rome, Italy

Correspondence: shiroma.sathyapala@fao.org

Healthy forests are essential for sustaining biodiversity, regulating climate and maintaining water cycles. They are critical for communities providing timber, non-timber forest products, clean air, water and habitat for wildlife. However, pest and disease outbreaks along with invasive plant species pose significant threats to forest ecosystems impacting human, animal and plant health alike. Traditional pesticide-centred management strategies for controlling forest pests, diseases and invasive plants are carbon-intensive and can have detrimental environmental impacts. To address this issue, innovative sustainable pest management solutions that rely on conservation and utilisation of biodiversity are of paramount importance. Biological control is a proven ecofriendly strategy that enhances the resilience and long-term health of forest ecosystems by utilising natural enemies such as predators, parasites or pathogens to manage insect pests, diseases and invasive plant species. Biological control aligns seamlessly with the One Health framework, which emphasises the interconnectedness of the health of humans, animals and ecosystems advocating for integrated solutions to sustainably balance and optimise this interdependent system. The Food and Agriculture Organization (FAO) plays a critical role in advancing biological control in forestry. It provides technical assistance to countries, develops educational materials, organises workshops and training courses, and collaborates with governments, the private sector, and civil society organisations to raise awareness on the use of biocontrol and to promote action. This presentation will explore the global perspectives of biological control in forestry with the context of One Health approach emphasising its vital role in safeguarding forest ecosystems and enhancing the health of people, animals and the environment.

Keywords: biodiversity sustainability; forest pests; invasive plants; wildlife habitat



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Session I

**Biocontrol Entrepreneurship:
Industries, Start-Ups and
Incubation Centres**

Biocontrol Entrepreneurship: Industries, Start-Ups and Incubation Centres

This session, which is scheduled for 25 February 2025, aims to bring together industry leaders, researchers and regulators to exhibit, promote and address the issues related to the commercialisation of biocontrol and biocontrol-compatible technologies.

Representatives from around 30 industries, officials from the Directorate of Plant Protection, Quarantine and Storage (DPPQS, Faridabad), the Indian Council of Agricultural Research (ICAR, New Delhi) and the ICAR–National Bureau of Agricultural Insect Resources (ICAR–NBAIR, Bengaluru) will participate in the deliberations.



Session II

Biodiversity, Biosecurity and Biosystematics of Crop Pests and Natural Enemies



Insect ecoacoustics: the state of the art

Rohini Balakrishnan

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

Correspondence: brohini@iisc.ac.in

Insects comprise the major component of terrestrial biodiversity and are critical to ecosystem functioning. As small poikilotherms, they are also particularly vulnerable to temperature changes accruing from anthropogenic land use change and climate change, making them good indicators of ecosystem health. Long-term monitoring of insect diversity across landscapes and levels of disturbance is crucial but poses a big challenge. Non-invasive, long-term, passive acoustic monitoring is one possibility for insect groups that produce species-specific sounds such as crickets, katydids and cicadas. Whereas ecoacoustic techniques are currently widely deployed for monitoring of vertebrate groups such as birds, bats and other mammals, monitoring of acoustic insects lags far behind. The problem is particularly acute in species-rich tropical ecosystems. I will discuss possible reasons for this, the state of the art, challenges and the way forward for reliable and effective acoustic monitoring of insect diversity.

Keywords: ecoacoustics; ecosystem health; indicators; insects; passive acoustic monitoring

Lead Speech



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Microbiome-mediated adaptation in insects feeding on ephemeral diets

Shantanu P. Shukla

Developmental Biology and Genetics, Indian Institute of Science, Bengaluru, India

Correspondence: sps@iisc.ac.in

Insects are a highly successful group of animals. Much of their success as pests, vectors of disease and pollinators can be attributed to their close symbiotic association with microorganisms. Symbiosis with microorganisms has allowed insects to use nutritionally imbalanced, recalcitrant and nutrient-deficient diets. Here we investigate the role of the microbiome in insect adaptation to ephemeral diets. Ephemeral diets are short-lived resources that are subject to intense competition. For example, carrion is a nutrient-rich resource that is vulnerable to rapid microbial degradation. Unregulated microbial growth can lead to depletion of nutrients, accumulation of toxic metabolites, and proliferation of parasites and pathogens. Despite carrion's susceptibility to putrefy and quickly turn unpalatable, the burying beetles (also known as carrion beetles) use carrion as a breeding resource and are seemingly immune to any ill effects of feeding on decaying carcasses. Here we demonstrate a role for its microbiome in facilitating carrion beetle adaptation to carrion. The principal selective forces associated with breeding on carrion can thus promote familial social interactions and aggregations as mechanisms to manage carrion microbial communities, making the burying beetles highly efficient feeders of a challenging resource such as carrion.

Keywords: burying beetles; carrion beetles; microorganisms; symbiosis





**Diversity and relative abundance of predators and parasitoids of
Spodoptera frugiperda (J.E. Smith) in the maize ecosystem**

Pratiksha B. Khedkar and V.K. Bhamare*

College of Agriculture, Vasantao Naik Marathwada Krishi Vidyapeeth, Parbhani, India

**Correspondence: drvijaybhamare@gmail.com*

Maize (*Zea mays* L.), a major cereal crop belonging to the Poaceae family, is heavily damaged by the invasive insect pest *Spodoptera frugiperda* (J.E. Smith) in India. The present study was conducted to investigate the diversity and relative abundance of predators and parasitoids of *S. frugiperda* infesting *Kharif* maize in the Marathwada region of Maharashtra. Observations were recorded at weekly intervals from randomly selected maize quadrats maintained under unsprayed conditions. The results revealed a total of seventeen species of predators and parasitoids across six insect orders: Hymenoptera, Diptera, Hemiptera, Coleoptera, Dermaptera and Araneae. The highest number of predators and parasitoids were found in the Hymenoptera order, followed by Coleoptera. The highest abundance was observed in Hymenoptera (52.94%), including families such as Trichogrammatidae, Ichneumonidae, Braconidae and Scelionidae. This was followed by Coleoptera (17.64%), which included Coccinellidae and Carabidae; Hemiptera (11.76%), with families Pentatomidae and Reduviidae; Diptera (5.88%), represented by Tachinidae; Dermaptera (5.88%), represented by Forficulidae; and Araneae (5.88%). The present findings not only enhance the understanding of the diversity of predators and parasitoids but also provide valuable insights for formulating an integrated pest management strategy for the maize ecosystem.

Keywords: diversity; maize; parasitoids; predators; *Spodoptera frugiperda*





**Cryptochetidae (Diptera): first record of parasitoid family from India or
is it a recovery?**

**Prabhu C. Ganiger*, Nagabhushana Reddy, K. Shravya Savithri,
P. Naveena, G. Mohanprasad and Siddamma**

University of Agricultural Sciences, Bengaluru, India

**Correspondence: prabhuganiger@gmail.com*

Cryptochetidae is a family of flies new to India, revealed in the Botanical Garden of UAS, GKV, Bengaluru, India. *Cryptochetum iceryae* (Williston) (Diptera: Cryptochaetidae) is found in India. It is one of the biocontrol agents of cottony cushion scale, *Icerya purchasi* Maskell (Hemiptera: Coccoidea: Monophlebidae). A brief review of literature on the identification key to species of Cryptochetidae is given.

Keywords: Cryptochetidae; *Cryptochetum iceryae*; Diptera; *Icerya purchasi*





Record of *Asphondylia* gall midge (Diptera: Cecidomyiidae) as a new species damaging fruit of mango in India

**B.S. Gotyal^{1*}, Peter Kolesik², K.J. David¹, D.S. Reddy³, R.S. Ramya¹,
K.T. Shivakumara¹ and D. Sagar¹**

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²South Australian Museum, Department of Terrestrial Invertebrates, Adelaide, Australia

³Citrus Research Station, Dr YSR Horticultural University, Tirupati, India

*Correspondence: gotyalento@gmail.com

Outbreak of gall midge-infesting mango fruit was recorded in Andhra Pradesh, India, during 2023. The larvae of the gall midge were feeding inside young fruits causing a substantial reduction in fruit set, resulting in considerable harvest loss. The infestation prompted an investigation into taxonomy, biology, and control of the pest. The morphology of adults among *Asphondylia* is rather uniform and it is mainly the pupa and the larva that are used in species diagnosis. Our morphological and *MtCOI* sequence comparisons show that the gall midge is a previously undescribed species of *Asphondylia* (Diptera: Cecidomyiidae) which we name here *A. mangiferi* Kolesik & David. The new species is named after the generic name of its host plant. This species is the first *Asphondylia* known to feed on mango and the third gall midge known to infest mango fruit worldwide with the other two occurring in the Philippines (*P. frugivora*) and southern China (*P. fructiculi*). The four COI sequences obtained for the new species (OQ657351, OQ657352, OQ672321, OQ681953) showed a pairwise intraspecific similarity of 99.62–100%. The sequences differed significantly from any Cecidomyiidae with COI sequences available in GenBank and BOLD (both accessed 22-vii-2023). In GenBank, the species closest to the new species was *Asphondylia yushimai* Yukawa & Uechi (GenBank accession OQ096699) with a pairwise interspecific similarity of 92.21–92.41%. In BOLD, the closest available sequence was a GenBank accession MN191251 belonging to BIN AED7387 representing *Asphondylia baca* Monzen with a pairwise interspecific similarity to the new species of 91.57%. The high intraspecific similarity and the low closest interspecific similarities indicate that *A. mangiferi* is an autonomous species, different from any congeners with published COI sequence.

Keywords: Cecidomyiidae; insect pest; *Mangifera indica*; mango fruit; South Asia





**Drawing phylogenetic relationships between completely parasitic and
entomophytophagous species of Braconidae with disparate morphologies and
cross-taxon hosts**

Ankita Gupta*, R. Gandhi Gracy and Rohit Pattar

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

**Correspondence: drankitagupta7@gmail.com*

The present study was undertaken under the SERB project CRG/2021/001523, wherein we investigate the phylogenetic relationships among representatives of a number of different Braconidae genera collected pan India, associated with concealed and non-concealed hosts, using mitochondrial cytochrome oxidase COI and nuclear large ribosomal subunit 28Sr genetic marker. We conducted Maximum Likelihood (ML) analyses using RaxML (GUI2.0) for 207 verified sequences of Braconinae. The vast majority of Braconidae, mainly *Bracon* species are idiobiont ectoparasitoids of moderately concealed immature hosts, such as gall inducers, leaf rollers, miners or wood-borers as deeply concealed hosts. The phylogenetic analysis reveals a distinct clade with closely allied taxa consisting of gall-associated *Bracon* species typically having exerted ovipositors, *Testudobracon* species which are ectoparasitoids of gall inducing asphondyline Diptera and *Syntomernus* species which thrives inside dipterocarp fruit larvae along with its generic synonym *Ficobracon* whose members have been reared from fig syconia. The *Bracon* species showing entomophytophagous behaviour forms a distinct subclade within the concealed host category. The *Crinibracon* clade comprising of pupal parasitoids share proximity with members of the subtribe Aspidobraconina (Braconini) which are also endoparasitoids of butterfly pupae, a distinctive mode of development. *Crinibracon* appears morphologically closely related to the Aspidobraconina in having densely setose mesoscutum and a midlongitudinal propodeal carina. The clades show strong support to species with common host behaviour pattern with similar morphological traits. This is the first-ever comprehensive study on Indian braconids which relates their morphological traits and ecological information leading to distinctive host–parasitoid phylogenetic relationships.

Keywords: concealed hosts; entomophytophagous; idiobiont ectoparasitoids; phylogenetic analysis





**Rice plant health management in diverse rice ecosystems of India —
impact on biodiversity and ecosystem services**

Gururaj Katti* and Chitra Shanker

ICAR–Indian Institute of Rice Research, Hyderabad, India

**Correspondence: gururajkatti@yahoo.com*

Rice, a vital food crop in India, supports sustainable livelihoods. It is grown across diverse ecosystems, including irrigated, rainfed upland, rainfed lowland, coastal and hill regions. The large-scale globalisation of agriculture, climate change and varying cultural and socioeconomic conditions have led to different farming systems, such as conventional, organic, natural and precision farming, each with distinct structure and function. These systems result in varying levels of quality and quantity of ecosystem services. Rice plant health management (PHM) practices have evolved to address these diverse ecosystems, and have a direct bearing on biodiversity and corresponding ecosystem services. Conventional rice farming, with introduction of input intensive high-yielding varieties and indiscriminate application of fertilisers and pesticides, resulted in substantial environmental impacts, including excessive water consumption, greenhouse gas emissions and biodiversity loss. In contrast, organic and natural farming emerged as sustainable alternatives to traditional agriculture prioritising ecological balance by reducing reliance on agrochemicals and enhancing ecosystem services. Precision farming, based on the rapid advances in scientific research and technology, aims to optimise pesticide and nutrient use while conserving water and energy. In this context, sustainable rice PHM should focus on applying ecological principles to conserve natural pest control mechanisms and promote in-situ biodiversity for long-term ecosystem services for human health and welfare. However, the challenge remains to integrate innovative and path-breaking market-friendly technologies that offer attractive profitability to farmers while maintaining sustainability.

Keywords: climate change; diverse ecosystems; precision farming; sustainable livelihoods



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



**Abundance and diversity of insect natural enemies in the
cultivated species of cotton**

**Prabhulinga Tenguri^{1,2*}, Babasaheb B. Fand¹, Shivaji H. Thube¹,
Richa Varshney² and Omprakash Navik²**

¹ICAR–Central Institute for Cotton Research, Nagpur, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: prabhulinga.tenguri@icar.gov.in

India is the world's largest producer of cotton and the only country that cultivates all four species of cotton. Despite this unique distinction, limited research exists on the diversity and abundance of natural enemies of cotton insect pests within these cultivated species. To address this gap, a study was conducted to evaluate the diversity and abundance of natural enemies hosted by different cotton species. The study examined five genotypes with distinct genetic backgrounds: Phule Dhanwantari, Suraj, Suvin, RCH-2 and DCH-32. Using the adiv 2.0.1 and vegan R packages, significant differences were identified in the diversity, richness, evenness, and abundance of natural enemies across these genotypes. Analysis of Similarity (ANOSIM) and Non-metric Multidimensional Scaling (NMDS) revealed notable variations in the community structure of natural enemies among the genotypes. A total of 17,279 natural enemies were collected and identified, belonging to seven predatory families and five parasitoid families. The percentage contribution of these families, in descending order, was as follows: Coccinellidae (28.23%), Tachinidae (19.23%), Braconidae (12.68%), Chrysopidae (11.65%), Chalcididae (9.41%), Aphelinidae (6.33%), Pentatomidae (3.29%), Ichneumonidae (2.37%), Syrphidae (2.33%), Vespidae (1.81%), Asilidae (1.79%) and Geocoridae (0.89%). Six major families, viz. Coccinellidae, Tachinidae, Braconidae, Chrysopidae, Chalcididae and Aphelinidae accounted for more than 85% of all recorded natural enemies. Notably, these families constituted a higher percentage share in Phule Dhanwantari (90%) compared to the other genotypes. The findings emphasise the importance of conserving and effectively utilising these natural enemies for the ecological and sustainable management of insect pests in cotton ecosystems.

Keywords: cotton; natural enemies; species diversity; species richness; yellow pan trap





Taxonomic notes on the predatory thrips in India

R.R. Rachana*, B. Amarendra and S.N. Sushil

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

**Correspondence: vavarachana@gmail.com*

Thrips constitute an economically important group of sucking insects and comprise around 6,500 extant species in 790 genera, of which, nearly 50 per cent are fungal feeders, another 40 per cent feed on plant tissues. Several thrips species are reported as predators of mites, thrips, scale insects and booklice. Hence, they can serve as biological control agents of arthropod pests. Obligate predation by thrips is rarely noticed, though the habit has evolved several times, and many species are facultative predators. Predatory thrips are reported in Aeolothripidae, Thripidae and Phlaeothripidae families. Among Thripidae, all species of *Scolothrips* Hinds are obligate predators on mites. *Frankliniella occidentalis* (Pergande), *Frankliniella fusca* Hinds, and *Thrips tabaci* Lindeman which are primarily phytophagous, have been observed predating on mites. Members of the family Aeolothripidae under the suborder Terebrantia exhibit a wide range of feeding diversity, from obligate phytophagous to facultative predators of small arthropods that live in flowers. In the Phlaeothripidae, all members of the genus *Leptothrips* Hood are presumed to be predators, and two species of *Karnyothrips* Watson predate on scale insects, although limited evidence is available for this habit among other species of this genus. Also Phlaeothripid, *Aleurodothrips fasciapennis* (Franklin) predate on the scale insect, *Aonidiella aurantii* (Maskell). Although predatory behaviour of several species has been documented, their potential as biocontrol agents has hardly been evaluated. Parameters like prey specificity and amenability for mass rearing need to be evaluated before selecting as potential biological control agents.

Keywords: Aeolothripidae; biological control; *Scolothrips*; Thripidae; Thysanoptera





Leafhopper diversity in the Andaman and Nicobar Islands: insights from the preliminary study

N.N. Rajgopal*, Ankita Gupta and S.N. Sushil

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

**Correspondence: raju924rg@gmail.com*

Leafhoppers (Hemiptera: Cicadellidae) are significant agricultural pests, causing damage to various crops both directly by sucking plant sap and indirectly by transmitting plant pathogens. Cicadellidae comprises nearly 23,500 recognised species worldwide. The Andaman and Nicobar Islands are renowned for their tropical hot and humid climate and rich biodiversity, these islands have historically received limited attention regarding leafhopper fauna. The leafhopper fauna documented from the islands includes *Aalinga brunoflava* Viraktamath & Webb, *Advikus andamanicus* Viraktamath & Yeshwanth, *Buloria gyponinoides* Distant, *Empoasca nara* (*Empoasca nara*) *benignalima* Dworakowska, *Paraidioscopus andamanicus* Viraktamath & Yeshwanth, *Phlogothamnus maculiceps* Ishihara, *Scaphoideus bifidus* Viraktamath & Mohan, *Signoretia takiyae* Viraktamath & Webb and *Webbolidia andamana* Viraktamath & Meshram. In the present study, preliminary surveys combined with an examination of National Insect Museum, ICAR–NBAIR specimens identified 23 species from 21 genera, representing 14 tribes across six subfamilies: Aphrodinae, Cicadellinae, Evacanthinae, Iassinae, Ledrinae and Tartessinae. With these findings, the total count of leafhopper fauna for the region now stands at 32 species in 30 genera. Among these, the subfamily Deltocephalinae was the most diverse, accounting for over 50% of the species. The currently recorded fauna was limited to the Andaman group of islands, while the Nicobar group remains unexplored. This preliminary study highlights the rich leafhopper diversity in the islands and underscores the need for systematic research to uncover the full extent of their diversity, including the species endemic to the region.

Keywords: Cicadellidae; distribution; genera; species; taxonomy





**Native parasitoids of the invasive pest fall armyworm,
Spodoptera frugiperda (J.E. Smith) (Lepidoptera: Noctuidae),
in southern Rajasthan, India**

**S. Ramesh Babu*, Beerendra Singh, Khushi Saini, S.R. Gayathri, K.K. Shruthi and
Divya Kumari Dhakar**

Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur, India

**Correspondence: babuento2018@gmail.com*

The invasive pest fall armyworm (FAW), *Spodoptera frugiperda*, is a polyphagous pest that causes severe losses in cereals. The study has been done on the prevalence of natural enemies and their abundance on FAW in Southern Rajasthan which could be potential biocontrol agents in the IPM programme. Based on the morphological and molecular analyses, we found about 10 species of different natural enemies recorded parasitoids were of egg, egg-larval and larval parasitoid species distributed in three different families: *Trichogramma chilonis* (Trichogrammatidae); *Telenomus remus* (Scelionidae); *Chelonus blackburni* and *C. formosanus*; *Cotesia ruficrus*; *Microplitis* cf. *prodeniae*; *Glyptapanteles* sp. (Hymenoptera: Braconidae); *Charops bicolor*; *Campoletis chlorideae* (Hymenoptera: Ichneumonidae); *Drino* sp./ tachinid species (Diptera: Tachinidae). The overall parasitism of FAW larvae, attributed to the distinct contributions of various parasitoid species was calculated as 7.35%. *Chelonus* sp. accounted for the majority of overall parasitism at 5.09%, followed by *Campoletis chlorideae* at 0.94%. *Chelonus* sp. and *Campoletis chlorideae* represented the two most prevalent species with the relative abundance values of 69.2 and 12.8, respectively. The different parasitoids found in this study will be useful for the development of sustainable management of FAW in the region-specific IPM programme.

Keywords: *Campoletis chlorideae*; *Chelonus*; *Drino*; *Spodoptera frugiperda*; *Trichogramma*





Characterisation of entomopathogenic nematodes from semi-arid areas of Rajasthan for their potential use as larvicides against mosquitoes

Istkhar Rao

Department of Bioscience and Biotechnology, Banasthali Vidyapith, Banasthali, India

Correspondence: istkharrao@gmail.com

Entomopathogenic nematodes (EPNs) are effective biological control agents of insect pests damaging crops throughout the globe. These nematodes are not only found effective against insect pests but also against other arthropods. The existence and potential of EPNs in India's high-temperature, semi-arid areas are still mostly unknown, and the present study was performed to search for EPN species from these areas for their future application as larvicides of mosquitoes (*Aedes* and *Anopheles* spp.). The soil samples were collected from different fields of Rajasthan and nematodes were isolated using the *Galleria*-baiting technique. Thirty-five samples were found positive for the presence of nematodes, out of which 19 were for EPNs while 16 were for other free-livings. All 14 steinernematids were identified up to the molecular level using conserved genes (ITS and D2D3) and their insecticidal properties were tested on insect larvae. Morphological and molecular characterisation revealed their identity as *Steinernema siamkayai* (4 isolates) and *S. pakistanense* (10 isolates). Five isolates of *Heterorhabditis* spp. are on the way to identification up to the species level. The insecticidal properties of these identified steinernematid isolates demonstrated significant pathogenicity against *Galleria mellonella* and *Tenebrio molitor* larvae, with high fecundity. The potential of isolated nematodes is promising not only for insect pest management but also for controlling mosquito larvae as a prospect, thereby reducing the incidence of diseases caused by pathogens carried by adult mosquitoes.

Keywords: *Galleria mellonella*; *Heterorhabditis* spp.; pathogenicity; *Steinernema* spp.; *Tenebrio molitor*





Exploring the taxonomy of Indian Tortricidae: past, present and future

**P.R. Shashank*, Santhosh Naik, Karthik M. Reddy, V.S. Aashiq Poon and
Kishore C. Sahoo**

National Pusa Collection, ICAR–Indian Agricultural Research Institute, New Delhi, India

**Correspondence: spathour@gmail.com*

The Tortricidae, known as leaf-roller moths, constitute one of the four largest lepidopteran pest families. Despite their ecological and economic significance, India's exploration of these moths remains relatively underexplored in comparison to other regions. These moths significantly contribute to biodiversity and are also economically important as pests of agricultural and horticultural crops; they also serve as model organisms for studying lepidopteran genetics, insect pheromones, and evolutionary biology. Out of the 11,365 known tortricid species worldwide, only 4.28% (487 species in 168 genera) have been identified from India in three subfamilies to date. Over the past six years, efforts to revise the taxonomy of Indian Tortricidae have significantly expanded our knowledge. A comprehensive study examined over 120 species collected from various regions and specimens deposited at the National Pusa Collection, ICAR–IARI, New Delhi. These efforts led to the discovery of 13 species new to science, 13 species newly recorded in India, and three newly recorded genera added to the country's Tortricidae faunal list. In addition to morphological identification, a DNA barcoding reference library for 31 species of tortricid moths has been developed, with 27 novel barcodes. Despite these advancements, challenges persist in characterising the Tortricidae in India. Limited taxonomic expertise, scarce genetic data, and underrepresentation in faunistic studies hinder progress. Our knowledge of the Tortricidae might be substantially improved by addressing these problems through thorough taxonomic surveys and molecular techniques, which could uncover previously unknown species and shed light on the evolutionary processes influencing lepidopteran diversity.

Keywords: DNA barcoding; discovery; insects; Lepidoptera; systematics



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



**Diversity and diagnostics of *Rhinyptia* spp. (Coleoptera: Scarabaeidae:
Rutelinae) of Indian fauna**

Kolla Sreedevi*, S. Jayashree and S.N. Sushil

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

**Correspondence: kolla.sreedevi@gmail.com*

The family Scarabaeidae comprises around 35,000 species (91% of all Scarabaeoids) worldwide and is the largest family under the superfamily Scarabaeoidea of Coleoptera. It includes both beneficial and phytophagous insects. The phytophagous beetles (Pleurosticti), also known as chafers, white grub, June beetle and root grubs, are pests of agricultural and horticultural crops, plantations and forest trees, while the saprophagous beetles (Laprosticti), also known as dung beetles, play a significant role in nature's sanitation and soil fertility by decomposing dung. The Pleurosticti Scarabaeidae comprises mainly five subfamilies, viz. Melolonthinae, Sericinae, Rutelinae, Dyanstinae and Cetoniinae, of which Rutelinae is one of the speciose subfamilies comprising nearly 200 genera and about 4,500 described species worldwide. Among several genera of Rutelinae, economically important *Rhinyptia* belonging to the subtribe Anisopliina and tribe Anomalini is less studied. Information on this genus is very scanty, inadequate and the Indian fauna is not fully explored. So, the present study is focussed on the less speciose genus, *Rhinyptia*, which comprises around 29 species globally. In India, nine species have been reported so far from different parts of the country. These are easily recognisable from other scarabs of Rutelinae by its clypeus extending into a rostrum anteriorly and strongly recurved. The larval stages of *Rhinyptia* spp. are known to feed on the roots and rootlets of field crops mostly rice, sugarcane, sorghum, niger, acacia, ber, etc. The present study provides species diversity, distribution, feeding behaviour, diagnostics and taxonomic keys of *Rhinyptia*, which can form a basis for further in-depth studies and explorations.

Keywords: diagnostic characters; distribution; *Rhinyptia*; species diversity





**Insect pests and natural enemy fauna of major fruits of Vijayapura district,
Karnataka, India**

N.D. Sunitha* and Narayana Chavadal

College of Agriculture, University of Agricultural Sciences, Vijayapura, India

**Correspondence: sunithand@uasd.in*

Vijayapura district is a leader in the production of many fruits, including grapes, pomegranate, citrus, papaya, sapota and custard apple. However, the cultivation of fruit crops in the district faces several challenges, of which insect pests are the major one. Studies were conducted during 2023–2024 in the district on major insect pests and their natural enemies in all the six fruit ecosystems of the district. While one or two species of insect pests were found to be the major pests in the fruit ecosystems studied, mealybugs were found to be major constraints in all the six fruit ecosystems due to their high multiplication rates, invasive nature, concealed habitat and pathogen transmission. *Planococcus* spp., *Maconellicoccus* spp. and *Ferrisia* spp. were recorded as dominant mealybug species and custard apple suffered maximum fruit damage to the tune of 43–70%. Two key predators, *Spalgus* spp. (Lycaenidae: Lepidoptera) and *Micromus* spp. (Hemerobiidae: Neuroptera), were identified as effective natural enemies in controlling mealybug populations in custard apple. *Spalgus epeus* in particular demonstrated significant suppression, suggesting its potential for integrated pest management programmes.

Keywords: fruit crops; mealybug; *Micromus* spp.; *Spalgus* spp.





Species richness and diversity of predatory spiders in *Bt*-cotton ecosystem

H. Latha¹, S.S. Udikeri^{1*}, Sachin R. Patil² and M. Sampathkumar³

¹College of Agriculture, University of Agricultural Sciences, Dharwad, India

²Zoological Survey of India, Western Regional Centre, Pune, India

³ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: ssudikeri@gmail.com

Spiders are often overlooked despite their diverse species range and pest control potential. To assess the species richness and diversity extensive survey has been undertaken during 2023–2024 in Haveri and Dharwad district *Bt*-cotton fields. Among the nine families, Araneidae showed a higher relative abundance in Haveri district, with six species (31.58%), compared to Dharwad district having four species (28.57%). Similarly, the Thomisidae family exhibited same results, as Dharwad district had a lower number of species (3 species) recorded whereas, Haveri district recorded five species. When evaluating the Oxyopidae family, Dharwad district recorded two species and Haveri district had one species recorded. Another family, Theridiidae, demonstrated a higher relative abundance in Haveri district with three species (15.79%), while Dharwad district documented only one species (7.14%). Thus, Haveri district displayed higher taxa richness with compared to Dharwad. The dominance index in Dharwad district was 0.112, whereas Haveri district had a lower index of 0.077. Haveri also showed a higher Simpson diversity index (0.922) compared to Dharwad district (0.887). The Shannon diversity index was 2.710 in Haveri district and 2.392 in Dharwad district, emphasising Haveri district's higher species diversity. Both regions had comparable evenness indices, with Dharwad district at 0.781 and Haveri district slightly elevated at 0.790. Margalef richness index was higher in Haveri district (4.010) than Dharwad district (3.687). Overall, Haveri district exhibited richer and more diverse spider fauna compared to Dharwad district. The diversity and richness urges for their conservation and deployment in biocontrol programmes for *Bt* cotton, especially against sucking pests.

Keywords: biocontrol; cotton; diversity; richness; spiders



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



***Gaeolaelaps* (Acari: Laelapidae) — a group of predatory mites as successful biocontrol agents**

Pritha Bandyopadhyay and Krishna Karmakar*

Department of Agricultural Entomology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India

**Correspondence: karmakar.krishna@bckv.edu.in*

Mites are tiny but mighty arthropodan organisms with four pairs of legs in adult and completely devoid of antenna and wings. They are ubiquitous and important mesofauna of soil food webs, shredders, predators as well as prey in the system. Cosmopolitan mite family Laelapidae includes both free-living predatory species and species associated with arthropods, mammals or birds. Free-living species have received significant attention as predatory bioagents of agri-horticultural pests that spending some parts of their life-cycle in the soil and litter, but they are less researched and used in biocontrol. Among the most commonly observed hypoaspidins in soils, *Gaeolaelaps* is a well-known group of predatory mites that can be mass cultured. Based on previous studies, they feed on nematodes, acarid mites and soft-bodied arthropods that abound in soil and decomposing organic matter. They may therefore play an important role in balancing the soil ecosystem. Recently, four *Gaeolaelaps* spp. are collected from parts of Eastern India. Also, a checklist of the Laelapidae of India with available information on the distribution and biology of 66 species belonging to 21 genera is published. Even though India is a vast biodiverse country, only a few laelapids have been reported and described to date. In India, knowledge is also lacked in the study of diversity and taxonomic aspects but equally so in bioecology, mass culture techniques and field utilisation. This highlights an important opportunity for in-depth exploration of voracious laelapids like *Gaeolaelaps*, their ecological roles and importance as biocontrol agents.

Keywords: biocontrol agents; Laelapidae; mesofauna; predators; soil-litter ecosystem





Occurrence of white grubs (Coleoptera: Scarabaeidae) in the vicinity of Pattambi rice fields, Palakkad, Kerala

Judith Corolin Correya¹ and K. Sreedevi^{2*}

¹Department of Zoology, Jain (Deemed-to-be-University), Bengaluru, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: kolla.sreedevi@gmail.com

The phytophagous scarab group includes white grubs, also known as June beetles or chafer beetles which belong to the family Scarabaeidae of Coleoptera. These beetles are significant pests of crops like sugarcane, groundnut, potato, arecanut, etc. White grub larvae feed on roots and underground stems, while adult beetles feed on foliage, causing stunted growth, reduced yields, and plant death. This group belongs to subfamilies Melolonthinae, Rutelinae, Sericinae, and partly Dynastinae of Scarabaeidae. A survey was taken up to document the species diversity of phytophagous scarabs in Pattambi, Palakkad district of Kerala, a significant agricultural area known for its extensive rice cultivation. Adult beetles were collected from March to August, 2021–2024 using light traps. Around 750 collected beetle specimens were sorted, cleaned, mounted, labelled, and identified up to the species level using available literature and identification keys. The collection included 22 species from 12 genera representing subfamilies Melolonthinae, Rutelinae, Sericinae, and Dynastinae. Melolonthinae had the most genera (5), followed by Dynastinae (4), Rutelinae (2), and Sericinae (1). The species, *Schizonycha ruficollis*, *Heteronychus annulatus*, and *Apogonia* sp. were prevalent throughout the four-year study, constituting 80% of the total population. This study provides critical insights into the diversity, distribution, abundance, and seasonal variations of white grubs in Pattambi area of Kerala. The collections aid in documentation of the species diversity and dynamics to understand the distribution and species range.

Keywords: Pattambi; rice fields; Scarabaeidae; species diversity; white grubs





Why are we ignoring shrubs? *Acraea issoria* (Hubner)—yellow coster defoliator of *Debregeasia hypoleuca* (Steud.) in the Western Himalaya

Romila Devi* and Pawan Kumar

KSCSTE–Kerala Forest Research Institute, Peechi, India

*Correspondence: romilaroma1122@gmail.com

The present study investigated the taxonomic, morphological details, and pest status of the yellow coster, which is a defoliator of *Debregeasia hypoleuca* (Steud.) evergreen shrub growing in shady forests of Western Himalaya (Himachal Pradesh). *Acraea* is a genus of brush-footed butterflies (Lepidoptera: Nymphalidae) of the subfamily Heliconiinae. The larvae are potential defoliators of *D. hypoleuca*, a lesser-known but ecologically significant species in the Himalayas. The species was examined in terms of taxonomy and external genital morphology. Significant differences between the males and females were noted in the description details. The fact that this species completely defoliates *D. hypoleuca* in the early stages of the growing season and that defoliator outbreaks are a yearly occurrence makes it a serious problem. Population dynamics study revealed habitual, short-range movements of emerging populations. In the current study, described morphometric characters could be used as a guide for taxonomic identification of this pest. We were therefore interested in investigating the temporal and spatial relationship among various population groups in Western Himalaya and addressing the cause of the outbreak at the landscape level. Understanding the life cycle and ecology of *Acraea issoria* (Hubner) is crucial for developing effective biocontrol management strategies. Management approaches can be used to control their populations while minimising harm to beneficial species.

Keywords: biocontrol strategies; spatial and temporal analysis; taxonomic identification; pest outbreak



Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources



Diversity and emerging threats of eriophyoid mites to food and biosecurity in Karnataka

**P. Dyamanagouda^{1*}, K. Rajashekharappa¹, C. Chinnamade Gowda², Vidya Mulimani²,
Renuka Hiremath² and Anna Jose²**

¹College of Agriculture, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences,
Shivamogga, India

²University of Agricultural Sciences, Bengaluru, India

*Correspondence: pdyamanagouda@uahs.edu.in

Eriophyoid mites are host-specific and significant vectors of phytoviruses, posing an increasing risk to diverse flora due to their adaptability and host manipulation capabilities. A survey conducted from 2022 to 2024 across various agro-ecosystems and agro-climatic zones of Karnataka aimed to document the diversity of eriophyoid mite species. The study identified 50 eriophyoid mite species from a range of hosts, including agricultural crops and forest tree species. Among the different mites collected seven species are new records to India, viz. *Aceria ficaria* Ueckermann on *Ficus racemosa* L., *Abacarus horseshoex* Lu & Xue and *Abacarus fuzhoubambusae* Lu & Xue and *Knorella gigantochloae* Keifer on *Bambusa* sp., *Vittacus bougainvilleae* (Keifer) on *Bougainvillea spectabilis* Willd., *Calacarus flagellisetia* Flechtmann, De Moraes & Barbosa on *Carica papaya* L. and *Jutarus benjaminiae* Boczek & Chandrapatya, on *Ficus benamina* L. Additionally, two significant pest mites were recorded, *Aculus (Aculops) lycopersici* (Tryon), which causes severe damage to the leaves and fruits of tomato (*Solanum lycopersicum* L.) and *Aceria boisi* (Gerber), which induces gall formation on cinnamon (*Cinnamomum verum* J. Presl) leaves, compromising leaf quality and market value. The study also highlights new host records, new records for Karnataka state and records of previously known species, with some identified as potential weed control agents. In conclusion, conducting timely inventory surveys is crucial for understanding eriophyoid mite pest fauna and assessing their potential future threats to food and biosecurity.

Keywords: *Aceria*; biosecurity; cinnamon; eriophyoid mites; tomato





Diversity and species richness pattern of predatory wasps in tasar ecosystem

**Hanamant Gadad^{1*}, Shreyansh¹, S.M. Mazumdar², Thirupam Reddy³, Vishal Mittal¹,
Jitendra Singh¹ and N.B. Chowdary¹**

¹Central Tasar Research and Training Institute, Central Silk Board, Ranchi, India

²Basic Seed Multiplication and Training Centre, Central Silk Board, Kathikund, India

³Basic Seed Multiplication and Training Centre, Central Silk Board, Bastar, India

*Correspondence: hsgadad@gmail.com

Despite wasps being regular predators of tasar silkworms, little is known about their diversity, species richness, and abundance in the tasar ecosystem. Traditionally, predatory wasps are considered minor pests of tasar silkworms. However, in recent years they have emerged as a major concern in some of the tasar-practicing regions. This study investigated wasp communities across major tasar-growing regions in Eastern India, including Jharkhand, Odisha, West Bengal, and Chhattisgarh. Field surveys were conducted during the silkworm rearing period (June–October) in *Terminalia arjuna* and *T. tomentosa* plantations. Data was analysed using ecological indices such as Shannon-Wiener, Simpson's diversity index, and Pielou's evenness, alongside richness estimators (Chao-1, iChao-1) and similarity metrics (Jaccard, Bray-Curtis). Seventeen wasp species were recorded, with Ranchi showing the highest species richness (11 species) and DhainkiNainjiya the lowest (1 species). Ranchi and Kathikund exhibited high species overlap, whereas DhainkiNainjiya recorded distinctively, low species diversity. Further rarefaction analysis revealed that sites with high plant diversity supported richer wasp communities, underscoring the role of habitat and environmental heterogeneity in enhancing biodiversity. Some of the wasp species were found to predate on tasar silkworms, while others may serve as potential natural enemies of herbivores of tasar food plants and nearby crops. These findings highlight the ecological complexity of the wasps community in the tasar ecosystem and their dual predatory role.

Keywords: ecological indices; environmental heterogeneity; predatory wasps; species richness; tasar silkworm





Soft scale (Hemiptera: Coccidae) fauna of Kerala and their associated natural enemies

Desavath Gouthami^{1*}, Haseena Bhaskar¹, Sunil Joshi², A. Rameshkumar³ and C.V. Vidya

¹College of Agriculture, Kerala Agricultural University, Vellanikkara, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

³Hymenoptera Section, Zoological Survey of India, Kolkata, India

*Correspondence: desavath-2021-21-071@student.kau.in

Soft scales are one of the most destructive insect pests across the globe with around 1,241 described species under 180 genera. Recently, several alien scale insect species have invaded and got established in India. In spite of the significance of soft scales in agricultural ecosystems, no systematic studies have been carried out to document the fauna of Coccidae of Kerala. Periodic surveys were conducted during 2021 to 2024 across different agricultural ecosystems of Kerala, and soft scale infested plant samples were collected. The associated ants and predators were also collected separately. In the laboratory, the scale infested plant samples were maintained in plastic containers for emergence of parasitoids, if any. Adult females of Coccidae, predators, parasitoids and ants collected were preserved in 70% ethanol for further identification. Specimens of scale insects were slide mounted for taxonomic studies. The ants and natural enemies were identified with the help of expert taxonomists. The study revealed 28 species of Coccidae under 17 genera belonging to three subfamilies viz. Cardiococcinae (Tribe: Cardiococcini), Coccinae (Tribes: Coccini, Saissetiini, Paralecaniini and Pulvinariini), and Ceroplastinae (Tribe: Ceroplastini). Seven species of hymenopteran parasitoids belonging to Aphelinidae, Eulophidae, Encyrtidae, Eunotidae and Pteromalidae and five species of predators in the family Coccinellidae, Lycaenidae and Cybocephalidae were recorded as natural enemies of the scale insects. In addition, 18 species of ants were found associated with Coccidae in Kerala. The study reports new geographical distribution as well as host records for different species of Coccidae from Kerala.

Keywords: ants; diversity; host range; natural enemies; taxonomy





**First report of non-bioluminescent cave dwelling keroplatid, *Chetoneura* sp.,
from Meghalaya, northeastern India**

K.H. Hans Austin^{1*}, Snata Kaushik¹, M. Ranjith², K.M. Sreekumar³ and K.R. Sudharshan¹

¹College of Post Graduate Studies in Agricultural Science, Central Agricultural University, Imphal, India

²Regional Plant Quarantine Station, Directorate of Plant Protection, Quarantine and Storage, Mumbai, India

³College of Agriculture, Padanakkad, India

*Correspondence: hansaustine@gmail.com

This study reports the first non-bioluminescent cave-dwelling species of Keroplatidae, *Chetoneura* sp. from Meghalaya, northeastern India, expanding knowledge of the ecological and taxonomic diversity of the understudied dipteran family Keroplatidae. The adults and larvae were collected from the caves of PedengShnog village of Sohra, Meghalaya. This non-luminescent larva was found on the roof of the caves hanging down horizontally in a silken hammock with long sticky mucous covered threads to lure and trap prey. The 300 m long limestone cave being situated on top of the mountain, characterised by the fossil remnant of crustaceans and fish and a continuous flowing stream. Colonies of larvae with their characteristic shimmering snares 9–10 cm long were observed nearly 50–70 m from the cave entrance in vicinity to the illuminated light source were intriguing. A single female adult and a few larvae were collected in 70% ethanol for the current studies. Absence of R_4 vein with long r-m fusion and costa extending $2/3^{\text{rd}}$ of the distance between R_5 and M_1 being the key diagnostic feature, the abdomen was adorned with distinctive hexagonal or polygonal sculpturing on tergites and sclerites, giving the appearance of interlocking protective plates. Within this family, the genus *Chetoneura* is particularly rare/ unexplored, currently comprising five known species: *C. cavernae*, *C. shennonggongensis*, *C. oligoradiata*, *C. davidi*, and *C. lagangensis*. The earlier studies have focused on bioluminescent species, such as *Arachnocampa luminosa* in New Zealand, this discovery highlights the presence of non-glowing members within the Oriental biogeographic region.

Keywords: cave-dwellers; *Chetoneura*; Keroplatidae; non-bioluminescent; Northeast India





Assessing the geographic distribution of *Ipomoea* and its association with insect diversity in southern India

M.N. Harish^{1*}, A.N. Shylesha², S.R.K. Singh¹ and A.A. Raut¹

¹ICAR–Agricultural Technology Application Research Institute, Jabalpur, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: harish9739@gmail.com

A comprehensive survey was conducted across 19 water resources in six districts of South Karnataka to evaluate the establishment of *Ipomoea aquatica* and its association with insect diversity. *Ipomoea aquatica*, a fast-spreading invasive aquatic plant, was observed to dominate these ecosystems, forming dense mats that disrupt native vegetation and aquatic biodiversity. The study identified six insect species interacting with *I. aquatica*, representing two orders (Coleoptera and Hemiptera) and five families. These include *Aspidimorpha miliaris* (Asian Spotted Tortoise Beetle), *Charidotella bicolor* (Golden Tortoise Beetle), *Eurybrachys tomentosa* (Squat Hoppers), *Acanthocoris scabrator* (Squash Bug), *Cylas formicarius* (Sweet Potato Weevil), and *Sternuchopsis* sp. (Weevil). Each insect species displayed unique host plant preferences, primarily focusing on members of the Convolvulaceae family, with some exhibiting generalist feeding habits. Their roles as potential biocontrol agents were evaluated, considering their feeding behaviours, natural enemies, and ecological adaptability. For instance, *A. miliaris* and *C. bicolor* demonstrated herbivory on *Ipomoea* spp. but faced limitations due to host specificity and vulnerability to predators. Generalist feeders like *E. tomentosa* and *A. scabrator* showed promise for broader pest control applications, albeit with a need for ecological monitoring. This study highlights the complexity of using insect diversity for integrated pest management (IPM) of invasive aquatic plants like *I. aquatica*. It underscores the need for further ecological assessments to optimise biocontrol strategies while minimising unintended impacts on non-target species and ecosystems.

Keywords: biocontrol agents; ecological assessment; IPM; *Ipomoea* sp.





Record of Cheyletidae mites from the eastern dry zone of Karnataka

**Renuka Hiremath^{1*}, Anna Jose¹, N. Srinivasa¹, C. Chinnamade Gowda¹, Vidya Mulimani¹
and P. Dyamanagouda²**

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

²Department of Agricultural Entomology, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, India

*Correspondence: renukahiremath18@gmail.com

Cheyletidae is one of the major mite families in the superfamily Raphignathoidea (Acari: Trombidiformes: Prostigmata). Cheyletids are small, yellow, orange or brown coloured mites, with a fairly flat body. These are mainly free-living predators that feed on various micro arthropods, particularly on herbivorous, frugivorous, and saprophagous acarid mites. A few species can be beneficial as biological control agents controlling acarid mites, which are serious pests damaging agricultural stored foods. The family includes over 440 species under 75 genera in the world and plant-associated cheyletid mites known from India are 15 species under 10 genera. Plant and leaf litter associated cheyletid mites were surveyed in the six districts (Bengaluru Urban, Bengaluru Rural, Kolar, Chikkaballapur, Tumakuru and Ramanagara) of the eastern dry zone of Karnataka during 2021–2023. Samples from major cultivated crops, orchard plants, weeds and forest trees were collected and observed for the presence of cheyletid mites under stereo-binocular microscope in the laboratory. The extracted mites were mounted on glass slides and studied using Axioscope phase contrast microscope with image analysis facilities. Totally, ten species of cheyletid mites viz. *Tutacheyla robusta* Corpuz-Raros, *Oudemans cheyladenmarki* (Yunker), *Hypopicheyla elongata* Volgin, *Dubininiola boonkongae* Vaivaniikul, *Cheletogenes ornatus* (Canestrini and Fanzago), *Kerpalmatus* Muma, *Cheletomorpha lepidopterorum* (Shaw), *Cheletomimus wellsi* (Baker), *Cheletomimus bakeri* (Ehara) and *Cheletomimus congensis* (Cunliffe) were recorded from 17 plant species belonging to 13 botanical families. Of these, seven mite species are new records to India and three are new records to Karnataka state.

Keywords: Cheyletidae; eastern dry zone; Karnataka; predator; Prostigmata





Dynamics and occurrence of predominant white grub species (Coleoptera: Scarabaeidae) across the country

S. Jayashree* and Kolla Sreedevi

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

*Correspondence: jayashreeraj467@gmail.com

Scarabaeidae is the largest family under the superfamily Scarabaeoidea, which constitutes about 35,000 species globally. It includes both beneficial (Laprosticti) and harmful (Pleurosticti) insects. Pleurosticti scarabs include white, which grubs mainly belong to subfamilies Melolonthinae, Sericinae, Rutelinae and partly Dynastinae of Scarabaeidae. In India, the predominant genera of white grubs are *Holotrichia*, *Brahmina*, *Leucopholis*, *Lepidiota*, *Maladera*, *Melolontha*, *Schizonycha*, *Sophrops*, *Apogonia*, *Anomala*, *Adoretus* and *Phyllognathus*, and these are the serious pests of several agricultural and horticultural crops. Among these, the most speciose group are *Holotrichia*, *Maladera*, *Anomala*, *Adoretus*, *Apogonia*. The species distribution of these genera varies with the crop, latitude and altitude. So, the present study is focused on the major white grub species, their geographic prevalence, species range and occurrence across the country over different time periods. To cite an example, *Holotrichia* is represented by nearly 50 species and the various species except *H. serrata*, exhibits distinct distribution across the country, as influenced by crop, latitude, soil factors, environmental variables, etc. The paper describes the dynamics and distribution of major predominant species of white grubs. By understanding their distribution, population dynamics trend and occurrence patterns, the study seeks to provide valuable insights to develop effective and sustainable pest management strategies to mitigate the significant damage these pests.

Keywords: dynamics; major species; after occurrence; pleurosticti white grub; Scarabaeidae





Diversity of *Typhlodromus* (*Anthoseius*) from eastern dry zone of Karnataka

Anna Jose*, Renuka Hiremath, C. Chinnamade Gowda and Vidya Mulimani

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

*Correspondence: annajose93@gmail.com

Predatory mites in the family Phytoseiidae (Acari: Mesostigmata) are of great importance for their potential as predators of phytophagous mites and certain small insects. Globally, the family exhibits remarkable diversity, comprising over 2,700 valid species, 261 of which are reported from India. The subgenus *Typhlodromus* (*Anthoseius*) De Leon is one of the largest groups of phytoseiid mites with more than 400 species including synonyms according to the online database on Phytoseiidae. Survey for phytoseiid mites during 2021–23 on different plants in the Eastern dry zone of Karnataka, revealed the presence of eight species of *Typhlodromus* (*Anthoseius*) viz. *T. (A.) bengalensis* Karmakar et al., *T. (A.) bulbosis* Karmakar et al., *T. (A.) bolpurensis* Bhowmik & Karmakar, *T. (A.) divergentis* (Chaudhri, Akbar & Rasool), *T. (A.) ghanii* (Muma), *T. (A.) rickeri* Chant, *T. (A.) serrulatus* Ehara and *T. (A.) transvaalensis* (Nesbitt). Among these 8 species, four are new records to Karnataka. The habitat (plant) of the aforementioned species and the prey associated with the predatory mites were also recorded. Prey include chilli thrips, spider mites, mealybugs, scale insects and eriophyid mites. Phytoseiid mites such as *T. (A.) bengalensis* and *T. (A.) bulbosis* were collected only on *Ficus* spp. showing their limited host plant association whereas the remaining species were collected from a wide range of plants in different botanical families.

Keywords: *Anthoseius*; biological control; Phytoseiidae; predatory mite





Annual fluctuations in the populations of spiders, chrysopids and lady bird beetles in mango and cashew orchards

S.N. Kale*, V.N. Jalgaonkar, M.S. Karmarkar, B.D. Shinde and R.S. Mule

Dr Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, India

**Correspondence: sameerakl@yahoo.com*

Fluctuations in the populations of predatory insects viz. spiders, chrysopids and lady bird beetles in mango and cashew orchards throughout the year were studied at Regional Fruit Research Station, Vengurle, Maharashtra during 2017–18. Out of three predators, only spiders were present more or less regularly throughout the year and its population ranged between 0.00 to 0.90 per shoot in mango and 0.05 to 1.40 per shoot in cashew. The highest population of spider was recorded in 2nd MW in mango and 1st MW in cashew while the lowest population was recorded in 27th MW in mango and 24th and 25th MW in cashew. The egg masses of spiders were recorded intermittently in both the orchards and the highest recorded in 39th and 40th MW (0.10/ shoot) in mango and 46th MW (0.20/shoot) in cashew. Unlike spiders, chrysopids were not observed throughout the year in mango and cashew. Eggs/egg masses and larvae of chrysopid were regularly observed only during initial meteorological weeks. In mango, the highest eggs/egg masses were observed in 5th MW (0.40/shoot) while in cashew in 1st and 2nd MW (0.35/shoot). The highest population of chrysopid larvae was recorded in 7th MW (0.45/shoot) in mango and 5th MW (0.40/shoot) in cashew. Pupal population of chrysopid was observed very haphazardly in mango while it was observed more or less regularly during 10th to 15th MW in cashew. Adults of chrysopids were observed only during 9th MW in mango while they were not recorded in cashew. In case of lady bird beetle, eggs, larval and pupal populations were not observed in mango while it recorded only during 1st to 5th MW in cashew. The adult ladybird beetle was observed only during 9th MW in mango while in cashew they were observed intermittently during 2nd MW to 22nd MW and 47th MW to 52nd MW while not observed during 23rd to 46th MW.

Keywords: cashew; chrysopids; lady bird; spider



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



**Shedding light on the importance of mites of genus *Cosmolaelaps*
(Acari: Laelapidae) as biocontrol agents**

Payel Kar and Krishna Karmakar*

Department of Agricultural Entomology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India

**Correspondence: kamakar.krishna@bckv.edu.in*

Mites are small, ubiquitous arthropods belonging to the class Arachnida, sub-class Acari, known for their ecological diversity. They play a significant role in biological control, a key element of integrated pest management. Predatory mites of the genus *Cosmolaelaps* in the family Laelapidae, have emerged as very important biocontrol agents in agricultural ecosystems. These mites are important members of the soil mesofauna and play a significant role in maintaining soil health. They are generalist predators which allow them to feed upon a broad range of organisms from nematodes to insects, which spend a part of their life cycle in soil. This contributes to their role in sustainable pest management strategies. Their importance lies in their adaptability to diverse habitats and resilience in varying environmental conditions. They exhibit rapid reproduction rates and a broad diet, allowing them to thrive in agricultural settings while effectively controlling pest populations. Furthermore, the use of these mites aligns with organic farming practices, supporting the increasing demand for eco friendly agricultural methods. Research into the biological characteristics and behaviour of *Cosmolaelaps* has revealed their potential for mass production and release in various crops. By harnessing their predatory capabilities, farmers can achieve long-term pest management solutions that mitigate their reliance on chemical pesticides, ensuring healthier agroecosystems. Continued research and field trials are essential to optimise their use and fully realise their benefits in diverse agricultural contexts.

Keywords: biological control; *Cosmolaelaps*; Laelapidae; soil mesofauna



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Morphological and molecular identification of earwigs (Dermaptera) of South India with insights into predatory potential against fall armyworm, *Spodoptera frugiperda*

C.M. Karthik* and C.M. Kalleshwaraswamy

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

*Correspondence: karthikcmag62@gmail.com

Surveys undertaken during 2020–2022 along the selected parts of South India yielded 32 species of earwigs belonging to 21 genera of eight families including one new species and two new records from India. Among the collected samples, the highest samples were represented by Anisolabididae (32.85%) with the highest generic and species diversity. A new species of earwig, *Diplatys sahyadriensis* Karthik, Kamimura and Kalleshwaraswamy was reported and an identification key to *Diplatys* species of India and Sri Lanka was given. *Chaetospania anderssoni* and *Dendroketes corticinus* were two new records from India. The specific region of mitochondrial COI (*mtCOI*) gene of 13 earwigs DNA was amplified and sequences were submitted to NCBI. Phylogenetic analysis using maximum likelihood method based on *mtCOI* gene revealed that species belonging to Labiduridae and Forficulidae formed the basal group, while Anisolabididae formed the sister group with Pygidicranidae and Spongiphoridae. The biology of *Euborellia annulata* was studied on artificial diet under laboratory conditions. The incubation period recorded was 10.60 days and total nymphal period was 32.26 days. The *Forficula gravelyi* was tested for its efficacy as potential biocontrol agent on the eggs of *S. frugiperda*. There was a significant egg predation ($t=19.95$) ($P<0.01$) indicating potentiality of *F. gravelyi* for exploitation as biocontrol agent of fall armyworm. Field evaluation of predator, *F. gravelyi* against *S. frugiperda* showed significant reduction in the number of egg masses ($t=-2.35$) ($P<0.01$), larval population ($t=-6.36$) ($P<0.01$) and increased number of earwigs ($t=16.90$) ($P<0.01$) per plant in augmented plots compared to control.

Keywords: *Diplatys sahyadriensis*; diversity; earwig; efficacy; potential





Allure of the overlooked: first report of *Ormyrus* sp., parasitoid of cecidomyiid gall midge on *Machilus bombycina* from Meghalaya

Snata Kaushik^{1*}, K.H. Hans Austin¹, Manju Mathew¹, M. Ranjith² and Angshuman Kar¹

¹College of Post Graduate Studies in Agricultural Science, Central Agricultural University, Imphal, India

²Regional Plant Quarantine Station, Directorate of Plant Protection, Quarantine and Storage, Mumbai, India

*Correspondence: snatakaushik97@gmail.com

This study presents the first documentation of *Ormyrus* sp., a parasitoid from the family Ormyridae (Hymenoptera: Chalcidoidea) in Meghalaya, India. The species was found emerging from galls caused by a gall midge (Diptera: Cecidomyiidae) on *Machilus bombycina* (King ex Hook. f.), known as Som, an essential host plant for the muga silkworm (*Antheraea assamensis* Helfer). This silkworm is responsible for producing the famous muga silk of the region. Gall midges are major pests of Som, damaging its leaves and negatively impacting silkworm growth and silk production. The genus *Ormyrus* consists of solitary idiobiontoparasitoids that attack gall-forming insects from various orders, including Hymenoptera and Diptera. Both male and female adults emerged from the galls of leaves were collected and morphological characters were studied. These wasps are recognizable by their vivid metallic green coloration characterised with a body length of ~3.70 mm, head with large reddish compound eyes with three ocelli, wings with short stigmal vein with relative length of veins sub-marginal: marginal: post-marginal: stigmal as 15:11:3:1, metasomal tergites (Mt₄–Mt₆) having distinct crenulated and foveate tergites ends with a single apical seta, a prominent hind coxa and two robust, curved metatibial spurs of unequal length. This report enhances the understanding of parasitoid diversity within muga silk ecosystems in Meghalaya and underscores the potential of *Ormyrus* sp. as a biological control agent.

Keywords: Cecidomyiidae; gall midges; muga silkworm; *Ormyrus*; parasitoid





Postabdominal structures and molecular evidence reveal an undescribed species of *Rhochmopterum* Speiser (Diptera: Tephritidae: Tephritinae: Schistopterini) from India

Hatwar Nikhil Khemrajji^{1*}, Karamankodu Jacob David², D.L. Hancock³, Mahadevan Raghuraman¹, R. Gandhi Gracy² and Srinivasa Narayana¹

¹Banaras Hindu University, Varanasi, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

³Yew Tree Court, Carlisle, Cumbria, United Kingdom

*Correspondence: nikhilhatwar@bhu.ac.in

Rhochmopterum Speiser is a fruit fly genus in the tribe Schistopterini of subfamily Tephritinae; larvae of which develop in flowers of plants belonging to tribe Vernoniaeae (Asteraceae). Out of 13 species recorded worldwide, six species have been reported in the Oriental region with a single species, *Rhochmopterum venustum* (de Meijere) from India. The genus is characterised by the presence of a pair of white, erect, submedial setae on each abdominal tergite, glossy textured last abdominal tergite and wing with dark rays without white filling. During our collection trips to northern plains and Northeast India, we had collected and reared an undescribed species of *Rhochmopterum* from flowers of *Vernonia* sp. It is very similar to *R. venustum* in external morphology and can be easily misidentified as latter but careful examination of a series of reared specimens revealed differences wing pattern, aculeus morphology and structure of glans of phallus. Our finding is further reinforced by the molecular evidence based on mt-COI, i.e. the new species showed only 92% similarity with *R. venustum*. Both species are illustrated, along with barcodes and key to species of *Rhochmopterum* from the Oriental region.

Keywords: new species; northern plains; *Rhochmopterum venustum*; Vernoniaeae





Diversity of foliage feeders in groundnut, *Arachis hypogaea* L. in different parts of Bikaner district of Rajasthan, India

Keshav Mehra*, Ramawtar Yadav, Veer Singh, M.L. Reager and Mukesh Kumar

Krishi Vigyan Kendra, Bikaner, India

*Correspondence: nikhilhatwar@bhu.ac.in

Groundnut (*Arachis hypogaea* L.) is an important leguminous oilseed crop of Bikaner District of Rajasthan, India. Low groundnut productivity is caused by a wide range of biotic factors; among these, foliage feeders pests viz. red hairy caterpillar, *Amsacta albistriga* Walker, tobacco caterpillar *Spodoptera litura* (F.), gram caterpillar, *Helicoverpa armigera* (Hübner), semilooper, *Thysanoplusia orichalcea* (F.), leaf miner, *Aproaerema modicella* (Deventer), are recognised as important foliage feeders of groundnut. Five species of insect pests were found to infest the different growth stages of groundnut crop at different blocks viz. Kolayat, Nokha, Bajju, Sri dungargarh and Lunkaransar in Bikaner district of Rajasthan during the *kharif* 2023. Among the per square meter (sq. m.) population of pest species, the pod borer (2.00–11.00 larvae/sq. m.), grass hopper (1.00–4.00 hoppers/sq. m.), castor semilooper (1.00–24.00 larvae/sq. m.), spotted pod borer (1.00–3.00 larvae/sq. m.), Hawk moth (1.00–3.00 larvae/sq. m.) and grey weevil (2.00–17.00 weevils/sq. m.) were found at different blocks of Rajasthan considered as the major pests, while the rests were of minor importance. Most of the major and minor pests infested during the vegetative to pre-maturity stages (47–97 DAS) and the maximum infestation occurred during pod formation and pod filling stages (51–85 DAS) of the crop.

Keywords: foliage feeders; groundnut; insect pests; larva; weevils





Taxonomy of two predatory stink bugs: natural enemies of certain lepidopteran and coleopteran pests

Amartya Pal^{1*}, Swetapadma Dash¹ and Rahul Mondal¹

¹*Zoological Survey of India, Kolkata, India*

*Correspondence: amartyapal08@gmail.com

Asopinae, a subfamily within the family Pentatomidae, are the only predatory stink bugs. They can be distinguished by a four-segmented strong rostrum: the first segment is incrassate, not concealed between bucculae. These predatory bugs mainly predate on larvae of lepidopteran, dipteran, and coleopteran insects, both in the juvenile and adult stages. Their effectiveness in controlling insect pests is increasingly recognised in South-east Asia, including India. Two species, *Eocanthecona furcellata* (Wolff) and *Perillus bioculatus* (Fabricius) have been observed preying on lepidopteran larvae and coleopteran grubs. Field photographs illustrate their interactions with these insect pests. These observations suggest their potential as biocontrol agents. This study provides illustrations of both the pentatomid species, including their male genitalia and discusses their distribution in India and globally.

Keywords: Asopinae; *Eocanthecona furcellata*; larvae; *Perillus bioculatus*; predatory stink bug





Morphomolecular characterisation of field collected trichogrammatids and their parasitisation potential

B. Prabhu¹, Johnson Thangaraj¹, Y.S. Edward^{1*}, S. Pradeep¹, K.M. Venugopal², P. Jyoti², Omprakash Navik² and T. Venkatesan²

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

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: johnte_ys@tnau.ac.in

Trichogrammatid egg parasitoids are important biological agents used to control the lepidopteran pests that infest crops. Differentiating *Trichogramma* species is challenging due to their small size and lack of differences in morphological characters, particularly in females. Correct identification is a prerequisite for successful biological control of insect pests using parasitoids. Attempt was made to collect the egg parasitoids from the sugarcane, mango, citrus, and banana ecosystem by exposing sentinel egg cards placed inside baiting device across the northern districts of Tamil Nadu. This study reports the occurrence of trichogrammatids in the sugarcane and citrus ecosystem. Trichogrammatids collected from sugarcane and citrus ecosystems were identified as *Trichogramma chilonis* Ishii using both morphological characteristics and molecular tools (CO1 and ITS-2 markers). The sequence was submitted in GenBank and accession number was obtained. Furthermore, phylogenetic and haplotype diversity study using CO1 sequences of the collected *T. chilonis* revealed that the OL958558.1_India_Tamil-Nadu_Chitteri shared the haplotype 4 (Hap_4), which is the largest haplotype in the present study, which includes 18 insects from India, Kenya, and Pakistan. Our study suggests that an integrated approach using both, morphological and molecular tools is ideal for the accurate identification of trichogrammatids, which can be utilised in augmentative biological control.

Keywords: DNA barcode; parasitoids; *Trichogramma chilonis*; trichogrammatids





First report of *Thrips subnudula* Karny (Thysanoptera: Thripidae) on chilli (*Capsicum annuum* L.) in India

C. Praveenkumar^{1,2}, Kesavan Subaharan^{2*}, V.R. Saminathan^{1*}, R.R. Rachana²,
R. Gandhi Gracy², Jagadeesh Patil², R. Tamilselvan³ and S. Saravanan^{1,2}

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

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

³Pandit Jawaharlal Nehru College of Agriculture and Research Institute,
Karaikal, India

*Correspondence: Kesavan.Subaharan@icar.gov.in

Thrips by their feeding damage and vectoral role in transmitting plant viruses causes severe yield losses. This study presents the first recorded occurrence of *Thrips subnudula* on chilli plants in Karaikal, Pondicherry, India. This new finding highlights a previously unreported association between *T. subnudula* and chilli, a vital crop in Indian agriculture. The species was identified through a detailed morphological analysis, revealing distinct features that differentiate *T. subnudula* from other species within the *Thrips* genus. Key diagnostic traits include ocellar setae III located within the ocellar triangle, pronotum with numerous discal setae, 4–5 pairs of posteromarginal setae, pleurotergites with 4–8 discal setae, and sternites III–VI featuring around 12 marginal and up to 18 discal setae. For confirmation, molecular analysis was conducted. DNA was extracted, and a barcode analysis using the mitochondrial cytochrome oxidase I (mtCOI) gene was performed. The resulting sequences were submitted to the NCBI database. The molecular data supported the morphological findings, ensuring accurate species identification. In addition, scanning electron microscopy was employed to capture high-resolution images of key morphological characteristics, offering detailed insights into the microstructure of *T. subnudula*. These images allow for precise comparisons with other species. The discovery of this new association raises concerns about potential outbreaks and economic losses in chilli cultivation, a key sector of Indian agriculture.

Keywords: chilli; identification and diagnosis; pest biology; pest report; *Thrips subnudula*





Diversity of natural enemy complex associated with major insect pests in pulse crop ecosystems of Gangetic basin

Sabyasachi Ray* and A. Banerjee

Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India

*Correspondence: sabyasachiray1997@gmail.com

The study was conducted at the District Seed Farm, Bidhan Chandra Krishi Viswavidyalaya (22°87'N, 88°20'E) during the *kharif* 2023 and *rabi* 2023–2024 considering two *kharif* pulse crops (greengram and blackgram) and four *rabi* pulse crops (chickpea, fieldpea, lentil and lathyrus). Analysing the weekly data recorded, the relative abundance of each natural enemy was assessed. Various diversity indices such as Simpson's index, Shannon-Wiener index, Margalef index, Pielou's Evenness index and Berger-Parker dominance index were calculated to quantify the diversity of natural enemies. Among the coccinellid beetles, the maximum relative abundance was observed for *Coccinella transversalis* followed by *Micraspis discolor*, *Chilomenes sexmaculata*, *Coccinella septempunctata* and *Brumoides suturalis*. The most abundant syrphids were *Episyrphus balteatus*, *Ischiodon scutellaris*, *Asarkina salviae* and *Mesembrius benghalensis*. Among the spider fauna, most dominant species were *Neoscona theisi*, *Pardosa pseudoannulata*, *Oxyopes* sp. and *Tetragnatha* sp. Other important predators encountered included staphylinid (*Paederus fuscipes*) and carabid beetles, reduviid bugs (*Rhinocoris* sp.), neuropterans (*Mallada* sp.), predatory wasps, robber fly, tachinid flies and odonatan predators. The mostly dominant parasitoids were *Charops annulipes*, *Campolestis chloridae*, *Xanthopimpla* sp. and *Brachymeria* sp. Analysis of variance suggested the existence of significant variation in the selected diversity indices among the prevailing pulse crops. Maximum species diversity and richness were noted in fieldpea followed by lathyrus, greengram, blackgram, lentil and chickpea. Correlation studies revealed negative association between natural enemies and pest population in different pulse crops.

Keywords: abundance; correlation; diversity; natural enemies; pulse crops





First documentation of the larval parasitoid *Drino* sp. (Diptera: Tachinidae) on fall armyworm, *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae), in southern Rajasthan

**Beerendra Singh*, S. Ramesh Babu, K.K. Sruthi, Khushi Saini,
S.R. Gayathri and Divya Kumari Dhakar**

¹Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur, India

*Correspondence: bsgento95@gmail.com

The invasive pest, fall armyworm (FAW), *Spodoptera frugiperda*, is a polyphagous pest that causes severe losses in cereals. We have conducted a study on the prevalence and abundance of natural enemies on FAW in Southern Rajasthan, which could serve as potential biocontrol agents in the IPM programme. During the study period, we collected dipteran larval parasitoids from 530 FAW larvae. We found a larval parasitoid from the family Tachinidae that is similar to *Drino* sp. based on morphological and molecular analysis. This is the first time that this species has been reported in India on FAW. However, further confirmation is required to identify the species. Around three tachinid adults emerged from the single FAW larva. The current study found a parasitism percentage and relative abundance for *Drino* sp. on FAW to be 0.18 and 2.56, respectively. The extensive distribution may be attributed to the diverse range of lepidopteran pests that act as hosts for tachinid species. In future, we can expand the present study to encompass the entire region of Rajasthan, enabling the development of a comprehensive management strategy that incorporates biocontrol agents for the sustainable management of FAW in the state.

Keywords: *Drino*; IPM; parasitoid; *Spodoptera frugiperda*; Tachinidae





**Taxonomic studies on fruit flies of tribe Dacini (Diptera: Tephritidae:
Dacinae) in India**

Abhishek Venkateshaiah^{1*}, K.J. David², J.K. Pavana³, S. Pradeep¹ and N.R. Noor²

¹Department of Agricultural Entomology, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

³Department of Entomology, University of Agricultural Sciences, Bengaluru, India

*Correspondence: abhinto97@gmail.com

Roving surveys undertaken during 2022–2024 across India led to the identification of 85 species of fruit flies belonging to 3 genera, viz. *Bactrocera* Macquart, *Dacus* Fabricius and *Zeugodacus* Hendel in 15 subgenera of tribe Dacini. 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 & Abhishek from Meghalaya; *Bactrocera ettinabhuja* Abhishek and David and *Dacus venkateshi* Abhishek and David from Karnataka; *Zeugodacus sinuvittatus* David & 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 abbreviate* (Hardy), *Bactrocera gombokensis* 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 species 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 GenBank. Phylogenetic analysis 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.

Keywords: host plant data; lure response; new records; new species; updated checklist





Session III

**Satellite Symposium on Insect Multi-Omics:
Molecular Insight Meets Pest Management
Solutions**



Indian context of insect genome editing vis-à-vis global scenario

R. Asokan

*ICAR–Indian Institute of Horticultural Research,
Bengaluru, India*

Correspondence: asokan.r@icar.gov.in

Achieving site-specific genomic mutation has long been a goal. ZFN and TALEN required expertise, but CRISPR/Cas revolutionised site-specific mutations. Cas9 enabled locus-specific mutations via non-homologous end joining, though genomic lesions and large deletions caused cancer in mammalian cells. Homology-dependent repair offered an alternative but with low efficiency. Advances in Cas proteins (Cas12a, Cas13a, Cas3, Cas14, engineered Cas9) and precision editing using base excision and mismatch repair expanded applications. Precision editing is achieved by adenine and cytidine base editors (Cas9 nickase fused with deaminase) and prime editing (Cas9 nickase fused with reverse transcriptase) utilising RNA templates. New additions to this toolbox include twin prime editing, PASTE and bridge RNA, enabling DNA and RNA editing across organisms. In India, genome editing in agriculture focusses on pest management, pollinators and natural enemies. Genes involved in sex determination and spermatogenesis were validated for precision-guided sterile insect technique (pgSIT) in multiple pest species, with pgSIT developed for *Bactrocera dorsalis*. Precision editing using adenine base editor and prime editor-2 was applied in *Spodoptera frugiperda*. CRISPR-based diagnostics using Cas12a and Cas13a were developed for DNA/RNA viruses, and non-embryonic genome editing using ReMOT was conducted in select pests. Globally, insect genome editing is pursued in a few laboratories in USA, Japan, China, Europe and Latin America, with research on gene drive models in *Drosophila suzukii* and *Ceratitis capitata*. In India, biosafety regulations permit research on insect genome editing at SDN-1, with field release requiring validated gene drive models. The key challenge is the lack of well-annotated genomes for target species. Host-plant editing may serve as an alternative, with SDN-1 and SDN-2 permitted for field release after regulatory clearance. Teething problems in this emerging technology can be overcome with consistent efforts and perseverance.

Keywords: CRISPR/Cas genome editing; gene drive; insect pest management; regulatory framework



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Silver anniversary of RNAi discovery: progress and promise to become a viable biocontrol method for pests and diseases

Subba Reddy Palli

*Department of Entomology, Martin-Gatton College of Food, Agriculture and Environment, University of
Kentucky, Lexington, USA*

Correspondence: rpalli@uky.edu

Since its discovery in 1998, RNA interference (RNAi), a Nobel Prize-winning technology, made significant contributions to advances in science. However, RNAi applications in medicine and agriculture have been explored with limited success. RNAi contributed to our understanding of the mechanisms of its action, target specificity and differential efficiency among insects. Thus, RNAi played a major role in advances in insect biology. Did RNAi technology fully meet insect pest control expectations? I will address this question and discuss recent advances in the mechanisms of RNAi and its contributions to insect science as well as remaining challenges, including delivery of dsRNA to the target site, differential efficiency and potential resistance development using fall armyworm management as a model. Possible solutions for the roadblocks to the successful implementation of RNAi technology for future widespread use of this method to control pests and diseases will also be presented.

Keywords: delivery; dsRNA; fall armyworm; pest control; target-specificity





Redefining pest control through silent strike — the tale of RNAi from lab to land

T. Venkatesan*, K. Ashok, R. Gandhi Gracy, M. Mohan, D. Sagar and R.S. Ramya

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

**Correspondence: Venkatesan.T@icar.gov.in*

RNA interference (RNAi) represents a cutting-edge gene-silencing technology for targeted pest management. By disrupting vital insect genes related to growth, reproduction and development, RNAi has emerged as a promising tool to mitigate crop damage. Despite its potential, the success of RNAi hinges on effective delivery mechanisms and insect-specific RNA uptake, which vary significantly across species and even within the same order. Given transgenic approaches' economic and regulatory hurdles, non-transformative delivery methods such as foliar sprays, trunk injections, irrigation and seed coatings have gained traction. These environmentally sustainable methods minimise resistance development by limiting exposure to double-stranded RNA (dsRNA). At ICAR–NBAIR, pioneering advancements have been achieved in leveraging RNAi against major pests, including *Spodoptera frugiperda*, *Leucinodes orbonalis*, *Amrasca biguttula biguttula*, *Phenacoccus manihoti* and *Maconellicoccus hirsutus*. Notably, biopolymer-based dsRNA nano-formulations targeting *V-ATPase* have demonstrated over 85 per cent mortality in *Bemisia tabaci*. Globally, regulatory frameworks for dsRNA-based formulations exist in regions like USA, Europe and Australia, yet gaps persist in addressing biopolymer and nano-based systems, off-target effects, and multi-target RNAi constructs. In India, ICAR–NBAIR is at the forefront of establishing standard operating procedures, generating foundational data and developing regulatory guidelines for dsRNA applications in pest management. Ongoing research and innovation at ICAR–NBAIR will play a pivotal role in addressing the challenges and unlocking its full potential.

Keywords: biopolymers; dsRNA; nano-formulations; pest management; regulatory guidelines



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Session IV

**Invasive Alien Pests, Diseases and
Weeds: Biocontrol Interventions**



Gall-inducing insects in classical biological management of weeds

Anantanarayanan Raman^{1,2}

¹*Commonwealth Scientific and Industrial Research Organisation, Floreat Park, Australia*

²*Charles Sturt University, Orange, Australia*

Correspondence: anant@raman.id.au

High host-specificity levels of gall-inducing insects are a major strength in considering them in weed biological-management efforts. Effects of gall-inducing insects on plants are subtle and discreet. Among the various groups of gall-inducing insects recruited to regulate and manage populations of weeds as biological agents, those of the Tephritidae (Diptera), Curculionidae (Coleoptera) and the Heterocera (Lepidoptera) impress as effective, mainly because of their specialised host relations and the level of irreversible damage they inflict to plants, viz. the weeds, by interrupting water and nutrient transport. By injuring the host plant and draining nutrients, the gall-inducing insects induce minor to moderate levels of stress in tissues and organs they infest. Nonetheless, what needs to be factored is that gall-inducing insects are parasitic organisms that utilise host tissues for nutrition and habitat. Importantly, they cannot annihilate weeds totally as a weedicide such as glyphosate would do, by inhibiting 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase, a vital intermediate in the shikimic-acid pathway. Because of their stronghold as monophagous plant feeders, the gall-inducing insects can be used as primary plant stressors to downgrade the plant's immunity levels. We suggest that those weeds are to be subsequently counterattacked with a species of a necrotrophic or a phytotoxin-producing fungus, verified in the laboratory for its death-inducing capability, to aggravate the plant stress further, culminating in whole-plant death.

Keywords: host specificity; parasitic insects; plant stressors; weed biocontrol





**Classical biological control of *Mikania micrantha* in the Asia–Pacific region:
current status and future prospects**

K.V. Sankaran^{1*}, M.D. Day² and Prakya Sreerama Kumar³

¹Kerala Forest Research Institute, Peechi, India

²Department of Primary Industries, Brisbane, Australia

³ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: sankarankv@gmail.com

Mikania micrantha, a fast-growing neotropical vine, is invasive in over 35 countries in the Asia–Pacific region. It threatens biodiversity in natural ecosystems and undermines the productivity of plantations and agricultural systems. As physical and chemical control of mikania is non-sustainable, costly and environmentally damaging, classical biological control was attempted using the microcyclic rust fungus *Puccinia spegazzinii* pathogenic to the vine, introduced from its native range. A Trinidadian pathotype of the rust was first introduced into the Indian states of Assam and Kerala in 2005–2006, followed by introductions into China in 2006. A pathotype from eastern Ecuador was introduced into Taiwan in 2007, and subsequently into numerous countries in the Pacific. In all, *P. spegazzinii* has been introduced into nine countries in the region from 2006 to 2019. The rust established in five countries: Taiwan, Papua New Guinea, Fiji, Vanuatu and the Cook Islands. It has also spread naturally into the Solomon Islands. Field monitoring has shown that the eastern Ecuador pathotype has reduced populations of mikania in many areas where it has established. Attempts are currently being made to introduce *P. spegazzinii* onto Christmas Island, an Australian territory. This paper discusses the impact of *P. spegazzinii* as a biocontrol agent for mikania in the various countries where it has established, and the possible reasons for its failure to establish in other countries. It also discusses the benefits of introducing the rust into new countries and wherever it has failed, and the probable constraints for introduction.

Keywords: Asia–Pacific region; biological control; *Mikania micrantha*; *Puccinia spegazzinii*; rust pathotypes





Evaluation of diet, host preference and feeding potential of *Apertochrysa astur* Banks (Neuroptera: Chrysopidae), a potential predator against rugose spiralling whitefly, *Aleurodicus rugioperculatus*, on coconut

**N.B.V. Chalapathi Rao*, V. Anoosha, B. Neeraja, V. Govardhan Rao and
A. Kireeti**

Horticultural research station, Dr Y.S.R. Horticultural University, Ambajipeta, India

*Correspondence: chalapathirao73@gmail.com

Coconut (*Cocos nucifera* L.) is widely grown in Andhra Pradesh in 1.06 lakh hectares producing 17.097 lakh nuts with a productivity of 14,500 nuts per hectare. During December 2016, exotic rugose spiralling whitefly (RSW), *Aleurodicus rugioperculatus* Martin has entered Andhra Pradesh. The predator, *Apertochrysa astur* (Banks) was identified as a potential predator for the same. For large-scale multiplication and field release, diet standardisation, host preference and field evaluation studies of *A. astur* were conducted at Ambajipeta and results revealed that highest fecundity (393), larval hatch (324.60), pupation (279.20), male (23.25) and female longevity (59.62) of *A. astur* were recorded when reared on adult diet comprising honey (15 g), protein-x (15 g), glucose (15 g), yeast (15 ml) and coconut pollen (1 g). Among the various hosts, the total developmental period of *A. astur* was maximum on RSW (33.02 days) followed by *Corcyra cephalonica*, *Opisina arenosella* and *Aphis craccivora* with 26.72, 25.75 and 25.56 days, respectively. Field evaluation of *A. astur* indicated significantly low population of RSW (19.96 nymphs) on coconut palms clipped with *A. astur* eggs than on un-released palms (158.5 nymphs) 28th day after clipping of eggs. Hence, large scale mass production and supply of the predator eggs can play a vital role in the biocontrol based successful management of *A. rugioperculatus*.

Keywords: *Aleurodicus rugioperculatus*; *Apertochrysa astur*; coconut; predator





Mapping the success of *Cecidochares connexa* inoculation in curbing *Chromolaena odorata* invasion in South India

Mudagadde G. Deeksha^{1*}, Yogita Gharde¹, A.N. Shylesha² and
Richa Varshney²

¹ICAR–Directorate of Weed Research, Jabalpur, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: deekshamudagadde@gmail.com

Chromolaena odorata, an invasive weed from the America, poses a significant threat to ecosystems and agriculture across India. Its rapid colonisation of disturbed areas and adaptability to various environmental conditions make it difficult to control using conventional methods. *Cecidochares connexa* (Macquart), a gall fly from the Tephritidae family, has emerged as a promising biological control agent against *C. odorata*. By inducing gall formation on *C. odorata* stems, the fly impairs growth, reduces seed production, and depletes carbohydrate reserves, ultimately inhibiting its spread. To assess the population dynamics and spatial distribution of *C. connexa*, a survey was conducted across 39 locations in Karnataka, Kerala, and Tamil Nadu. The results showed the establishment of *C. connexa* in 28 locations, with 12 locations in Karnataka and Kerala exhibiting high densities of the gall fly. However, no *C. connexa* infestations were observed in Tamil Nadu, despite the presence of *C. odorata*, indicating either the absence of release or failure of establishment in this region. Spatial analysis using an interpolated surface map further confirmed the spatial distribution of *C. connexa* in Karnataka and Kerala, while its absence in Tamil Nadu highlights the need for future releases of the biocontrol agent in this region. These findings underscore the biocontrol agent's effectiveness in certain areas and the necessity for targeted efforts to expand its distribution.

Keywords: biocontrol; gall fly; invasive weed; survey





**Entomopathogenic fungi — potential alternatives to combat the invasive thrips
Thrips parvispinus (Karny) in chilli ecosystem of northeastern Karnataka**

Arunkumar Hosamani*, K. Veena, M. Mamatha, E. Sowmya and Vijayakumar Ghante

University of Agricultural Sciences, Raichur, India

*Correspondence: arunent@uasraichur.edu.in

Chilli (*Capsicum annuum* L.), commonly known as red pepper, is an important and indispensable condiment as well as vegetable grown in many parts of the world. The cultivation of chilli in Northern Karnataka has expanded to many folds with low productivity due to biotic stresses like insect pests and diseases. To the list of insect pests one more addendum of invasive pest, i.e. thrips, *Thrips parvispinus* (Karny) was noticed during 2021–2022 which caused severe damage and, in some instances, the entire crop was vanished (2022–2023). To combat this pest farmers solely dependent on pesticides and many of them were not effective. The preliminary studies on evaluation of biopesticides like, *Beauveria bassiana*, *Lecanicillium lecanii*, *Isaria fumosorosea* and *Metarhizium anisopliae* were found to be very effective in suppressing the invasive pest. Demonstration of bioagents in a few farmers' fields showed significant reduction (50–60%) of invasive thrips population after two to three rounds of sprays. To meet this huge demand of biopesticides in last three years scaled up from few quintals to 50 tonnes which indicated that there is a need to create awareness among the farmers to use the biocontrol agents for sustainable chilli production. During the crop season, weekly on an average 1.5 tonnes of biocontrol agents were produced and distributed to the farmers of Karnataka, Telangana and some parts of Andhra Pradesh.

Keywords: *Beauveria bassiana*; chilli; *Lecanicillium lecanii*; *Thrips parvispinus*





Reviving an old ally: deploying *Podisus maculiventris* to control *Nezara viridula* in Dutch greenhouses

Raghavendra Reddy Manda^{1,2*}, Hessel van der Heide¹ and
Gerben Messelink^{1,2}

¹Business Unit Greenhouse Horticulture & Flower Bulbs, Wageningen University & Research, Wageningen, The Netherlands

²Laboratory of Entomology, Wageningen University & Research, Wageningen, The Netherlands

*Correspondence: raghavendrareddy.manda@wur.nl

Greenhouse horticulture in the Netherlands faces a persistent threat from *Nezara viridula* (Hemiptera: Pentatomidae), which causes extensive damage, primarily to sweet peppers. Since 2022, *Trissolcus basalis* has been commercially available in the Netherlands as a biocontrol agent for *N. viridula*, but growers report that parasitism rates remain inconsistent. Targeting only one life stage of *N. viridula*, or relying on single natural enemy may not ensure sustainable pest management. Enhancing diversity of natural enemies could improve pest suppression, especially when different predators or parasitoids exploit complementary ecological niches. Such complementarity arises when they specialise in targeting different life stages of a pest, occupying distinct habitats, or employing different foraging strategies. Previous studies have shown that spined soldier bug, *Podisus maculiventris* preys on multiple life stages of *N. viridula*, highlighting its potential as a versatile predator. In this study, we evaluated the establishment and efficacy of *P. maculiventris* in greenhouse trials, using larvae of yellow mealworm beetle, *Tenebrio molitor*, as supplemental prey. Weekly provisioning of mealworms fostered a stable *P. maculiventris* population, leading to significant suppression of *N. viridula* nymph densities. Conversely, predator populations declined in the absence of supplemental prey, underscoring the necessity of alternative food sources for sustained biocontrol efficacy. These findings indicate that integrating *P. maculiventris*, supported by alternative prey, can enhance biocontrol of *N. viridula*, reduce pesticide dependence and promote integrated pest management in greenhouse-grown sweet peppers.

Keywords: biological control; invasive stink bugs; predator establishment; predator–prey dynamics; standing army





Fostering sustainable agriculture: the role of CABI's PlantwisePlus programme in promoting biological practices

Akanksha Nagpal¹, Manju Thakur^{2*}, Vinod Pandit³ and Malvika Chaudhary⁴

¹*Project Coordinator, CABI, India*

²*Crop Health Advisor, CABI, India*

³*Regional Director, CABI, India*

⁴*PlantwisePlus Global Team Leader, CABI, India*

**Correspondence: m.thakur@cabi.org*

PlantwisePlus is a global flagship programme enhancing food security and farmer livelihoods by reducing crop losses through plant clinics worldwide. These clinics provide farmers with tailored, science-based recommendations to address crop health issues. The Farmer Advisory pathway is focussed on enhancing knowledge and uptake of integrated pest management practices through responsive digital advisory tools focusing on promoting biological interventions over chemical solutions, fostering sustainable and environmentally friendly agricultural practices. To evaluate the programme's effectiveness and focus, we analysed data from the Plantwise Online Management System (POMS), a data management tool to store, manage, and analyse plant clinic data. A year-wise trend analysis from 2013 to 2024 for India reveals a significant shift toward biological recommendations. In 2013, 6.1% of recommendations were biological, rising to 79.8% by 2024. On average, 40.9% of recommendations during this period were biological, showcasing the programme's commitment to reducing reliance on chemical inputs and supporting sustainable farming practices. An example of this approach is the management of the fall armyworm, a major pest affecting maize crops globally. Of 455 recommendations for the fall armyworm diagnoses in India, 79.5% were biological interventions. The clinics' consultation was supported by complementary approaches like preparation of extension materials, mass activities such as radio broadcasts, and plant health rallies followed by qualitative surveys to measure the impact of these activities on adopting sustainable practices, including biocontrol by smallholder farmers. The PlantwisePlus programme supports global efforts to achieve resilient agricultural systems, safeguard the environment and improve livelihoods.

Keywords: biological interventions; integrated pest management; plant clinics; PlantwisePlus





Assessing the impact of the classical biological control agent *Anagyrus lopezi* against *Phenacoccus manihoti* in cassava plantations of India

M. Sampathkumar^{1*}, M. Mohan¹, A.N. Shylesha¹, S. Jayasekhar²,
Sunil Joshi¹, Ankita Gupta¹, T. Venkatesan¹, S.N. Sushil¹ and Georg Goergen³

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²ICAR–Central Plantation Crops Research Institute, Kasaragod, India

³International Institute of Tropical Agriculture, Cotonou, Republic of Benin

*Correspondence: ento_sam@yahoo.co.in

The recently invaded cassava mealybug, *Phenacoccus manihoti*, threatens the livelihood of cassava farmers in the country. To tackle the pest, ICAR–NBAIR has imported a parasitoid wasp, *Anagyrus lopezi*, from IITA, Republic of Benin, West Africa, as per Government of India guidelines during August 2021. After completion of the satisfactory pre-release mandatory protocols, the host specific parasitoids were first field released in Tamil Nadu during 2022, subsequently the Bureau also organised several release programmes in Tamil Nadu, Kerala and Puducherry in 2023–2024 and ensured the parasitoids have released all the sites where cassava mealybug menace was reported in the country. The field efficacy studies of *A. lopezi* in the farmers' fields of the released sites in Tamil Nadu and Puducherry revealed, *A. lopezi* have established very well in the released sites. Field parasitism rate was worked at fortnightly basis, one month post release of parasitoids till crop harvest. Increase in parasitism was witnessed during each observation and achieved maximum at six months post release of *A. lopezi* with tuber yield of 25 tonnes/ha in the cassava growing belts of Tamil Nadu. The per cent parasitism rate of *A. lopezi* in released fields at different districts of Tamil Nadu ranged between 28.02 and 60.23%, in the case of Puducherry and Kerala, the parasitism rate recorded were 42.00 and 50.12%, respectively, suggesting effective management of cassava mealybug by its classical biological control agent, *A. lopezi*. The impact of *A. lopezi* in suppression of the mealybug in cassava plantations is also being carried out by the bureau employing different methods, and quantified the net benefits of the biological control programme.

Keywords: *Anagyrus lopezi*; classical biological control; invasive; parasitoids



Alternate hosts of fall armyworm (*Spodoptera frugiperda*) in maize fields: an opportunity for conservation biological control

S.B. Suby*, V.D. Pashupat, N. Kumar, S.L. Jat, P.L. Soujanya and
J.C. Sekhar

ICAR–Indian Institute of Maize Research, Ludhiana, India

*Correspondence: subysb@gmail.com

Understanding the host preferences of the fall armyworm (FAW) in its invasive range, especially its interactions with weed hosts, is crucial for devising effective integrated crop protection strategies. Field observations during kharif seasons of 2020–2024, in maize crop, in north-west India revealed the presence of FAW damage and its larvae on 13 weed hosts, where *Acrachne racemosa*, *Dactyloctenium aegypticum*, *Digitaria sanguinalis*, *Dinebra retroflexa*, *Echinochloa colonum*, *Eleusine indica* and *Leptochloa chinensis* harboured I–IV instars of FAW, though egg masses were observed only on two weed species. Additionally, weed abundance data showed the fluctuating prevalence of certain weed species throughout the growing season, and across years, with some weed hosts consistently supporting FAW populations along with its natural enemies. The natural enemies included parasitoids, viz. *Chelonus* spp., *Temelucha* sp., *Coccygidium* sp., *Campoletis* sp. etc., and predatory beetles, bugs, ants, and spiders. The study suggests that managing weeds, rather than eliminating them, can support natural enemies of pests and enhance conservation biocontrol, contributing to sustainable crop production.

Keywords: conservation biocontrol; fall armyworm; maize; natural enemies; weed hosts





Biocontrol potential of the generalist predator *Chrysoperla zastrowi sillemi* (Esben-Petersen) against South American tomato pinworm, *Phthorimaea absoluta* (Meyrick) (Lepidoptera: Gelechiidae)

Kumar Surjeet*, Sharma Devika and A.K. Sood

Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur, India

*Correspondence: skumarhpau@gmail.com

Tomato is one of the most important vegetable crops grown widely both for fresh consumption and processing in India. The production and quality of tomato fruits are considerably affected by an array of insect-pests however, in recent years an invasive insect, *Phthorimaea absoluta* (Meyrick) has become one of the most devastating pests of tomato crop under greenhouse and open field conditions globally. High biotic potential, oligophagous nature and superior climate adaptation has led to successive invasions of the pest in different locations. In response to *P. absoluta* infestations, chemical control is often taken up as the first line of defence, providing a quick action against the pest pressure. However, the overuse of these chemicals may have several harmful side-effects and the pest has also shown reduced levels of susceptibility to commonly employed insecticides. Therefore, the alternative options including the use of effective biological control agents against this pest are urgently needed. In the present study biocontrol potential of the generalist predator, *Chrysoperla zastrowi sillemi* (Esben-Petersen) was assessed against *P. absoluta* by determining its comparative biology and feeding potential using eggs of *P. absoluta* and *Corcyra cephalonica* as preys. Studies revealed that the predator successfully completed its developmental and reproductive biology on *P. absoluta* and the feeding potential of its third larval instar was maximum (average 51.66 eggs/day). It is concluded that the predator could be a promising biocontrol agent for the management of *P. absoluta*. However, its effectiveness needs to be validated in trials under open field and protected conditions.

Keywords: biocontrol potential; biology; *Chrysoperla zastrowi sillemi*; tomato





Efficacy of native *Metarhizium rileyi* isolates from field evaluation against fall armyworm in maize

M. Visalakshi^{1*}, Arunkumar Hosmani², A. Kandan³ and P. Kishore Varma⁴

¹Regional Agricultural Research Station, Acharya N.G. Ranga Agricultural University, Anakapalle, India

²University of Agricultural Sciences, Raichur, India

³ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

⁴Regional Agricultural Research Station, Acharya N.G. Ranga Agricultural University, Lam, India

*Correspondence: m.visalakshi@angrau.ac.in

Epizootics of *Metarhizium rileyi* on fall armyworm, *Spodoptera frugiperda*, was noticed in 2019 at the Regional Agricultural Research Station, Anakapalle, India. *Metarhizium rileyi* was isolated from *S. frugiperda* cadavers and was characterised. A PCR technique for detection of DNA was developed by using internal transcribed spacers (ITS 1, ITS 4) as the primers for amplification. The amplified products of 650 bp were purified and sequenced. Sequence was submitted in NCBI GenBank and accession number was obtained (MN 960559). Blast analysis of revealed 100% match with the reference GenBank sequence from the NCBI database. Bioassay studies with the concentration of 1×10^9 spores/ml, showed larval mortality of 92.54% whereas, 1×10^8 spores/ml, showed 87.87%. The LT_{50} and LC_{50} values of *M. rileyi* at 1×10^8 spores/ml against *S. frugiperda* larvae were 84.4 hours. Over two years, two sprays of *M. rileyi* AKP Nr-1 ANGRAU strain at a concentration 1×10^8 spores/ml at a dosage of 5g/L reduced FAW incidence (7.45% and 4.83%) followed by *M. rileyi* Mr18 UAS, Raichur strain (11.46% and 4.82%). This strain reduced damage by an average of 54.97% in 2020 and 60.15% in 2021. In 2022, *M. rileyi* AKP Nr-1 strain reduced the damage by 3.88% as compared to emamectin benzoate with 2.05% reduction. Anakapalle strain showed yield of 63.22 q/ha, 66.83% increase over the control, Raichur strain showed 58.22 q/ha with 66.15% increase. This study assessed the potential of *M. rileyi* in ecofriendly pest management, offering a viable alternative to toxic chemical insecticides.

Keywords: maize; *Metarhizium rileyi*; *Spodoptera frugiperda*





First record of *Brithys crini* as crinum lily borer from northeastern region of India

K.M. Ajaykumara^{1*}, Denisha Rajkhowa¹, Ningthoujam Kennedy², Mahesh Pathak¹ and
Varun Hiremath¹

¹College of Horticulture and Forestry, Central Agricultural University, Imphal, India

²School of Crop Protection, College of Post Graduate Studies in Agricultural Sciences, Umiam, India

*Correspondence: ajaykumarakmath@gmail.com

The *Brithys crini* (Fabricius) (Lepidoptera: Noctuidae) known as crinum lily borer is widely distributed in the world and reported from Gujarat and West Bengal in India. The pest is known to occur in the months of July, September and December. *Crinum* (Amaryllidaceae) is a landscape plant cultivated even in small gardens which provide a regular dramatic focus point with their large, bright inflorescences. Because of its poisonous alkaloids, its only real pest is the specially adapted black-and-yellow-striped amaryllis caterpillar (*Brithys pancratii*) and occasionally snails and slugs. The bulbs of large plants are seldom entirely destroyed by *B. pancratii* and new leaves grow out quickly. However, during the field surveys *B. crini* caterpillars was recorded on both leaves and bulbs of *Crinum* sp. leading to mere destruction of whole plants in the farmer's home gardens at Silluk village of East Siang district, Arunachal Pradesh in the month of July, 2024. This preliminary study documented the eggs, larvae, pupae and adults of *B. crini* both under field and laboratory conditions. The eggs were pale yellow mass (30–40) on underside of leaf, caterpillars are dark coloured with series of white spots and pupates in leaf whorls and within bulbs. This is the first report of the crinum lily borer from Northeastern region of India indicating the need for further research on host plants, creating awareness about its early identification and management practices among farmers.

Keywords: Arunachal Pradesh; *Brithys crini*; crini lily borer; first record





***Cladosporium cladosporioides*: a new fungal bioagent of South-East Asian thrips,
*Thrips parvispinus***

M.C. Keerthi*, N.R. Prasannakumar, V. Sridhar, R. Dhinesh and K.N. Harshitha

Division of Crop Protection, ICAR–Indian Institute of Horticultural Research, Bengaluru, India

**Correspondence: keerthi.mc@icar.gov.in.*

Thrips parvispinus (Karny) is a notable polyphagous pest native to Southeast Asia. It invaded India in 2015, causing severe economic losses in chilli cultivation. Farmers have relied heavily on indiscriminate pesticide applications to control the pest. Identifying vulnerable life stages is critical for effective management. Further exploration of novel bioagents and its efficacy is essential for designing bio-intensive pest management strategies. *Cladosporium* sp. was isolated from the dead cadaver of *T. parvispinus* and identity of fungal bioagent was confirmed based on the morphological and molecular techniques. The *Cladosporium* sp. was a slow growing fungus and took 17 days to reach a colony diameter of 7.5 cm. The colony on PDA looks grey-olivaceous to dull green or olivaceous-grey. The conidiophores are solitary, macronematous or semimacronematous, narrowly cylindrical to cylindrical-oblong, with average spore length and width of 9.40 and 3.17 μm , respectively. The bioassay was conducted against *T. parvispinus* at various concentrations. The highest mortality (69.10 %) of *T. parvispinus* was recorded at 1×10^8 conidia/mL of *C. cladosporioides*, however lowest mortality was recorded at 1×10^5 post 7 days after treatment. The di-trophic interaction was analysed using SEM imaging, revealing multiple penetration points from a germinating conidium at 72 hours post-inoculation (hpi) and extrusion from the oral opening at 120 hpi. These findings highlight the potential of targeting the vulnerable immature stages of *T. parvispinus* and incorporating entomopathogens such as *Cladosporium* spp. into sustainable pest management strategies. This approach could reduce dependence on synthetic insecticides and minimise their ecological impact.

Keywords: biocontrol; *Cladosporium* spp.; entomopathogen; survival rate; *Thrips parvispinus*





**Evaluation of sustainable IPM approaches for *Phthorimaea absoluta* with
economic analysis in semi-arid tomato regions in India**

**Rajashekhar Mandla^{1*}, O. Shaila¹, B. Rajashekar¹, T.P. Reddy¹, M.C. Keerthi²,
K. Ramakrishna¹, A. Shankar¹, E. Jyoshna¹ and C.V. Sameer Kumar¹**

¹Professor Jayashankar Telangana Agricultural University, Hyderabad, India

²Division of Crop Protection, ICAR–Indian Institute of Horticultural Research, Bengaluru, India

*Correspondence: razshekarm@gmail.com

The invasive tomato pinworm, *Phthorimaea absoluta* (Lepidoptera: Gelechiidae), threatens tomato production in greenhouses and open fields. This study compares integrated pest management (IPM) approach with conventional farmer practices (FP) over 2022–23 and 2023–24. Monitoring using pheromone and yellow sticky traps indicated a seasonal trend, with peak captures of 40–65 adults per trap in November 2022–2023, and 35–55 adults per trap peaking earlier in October 2023–2024. Yellow sticky trap catches peaking from late September to mid-October, with overall higher catches in 2023–2024, highlighting the need for seasonally adapted monitoring. Fruit damage analysis showed the damage levels of 15–25% in IPM plots versus 30–45% in FP plots during 2022–2023, and a 40–60% reduction in 2023–2024. Key pest phases were identified: build up (September–October), peak (November), and maintenance (December–January), establishing November as a critical intervention period. T-statistics confirmed the efficacy of IPM treatments, with values ranging from 14.78 to 93.47 in 2022–2023 and 11.00 to 31.59 in 2023–24, demonstrating Emamectin benzoate's superior effectiveness. Economic analysis revealed a yield increase from 59.13 to 67.92 tonnes/ha in 2022–2023 and from 81.71 to 99.98 tonnes/ha in 2023–2024, with a benefit-cost ratio improvement from 2.13 to 2.59 and 3.44 to 5.11, respectively. These findings affirm IPM as an effective, sustainable approach, enhancing crop protection, yield, and economic resilience for farmers.

Keywords: invasive pests; pheromone traps; sticky traps; technology adoption; tomato pinworm



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Maize yield sensitivity and determinants of IPM adoption against invasive fall armyworm in Karnataka, India

K.N. Prakash^{1,2*}, M.N. Venkataramana¹, Manjanagouda S. Sannagoudar³, G.M. Gaddi¹,
K. Murali Mohan¹ and Siddayya¹

¹University of Agricultural Sciences, Bengaluru, India

²Directorate of Plant Protection, Quarantine, and Storage, Faridabad, India

³ICAR–Indian Institute of Seed Science, Regional Station, India

*Correspondence: ppp732@gmail.com

The invasive fall armyworm (*Spodoptera frugiperda* J.E. Smith) poses a growing threat to global food security, particularly as maize constitutes 36% of the world's grain production. India, ranked as the fifth-largest maize producer, is strategically positioned to meet rising global demand. This study investigates the impact of *S. frugiperda* infestation on maize yields and explores the determinants of Integrated Pest Management (IPM) adoption in Karnataka, the state with the highest maize production in India. Using the Cobb-Douglas production function, the analysis found that FAW infestation reduced maize productivity by 407 kg/ha, although the effect was statistically insignificant. To examine IPM adoption, a Probit model identified key factors influencing farmers' decisions, while the intensity of adoption was analysed using a negative binomial regression model. Key drivers for both adoption and its intensity included higher maize productivity, larger farm size, off-farm income, education level, training participation, and farming experience. The findings underscore the importance of targeted interventions, such as improving farmer education, expanding training programs, and enhancing resource access, to promote IPM adoption. Such measures are essential to mitigating the risks posed by FAW infestations and safeguarding maize productivity in Karnataka and beyond.

Keywords: adoption factors; fall armyworm; IPM; Karnataka; maize; negative binomial regression





**Ecofriendly management of fall army worm, *Spodoptera frugiperda* (J. E. Smith),
and cost benefits in maize crop ecosystem in Telangana**

A. Ramakrishna Babu* and K. Vani Sree

Agriculture Research Institute, Professor Jayashankar Telangana Agricultural University Hyderabad, India

**Correspondence: dr.arkrishnababu2023ew@gmail.com*

Maize (*Zea mays* L.) ranks third in cultivated area across Telangana. The major biotic production constraint in maize is fall armyworm (FAW), *Spodoptera frugiperda* (J.E. Smith) causing significant yield losses ranging from 8.0–58.0%. To curtail the chemical load and indiscriminate use of chemicals, the present study was conducted in farmers fields of Siddipet district of Telangana during rabi 2023–24. Eco-friendly management practices, viz. pheromone traps @ 10 traps/acre installed for mass collection + one week after sowing released two times egg parasitoid, *Trichogramma chilonis* (1,00,000 eggs/ ha) at 10 days interval one week after sowing + *Bacillus thuringiensis* NBAIR Bt-25 @ 2ml/L (20 days after sowing, two sprays with 10 days interval) + ICAR–NBAIR *Metarhizium anisopliae* (Ma-35) @ 5g/L (2 sprays with 10 days interval) as one set of treatment against farmers practice (emamectin benzoate @ 0.4 g/l, chlorantraniliprole 0.4 ml/l, lambdacyhalothrin @ 1 ml/l) and compared with untreated check plot in the farmers field. There is no significant difference between eco friendly practice and farmers practice in reduction of per cent damaged plants and dead larvae per plant and significantly differed with untreated control. Whereas, ecofriendly practices recorded highest number of predators (4.65) with egg parasitisation (4.79) per plant when compared with farmers practice (0.52 and 0.58). The grain yield was more in farmers practice (49.94%) followed by ecofriendly management (41.96%) than untreated check. Overall, eco-friendly management provides a holistic, sustainable solution that helps to manage FAW effectively while maintaining agricultural and ecological balance.

Keywords: adoption factors; fall armyworm; IPM; Telangana; maize





Decrypting the reproductive behaviour in an invasive alien pest,
Spodoptera frugiperda

N. Ramya^{1,2*}, Vinod K. Padala^{1,3} and D. Sagar^{1,4}

¹Division of Entomology, ICAR–Indian Agricultural Research Institute, New Delhi, India

²ICAR–Indian Institute of Agricultural Biotechnology, India

³ICAR–National Research Centre for Makhana, Darbhanga, India

⁴ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: ramya.n1@icar.gov.in

The fall armyworm, *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae), is an invasive pest originally native to tropical and subtropical regions of the Americas. Over the decades it spread to many parts of world and its rapid expansion is largely due to its exceptional reproductive capacity. Reproduction is a key physiological process that drives population growth in insects, and in *S. frugiperda*, it is particularly important. However, this reproductive period is limited in duration, with physiological changes over time affecting reproductive success. The main reproductive behaviours like calling, copulation, and oviposition evolve as the insect ages. These changes can influence the insect's overall reproductive success and the fitness of its progeny. Understanding the reproductive physiology of *S. frugiperda* is vital for developing effective pest control strategies. By targeting key reproductive behaviours like, calling copulation, egg-laying and their interrelationships, pest control methods can be developed to specifically disrupt reproduction, offering more sustainable and focused ways to manage the pest. In this context, we looked at the reproductive behaviour in the Indian population of *S. frugiperda* by conducting the experiment according to their natural circadian rhythm. We documented the calling behaviour, copulation duration, copulation frequency and effect of mating on the female calling behaviour, fecundity, fertility, etc. Our results indicated that the calling and mating took place in the first scotophase which is in contrast to mexican population. They were at peak in the second scotophase. This data can be used in formulating biorational molecules, which can modulate calling behaviour and improve mating disruption in *S. frugiperda* for its management.

Keywords: calling bouts; copulation; fecundity; mating success; temporal changes





Survey, isolation, and characterisation of entomopathogenic fungi associated with the mealybug complex in cassava

Smitha Revi^{1*}, Madhu Subramanian², K. Fasna Sherin² and C.V. Vidya²

¹ICAR–Krishi Vigyan Kendra, Kumarakom, India

²College of Agriculture, Vellanikkara, India

*Correspondence: smitha.revi@kau.in

Cassava, an important industrial crop has recently faced an invasion by the cassava mealybug, *Phenacoccus manihoti* Matile-Ferrero (Hemiptera: Pseudococcidae). This invasive pest was first reported in India on cassava in Thrissur, Kerala, in April 2020. As part of the AICRP programme, extensive surveys over two consecutive years, from 2020 to 2022 were conducted to assess the composition of mealybug species and their associated natural enemies. Surveys to determine the prevalence of cassava mealybug were conducted at over 300 locations in Thrissur district from May 2020 to March 2022. Taxonomic identification of mealybug samples showed that four mealybug species, viz. *Paracoccus marginatus*, *Ferrisia virgata*, *Phenacoccus manihoti* and *Pseudococcus jackbeardsleyi* infested the cassava plants simultaneously, forming a complex. During the survey, natural enemies of the mealybug complex were collected. Six isolates of entomopathogenic fungi were obtained from mummified cadavers of the mealybug complex. These isolates were subjected to molecular characterisation to confirm the identity. The sequences of five entomopathogenic fungal isolates were analysed in the BLASTn programme of NCBI to examine the nucleotide homology of each isolate. After BLASTn analysis, the sequences of all isolates were submitted at NCBI GenBank, and accession numbers were obtained. They were identified as two isolates of *Simplicillium aogashimaense*, two isolates of *Purpureocillium lilacinum*, one isolate of *Lecanicillium araneicola* and one isolate of *Lecanicillium psalliotae*. These isolates can be utilised for the ecofriendly management of mealybug complex in cassava.

Keywords: cassava mealybug; characterisation; entomopathogenic fungi; invasive pest; survey





Assessment of IPM strategies for South East Asian thrips in chilli in Nagarkurnool district

**O. Shaila^{1*}, M. Rajashekhar², T. Prabhakar Reddy¹, Adhi Shankar¹, B. Rajashekar¹,
K. Ramakrishna¹ and E. Jyoshna¹**

¹ Krishi Vigyana Kendra, Professor Jayashankar Telangana Agricultural University, Hyderabad, India

² Institute of Biotechnology, Professor Jayashankar Telangana Agricultural University, Hyderabad, India

*Correspondence: shaila08agri@gmail.com

Chilli (*Capsicum annuum*) is cultivated across 18,000 to 20,000 acres in the Nagarkurnool district. Despite its economic importance, chili production faces severe challenges from various pests and diseases, particularly the invasive thrips, *Thrips parvispinus*, which has emerged as a significant pest in the southern states of Andhra Pradesh, Karnataka, and Telangana. Thrips infestations have resulted in substantial damage to chili crops, with reported losses between 50% and 80%. To address this threat, current study was implemented and evaluated IPM practices on farmers' fields from 2022 to 2024. Monitoring revealed that thrips populations initially appeared around the 38th Standard Meteorological Week (SMW), peaking by the 47th SMW, which coincided with the first harvest, before gradually declining. Fields where IPM practices were implemented showed a marked reduction in thrips density (8.0 thrips/flower) compared to fields with conventional practices (13.5 thrips/flower). Consequently, flower and fruit damage in IPM fields was significantly lower (15.2% and 20.5%, respectively) than in fields using standard practices (44.4% and 43.5%). Implementing IPM also enabled farmers to reduce the four pesticide applications, resulting in savings of Rs. 8,500 per hectare. Furthermore, the technology yielded a high benefit-cost (B: C) ratio of 5.8, increased yields by 19.87%, and generated an additional net return of Rs. 89,037 per hectare for farmers compared to conventional practices. This IPM technology has now been adopted across 3,500 acres in selected villages and has expanded to cover 7,500 acres throughout the Nagarkurnool district, demonstrating its effectiveness in managing invasive thrips and enhancing economic returns for chilli farmers.

Keywords: chilli; economic analysis; invasive thrips; IPM; pest dynamics





**Bioefficacy of different biopesticides against fall armyworm,
Spodoptera frugiperda (J. E. Smith), on maize**

P.K. Waykule^{1*}, D.R. Kadam¹ and M.V. Ugale¹

¹Department of Agricultural Entomology, College of Agriculture, Vasantrao Naik Marathwada Krishi
Vidyapeeth, Parbhani, India

*Correspondence: waykulepk123@gmail.com

The field evaluation of various biopesticides against Fall armyworm of maize indicated superiority of the treatment *Metarhizium anisopliae* (Ma) with the lowest larval population and damaged plants of Fall armyworm. It was at par with *Nomuraea rileyi* (Nr), Ma+Nr. The least effective treatment with highest larval population of Fall armyworm among all biopesticides was *Lecanicillium lecanii* (Ll). Treatment Ma+Bb, Ma+Bb+Nr+Ll, Ma+Ll were found comparatively effective over untreated control. The highest yield of maize grains was harvested from *M. anisopliae* (Ma) sprayed plots, due to its higher efficiency. It was followed *N. rileyi* (Nr) and Ma+Nr. The order of superiority of the next best treatments were *Beauveria bassiana* (Bb), Ma+Bb, Ma+Bb+Nr+Ll, Ma+Ll and *L. lecanii* (Ll). The lower yield was recorded with untreated control.

Keywords: bioefficacy; Fall armyworm; *Spodoptera frugiperda*





Invasive whiteflies and their secret saviours in India on custard apple

G.A. Kavya Yadav^{1*}, J. Vasundhara¹, K. Selvaraj¹ and A. Rameshkumar²

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Zoological Survey of India, Kolkata, India

*Correspondence: g.a.kavya@gmail.com

Custard apple or sweetsop, *Annona squamosa* L., is a key tropical fruit crop in India, vulnerable to several insect pests, with whiteflies being a major concern. Whitefly nymphs and adults colonise underside of host plant and suck sap, results in significant impact on the crop yield and warrant control measures. Surveys were conducted in 2023–2024 across Andhra Pradesh, Karnataka, Kerala, Tamil Nadu, Maharashtra, and Odisha to document whitefly infestation and their natural enemies. Invasive whiteflies, viz. rugose spiraling whitefly, *Aleurodicus rugioperculatus*, spiraling whitefly, *Aleurodicus dispersus*, Bondar's nesting whitefly, *Paraleyrodes bondari*, nesting whitefly, *Paraleyrodes minei* and annona whitefly, *Aleurotrachelus anonae* were reported to infest the crop. It was found that colonies of invasive whiteflies also coexist with other native whitefly species, viz. *Aleurocanthus woglumi*, *Aleuroclava psidii*, *Dialeuropora decempuncta* and *Pealius nagercoilensis*. Aphelinid parasitoids, viz. *Encarsia guadeloupae* and *E. dispersa* on *A. rugioperculatus* and *A. dispersus*; *E. sophia*, *Encarsia* sp. and *Eretmocerus* sp. on *A. anonae* were reported to parasitise whiteflies. Predators, viz. *Acletoxenus indicus* (Diptera), *Apterochrysa astur* (Neuroptera), *Cybocephalus indicus* and *Scymnus latemaculatus* from Coleoptera were reported to predate on whiteflies. The surveys confirm the first occurrence and establishment of *A. anonae* and its parasitoids and predators from Bengaluru, Karnataka, India on custard apple. However, globally there is no record of any parasitoid/predator so far on *A. anonae*. The present study paved a way for natural pest regulation of whiteflies with existing parasitoids and predators through augmentation and conservation strategies.

Keywords: coexistence; custard apple; invasive; natural enemies; whitefly





Session V

**Biocontrol-Compatible Technologies,
Conservation Strategies and Pollinators**



Keeping crop protection relevant to modern times with the new IPM model

Surendra K. Dara

Oregon State University, Corvallis, USA

Correspondence: surendra.dara@oregonstate.edu

The concept of integrated pest management (IPM) evolved from primarily promoting the use of synthetic pesticides as the last option to a comprehensive system that promotes an economically viable, environmentally sustainable and socially acceptable crop production system. The new IPM model explores many aspects of agribusiness by taking advantage of various control options, integrating modern technology, data management, and decision-making based on logistics, market issues and operational needs. It also emphasises the importance of communication and outreach, regulatory influences, and various social and economic factors on pest management and reorganises various control option categories based on recent advancements. For example, the new model separates microbial control from the general category of biological control due to the complexity of microbial control, various organisms involved and their modes of action/infection, and to expand the applicability to multiple groups of pests. Additionally, with the growing threat of invasive pests, increasing crop production costs, impact of climate change on global food security, we need a comprehensive approach that is relevant to modern times, offers effective pest suppression, optimises production costs, and ensures environmental and human safety.

Keywords: climate change; crop protection; food security; invasive pests

Lead Speech



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



From Southeast Asia to West Africa: two decades of biocontrol innovation against the legume pod borer

Ramasamy Srinivasan^{1*} and Manuele Tamò²

¹World Vegetable Center, Tainan, Taiwan

²International Institute of Tropical Agriculture, Cotonou, Benin

*Correspondence: srini.ramasamy@worldveg.org

The legume pod borer, *Maruca vitrata*, is a major pest of food legumes in Asia and Africa, attacking 73 legume species, including cowpea, which is extensively cultivated across millions of hectares in Africa. Unfortunately, no *Maruca*-resistant cowpea varieties are available, compelling farmers to rely heavily on chemical pesticides, often applied indiscriminately and without adherence to crop-specific registration guidelines. This practice has led to pesticide resistance, elevated production costs, and significant human and environmental health risks. As a result, biocontrol has emerged as a sustainable alternative to reduce pesticide reliance. Biocontrol efforts for *M. vitrata* in West Africa were pioneered by the International Institute of Tropical Agriculture (IITA). Despite the presence of native parasitoids such as *Phanerotoma leucobasis* and *Braunsia kriegeri*, their impact on *M. vitrata* populations was insufficient. Consequently, the World Vegetable Center (WorldVeg) explored more effective, species-specific parasitoids in Southeast Asia, which is considered the potential centre of origin for *M. vitrata*. Collaborative efforts between IITA and WorldVeg led to the introduction of *Apanteles taragamae* from Taiwan into Benin. Although this parasitoid showed high parasitism rates in Taiwan, it failed to establish in West Africa due to poor ecological adaptation. Further explorations identified three additional parasitoids in Southeast Asia: *Phanerotoma syleptae* (an egg-larval parasitoid), *Therophilus javanus*, and *Therophilus maruca* (larval parasitoids). Among these, *P. syleptae* and *T. javanus* were introduced into Benin and Burkina Faso in 2016. Their successful establishment, including survival during the dry season on alternative host plants in the absence of cowpea, was confirmed the following year. Additionally, *Maruca vitrata* multiple nucleocapsid nucleopolyhedrovirus (MaviMNPV), a biopesticide, was introduced by IITA and effectively deployed across several West African countries, including Benin, Burkina Faso, Niger and Nigeria. The use of MaviMNPV has significantly boosted cowpea yields in these regions. The combined introduction of parasitoids (*P. syleptae* and *T. javanus*) and MaviMNPV can potentially enhance the classical biological control of *M. vitrata* across Asia and Africa. However, integrating these biocontrol agents into comprehensive pest management strategies remains challenging. Future efforts must address these challenges while leveraging opportunities to develop sustainable integrated pest management packages for *M. vitrata*. These aspects will be discussed in detail, highlighting pathways to improve pest management and reduce reliance on chemical pesticides.

Keywords: classical biocontrol; cowpea; *Maruca vitrata*; parasitoids





Diversified cropping systems for pest resilience and enhanced efficacy of biocontrol agents

Sevgan Subramanian

International Centre of Insect Physiology and Ecology, Nairobi, Kenya

Correspondence: ssubramania@icipe.org

Increasing demand and awareness among consumers for safe and healthy foods, declining pipeline of new pesticide molecules and development of pesticide resistance among major pests has contributed to growing use of biocontrol agents in pest management. Current market share of biocontrol agents globally is valued at US\$ 5 billion (approximately 6–7% of the world pesticide market) with a projected annual growth rate of 8%. Hence, significant potential exists for biocontrol agents to contribute to pest management globally. However, the inherent nature of biocontrol agents makes them effective only against specific stages of insects, vulnerable to abiotic stresses and influenced by negative interactions with other trophic levels in the environment. Further, large-scale monocropping makes the crops susceptible to pest outbreaks, while they do not favour biocontrol agents. However, with the right choice of crop mixtures, diversified cropping systems, such as maize–legume intercropping, push–pull and vegetable integrated push–pull systems have the potential to effectively control pests such as the fall armyworm and thrips. Mixed cropping systems further contribute to conservation of their natural enemies. Effective monitoring tools such as pheromone-based traps can also contribute to better timing and enhance effectiveness of the biocontrol interventions. Beyond pest management, diversified cropping systems also contribute to additional value creation through product diversification, climate resilience and crop–livestock integration.

Keywords: biological control; crop–livestock integration; mixed cropping; pest management



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Sublethal effects of pesticides on parasitoids: harm or hormesis?

G. Basana Gowda*, Aishwarya Ray, Totan Adak, G. Guru-Pirasanna-Pandi,
Naveenkumar B. Patil and Shyamaranjan Das Mohapatra

ICAR–Central Rice Research Institute, Cuttack, India

*Correspondence: basanagowda.g@icar.gov.in

Pesticides can have both lethal and sublethal effects on exposed organisms. While pesticides are generally applied at effective concentrations to target pests, various spatio-temporal changes driven by abiotic and biotic factors can alter these concentrations. These sublethal concentrations often influence demographic and biological traits, affecting the growth and development of organisms, a phenomenon known as ‘hormesis,’ characterised by stimulation at low concentrations and inhibition at high concentrations. Such positive effects may enhance the production performance of parasitoids, making them more suitable for mass rearing and biological control programs. Adult longevity ($P < 0.01$), fecundity ($P < 0.01$), reproductive days ($P < 0.01$), net reproductive rate ($P = 0.011$), and gross reproductive rate ($P = 0.002$) of F_5 individuals of *Trichogramma chilonis* were significantly enhanced by exposure to imidacloprid (LC_5). Furthermore, functional response parameters, such as searching efficiency and handling time of the adult parasitoid were also improved. Deltamethrin-induced hormesis in the host insect, *Corcyra cephalonica* at LC_{15} exposure, stimulated the development of its parasitoid, *Habrobracon hebetor* without significant trade-offs. Nutrient reserves and microbial diversity in the larval gut were significantly higher in phosphine (LC_5)-treated *C. cephalonica* larvae. In general, sublethal concentrations that stimulate the development of parasitoids could be leveraged in scenarios involving low pesticide exposure in the field and for mass rearing purposes. However, long-term studies are essential to evaluate if these stimulations can provide economic benefits in mass-rearing programmes and to identify any potential trade-offs.

Keywords: *Corcyra cephalonica*; *Habrobracon hebetor*; hormesis; *Trichogramma chilonis*





**Biology, life table parameters and feeding potential of the predator
Sycanus versicolor Dohrn (Hemiptera: Reduviidae)**

B. Gundappa^{1*}, S.N. Bhagyashree², Mahesh Yandigeri¹, B.S. Gotyal¹ and S.N. Sushil¹

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²ICAR–Indian Institute of Horticultural Research, Bengaluru, India

*Correspondence: Gundappa@icar.gov.in

This study investigated biology and life table parameters of general predator *Sycanus versicolor* on three hosts, *Corcyra cephalonica*, *Hermetia illucens* and *Galleria mellonella*. The life cycle was very short on *G. mellonella* compared to the *C. cephalonica* and *H. illucens*. On *G. mellonella* bug completed its incubation period, I, II, III, IV nymphal instars in 8.30±1.30, 9.30±1.17, 10.15±1.60, 10.40±1.57, 12.55±1.88 days, respectively. Male and female bugs of fifth instar completed in 12.86±1.95, 13.92±2.06 days, respectively. Adult male and female completed their life span in 21.29±2.98 and 27.46±2.40 days, respectively. Life table studies of *S.versicolor* focussing on its demographic parameters were carried out on different hosts. *S. versicolor* exhibited variations in demographic parameters and survivorship curves across different hosts. Among the hosts studied, high intrinsic rate of increase (*r*) was observed on *G. mellonella* (0.333). Survivorship curves indicated that *S. versicolor* populations on *H. illucens* exhibited prolonged longevity (23.69 days) and enhanced survival rates compared to other hosts. Adult female of *S. versicolor* demonstrated a high feeding potential on okra fruit borer (*Earias vitella*) (24.12±2.12/day) compared to mango leaf webber (*Orthaga eudrusalis*) and tobacco caterpillar (*Spodoptera litura*). This study signifies the importance of host-specific considerations in understanding the life table dynamics of *S. versicolor* and its application in IPM.

Keywords: biology; life table; predator; Reduviidae; *Sycanus versicolor*





Optimisation of sterility dose of gamma radiation for the management of guava fruit fly, *Bactrocera correcta* (Bezzi) (Diptera: Tephritidae), and its field performance

**Basavaraj Kalmath^{1*}, Ashok Hadapad², Rachappa Haveri³,
Ramesh S. Hire², Ashwini⁴ and K.S. Ashoka⁴**

¹College of Agriculture, Raichur, India

²Bhabha Atomic Research Centre, Mumbai, India

³College of Agriculture, Kalaburagi, India

⁴College of Agriculture, Bheemarayanagudi, India

*Correspondence: bskalmath@gmail.com

Effect of gamma radiation on the reproductive performance of *Bactrocera correcta* was studied to explore the potential of the sterile insect technique for the management of the pest. Among different gamma radiation dose, adult emergence was recorded maximum at 10 Gray (89.99 %) exposure. Among different crossing studies, IM × UF recorded lowest egg hatching of 0.52 per cent at 30 Gray, followed by 20 Gray (7.61 %) and 10 Gray (26.22 %). Results of adult flight activity revealed that, there was no significant difference in percent flight activity at 30, 40 Gray and control treatments at different heights. Mating competitiveness of the sterile males at 30 and 40 Gray indicated that, significantly maximum mating competitiveness was recorded with 2.5 and 2.02, respectively at 1:1:9 combination. Study of performance of sterile males on guava fruits indicated that, per cent reduction in pupae obtained over control (%) was 91.99 per cent in 30 Gray and 90.24 per cent in 40 Gray at 1:1:9 combinations. Per cent reduction in adults over control (%) was 97.94 per cent in 30 Gray and 98.42 per cent in 40 Gray at 1:1:9 combinations. Per cent pupal reduction over control was 79.97 and 68.41 percent at 30 and 40 Gray, respectively. Similarly, average per cent adult reduction over control was 96.21 and 95.45 percent at 30 and 40 Gray, respectively. Irradiation of seven-day old pupae at 30 to 40 Gray and releasing sterile males at 1:1:9 ratio would suppress the fruit fly in the field successfully.

Keywords: flight activity; gamma radiation; insect sterility; mating competitiveness



Development and validation of an integrated pest management strategy in winter maize

M.K. Khokhar^{1*}, Mukesh Sehgal¹, Anoop Kumar¹, D. Sreelatha¹, S.B. Suby²
and Richa Varshney³

¹ICAR–National Research Institute for Integrated Pest Management, New Delhi, India

²ICAR–Indian Institute of Maize Research, Ludhiana, India

³ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: khokharmk3@gmail.com

The fall armyworm, *Spodoptera frugiperda* (J. E. Smith), an invasive pest and is difficult to control, manage or eradicate, because it is polyphagous and trans-boundary, multiplies fast, has a short life cycle and migrates easily. Therefore, the IPM strategy was formulated and a validation trial was carried out in winter maize at Telangana during 2019–2022. The findings revealed that the effect of the IPM package in reducing *S. frugiperda* infestation was quite promising in all the experimental trials. The performance of the IPM module was on par with the farmers' practice (calendar-based application of chemical pesticides) in reducing *S. frugiperda* infestation, without any compromise in the marketable yield. The FAW infestation was recorded 23–28% in IPM field, 38 per cent in FP (farmers' practice) and 68 per cent in untreated control. Population of natural enemies (predatory insects) were recorded highest in the untreated control (>10.7/50 plants) followed by IPM (1.28 to 2.0 predators/50 plants) and FP (<0.30/50 plants) fields. The data on yield and economics indicated the highest yield in IPM (72 q/ha), followed by FP (65 q/ha), and in control (36 q/ha). IPM fields recorded benefit-cost ratio of 6.24 where in FP the ratio was 4.84 and in untreated control it was 3.37. Hence, the IPM package was proved to be effective can be considered as effective and economical in managing invasive *S. frugiperda* in winter maize along with conservation of natural enemies.

Keywords: fall armyworm; invasive pest; maize; natural enemies





Potential of the green lacewing (*Chrysoperla* sp.) for the control of red spider mites in *Acacia crassicaarpa* mother plants in commercial nurseries of Indonesia

Srikumar Koda Kkadan*, H.Br.S. Nike Grace, Br.G. Irma Yunara,
L.S. Ika Feronika, P. Hengki Marantika, Marthin Tarigan and
Álvaro Durán

Asia Resources Pacific International Holdings Limited, Riau Andalan Pulp and Paper,
Pangkalan Kerinci, Riau, Indonesia

*Correspondence: sreeku08@gmail.com

Acacia crassicaarpa Mill. (Fabales, Fabaceae) has been planted in peatland areas with acidic soil in Indonesia for use in paper, pulp and viscose materials. *Acacia crassicaarpa* plants grown in nursery have been attacked by several pests and mite pests. Among them the red spider mite, *Tetranychus* sp., is an important pest causing considerable production loss in commercial nurseries. Their infestation is mainly confined to the upper surface of the mature leaves and identified by a pale spot that turns brown or reddish colour on the upper surface of leaves. There are several naturally occurring insect predators against red spider mite and green lacewing (*Chrysoperla* sp.) is most important. *Chrysoperla* sp. has been successfully reared with *Corcyra cephalonica* eggs and larva as alternate hosts in the biocontrol facilities of the PT. Riau Andalan Pulp and Paper (RAPP), Pangkalan Kerinci, Riau, Sumatra. Inundative release of *Chrysoperla* sp. eggs were conducted in commercial nurseries. A total of 400 green lacewing eggs were released per bed in nurseries accounting 5000–7000 eggs per block. The red spider mite infestation was reduced to 1.4% in five weeks after release compared to the 7% in unreleased area. Two rounds of acaricide applications were lower in *Chrysoperla* sp. released blocks compared to unreleased. The study showed that green lacewing can be successfully utilised in integrated pest management programme for red spider mite.

Keywords: *Acacia*; biological control; forestry; mites





Selection of biocontrol-compatible insecticides for the conservation of natural enemies

Anoop Kumar* and Mukesh Sehgal

ICAR–National Research Institute for Integrated Pest Management, New Delhi, India

**Correspondence: anooptiwariant@gmail.com*

Climate change leads to the change in the agroecology of a region, consequently the status of minor pests' changes into the major pest and pest outbreaks. The selection of insecticides compatible with natural enemies and effective against target pests is a key to the success of the IPM programme. Based on the toxicity to natural enemies, insecticides have been classified into four different categories by the International organisation for biological control (IOBC) i.e. class-1: harmless, class-2: slightly harmful, class-3: moderately harmful, and class-4: harmful. Available databases shows that a large number of insecticides belonging to the newer groups are relatively safer to particular biocontrol agents but harmful to others and some insecticides are harmful to most of the natural enemies. Azadirachtin from neem, generally recommended in biocontrol-based pest management programmes was reported to be harmful to 18 natural enemies. So, the blanket application of botanicals such as azadirachtin can also be dangerous to natural enemies in biocontrol programmes where control is expected from released and natural populations. Therefore, the proper use of available databases for the selection of insecticides based on the IOBC categories will be of great help in the conservation of natural enemies.

Keywords: biocontrol; conservation of natural enemies; IOBC categories; safer insecticides



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Pectin extracted from pomelo peel and coconut or arecanut shell as biopesticide

Niranjan Kumar^{1*} and Shannon N. Sangma¹

¹ICAR–Indian Agricultural Research Institute, Barhi, India

*Correspondence: niranjan.kumar1@icar.gov.in

Pomelo peel, coconut and arecanut shells are valuable agro-waste materials, rich in pectin, a polysaccharide known for its bioactive properties. Pectin has demonstrated notable antimicrobial and insecticidal activities, positioning it as a promising candidate for biopesticides. The extraction process of pectin from these materials involves acid hydrolysis, enzymatic extraction, microwave extraction, steam extraction, solvent extraction, etc. followed by characterisation techniques such as FTIR, XRD and HPLC. Once extracted, the pectin can be encapsulated for application against various fungal pathogens, including *Fusarium oxysporum* and *Alternaria solani*, as well as insect pests like aphids and whiteflies. Research has shown that pectin-based biopesticides can significantly inhibit fungal growth and increase insect mortality, highlighting their potential as sustainable and eco-friendly alternatives to conventional chemical pesticides. While the initial findings are encouraging, further studies are essential to optimise extraction methods, scale up production and refine formulation techniques for field application. Additionally, exploring the commercialisation of encapsulated pectin products for the slow and controlled release of active ingredients will enhance their viability in agricultural practices. Overall, pectin derived from pomelo leaves and arecanut shells offers a promising pathway towards more sustainable pest management solutions.

Keywords: biopesticide; coconut shell; extraction; pectin; pomelo





***Fusarium* spp.: new entomopathogenic fungi on tea mosquito bug,
Helopeltis theivora (Hemiptera: Miridae)**

T.N. Madhu^{1*}, R. Thava Prakasa Pandian¹, B.J. Nirmal Kumar¹ and H. Skanda²

¹ICAR–Central Plantation Crops Research Institute, Regional Station, Vittal, India

²St. Aloysius College, Mangaluru, India

*Correspondence: madhuentomology@gmail.com

Tea mosquito bug (TMB), *Helopeltis theivora*, is a serious pest on cocoa that causes huge economic losses by feeding on shoots, cherelles and mature pods. Management of TMB through chemical measures affects on non-target organisms. Hence, use of entomopathogenic fungi (EPF) is an effective and alternate approach for the management of TMB. *Fusarium* spp. are the most common fungus reported as EPF on various insects but has not been documented on TMB. We collected the naturally infected TMB from cocoa field during our survey in March 2024 at ICAR–CPCRI, Vittal, India, and the pure culture was isolated from the infected adults. Based on morphological characters (sickle-shaped and segmented spores), ITS sequence and partial sequencing, the isolates were confirmed as *Fusarium* spp. Pathogenicity tests were conducted under *in-vitro* condition and positive results recorded. The results showed that the collected isolate was found to be highly effective and caused up to 80% mortality at 2×10^8 conidial suspension on 6 days after inoculation. This is the first record of natural infection caused by *Fusarium* spp. in TMB and it could be used as a good biocontrol agent against mirids in cocoa ecosystem.

Keywords: entomopathogenic fungi; *Fusarium* spp.; *Helopeltis theivora*; management





Influence of habitat manipulation on incidence and severity of pest damage in cabbage

N.B. Patel*, B.L. Raghunandan and Neha M. Patel

Anand Agricultural University, Anand, India

**Correspondence: nainesh@aau.in*

Cabbage (*Brassica oleracea* var. *capitata* L.) is a commercially important cruciferous vegetable crop. The insect-pests on cabbage alone causes a yield loss to the extent of 57 to 97 % from transplanting to till harvesting. The conservation of biocontrol or habitat management aims at preserving the natural enemies in the crop ecosystem to bring about effective management of the pests of cabbage instead of using insecticides. An experiment was conducted to assess the influence of mustard and cowpea as intercrop and oats as border crop with sole crop cabbage on major insect pests and natural enemies of cabbage. The treatment wherein mustard and cowpea were intercropped (5:1:1 rows), showed the lowest number of aphids per plant (7.40/plant). With regard to the data on larval population of diamondback moth (DBM), the recommended check treatment i.e. cabbage with cress crop as border crop recorded the lowest population (2.06/plant). Cabbage with cowpea as intercrop (5:1 rows) and oats as border crop recorded the lowest population of aphid and DBM with highest net income. This treatment was found statistically at par with the recommended check i.e. cabbage with cress as border crop. The reduced aphid population was witnessed due to the presence of more coccinellids/plant as a result of the intercrops, mustard and cowpea, which served as aphid trap crops. The highest population was documented in the treatment comprising the mustard and cowpea as intercrops (coccinellid population of 3.30/plant). The recommended check treatment, cabbage with cress as a border crop documented the highest head yield of 256 q/ha, which was statistically comparable to the yield of 243 q/ha recorded in the treatment wherein the main crop cabbage intercropped with cowpea and oats as a border crop.

Keywords: aphids; cabbage; coccinellids; diamondback moth; habitat manipulation





Biosafety of the entomopathogenic fungus *Lecanicillium saksenae* to non-target organisms

O.P. Reji Rani^{1*} and R.S. Karthik²

College of Agriculture, Thiruvananthapuram, India

*Correspondence: reji.rani@kau.in

Lecanicillium saksenae (NCBI Accession MN 545844.1), is an indigenous entomopathogenic fungus from soils of Kerala, India, proven to be an effective biocontrol agent to sucking pests of rice and vegetables @ 10^7 conidia/mL. In this investigation we undertook its biosafety evaluation in non target organisms. The test dose was 10^9 conidia/mL of the spore suspension and the test organisms were crop plants, pollinators, beneficial insects, parasitoids, predators, birds and mammals. Leaf inoculation and soil inoculation of *L. saksenae* in crop plants such as cowpea, okra, brinjal and tomato did not develop any symptoms of disease. Topical application of the spore suspension in the larval and adult stages of *Apis cerana indica* and adults of *Tetragonula iridepennis* did not cause any morbidity or mortality. Adult and larval stages of coccinellids completed their normal life cycle both in the treated and untreated insects. The egg parasitoids, *Trichogramma chilonis* and *T. japonicum* were found to be unaffected when tested using dry film technique. The life cycle of the larvae of silkworm, *Bombyx mori* treated with the fungus did not vary from that of control. The common quail, *Coturnix coturnix* and earthworm, *Eisenia andrei*, were observed to be healthy after exposure to *L.saksenae*. Acute toxicity studies carried out in guinea pigs, *Cavia porcellus*, New Zealand white rabbits and rat, *Rattus norvegicus*, revealed normal clinical parameters and blood values when administered orally, dermally and intranasally. Histopathological investigations did not reveal any necrotic tissues or lesions in any of the vital organs such as liver, kidney, lungs, heart or brain. Therefore, *L. saksenae* can be recommended and included in the IPM programme for sucking pests.

Keywords: biosafety; entomopathogenic fungus; *Lecanicillium saksenae*; mammalian toxicity





Influence of age of factitious host egg on parasitic potential of *Anastatus* sp., an egg parasitoid of coconut coreid bug, *Paradasynus rostratus* Distant

Jilu V.Sajan^{1*}, Merin Babu¹, P.S. Prathibha², K.M. Anes¹ and A. Josephraj Kumar¹

¹ICAR–Central Plantation Crops Research Institute, Regional Station, Kayamkulam, India

²ICAR–Central Plantation Crops Research Institute, Kasaragod, India

*Correspondence: jilu.sajan@icar.gov.in

Augmentative biological control has been very successful in the area-wide bio-suppression of coconut pests. Coreid bug, *Paradasynus rostratus* is an emerging pest of coconut, which cause direct yield loss as high as 65% in certain endemic tracts. An egg parasitoid, *Anastatus* sp., is identified as potential biocontrol agent against coreid bug from Kayamkulam, Kerala. The parasitoid could be successfully mass reared in the laboratory on eri silkworm eggs. The current study aimed to collect baseline information on the parasitic capabilities vis-à-vis progressing age of the factitious host eggs. The laboratory experiments were conducted with eri silkworm eggs of different ages. Host eggs glued to paper strips (1 × 1 cm) were offered to *Anastatus* sp. females for parasitisation at the parasitoid: host ratio (1:10) in laboratory conditions. Highest level of parasitism (70%) was registered on those eggs that are <1day old following by 1-day-old eggs and 2-day-old eggs, respectively. From 6th day onwards, the host eggs were avoided by the parasitoid and hence no parasitism occurred. The developmental duration of *Anastatus* sp. on eri-silk worm eggs was around 20 ± 2 days. The parasitoid exhibited selective preference for fresh eggs than the matured ones. This necessitated storage of fresh eggs, which can lead to uninterrupted production and supply of egg cards, especially during pre-monsoon showers coinciding the peak pest incidence. Thus, an environmentally responsible technology has been evolved for the sustainable management of nut crinklers.

Keywords: *Anastatus* sp.; coreid bug; egg parasitoid; eri silkworm





**Evaluation of dietary constituents on the survival and fitness of adult syrphid fly,
Ischiodon scutellaris (Fabricius, 1805)**

H.S. Venu* and Amala Udayakumar

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

*Correspondence: venuhs5072@gmail.com

Syrphids are an important group of predators that voraciously feed on the aphids infesting agricultural and horticultural crops. Yellow-shouldered hover fly, *Ischiodon scutellaris*, is an efficient predator of different species of aphids infesting agricultural and horticultural crops. Culture establishment of the syrphid predator, *I. scutellaris* is dependent on the availability of healthy aphids for the predatory larvae and an appropriate diet for the adult flies favouring their mating and oviposition. An experiment was conducted to evaluate different diets, viz. yeast (10%) + sugar/jaggery solution (10%) + pollen (1 g), yeast (10%) + pollen (1 g), pollen (1 g) + honey solution (10%), 1% vitamin E + honey solution (10%) + pollen (1 g) and yeast (10%) + honey solution (10%) + pollen (1 g) over the survival rate, mating, rate of oviposition and egg hatchability of the fly, *I. scutellaris*. A significantly higher number of mating events/day (2.11 ± 0.06 mating events/day) and egg hatchability (65.59%) was recorded in the adult flies supplied with 1% vitamin E (5 ml) + 10% honey solution (5 ml) + pollen (1 g) diet. The survival rate of the adult flies was significantly higher in yeast + honey + pollen diet (72.8%) followed by vitamin E + honey + pollen diet (72.4%). Vitamin E added to the honey + pollen could be a modified standard promising diet source for rearing the adults of the syrphid predator, *I. scutellaris*.

Keywords: egg hatchability; *Ischiodon scutellaris*; pollen; survival rate; vitamin E





**Biology, population growth parameters and foraging behaviour of the
parasitoid *Encarsia formosa* against the greenhouse whitefly,
Trialeurodes vaporariorum, in tomato**

**S.C. Verma^{1*}, Vibhuti Sharma¹, V.G.S. Chandel¹, P.L. Sharma², R.S. Chandel¹,
Chander Singh¹ and Anshuman Semwal¹**

¹Dr Y.S. Parmar University of Horticulture and Forestry, Nauni, India

²College of Horticulture and Forestry, Dr Y.S. Parmar University of Horticulture and Forestry, Thunag, India

*Correspondence: scvermaento@gmail.com

The biology, population growth parameters and foraging behaviour of *Encarsia formosa* against *Trialeurodes vaporariorum* was investigated under laboratory conditions ($25 \pm 0.5^\circ\text{C}$, $70 \pm 5\%$ RH, 14L:10D photoperiod) on tomato plants. The study reveals that the nymphal period was 12.1, 11.0, and 8.6 days for 2nd, 3rd, and 4th instars of *T. vaporariorum*. Pupal period was 8.0, 8.17, and 7.25 days for 2nd, 3rd, and 4th instars of *T. vaporariorum*. Parasitoid developed in 19.92, 19.25 and 16.08 days on 2nd, 3rd, and 4th instars of *T. vaporariorum*. Female adult lived for 7.71, 7.23 and 8.69 days on 2nd, 3rd, and 4th instar of *T. vaporariorum*. Gross reproductive rate was 10.43 on 2nd instar, 25.97 on 3rd instar and 30.48 on 4th instar of *T. vaporariorum*. Intrinsic rate of increase (r) showed an upward trend, with 0.07, 0.11, and 0.13 per day for 2nd, 3rd, and 4th instars *T. vaporariorum*. Parasitoid population doubling time was 9.24, 6.08, and 5.07 days while preying on 2nd, 3rd, and 4th instars of *T. vaporariorum*, respectively. Present study revealed Type II functional response across all host nymphal instars. Attack rate (a) was highest for 4th instar (0.121/h), followed by 3rd instar (0.103/h) and 2nd instar (0.037/h). Whereas, the shortest handling time (T_h) duration was observed for 4th instar (0.631 h), 3rd instar (0.767 h), and longest for 2nd instar (3.201 h). These findings elucidate valuable insights of *E. formosa* in relation to *T. vaporariorum* nymphal instars for optimising biological control strategies in tomato ecosystem.

Keywords: biology; *Encarsia formosa*; functional response; greenhouse whitefly; handling time





Validation of biointensive pest management practices for the management of brinjal pests

G. Anitha

Department of Entomology, Agricultural College, Adilabad, India

Correspondence: anithabiocontrol@gmail.com

Experiments were conducted in farmers' fields in Ranga Reddy district, Telangana for three years from kharif 2020 to 2023 to study the efficacy of biointensive pest management (BIPM) practices on pests of brinjal in comparison with farmers' practices and untreated control. Components of BIPM included the use of pheromone traps, 6 releases of *Trichogramma chilonis* @ 2 cc/acre, spraying *Bt* at 2ml/L, *Lecanicillium lecanii* VI8 (1×10^8 spores/ ml @ 5g/L) for sucking pests, Azadirachtin 1500 ppm (5ml/L). Results revealed that untreated control plots recorded highest incidence of shoot and fruit borer (25.72% shoot damage and 35.40% fruit damage, respectively, while the BIPM package plots recorded lesser incidence (16.84% shoot damage and 13.9% fruit damage, respectively) and the damage was least in the farmers' practice plots (12.19% shoot damage and 10.90% fruit damage). Fruit yield was highest in the farmers' practice plots (43.99 t/ha), while it was 39.38 t/ha in the BIPM package, while the untreated control plot recorded 14.25 t/ha. Overall results indicated that the BIPM package was effective in managing the pests on brinjal and also recorded good fruit yield. However, farmers' practice plots recorded higher benefit: cost ratio (3.95) compared to the BIPM package (3.59). On the other hand, higher yields and benefit: cost ratios at the cost of environmental safety may be risky for the agroecosystem in the long run. Hence, BIPM practices have to be given importance in the wake of depleting ecological services and increasing pesticide residues in foods.

Keywords: BIPM; brinjal; shoot and fruit borer; leafhoppers





Impact of biorational integrated pest management module against major pests of sugarcane in north coastal region of Andhra Pradesh, India

B. Bhavani* and M. Visalakshi

Regional Agricultural Research Station, Anakapalle, Acharya N.G. Ranga Agricultural University, Andhra Pradesh, India

*Correspondence: b.bhavani@angrau.ac.in

Field studies were conducted to evaluate the impact of BIPM module against major pests of sugarcane from 2017–2020 at Regional Agricultural Research Station, Anakapalle, and the results revealed that the incidence and intensity of major insect pests of sugarcane, viz. early shoot borer (13.75 %DH), internode borer (36.16; 1.70 %) and scale insect (9.40%; 1.30 %) were significantly reduced and resulted in superior cane yield (70.50 t/ha) by adopting BIPM module which comprises dipping of setts in chlorpyrifos 20 EC @ 0.05 % solution for 15 minutes before planting; application of chlorantraniliprole 0.4G @ 20 kg /ha at the time of planting, trash mulching @ 3t /ha on 3rd day after planting (DAP); installation of pheromone traps @ 27 traps /ha from 20 DAP for mass trapping of borer moths; field release of *Trichogramma chilonis* @ 50000/ha at weekly interval for four times commencing from 30 DAP and 120 DAP at weekly interval against borers; need based spray of chlorantraniliprole 18.5 SC @ 375 ml/ha at 60 DAP against early shoot borer, detaching of the lower leaves and removal of water shoots at 150 and 180 DAP followed by spray of clothianidin 50WDG @ 250 g/ha against sucking pests. The plot that received BIPM module (70.50 t/ha) produced an additional yield of 12 t/ha with a cost benefit ratio of 1: 1.63 over farmers' practice (58.33 t/ha). In addition to its efficacy against early shoot borer, chlorantraniliprole with new mode of action makes it a valuable option for IRM strategies, safety to key beneficial insects confer a strong fit within integrated pest management.

Keywords: chlorantraniliprole; mass trapping; pheromone traps; scale insect; sugarcane borers





Functional response of predatory mite *Neoseiulus longispinosus* (Evans) to different stages of *Tetranychus urticae* Koch on Carnation

V.G.S. Chandel*, Pankaj Sharma, S.C. Verma, P.L. Sharma, R.S. Chandel,
Anshuman Semwal, Chander Singh and Nikita Sharma

Dr Yashwant Singh Parmar University of Horticulture and Forestry,
Nauni, India

*Correspondence: vishv.chandel@gmail.com

Tetranychus urticae (Acari: Tetranychidae) is the most significant pest of carnation (*Dianthus caryophyllus* L.). *Neoseiulus longispinosus* (Evans) is an effective predatory mite against tetranychids. The functional response of different feeding stages of *N. longispinosus* was studied against the eggs, protonymphs and deutonymphs of *T. urticae* on Kleos cultivar of carnation. The predatory mites were offered with five different densities ranging from 3 to 40 individuals of different prey stages *T. urticae*. Consumption of predator increased with increase in prey density and then levelled off or declined slightly. The attack rate of predatory protonymphs, deutonymphs, male and female adults against prey eggs was calculated as 0.2040, 0.2961, 0.2865, 0.3041 h⁻¹, respectively. While, the handling time of respective predator stages was 3.789 h, 3.9147 h, 3.7695 h and 1.4301 h, against prey eggs. The handling time of respective predator stages against similar densities of *T. urticae* protonymphs was calculated as 4.5138 h, 4.2884 h, 3.9546 h and 1.5896 h, respectively, whereas, it was 4.5266 h, 4.2396 h, 4.1415 h and 1.6391 h, respectively against the deutonymphs of the prey. The highest attack rate and shortest handling time was shown by adult female of *N. longispinosus* on *T. urticae* eggs followed by protonymphs and deutonymphs, respectively. Significantly negative linear coefficients were obtained in all the predator stages which confirm the type-II functional response of the predatory mite. Hence, it can be concluded that *N. longispinosus* may be utilised as an effective biocontrol agent against *T. urticae* on carnation crop.

Keywords: carnation; functional response; *Neoseiulus longispinosus*; *Tetranychus urticae*





Sustainable control of bacterial diseases using novel bacteriophage formulations

Manoj Choudhary^{1,2*}, Jeffrey B. Jones² and Mathews L. Paret²

¹ICAR–National Research Institute for Integrated Pest Management, New Delhi, India

²Plant Pathology Department, University of Florida, Gainesville, USA

*Correspondence: manoj04444@gmail.com

Bacteriophages have been extensively explored for managing phytopathogenic bacteria. Their application in sustainable disease management is constrained by factors like limited persistence under field conditions due to rapid inactivation by ultraviolet (UV) radiation. Currently there are no commercially viable formulations that effectively shield phages from such degradation. Bacteriophage ΦXp06-02-1, used in this study, lyses *Xanthomonas perforans*, casual agent of tomato bacterial spot, was combined with varying concentrations of the nanomaterial N-acetylcysteine surface-coated manganese-doped zinc sulfide (NAC-ZnS; particle size: 3.5 nm). Under in vitro conditions, phages formulated with NAC-ZnS at 10,000 µg/ml exhibited UV resilience, maintaining plaque-forming unit (PFU) recovery rates comparable to non-UV-exposed phages following 1-minute UV irradiation. NAC-ZnS demonstrated no adverse effects on the lytic efficiency of the phage against bacteria. N-acetylcysteine-coated zinc oxide (NAC-ZnO) did not confer similar protective benefits. Under natural conditions, NAC-ZnS significantly enhanced persistence within the phyllosphere, achieving a 15-fold increase in phage longevity compared to non formulated phages. NAC-ZnO-formulated phages were undetectable within 32 hours post-application, whereas NAC-ZnS-formulated phages remained viable at 10³ PFU/g. The NAC-ZnS-phage formulation exhibited no phytotoxic effects when applied to tomato plants. Under sunlight exposure for 4 hours, NAC-ZnS-formulated phages at 1,000 µg/ml significantly suppressed bacterial spot disease severity, achieving a 16.4% reduction compared to non formulated phages. These findings underscore the potential of NAC-ZnS as an innovative nanomaterial-based approach to enhance phage stability and efficacy, offering a promising strategy for the biocontrol of bacterial diseases in crops.

Keywords: bacterial disease; bacteriophage; ultraviolet degradation; *Xanthomonas perforans*





Natural parasitism of citrus butterfly, *Papilio demoleus* by *Distatrix papilionis* (Hymenoptera: Braconidae) on acid lime

N.T. Dileep Kumar* and A.P. Biradar

College of Agriculture, University of Agricultural Sciences, Dharwad, India

*Correspondence: entodileep15@gmail.com

Citrus butterfly, *Papilio demoleus* L., is an economically important pest of citrus. The larval forms of this pest cause significant damage to citrus by devouring large quantity of foliage during their development. The caterpillars feed voraciously on young seedlings and cause death of the seedling. Severe infestation of pest results incomplete defoliation of the young trees and decreases photosynthetic activity leading to reduction in vigour, plant growth and fruit yield. The biological control of this pest involves exploitation of native predators, parasitoids and entomopathogens. A fixed plot survey was carried out during November 2020 to June 2022 to record the parasitism of citrus butterfly by an endolarvalparasitoid, *Distatrix papilionis* (Braconidae: Hymenoptera) on acid lime, *Citrus aurantifolia* Swingle. The larvae of citrus butterfly were collected from the lime orchard and kept under the observation for recording the parasitism. Braconid parasitoid, *D. papilionis* was found parasitising the larvae of citrus butterfly in acid lime orchards. During the study, parasitisation of larval stage of pest by *D. papilionis* was ranged from 0.00 to 44.00 per cent. The maximum parasitisation was recorded during second fortnight of July 2021 (44.00 %) and first fortnight of December 2021 (44.00 %), which coincided with peak activity of the pest. Overall, 24.87 per cent parasitisation of citrus butterfly larvae by *D. papilionis* was recorded. The efforts can be made to utilise identified endolarvalparasitoid in biological control of citrus butterfly on acid lime.

Keywords: acid lime; biological control; citrus butterfly; *Distatrix papilionis*; endolarval parasitoid





**Studies on nesting habitat and nest architecture of stingless bee,
Tetragonula ruficornis (Smith) (Hymenoptera: Apidae: Meliponini), from India**

Basavaraj N. Hadimani^{1*}, K. Chandrakumara² and Debjani Dey¹

¹Division of Entomology, ICAR–Indian Agricultural Research Institute, New Delhi, India

²Silkworm Division, Central Muga Eri Research & Training Institute, Lahdoigarh, India

*Correspondence: hadimanibasavaraj6@gmail.com

Stingless bees play a key role in natural environments and human economy because of their pollination services and high-value products. Understanding the intricacies of their nesting habitat and architecture is vital for preserving their ecological significance. Thus, current study was aimed to investigate the nesting habitat and architecture of the stingless bee, *Tetragonula ruficornis* Smith, at the ICAR–Indian Agricultural Research Institute, New Delhi, during 2021–2022. Among the 47 feral colonies studied, bees preferred tree trunk cavities (27 colonies) over building walls (20 colonies). The internal nest structure revealed the arrangement of brood cells in clusters at the centre surrounded by pollen and honey pots. Brood cells were light brown, oval-shaped with an average length of 3.48 ± 0.08 mm and a width of 2.48 ± 0.09 mm. Pollen pots were dark brown, spherical to polygonal-shaped with an average length of 8.10 ± 0.14 mm and a width of 6.73 ± 0.73 mm, composed of soft cerumen. Honey pots were dark brown, spherical to polygonal-shaped with an average length of 8.52 ± 0.46 mm and width of 7.36 ± 0.56 mm, located at the inner periphery. Further, the nesting cavity dimensions ranged from 105 to 168 mm in length, 129 to 216 mm in width and 283 to 472 mm in height, with an average volume of $136.67 \text{ mm} \times 171.33 \text{ mm} \times 365.67 \text{ mm}$. The study provides crucial information on nesting habitat and nest architecture, which could be exploited for designing bee hives and utilisation in directed pollination services.

Keywords: meliponiculture; nest architecture; nesting habitat; stingless bee; *Tetragonula ruficornis*





In vitro* bioefficacy of fungal endophytes against *Rhizoctonia bataticola

S.S. Kadam^{1*}, S.N. Banne², D.G. Hingole³ and S.J. Magar⁴

¹Department of Plant Pathology, Sadguru College of Agriculture, Mirajgaon, India

²Department of Plant Pathology, College of Agriculture, Pathri, India

³National Agricultural Research Project, Sambhajinagar, India

⁴Department of Plant Pathology, College of Agriculture, Latur, India

*Correspondence: shrutisk0143@gmail.com

Dry root rot of chickpea is an emerging disease posing threat to chickpea cultivation around the world. It is caused by the soil borne pathogen, *Rhizoctonia bataticola*. The current study was conducted to investigate the potential of employing endophytic microorganisms that are antagonistic to *R. bataticola* to manage dry root rot. A total of 20 fungal endophytes were isolated from healthy chickpea plant (roots, stem and leaves). The isolated fungal endophytes were tested against *R. bataticola* by dual culture technique under *in vitro* conditions. Among all, *Trichoderma asperellum* (CLEF18) exhibited the maximum inhibition of test pathogen, followed by *Aspergillus fumigatus* (CREF4) and *Acremonium* sp. (CREF1). The least mycelial inhibition of *R. bataticola* was observed in *Colletotrichum* sp. (CLEF6), followed by *Rhizoctonia* sp. (CREF17). These endophytes thus; could be efficient biological control agent in sustainable crop production and offer unique opportunity for crop protection and biological control.

Keywords: dry root rot; endophytes; inhibition; *Rhizoctonia bataticola*





Impact of new insecticides on natural enemy complex of cotton ecosystem

Ashish Kamal^{1*}, Shivaray Navi² and N. Sheela³

¹College of Agriculture, Mandya, India

²All-India Coordinated Research Project on Cotton, Chamaraajanagara, India

³ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: parisapoguashish@gmail.com

Cotton (*Gossypium* spp.), is a member of the Malvaceae family and one of the most widely used fibre crop, is essential to global economic, political, and social events. It is a crucial crop for trade and is referred as the “king of fibre” by many. The usage of insecticides is among the most dependable techniques for eradicating these infamous pests. To combat the sucking pests’ incidence, newer molecules which are ecofriendly, safer to natural enemies and have less risk on human being are to be integrated in pest management. Observations on population of natural enemies [(*Chrysoperla carnea* (adults), spiders and coccinellids (grubs and adults)] per plant were recorded from randomly selected 5 plants 1 day before the spray and 14 days after third spray in an experiment to evaluate the effect of newer molecules on natural enemies’ population. The mean data on natural enemies were reported that higher population of natural enemies were observed in the plot treated with pyriproxyfen 10EC @ 2 ml/L with 28.66 % and found safer to natural enemies followed by flonicamid 50 WG @ 0.3 g/L (30.29 %), dinotefuran 20SG @ 0.3 g/L (30.61%) followed by spinetoram 11.7SC @ 0.5 ml/L (34.52%), spiromesifen 22.9SC @ 1.2 ml/L (37.45%) and diafenthiuron 50 WP @ 0.8 g/L (38.43 %) reduction over control. Imidacloprid 17.8SL @ 0.3 ml/L has recorded lesser population of natural enemies, which was found toxic comparatively with higher per cent reduction over control of 43.97.

Keywords: natural enemies; new insecticides; pyriproxyfen; safe insecticides; sucking pests





**Non-predatory effects of *Neoseiulus longispinosus* (Evans) on
Tetranychus urticae Koch**

**Shashank Kaundal*, P.L. Sharma, S.C. Verma, V.G.S. Chandel, R.S. Chandel,
Nikita Chauhan, Chander Singh, Anshuman Semwal, Sushmita and Simran Sharma**

*Department of Entomology, Dr Yashwant Singh Parmar University of Horticulture and Forestry,
Nauni, India*

**Correspondence: shashank.kaundal18@gmail.com*

Two spotted spider mite, *Tetranychus urticae* Koch, is a highly polyphagous pest with a global distribution. Due to its high biotic potential and ability to develop pesticide resistance, alternatively predatory mites have been recommended and used against this pest worldwide. Among predatory mites, *Neoseiulus longispinosus* (Evans) has been used successfully against *T. urticae* especially under polyhouse conditions. Predators are generally assessed for their predatory potential against the target pests. However, there are prey individuals that escape predation and the predators may induce a range of responses including behavioural, morphological and life history changes in the target pest. Accordingly, there are many reports on the predatory efficiency of *N. longispinosus* against *T. urticae*, but its non-predatory effects on the prey mites that escape predation remains unknown. Therefore, the present study was conducted to measure the non-predatory effects of the predator on biology, reproduction and population growth parameters of the prey mite. We studied these parameters by rearing the prey mite in the presence of the predator or in an arena having predator cues and compared with the normally reared cohort. The results showed that all the tested parameters were negatively impacted in cohorts reared in the presence of the predator or predator cues as compared to the control cohort. This indicates a strong influence of the presence of natural enemy and its cues on the biology of the prey species suggesting the utilisation of these techniques in managing *T. urticae* populations in fields using biological control.

Keywords: *Neoseiulus longispinosus*; non-predatory effects; predation; semiochemicals; *Tetranychus urticae*





Acceptability and adaptability of *Trichogramma* spp. on eggs of *Samia cynthia ricini* (Drury)

Harpreet Kaur¹, Rabinder Kaur¹, P.S. Shera¹, K.S. Sangha¹ and Richa Varshney²

¹Department of Entomology, Punjab Agricultural University, Ludhiana, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: harpreet_flora@yahoo.com

Trichogramma spp. are among the most significant egg parasitoids utilised in biological control globally, capable of parasitising over 400 insect species. This study evaluates the acceptability with respect to parasitism potential of *T. chilonis*, *T. japonicum*, and *T. embryophagum* on factitious host, eri silkworm (*Samia cynthia ricini*) eggs, intending to develop a cost-effective production technology of trichogrammatids for their augmentative biocontrol programme. A comprehensive analysis of the biological attributes of these species was conducted on the eggs of *S. cynthia ricini* and compared with other most common factitious hosts, *Corcyra cephalonica* Stainton. The mean developmental time of *Trichogramma* on eri eggs ranges from 10.51 to 14.21 days, significantly longer than that of *Corcyra* (7.12 to 9.47 days) with adult longevity of 4–7 days. However, parasitisation was observed around 55.6 to 67.4 per cent with a greater number of female emergences, resulting in an average of 2–7 adult wasps per egg as compared to a single adult per egg as in the case of *Corcyra*. Importantly, no significant differences were noted in the female-to-male ratios among the parasitoid species developing on eri silkworm eggs. Thus, these findings suggest that eri silkworms can serve as an alternative host to rice moth for the mass production of *Trichogramma* as it yields a higher benefit-cost ratio due to superior biological traits. This production technology would also be suitable and helpful for promoting localised production of eri silkworm for silk as well.

Keywords: acceptability; adaptability; eggs; eri silkworm; *Trichogramma*



**Evaluation of predation potential and behavioural preferences in
Chrysoperla zastrowi sillemi under intraspecific and interspecific interactions**

Sahilpreet Kaur* and K.S. Sangha

Department of Entomology, Punjab Agricultural University, Ludhiana, India

**Correspondence: sahilpreet.dadhyal@gmail.com*

Sucking pests inflict substantial economic damage on diverse crops, such as cereals, vegetables, forage, fruits, nuts, fiber crops, ornamentals, greenhouse crops, and forest species. Controlling these pests with chemical pesticides poses significant environmental and health challenges, making biological control a sustainable alternative. *Chrysoperla zastrowi sillemi* (Esben-Peterson 1935) effectively manages these pest populations through a density-dependent response, where increased prey density supports higher predator populations, thereby suppressing pest numbers. However, *C. zastrowi sillemi* exhibits cannibalistic behaviour in prey-scarce conditions, especially during its third larval instar, a voracious feeding stage. This study evaluated its predation potential and prey preferences, focusing on jassid nymphs, aphids, and conspecific larvae. The first, second, and third larval instars of *C. zastrowi sillemi* consumed an average of 5.88 ± 1.81 , 10.88 ± 5.89 , and 27.88 ± 2.64 jassid nymphs, respectively, and 29.63 ± 7.65 , 48.75 ± 6.23 , and 72.75 ± 3.62 aphids. In the case of cannibalism, the third larval instar consumed 27.8 ± 1.92 first instar larvae and 7.2 ± 1.30 second instar larvae. The behavioural preference study revealed that the third larval instar preferred cannibalism when prey and conspecific larvae were equally available. In this scenario, the conspecific larvae also fed on the prey, resulting in prey scarcity for the third instar. However, when prey was provided and conspecific larvae were limited, cannibalism was absent, indicating that sufficient prey availability can suppress cannibalistic behaviour in *C. zastrowi sillemi*.

Keywords: cannibalism; host preference; interspecific predation; predation potential; sucking pests





Prospects and challenges of biopesticide use in Nepal

Debraj Adhikari¹, H.M. Mahesh^{2*}, Vinod Pandit² and G.C. Yubak Dhoj³

¹*Plant Quarantine and Pesticide Management Centre, Nepal*

²*CABI, South Asia, New Delhi, India*

³*Food and Agriculture Organisation, Bangkok, Thailand*

**Correspondence: m.mahesh@cabi.org*

Agriculture contributes approximately 24.1% to GDP and employs 64.8% of the population in Nepal. To prevent an estimated 35% crop loss due to insect pests and diseases, farmers generally depend on agrochemicals. Despite the introduction of pesticides in the 1950s, primarily for malaria eradication, their use has expanded significantly, particularly in high-value crops and vegetables. However, issues such as improper handling, storage, and disposal, along with limited farmer knowledge and inadequate training, pose significant challenges. The harmful effects were more evident in the recent chronic disease cases due to conventional pesticides. The use of bio-pesticides in Nepal presents a promising alternative to conventional chemical pesticides, aligning with sustainable agricultural practices, safety to users, and environmental protection. The study explores the status, challenges, and prospects of bio-pesticide use in Nepal. This employs a literature review, a questionnaire-based survey with agro-advisory service providers, and data analysis from the Plantwise Online Management System (POMS) to assess the awareness, adoption, and challenges of bio-pesticide use in Nepal. Findings indicate that bio-pesticides constitute a mere 0.015% of total pesticide import in Nepal. Key challenges include limited availability, perceived lower efficacy compared to chemical pesticides, high costs, and insufficient training on application and dosage. The study underscores the need for enhanced awareness, robust regulatory frameworks, and collaborative efforts among government agencies, research institutions, private sector stakeholders, and farmer organisations to promote the effective use of bio-pesticides. Addressing these challenges through capacity-building initiatives and supportive policies is crucial for the successful integration of bio-pesticides into Nepalese agriculture.

Keywords: bio-pesticides; challenges; Nepal; POMS



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



**Sustainable management of *Tetranychus truncatus* using native
Photorhabdus luminescens isolates**

Athira G. Menon^{1*}, Haseena Bhaskar¹, M.S. Smitha¹ and K. Surendra Gopal²

¹Department of Agricultural Entomology, College of Agriculture, Vellanikkara, India

²Department of Agricultural Microbiology, College of Agriculture, Vellanikkara, India

*Correspondence: athiragmenon94@gmail.com

Spider mites are major pests of agricultural and horticultural crops globally. *Tetranychus truncatus* Ehara, a polyphagous species, causes significant damage to vegetables and ornamentals in Kerala. Resistance to synthetic acaricides, such as fenazaquin and spiromesifen, underscores the need for sustainable alternatives. The symbiotic bacterium, *Photorhabdus luminescens* (associated with entomopathogenic nematodes, *Heterorhabditis* spp.) has shown promise as a biocontrol agent against various arthropods, including mites. Soil samples from five districts in Kerala yielded 14 bacterial isolates, including two *P. luminescens* strains (ODA and CNT1), identified through molecular and cultural characterisation. Laboratory bioassays demonstrated significant ovicidal and adulticidal activity, with the ODA isolate showing 100% adult mortality using cell-free supernatant at 10⁸ cells/ml. Bioformulations were developed as liquid (glycerol, trehalose, PVP-based) and solid (starch, talc-based) products. Laboratory assays revealed that the PVP-based liquid formulation achieved 100% adult and 97.33% egg mortality, outperforming the starch-based solid formulation. Shelf-life studies indicated bacterial populations declined over 90 days under refrigerated and room-temperature conditions. Field trials on cucumber in polyhouse showed a 99.15% mite population reduction with the liquid formulation by day 7, comparable to synthetic acaricides like spiromesifen. The study highlights the potential of native *P. luminescens* strains for developing effective, sustainable alternatives to manage *T. truncatus* infestations, reducing reliance on synthetic chemicals in pest management systems.

Keywords: bacterial bioformulations; bioefficacy; *Heterorhabditis indica*; *Photorhabdus luminescens*; *Tetranychus truncatus*





Foraging activities of *Apis florea* Fab. and *Apis cerana indica* L. on Indian mustard

S.A. More* and Sushma Tamgond

College of Agriculture, Pune, India

*Correspondence: ento3655@gmail.com

Mustard has bright yellow-coloured flowers and are good source of nectar. Being a valuable source of pollen and nectar, pollinating insects prefer to visit them and mostly pollinated by them. The foraging activity of honey bees, *Apis florea* Fab. and *Apis cerana indica* L. on flowers. Maximum and minimum foraging activities of both species were recorded 10.87 ± 2.59 and 6.87 ± 2.19 bees/m²/2 min at 10:00–12:00 hrs of the day and at 18:00–18:30 hrs of the day with 1.73 ± 0.55 and 0.60 ± 0.28 bees/m²/2 min, respectively. Both species were not recorded at 6:00–8:00 hrs of the day. The mean foraging activity recorded during 8:00–10:00 hrs, 12:00–14:00 hrs, 14:00–16:00 hrs and 16:00–18:00 hrs were 1.93 ± 1.69 , 9.33 ± 0.75 , 6.60 ± 1.16 and 4.53 ± 1.26 bees/m²/2 min, respectively in *A. florea* and 1.13 ± 0.96 , 6.53 ± 1.07 , 3.93 ± 1.16 , 2.93 ± 0.86 bees/m²/2 min, respectively in *A. cerana*. Thus, *A. cerana* is the most efficient pollinator, as its foraging speed was less with $2.530.38 \pm$ sec/flower, and hence it visited more number of flowers per minute (24.67 ± 3.81) in non-sprayed mustard crop. Effect of three sprays of insecticides, viz. imidacloprid 17.8%SL, buprofezin 25SC, thiamethoxam 25WG, lambda cyhalothrin 5EC, *Metarhizium anisopliae* and NSE (5%) on both species showed reduced foraging activity. It was observed that imidacloprid and thiamethoxam treated plots exhibited maximum repellent effects on the foraging activity of the bees. Whereas, the maximum bee activity was recorded in NSE (5%) treated plots. Moderate repellent effect was recorded on spraying of ibuprofen 25SC, lambda cyhalothrin 5EC and *M. anisopliae* treated plots. Hence, it is suggested to use the insecticides in following order: NSE > *M. anisopliae* > lambda cyhalothrin > buprofezin > thiamethoxam > imidacloprid, to avoid toxic effects on the bees. The differences in the present findings and those reported by various workers may be due to the difference in the concentration of insecticides, crop and agro climatic conditions.

Keywords: foraging activity; mustard; pollinators; spraying





***Cheletomimus berlesei* (Oudemans) (Acari: Cheyletidae): interesting life history,
intriguing predatory behaviour and an indeterminate prey range**

Nanjundaiah Sheela and Prakya Sreerama Kumar*

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

*Correspondence: psreeramakumar@yahoo.co.in

Predatory mites are essential arthropods in commercial biological control, crucial for sustainable pest management. By preying on pests like spider mites, whiteflies and thrips in agricultural and horticultural ecosystems, they reduce the need for chemical pesticides, mitigating environmental risks. Species within the Cheyletidae family (Acari: Acariformes: Trombidiformes) have largely been overlooked, despite their notable predatory behaviour, which makes them valuable assets in biological pest control. Approximately 75% of cheyletid mites are predators that target other arthropods, while the remaining 25% are parasitic on birds and mammals. Recently, we have turned our attention to *Cheletomimus berlesei*, a versatile predatory mite known for its active searching and ambush predation strategies. Investigations on its biological characteristics, targeting the storage mite *Tyrophagus putrescentiae* and the spider mite *Tetranychus urticae*, indicated that its average lifespan varies significantly depending on the prey. It preyed on the larval, nymphal and adult stages of various spider mites, as well as on *Polyphagotarsonemus latus*, *Raoiella indica* and early-instar thrips. In field studies, *C. berlesei* could sustain under protected conditions and reduced the pest population.

Keywords: biological control; *Cheletomimus berlesei*; phytophagous mites; predatory mites





Observations on immature stages of aphidophagous hoverflies (Diptera: Syrphidae) in India

P. Naveena^{1*}, K.S. SaiTeja¹, Prabhu C. Ganiger², K. Shravya Savithri¹,
Nagabhushana Reddy², G. Mohanprasad¹ and Siddamma¹

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

²Zonal Agricultural Research Station, University of Agricultural Sciences, Bengaluru, India

*Correspondence: naveenapandi7@gmail.com

The family Syrphidae (Insecta: Diptera), comprising over 6,300 species globally, has been primarily studied for adult morphology, with limited research on their immature stages. Adult hoverflies, or flower flies, are important pollinators, while their larvae play various ecological roles, such as predation on insects, decomposition of organic materials, and herbivory on plants. In India, approximately 371 syrphid species have been reported. This study focuses on identifying aphidophagous syrphid species and their hosts by rearing larvae in the laboratory. Observations revealed *Serratoparagus serratus* feeding on Ragwort aphid, *Tetraneura nigriabdominalis* and *Ischiodon scutellaris* preying on Cabbage aphid, *Brevicoryne brassicae*. In the pigeon pea ecosystem, *Dideopsis aegrotus*, *Betasyrphus linga*, and *I. scutellaris* were recorded feeding on *Aphis craccivora*. Among these, *I. scutellaris* was the most abundant, followed by *B. linga* and *D. aegrotus*. Identification of larvae was based on distinct features: *I. scutellaris* larvae had a yellowish mid-dorsal line on a green body, while *S. serratus* larvae were recognised by serrations. *Betasyrphus linga* larvae, resembling bird droppings, had three lateral stripes, leading to the species name “linga.” Pupae were identified by unique characteristics, such as the eye-like water droplets; *I. scutellaris* pupae were green with brown spots, while *B. linga* pupae were dark brown with elongated appendages. This study improves our understanding of syrphid biology and their ecological role in pest control.

Keywords: aphidophagous; hoverflies; immature stages; Syrphidae; taxonomy



**Suppression of host egg development during *Trichogramma* parasitisation:
are polydnviruses not the sole molecules involved?**

P. Niranjana*, M.C. Meghashree, S. Gagana and G.M. Shubha

Kuvempu University, Shivamogga, India

**Correspondence: bpniru@gmail.com*

Insects are dominant among all organisms and approximately 10% of all insects are parasitoids. The successful ecological adaptations of parasitoids on their hosts, attracted and promoted them as biocontrol agents in the management of pesticide resistant strains of agricultural pests. In an antagonistic co-evolution, parasitoids build powerful strategies to make successful parasitism, though hosts spurred resistance counter mechanism of avoidance. Even now, with varied drastic climatic niche, many of the parasitoids build foster arms of race to adopt broader range of hosts species. Among egg and larval parasitoids deployed in the management of agricultural pests, *Trichogramma chilonis* is most commonly used biocontrol agent in India. Fundamental to the parasitism efficiency of many parasitoid wasps are polydnviruses (PDVs), which facilitate successful host manipulation by suppressing immune responses. In nature, larval parasitoids like *Cotesia* lays its eggs into the larva of the host insect, and at the same time introduces PDVs. The PDVs play an important role in the developmental arrest of the host and in nature its mechanism is well established. However, in laboratory conditions, we hypothesise that, during *T. chilonis* parasitisation into UV killed *C. cephalonica* host eggs, the released PDVs may not have any role. Because *C. cephalonica* eggs are UV inactivated, *T. chilonis* must be introducing other defensive molecules or antimicrobial agents to protect the invaded microbes at the time of parasitisation. Our cloning and characterisation studies using in-house *T. chilonis* transcriptome data confirms the presence of other defensive related proteins which may be functioning as alternatives to PDVs.

Keywords: parasitism; parasitoids; polydnviruses; *Trichogramma chilonis*





Integrated pest management — an ecological approach for pest suppression in tomato

**K.V. Raghavendra^{1*}, Balodi Rekha¹, Ramakrishnappa Manjunatha²,
Maddireddy Papireddy³, Mukesh Sehgal¹ and Subhash Chander¹**

¹ICAR–National Research Institute for Integrated Pest Management, New Delhi, India

²College of Sericulture, University of Agricultural Sciences, Bengaluru, India

³Krishi Vigyan Kendra, Chintamani, University of Agricultural Sciences, Bengaluru, India

*Correspondence: raghavendra.kv@icar.gov.in

Current study illustrates results of validation of Integrated Pest Management strategy in tomato under farmers' participatory approach at two agro-ecologies in India (Chikkaballapura, Karnataka and Karnal, Haryana). Validated IPM strategy included cultural, mechanical, biological methods and need-based chemical pesticides with label claims. IPM resulted in overall reduction in pest population at both the locations. There was 17.55% and 9.02% reduction in pinworm and fruit borer damage, respectively in Karnataka, while 14.33% reduction in fruit damage due to borer was recorded in Haryana. Similarly, 7.76% and 21.34% reduction in whitefly and 10.66% and 38.36% reduction in leaf miner compared to Non-IPM-Farmers' Practice was observed in Karnataka and Haryana, respectively. Regarding early blight, an average PDI of 276.78% and 378.91% (IPM) and 287.16% and 409.84% (FP) was recorded in Karnataka and Haryana, respectively. An average PDI of 43.35% and 206.35% (IPM) and 44.29% and 260.96% (FP) was recorded at two locations in case of late blight. There was an enhancement of up to 75% in chrysopid, 87.50% in coccinellids and 66.66% in predatory spiders population in IPM fields. IPM thus helped in maintaining more favourable P:D ratio and reduced insecticide applications. Farmers adopted IPM could significantly reduce cost of cultivation i.e. input cost (19.95% and 15.52%) and increase in the average yield (4.75% and 7.36%) at Karnataka and Haryana, respectively. IPM farmers received 1.05 and 0.69 rupees more per rupee invested over FP at Karnataka and Haryana, respectively. IPM strategy was effective in curbing the pest menace, and proved farmer friendly, economical and environmentally safe.

Keywords: diseases; ecological approach; insect pests; IPM



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Andrographolide-based biopesticide for aphid management in vegetable cowpea

Neethu G. Raj^{1*}, T. Santhoshkumar² and K. Anoop Krishnan³

¹Department of Agricultural Entomology, Kerala Agricultural University, Thrissur, India

²Department of Nematology, Kerala Agricultural University, Thrissur, India

³Hydrological process group, National Centre for Earth Science Studies, Thiruvananthapuram, India

*Correspondence: neethug21@gmail.com

The study aimed to develop an andrographolide-based biopesticide against cowpea aphid, *Aphis craccivora*. Andrographolide was isolated from *Andrographis paniculata*, yielding 0.20g per 50g of plant powder. Identification of the bioactive compound was done through FTIR and LC-MS analysis. The effectiveness of andrographolide based compound on aphids demonstrated concentration-dependent mortality. The LC_{50} and LC_{90} values recorded at 24 hours after treatment were 2064.51 and 3206.52 ppm, respectively. The development of stable formulations utilising andrographolide as the active ingredient alongside appropriate solvents, carrier oils and emulsifiers was carried out. The study selected two optimal formulations, namely Formulation A (andrographolide+neem oil+Triton X-100) and Formulation B (andrographolide+pungam oil+Triton X-100), based on their efficacy against *A. craccivora*. The *in vitro* evaluation showed that the LC_{50} of formulations A and B were 1.51 and 1.42%, respectively and the LC_{90} of formulations A and B were recorded as 4.52 and 4.40%, respectively. The field evaluation showed that both formulations effectively reduced aphid populations, achieving significant reduction at 1 day after spraying (DAS) and sustained impact through 14 DAS at higher concentrations. Both formulations A and B were found to be safe for natural enemies compared to chemical checks. The shelf-life assessment of the formulations revealed stable and sustained properties over six months after the preparation of the formulations. These findings highlight the potential of andrographolide-based biopesticides as sustainable alternatives in integrated pest management (IPM) strategies for cowpea aphids.

Keywords: andrographolide; *Aphis craccivora*; biopesticide; cowpea; IPM





Bee pollination in greenhouse and its efficacy in yield enhancement

T.N. Rakshitha^{1*}, S.T. Prabhu¹, P.S. Tippannavar¹, R.V. Hegde² and G.K. Naidu³

¹Department of Agricultural Entomology, University of Agricultural Sciences, Dharwad, India

²Department of Horticulture, University of Agricultural Sciences, Dharwad, India

³Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, India

*Correspondence: tnrakshitha@gmail.com

Agricultural practices gradually evolved to rise the production and productivity of crops without expanding the area, lead to protected cultivation but, this condition creates a physical barrier which prevents the access of natural pollinators to flowers. Role of pollinators play an important role in vegetable seed production. Comparative study was carried out between Indian honey bee, *Apis cerana* F. and Stingless bee, *Tetragonula irridipennis* S. on Gherkin (savory pickled cucumber) raised undergreenhouses of Hitech Horticulture Unit, University of Agricultural Sciences, Dharwad. *Tetragonula irridipennis* were late foragers (08:00 h) compared to *A. cerana* (06:00 h) while, maximum foraging activity observed between 11:00–12:00 h (11.45 bees/m²/10 min) and 09:00–10:00 h (20.18 bees/m²/5 min) in *T. irridipennis* and *A. cerana*, respectively. The flower sex type selection index of *T. irridipennis* and *A. cerana* on gherkin flower was 0.48 and 0.78, respectively, indicating strong preference for male flower. *Tetragonula irridipennis* (15.40%) had a high pollen carrying capacity compared to the *A. cerana* (10.02%). The per cent fruit set was significantly enhanced to 90.72 per cent and 89.11 per cent in *T. irridipennis* pollinated crop and *A. cerana* pollinated crop, respectively compared to crop without bee pollination (3.04%). Bee pollination enhanced gherkin yield both quantitatively and qualitatively. *Tetragonula* sp. adapt to enclosed structure easily while compared *Apis* sp. because of its smaller effective foraging range and are considered as good candidates for future alternatives in commercial pollination. Crop growers under greenhouses may have the option of selecting stingless bees as most suitable pollinator.

Key words: foraging; fruit set; gherkin; greenhouse; pollination





Biology and morphometrics of *Apis cerana himalaya* Fabricius under Manipur conditions

Pranita Roy*, Shravan M. Haldhar, C.N. Nidhi and Om Prakash Mishra

Department of Entomology, Central Agricultural University, Imphal, India

**Correspondence: roypranita2899@gmail.com*

A comprehensive study was conducted on the biology and various morphometrics traits of *Apis cerana himalaya* at the Apiary, Department of Entomology, College of Agriculture, Central Agricultural University, Manipur. The studies on the biology of *A. cerana himalaya* revealed developmental timeline of 18.20 days for workers and 22.66 days for drones during honey flow, and slightly longer times during the dearth period. Morphological measurements were recorded for workers, drones and queens. Key findings included mean lengths of middle leg segments: coxa (0.21 ± 0.06 mm), trochanter (0.53 ± 0.09 mm), femur (1.15 ± 0.20 mm), tibia (1.05 ± 0.08 mm), and tarsus (1.20 ± 0.09 mm). In the hind leg, measurements highlighted structural adaptations for pollen collection, with a tibial pollen basket size of 0.39 ± 0.11 mm. The queen's morphology was also documented, with the head measuring 2.45 ± 0.05 mm in length and the thorax 3.36 ± 0.06 mm. Total body lengths of different castes were recorded, with workers at 8.17 ± 0.34 mm, drones at 9.80 ± 0.38 mm, and the queen at 11.10 ± 0.08 mm. These findings provide insights into the specific adaptations of *A. cerana himalaya* to its environment and underscore the value of morphological data in honeybee conservation. By adding to the knowledge of honeybee diversity, this study supports the broader goals of biodiversity preservation and ecological resilience, promoting an understanding of how different honeybee subspecies can contribute to ecosystem health.

Keywords: *Apis cerana himalaya*; biology; drone; morphometrics; queen; worker



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Observation on larval and larval-pupal parasitoids of the serpentine leaf miner, *Liriomyza* sp. (Diptera: Agromyzidae), in tomato and common bean ecosystem

K. Shravya Savithri^{1*}, Prabhu C. Ganiger², P. Naveena¹, Nagabhushana Reddy²,
G. Mohanprasad¹ and Siddamma¹

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

²All-India Coordinated Research Project on Small Millets, Zonal Agricultural Research Station, University of Agricultural Sciences, Bengaluru, India

*Correspondence: shravyasavithri@gmail.com

The serpentine leaf miner, *Liriomyza* sp. is an important polyphagous pest infesting over 70 host plants representing vegetables, ornamentals, field crops and weeds. Damage is mainly caused by the maggots which feed by mining into the leaves and affect the photosynthesis of the plant drastically. The pest has caused considerable damage to tomato and common/french bean, *Phaseolus vulgaris* L. at Bengaluru, India. Here, attempt was made to know parasitoids associated with *Liriomyza* sp. and their role in suppressing this pest. A total 20 infested leaves were collected from each stratum. These leaves were brought to the laboratory and examined under microscope for empty mines, dead mines, live mines and parasitised mines. These leaves were then kept in plastic jars in the laboratory for the emergence of either miner flies or the parasitoid adults. During 2024, one species of larval parasitoid belonging to the family Eulophidae and one larval-pupal parasitoid belonging to the family Braconidae were collected. The larval-pupal parasitoid recorded during the study was identified as *Opius* sp. (Hymenoptera: Braconidae) whereas larval parasitoid as *Hemiptarsenus* sp. (Hymenoptera: Eulophidae). Total parasitisation ranged from 2 to 22.5 per cent and 10 to 15 per cent by *Opius* sp. and *Hemiptarsenus* sp., respectively. Further studies are necessary for the conservation of these natural enemies through suitable habitat management techniques and reduction in pesticide use.

Keywords: common bean; *Liriomyza* sp.; parasitoids; *Phaseolus vulgaris*; tomato





**Deciphering the gut bacterial diversity associated with *Apis cerana indica* from
the southern regions of Karnataka**

**J. Jenifer Sheeba^{1,2}, Selva Babu Selvamani¹, Venkatesan Thiruvengadam^{1*},
R. Gandhi Gracy¹, Jyoti Pathak¹, Sabtharishi Subramanian³,
Gopalakrishnan Menon², G. Sivakumar¹, C. Manjunatha¹, U. Amala¹ and S.N. Sushil¹**

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Department of Microbiology, Jain (Deemed-to-be-university), Bengaluru, India

³Division of Entomology, ICAR–Indian Agricultural Research Institute, New Delhi, India

*Correspondence: tvenkat12@gmail.com

In general, the insect gut microbiota influences important features and metabolic processes such as feeding, digestion, detoxification, and immunity. However, data on the gut bacterial diversity of the Asian honeybee, *Apis cerana* Fabricius is scarce. In this study, the gut bacterial diversity of honeybee samples taken from the Southern regions of Karnataka (Shivamogga and Kodagu) was investigated using culture-dependent and culture-independent techniques, and the positive results were presented. The 16S rRNA amplicon sequencing analysis indicated an extremely complex bacterial makeup, with 14 distinct types of bacteria. Similarly, culturable tests showed significant variations in gut bacteria between the two areas. The cultured gut homogenates of bees from the Shivamogga area included three distinct bacterial phyla: *Firmicutes*, *Proteobacteria*, and *Actinomycetota*. In contrast, Kodagu bees contain two phyla: *Firmicutes* and *Proteobacteria*. The gut flora of Kodagu bees was relatively diverse and rich in microorganisms. This study emphasised the discovery of gut bacteria that might have a substantial impact on colony health and function. Our research emphasises the importance of honey bee-bacteria symbioses, as well as how these symbioses are connected to genetic diversity, bacterial co-occurrence patterns, disease burden, and nutrition all of which are expected to have a role in honey bee decline. Overall, our study demonstrated the complex link between *A. cerana* and gut microbiota diversity in the two biodiversity hotspots.

Keywords: *Apis cerana*; culture dependent; diversity; gut microbiota; honey bees; metagenomics





Exploration of entomopathogenic fungi as potential biocontrol agents of *Spodoptera litura* in soybean (*Glycine max* L. Merrill)

Hemant Swami* and M.K. Mahla

*Maharana Pratap University of Agriculture and Technology, Udaipur, India

*Correspondence: hemantswamy@gmail.com

The bioefficacy of entomopathogenic fungi, viz. *Metarhizium anisopliae* (NBAIR strain) @ 5g/lit, *M. anisopliae* (UAS, Dharwad) @ 2g/lit, *Beauveria bassiana* (UAS, Dharwad) @ 2g/lit, *Metarhizium rileyi* (UAS, Dharwad) @ 2g/lit was evaluated and compared with neem oil @ 3ml/lit, chlorantraniliprole 18.5SC w/w @ 0.3 ml/lit and untreated control, in randomised block design with three replications. The observations recorded on the efficacy of different treatments against the tobacco caterpillar of soybean during kharif 2023 revealed that among all the treatments, application of chlorantraniliprole 18.5SC w/w @ 0.3 ml/lit proved to be most effective in reducing the population of tobacco caterpillar with mean per cent larval reduction of 46.23, 58.44, 75.16 (1st spray), 54.03, 64.55, 82.38 (2nd spray), 62.67, 75.09, 82.50 (3rd spray) per cent at three, five and seven days after treatment, respectively during kharif 2023 whereas among the entomopathogenic treatments, the application of *M. anisopliae* (UAS, Dharwad) @ 2g/lit and *B. bassiana* (UAS, Dharwad) @ 2g/lit were proved to be next effective and superior to other treatments except Chlorantraniliprole in reducing the population of tobacco caterpillar with mean per cent larval reduction of 35.05, 41.76, 46.19; 34.62, 43.02, 48.51 (1st spray), 36.12, 49.90, 57.51; 40.16, 50.47, 55.77 (2nd spray), 43.60, 57.08, 62.57; 46.60, 53.02, 59.14 (3rd spray) per cent, respectively at three, five and seven days after treatment, respectively. The application of *M. anisopliae* (NBAIR strain) @ 5g/lit and *M. rileyi* (UAS, Dharwad) @ 2g/lit were to be next in order of effectiveness. The treatment application of neem oil resulted in minimum mean per cent larval reduction of tobacco caterpillar are 25.05, 31.29, 35.43 (1st spray), 29.03, 37.56, 42.64 (2nd spray) and 34.08, 46.38, 49.14 (3rd spray) per cent at three, five and seven days after the treatment, respectively and proved to be the least effective treatment.

Keywords: chlorantraniliprole; entomopathogenic fungi; neem oil; soybean





Scope of biological control in tasar sericulture

**B. Thirupam Reddy^{1*}, C. Selvaraj², S.M. Mazumdar², H.S. Gadad³,
D.M. Bawaskar², G.V. Vishaka², H. Nadaf² and T. Selvakumar²**

¹Basic Seed Multiplication and Training Centre, Central Silk Board, Bastar, India

²Basic Tasar Silkworm Seed Organisation, Central Silk Board, Bilaspur, India

³Central Tasar Research and Training Institute, Central Silk Board, Ranchi, India

*Correspondence: entomophily@gmail.com

The tasar silkworm (*Antheraea mylitta* Drury) is a wild sericigenous insect famous for producing tasar silk, which holds significant commercial value both domestically and internationally. Due to its economic importance, tasar sericulture is widely practiced in the tribal and rural regions of Central India, providing livelihoods to tribal and rural population. Unlike mulberry sericulture, tasar silkworm rearing is conducted in outdoor conditions, making it vulnerable to various insect pests and diseases. Common insect pests include *Ichneumon* wasps, uzi flies, stink bugs, assassin bugs and paper wasps. Additionally, the host plants of tasar silkworm, namely *Terminalia arjuna* and *T. tomentosa*, are severely affected by herbivores such as gall flies, defoliators, stem borers and termites. The use of chemical measures for pest management is limited due to the safety concerns associated with tasar silkworms. As a sustainable alternative, biological control could be a prominent solution, as it is an ecofriendly strategy mainly depends on predators, parasites, and pathogens to manage pests. While the application of entomopathogens remains limited, the use of predators, parasitoids and hyperparasitoids shows considerable potential. This article highlights various natural enemies of tasar silkworm pests and their host plants. Examples include *Aprostocetus* sp. and *Trechnites aligharhensis*, which parasitise gall flies on host plants, and *Theronia karthiki*, a novel hyperparasitoid of *Ichneumon* wasps and a pupal parasitoid of tasar silkworms. Additionally, other natural enemies targeting various pests are also discussed.

Keywords: biological control; hyperparasitoids; natural enemies; pests; tasar sericulture





Session VI

**Ecological Chemistry in Biological
Control: Pheromone Synthesis,
Sensors and Nanotechnology**



Smart optical sensors for sustainable pest management in agriculture

Nilanjan Dey

Department of Chemistry, BITS Pilani, Hyderabad, India

Correspondence: nilanjan@hyderabad.bits-pilani.ac.in

Optical sensing of nuclear polyhedrosis viruses (NPVs) is essential for efficient pest management in Indian agriculture, where pests like *Helicoverpa armigera* and *Spodoptera litura* pose significant threats to crop yields. Rapid and precise detection enables the timely application of biopesticides, reducing dependence on chemical pesticides, improving crop quality, and supporting sustainable farming practices. To address these challenges, three innovative luminescent probes have been developed for NPV detection in crops. A carbazole-based amphiphilic probe was designed to identify *Helicoverpa armigera* NPV (HaNPV) through fluorescence colour changes from blue to cyan at pH 7.4, with a detection limit of $\sim 10^3$ POBs/mL. Reusable paper strips allow cost-effective, on-field detection and differentiation of fresh versus aged pesticide solutions. Similarly, a ruthenium (II) polypyridyl complex enables ratiometric detection of *Spodoptera litura* NPV (SLNPV) with a luminescence shift from red to blue, achieving a detection limit of 5.6×10^3 POBs/mL via electrostatic interaction with the negatively charged amino acid residues of SLNPV. Finally, a pyrene-based chromogenic probe was developed for quantitative analysis of *Spilosoma obliqua* NPV (SpobNPV) in aqueous medium through imidazole-mediated ester hydrolysis, with a detection limit of 2.305×10^3 OBs/mL. These advancements in NPV detection offer practical, efficient, and sustainable solutions to minimise crop losses and ensure better pest management in Indian agriculture.

Keywords: *Helicoverpa armigera*; luminescent probes; nuclear polyhedrosis viruses; *Spilosoma obliqua*; *Spodoptera litura*





Mating disruption trials of brinjal fruit and shoot borer in Bangladesh

Rangaswamy Muniappan^{1*}, Madhab Chandra Das², Hedyet Ullah²,
Md. Masudur Rahman², Markandeya Gorantla³ and Shahela Alam⁴

¹CIREC, Virginia Tech, Blacksburg, USA

²IPM Activity, Virginia Tech, Bangladesh

³ATGC, ATGC Biotech, Genome Valley, Hyderabad, India

⁴Dhaka Commerce College, Mirpur, Dhaka, Bangladesh

*Correspondence: rmuni@vt.edu

Brinjal fruit and shoot borer (BFSB), *Leucinodes orbonalis* (Lepidoptera: Crambidae) is one of the destructive pests of eggplant in Bangladesh and in South and Southeast Asia. Farmers in Bangladesh routinely spray broad spectrum of insecticides two to three times a week to combat this pest, and despite of it, 30–60% of yield loss is encountered. Also, it leads to pesticide resistance, higher pesticide residues on fruits, outbreaks of secondary pests and adverse impact on non-target species. Ultimately, the cost of insecticide treatments accounts for a substantial portion of the total cost of cultivation of brinjal. While the country has approved the development of *Bt* brinjal to resist BFSB — only four winter season varieties were produced with genetically modified constructs which are not commonly cultivated all over the country. Additionally, there is a preference for a particular variety of brinjal in each region, resulting in several non-*Bt* varieties cultivated around the country. Recognising the need to address BFSB menace by adopting a safe and effective method, IPM Activity, a project funded by USAID Mission in Bangladesh conducted three mating-disruption trials in farmers' fields in Magura, Mymensingh and Satkhira districts of Bangladesh. We present the findings, lessons learned and recommendations from these trials.

Keywords: brinjal; eggplant; *Leucinodes orbonalis*; mating-disruption trials





**Ecofriendly pest management: innovations in pheromone formulations,
nanosensors and nanotechnology for sustainable agriculture**

Deepa Bhagat

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

Correspondence: deepa.bhagat@icar.gov.in

The integration of ecological chemistry, pheromone technologies and nanotechnology offers promising solutions for sustainable pest management by minimising the adverse environmental and health impacts of synthetic pesticides. Recent advancements include nanogel-loaded slow-release pheromone formulations that improve the stability and longevity of semiochemicals in field conditions, providing effective and targeted pest control. Surface-functionalised nanosensors capable of early detection of key pests such as *Helicoverpa armigera*, *Spodoptera litura* and *Bactrocera dorsalis* have demonstrated high sensitivity and reliability, enabling data-driven pest management. National efforts led by ICAR–NBAIR, IISc (Bengaluru) and IARI have contributed to the development of pheromone nanogels and MEMS-enabled nanosensors. Internationally, companies such as *Provivi* and *ISCA Technologies* are driving commercial adoption with products like *ProviviFAW* and *SPLAT®*, which have shown field efficacy in large-scale pest management. European firms like *NanoBioMatters* and *Agrosavfe* are advancing nanoencapsulation for controlled agrochemical release. These technologies signify a paradigm shift towards eco-friendly pest management, with future directions involving multi-target formulations, hybrid nanosensors, and IoT-enabled smart agricultural systems. Collaborative efforts among researchers, agro-tech companies, and policymakers will be key in scaling these innovations for global adoption.

Keywords: ecological chemistry; MEMS sensors; nanosensors; pheromone nanogels; sustainable pest management





Slow-release pheromone formulations for the management of insect pests in rice

Padmavathi Chintalapati*, M.M. Azam, D. Sanjeeva Rao, Chinna Babu Naik and R.M. Sundaram

ICAR–Indian Institute of Rice Research, Hyderabad, India

*Correspondence: chintalapatipadmavathi68@gmail.com

Rice (*Oryza sativa* L.) is one of the world's most important crops, providing a staple food for nearly half of the global population. More than 100 species of insects can attack rice crop, and 20 of them can cause serious economic loss. Yellow stem borer (YSB), *Scirpophaga incertulas* Walker is the dominant species in India and causes a yield loss of 38 to 80% in late-transplanted rice crops. Rice Leaf folder (RLF), *Cnaphalocrocis medinalis* Guenee has now drawn attention and damage may sometimes go as high as 60%. Among various alternatives to toxic chemical pesticides, pheromones offer the best solution. However, the present technology remains pheromonically active only for two-three weeks. Keeping this in view, we developed a sustained release system, which includes a pheromone formulation comprising a biodegradable base matrix and a blend of pheromones of a specific insect in a natural ratio. The sustainable release behaviour of pheromone components was established by GC analysis and was found effective for more than 16 weeks. Field evaluation of pheromone formulations of YSB and RLF for three years revealed that adults' mean cumulative catches were higher in traps with slow-release formulation compared to traps with the normal formulation. The system of the present invention can be utilised in rice fields for monitoring and mass trapping YSB and RLF. There was a 53.32% reduction in white ear damage caused by YSB compared to control (farmers' practices). There was a yield advantage of 2.13 t/h. One spray was reduced due to the placement of pheromone traps for mass trapping.

Keywords: behaviour; mass trapping; monitoring; pheromones; sustained release





Role of brown planthopper-induced rice volatiles on behavioural response of wolf spider

Vinod K. Padala^{1,2}, Suresh M. Nebapure¹, S. Rajna¹ and Subash Chander^{3*}

¹ICAR–Indian Agricultural Research Institute, New Delhi, India

²ICAR–National Research Centre for Makhana, Darbhanga, India

³ICAR–National Research Institute for Integrated Pest Management, New Delhi, India

*Correspondence: schanderthakur@gmail.com

Brown planthopper (BPH), *Nilaparvata lugens* is a destructive insect pest causing severe yield loss in rice crop. Spiders play a vital role as natural predators of BPH. We investigated the response of wolf spiders to different odour sources from rice plants subjected to various treatments, viz. undamaged plants, mechanically damaged plants and plants damaged by nymphs, males and females of BPH for different durations (24 h, 48 h and 72 h) using Y-olfactometer. Spider response showed a significant preference for olfactometer arms treated with volatiles from plants damaged by BPH over undamaged plants and mechanically damaged plants. Spider response was non-significant between undamaged and mechanically damaged plant. Notably, the highest per cent response was observed towards plants damaged by females for 48 h (85.19%) and nymphs for 72 h (84.00%) than undamaged plant and the highest per cent response was observed towards plants damaged by nymphs for 72 h (86.36%) and females for 72 h (83.33%) than mechanically damaged plants. So, spiders can differentiate BPH induced HIPVs from undamaged and mechanically damaged plants and they are more attracted to plants damaged by BPH for 48 h, 72 h duration. No significant difference of spider response was observed among the BPH damage with equal duration. However, spider showed more preference towards the volatiles of 48 h and 72 h of damage by nymph, male and female over to 24 h damage, but between the 48 h and 72 h of damage was non-significant across the treatments except between 48 h damage by nymph and 72 h damage by male and female. The findings indicate that herbivore-induced rice volatiles can attract wolf spider and enhance their predatory abilities, offering a potential method for improved rice pest control.

Keywords: bioassay; brown planthopper; HIPVs; predator; Y-olfactometer





Use of essential oil repellents and pheromone trap for the management of rhinoceros beetle in endemic area — a push–pull strategy

P.S. Prathibha^{1*}, K. Subaharan², Jilu V. Sajan¹ and A. Josephraj Kumar¹

¹ICAR–Central Plantation Crops Research Institute, Kasaragod, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: prathibha.ps@icar

Rhinoceros beetle is a devastation pest in coconut seedlings as it bore through collar region and cause dead heart. Though the infestation in adult palms is not fatal, it predisposes the incidence of red palm weevil and bud rot disease. So prophylactic palm protection could be the chief management strategy. A set of essential oils were evaluated for its repellency against it under *in vitro* condition. In 'y' tube olfactometer bioassay, the maximum repellency recorded with citriodora oil where, 28% of beetles oriented towards treatment arm and remaining 72% moved towards control arm. However, when the other essential oils placed in treatment arm 60–70% of weevils moved towards the odour arm. Repellent property of citriodora was confirmed by wind tunnel assay in which only 13.33% beetles exhibited up wind flight response and 23.33% beetles moved up to mid point and then exhibited downwind flight response. 63.33% beetles remained at the point of release itself in the wind tunnel. GC-MS analysis of citriodora oil indicated presence of citronellal (79.66%) as the major component, which retained at 20.056 min. Gel based slow released matrix was developed by impregnating citriodora oil (2.5%) in calcium alginate beads. Its field efficacy on prophylactic protection was evaluated by leaf axil placement at 6 weeks interval (June–Nov) on 1.5 years old coconut seedlings and a pheromone trap outside the garden at Bayar in Kasaragod district. It indicated a reduction of spindle leaf damage from 50% to 8.8% over a period of 18 weeks. The total number of beetle captured was 321, with an average of 53.5±20.9 beetles/month.

Keywords: calcium alginate beads; citriodora; coconut; rhinoceros beetle



**Innovative climate-resilient liquid lure and trapping system: enhancing fruit fly
(*Bactrocera* spp.) management as a biocontrol component**

M.A. Rashmi¹, Abraham Verghese^{1*}, K.J. David² and B. Gundappa²

¹Rashvee International Phytosanitary Research and Services, Bengaluru, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: rashmigowda.ento@gmail.com

Conventional fruit fly traps faced significant drawbacks in changing climatic conditions. Earlier traps using malathion or dichlorvos were banned and has regulatory issues with newer chemicals. Additionally, the lures used in these traps evaporated at high temperatures, high winds and diluted in heavy rains creating an urgent need for a climate-resilient lure and trapping system. A novel trap was developed, featuring both liquid lure and trap cap designed to withstand varying climatic conditions funded by BIRAC, DBT. The climate-resilient cap for the trap incorporates parachute technology with stilts to reduce air drag, a skirt rain-hood to guard against heavy rain, and liquid lures with anti-evaporants and gums. These lures when tested in field trials showed stability and excellent efficiency under high temperatures, rainfall, and wind velocities and effective in the field for over 60 days. These liquid lure traps have proven superior to commercial traps in attracting diverse *Bactrocera* species and cost 70% less than commercially available options, making them economical for farmers. Over 5,000 traps were distributed to farmers and tested in different agro-climatic regions. Rashvee herbal liquid soap adjuvant (RHLSA) with eco-friendly neem showed excellent repellent, deterrent, and antifeedant properties. RHLSA is rain fast and retains neem molecules on the fruits, deterring females from oviposition by disrupting their ovipositional orientation. Farmers expressed high acceptability, efficacy and user-friendliness of these traps in diverse crops. The above two Rashvee products have been approved by DBT, BIRAC and validated by ICAR–NBAIR and UAS, Bengaluru, in 2024. Both these products showed resilience to different erratic climatic phases in southern India in experimental fields.

Keywords: *Bactrocera* spp.; biocontrol; climate-resilience; fruit fly trap





Evaluation of suitable traps, dispenser and sex pheromone against the stored grain pest *Sitotroga cerealella* (Lepidoptera: Gelechiidae)

G. Sainath, T. Nagaraju, B. Kariyanna*, B.V. Subba Reddy and B. Nagendra Babu

Fluoro-Agrochemicals, CSIR–Indian Institute of Chemical Technology, Hyderabad, India

*Correspondence: kariyanna@iict.res.in

The Angoumois grain moth, *Sitotroga cerealella* (Olivier), is a highly destructive stored grain pest, causing severe grain loss through larval feeding and contamination. Pheromone traps offer an ecofriendly management solution by attracting and disrupting pests life cycles, reducing the need for chemical pesticides while maintaining grain quality and promoting sustainable storage practices. A study at the National Seed Corporation (NSC) in Warangal evaluated the efficacy of sleeve and multi-holed cup traps, doses of sex pheromone compounds (3 mg and 5 mg of sex pheromone (Z,E-7,11-hexadecadien-1-ylacetate) and dispensers (silica, rubber and pellets) against *S. cerealella*. The silica and rubber dispenser loaded with 5 mg sex pheromone installed in sleeve traps displayed mean moth captures of 258.88 and 241.68, followed by 103.76 in tablet formulation during the first phase. Similarly, in second phase the sleeve traps displayed mean moth catches of 201.78 and 198.22 in silica and rubber septa followed by tablet dispenser (110.12). On the other hand, the multi-holed cup traps with 5mg of pheromone loaded in silica, rubber and pellets dispenser displayed moth catches of 77.16, 46.04 and 17.67 in first phase and 54.31, 32.61 and 10.35 in second phase, respectively. In all trap types and dispensers loaded with 3mg of sex pheromones displayed significantly lower moth captures. The study concluded that the sleeve traps containing silica dispenser loaded with 5 mg sex pheromone displayed more number of moths, *S.cerealella* captures.

Keywords: Angoumois grain moth; dispenser; pheromone; *Sitotroga cerealella*; traps





Carvone-rich *Mentha spicata* essential oil: a natural alternative to synthetic fumigants against rice weevil, *Sitophilus oryzae*

M. Shanthi^{1*}, K. Aarthi², G. Srinivasan², S. Vellaikumar³, G. Hemalatha⁴ and K. Naveena¹

¹Centre for Plant Protection Studies, Tamil Nadu Agricultural University, Coimbatore, India

²Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai, India

³Department of Plant Biotechnology, Tamil Nadu Agricultural University, Coimbatore, India

⁴Community Science College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, India

*Correspondence: mshanthiento@tnau.ac.in

Sitophilus oryzae (L.) (Curculionidae: Coleoptera), commonly known as the rice weevil, is a small snout-bearing insect and a significant pest of stored grains. Botanical pesticides offer a promising alternative to synthetic fumigants, associated with pest resurgence, pesticide resistance, and environmental hazards. Plant vital compounds have a wide range of biological activity against pests, acting as contact insecticides, oviposition deterrents, antifeedants, repellents, fumigants, disrupting behaviour and growth rate. This study evaluated the toxicity of essential oils from various mint species, including spearmint (*Mentha spicata*), peppermint (*Mentha piperita*), corn mint (*Mentha arvensis*), and bergamot mint (*Mentha citrata*) at different concentrations against the rice weevil. All the mint oils were found to be efficacious in minimising the population of rice weevil, among which, *M. spicata* oil exhibited the highest contact toxicity (LC_{50} : 6.65 nL/cm²), repellence (RC_{50} : 5.90 nL/cm²), and fumigant toxicity (LC_{50} : 13.68 nL/cm³). Gas Chromatography-Mass Spectrometry (GC-MS/MS) analysis identified carvone (63.35%) as the major bioactive compound in *M. spicata* essential oil, further confirmed by High-Performance Liquid Chromatography (HPLC), which recorded carvone at an area of 1,688.57 mg/L. These findings highlight the potential of *M. spicata* oil for development as a botanical pesticide formulation suitable for application in storage godowns.

Keywords: GC-MS/MS; HPLC; rice weevil; mint oil; storage





Advanced delivery systems for controlled release of fall armyworm (*Spodoptera frugiperda*) pheromone

Kesavan Subaharan^{1*}, M. Eswaramoorthy² and Vinay Kumar¹

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Jawaharlal Nehru Centre for Advanced Scientific Research, Bengaluru, India

*Correspondece: Kesavan.Subaharan@icar.gov.in

The fall armyworm (FAW), *Spodoptera frugiperda*, poses a significant threat to maize worldwide due to its destructive nature. Utilising semiochemicals presents an environmentally friendly strategy for FAW management, especially given its compatibility with natural pest control agents. The female sex pheromone of *S. frugiperda* consists of Z-9-tetradecenyl acetate, Z 11-hexadecenyl acetate, and Z-7-dodecenyl acetate. Currently, pheromones loaded into silicone septa have a high release rate, necessitating frequent replacement of lures and proving costly for farmers. Carbon nanomatrix serves as an innovative dispenser for these volatile signalling molecules, offering controlled release rates over time and space. Characterisation via field scanning electron microscopy (FESEM) and thermal gravity analysis (TGA) confirms the suitability of the carbon nanomatrix for delivering FAW pheromones. Compared to silicone septa, the nanomatrix-loaded pheromones exhibit a more controlled release. The physiological and behavioural response of the male moths to the pheromone released from nanomatrix was ascertained. Field trials employing pheromone-loaded nanomatrix demonstrated significant reductions in pest damage.

Keywords: mass trapping; nanomatrix; *Spodoptera frugiperda*





Biocontrol through scent: the role of odours in parasitoid wasp host selection

Radhika Venkatesan

Indian Institute of Science Education and Research, Kolkata, India

Correspondence: rv@iiserkol.ac.in

Host selection is vital for parasitoid wasps, with odours playing a key role in this process. Parasitoid wasps rely on herbivore-induced plant volatiles as long-range cues to locate hosts. However, these cues alone often do not guarantee successful parasitisation. In this study, we examined how both long- and short-range cues influence the parasitisation preferences of *Bracon brevicornis*, a generalist ectoparasitoid, and *Cotesia vestalis*, a specialist endoparasitoid. Our findings reveal that parasitoids can detect larval body odour at close range, allowing them to identify the most suitable host. This body odour, derived from plant metabolites, varies based on the larval diet. We found that *Plutella xylostella* larvae feeding on *Brassica juncea* plants released isothiocyanates, while larvae feeding on *B. oleracea* emitted sulfides. These odours not only reflect dietary differences but also signal the immune status of the larvae, aiding parasitoids in selecting healthier and more viable hosts. This selection is crucial, as parasitising an unsuitable host negatively impacts the wasp's fitness. Additionally, we investigated whether parasitoids can distinguish between *Bt*-infected and healthy hosts. Our results confirm that parasitoids use olfactory cues to make this distinction, further highlighting the sophistication of their host selection process. Overall, this study emphasises the critical role of plant and larval odours in shaping parasitoid host selection. These insights deepen our understanding of host-parasitoid dynamics and offer potential avenues for developing pest control strategies that support beneficial parasitoids, promoting sustainable agricultural practices.

Keywords: *Bracon brevicornis*; *Cotesia vestalis*; herbivore-induced plant volatiles; *Plutella xylostella*





Biosynthesis and evaluation of *Polygonum hydropipper* based Ag-nanoparticles against *Callosobruchus chinensis* (Coleoptera: Bruchidae)

C.R. Chandana^{1*} and Surajit Kalita²

¹Department of Entomology, University of Agricultural Sciences, Raichur, India

²Department of Entomology, Assam Agricultural University, Jorhat, India

*Correspondence: chandanacr25@gmail.com

The investigation on biosynthesis and toxicity of Silver-Nanoparticles (AgNPs) using aqueous leaf extract of *Polygonum hydropipper* was carried against *Callosobruchus chinensis* (Coleoptera: Bruchidae). The biosynthesis of PhAgNPs was confirmed through physicochemical methods, viz. UV-Vis spectrophotometer, Dynamic Light Scattering (DLS) analysis, Zeta potential analysis, Transmission Electron Micrograph (TEM) and Scanning Electron Micrograph (SEM). The bioefficacy test of PhAgNPs at different concentrations, viz. 100, 150, 200, 250 and 300 ppm and dosages, viz. 0.5, 1.0, 2.5, 5.0 and 7.5 ml/kg seed against *C. chinensis* revealed that the highest mortality (90.00%), the lowest seed damage (0.13%), and the lowest seed weight loss (1.83%) was recorded at 300 ppm concentration and a dosage of 7.5 ml/kg after 14 days of treatment. The lowest LC₅₀ value of 0.392 ml/kg of *C. chinensis* was also recorded at 300 ppm concentration after 14 DAT. It was also evident that green gram seeds infested by *C. chinensis* and treated with AgNPs showed the highest germination (96.67%) and the highest vigour (1434.67) at 200 ppm with a dosage of 0.50ml/kg, along with the highest moisture content (8.93%) at 300 ppm concentration @ 7.5ml/kg of seed. In our present investigation, we confirmed biosynthesised AgNPs from *P. hydropipper* and their suitability in managing *C. chinensis* ensuring the qualitative parameters of green gram seeds. Therefore, it could be concluded that the use of PhAgNPs could be a promising strategy of storage insect pest management in years to come.

Keywords: bioefficacy; biosynthesis; *Callosobruchus chinensis*; *Polygonum hydropipper*





Chemical ecology of rice — *Meloidogyne graminicola* interaction: insights from root exudates and metabolite profiling

Suvasri Dutta^{1*}, Abhishek Mukherjee¹ and Totan Adak²

¹Agriculture and Ecological Research unit, Indian Statistical Institute, Kolkata, India

²Crop Protection Division, ICAR–National Rice Research Institute, Cuttack, India

*Correspondence: suvasri1995@gmail.com

Chemical signals play a crucial role in plant-nematode interactions. Manipulation of the semiochemicals modulating this interaction may enable the development of novel biological control strategies for nematode management. The rice root-knot nematode, *Meloidogyne graminicola*, is a major plant-parasitic nematode affecting rice, causing significant yield and economic losses in rice-growing countries, particularly in India. Available control methods for this nematode, including soil flooding and nematicide applications, are of increasingly limited utility. In our study, two rice cultivars, Pusa Basmati 1121 (PB1121, nematode-susceptible) and Kalo Bhutia 213 (KB213, nematode-resistant), were used to elucidate the role of root exudate chemical constituents influencing rice-*M. graminicola* interactions. Initial olfactometer studies confirmed that *M. graminicola* was significantly more attracted to PB1121 compared to KB213. Attraction assays with intact roots under choice and no-choice conditions corroborated these observations. Root exudates were fractionated, and bioactive secondary metabolites and volatile organic compounds (VOCs) were analysed using GC-MS. Compounds such as diethyl phthalate, lactic acid, and 1-nonanol were identified as modulators of nematode chemotactic behaviour. The identification of these bioactive semiochemicals offers an avenue for developing cost-effective and environmentally sustainable solutions for nematode management in rice cultivation.

Keywords: biological control; chemical ecology; *Meloidogyne graminicola*; root volatiles





**Electrophysiological and behavioural responses of tobacco cutworm,
Spodoptera litura, to sex pheromone and plant volatiles for its management**

**Subrata Goswami^{1,2}, K. Subaharan^{2*}, M. Raghuraman¹, M. Eswaramoorthy³,
Manish Gadekar⁴, Ujjwal Vidyarthi³, T.M. Vinay Kumar², Richa Varshney² and
S. Saravanan^{5,2}**

¹Banaras Hindu University, Varanasi, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

³Jawaharlal Nehru Centre for Advanced Scientific Research, Bengaluru, India

⁴Jawaharlal Nehru Krishi Vishwa Vidyalyaya, Jabalpur, India

⁵Tamil Nadu Agricultural University, Coimbatore, India

*Correspondence: subaharan_70@yahoo.com

Spodoptera litura is a polyphagous and destructive pest inflicting serious damage to around 87 economically important crops. Confronted with the ill effects of chemical pesticides and the incidence of *Bt* resistance, environmentally benign alternatives seem to be promising in its management. An experiment was conducted to identify behaviourally active phytochemicals for adult males of *S. litura*. The attractive VOCs were further tested for their synergistic effects, if any, with *S. litura* sex pheromone. Esters and phenylpropanoids blend with synthetic sex pheromone elicited elevated antennal response as compared to pheromone alone thereby providing the theoretical basis for combining pheromones with synergistic HPVs for the development of more efficient and competitive lures for *S. litura*. Blends of these two VOCs along with sex pheromone were tested for their efficacy in trapping moths in field. Mesoporous silica nanomatrix was used as the dispensing medium. Thermogravimetric analysis showed that the nanomatrix dissipated the volatiles slower than the commercial rubber septa and that too in behaviourally relevant aerial concentration for around two months as confirmed by the field experiments. The trap catches indicated that both the ester and phenylpropanoid significantly enhanced the attraction of male *S. litura* moths to the sex pheromone. Leveraging SBA-15 as a controlled-release dispenser to deliver the synergistic blend of sex pheromone and HPVs could serve as an efficient as well as sustainable management option to combat this notorious pest.

Keywords: controlled-release dispenser; plant volatiles; sex pheromone; *Spodoptera litura*





Electrophysiological responses of rice leaf folder, *Cnaphalocrocis medinalis*, to green leaf volatiles: implications for pest management

K. Lokesh*, Ch. Padmavathi, Chitra Shanker, M.B. Kalyani and D. Sanjeeva Rao

ICAR–Indian Institute of Rice Research, Hyderabad, India

**Correspondence: lokeshphd2002@gmail.com*

Green leaf volatiles (GLVs), emitted by plants in response to herbivory or mechanical damage, play a crucial role in mediating plant-insect interactions. The rice leaf folder (RLF), *Cnaphalocrocis medinalis* Guenee is now drawing attention to a greater extent and damage may sometimes go as high as 60%. This study investigates the electrophysiological responses of *C. medinalis* to 15 plant volatiles, including GLVs, at five doses across three physiological stages of both male and female insects using electroantennography (EAG). Results revealed significant variations in antennal sensitivity based on the compound, dose, sex, and physiological stage. Antennal responses followed a distinct stage-dependent pattern, peaking at 3-day-old insects and decreasing in 1 and 5 day old insects, suggesting a physiological modulation of olfactory perception. Males exhibited higher responsiveness to certain GLVs at specific doses compared to females, while specific GLVs elicited strong electrophysiological responses, highlighting their role as key olfactory activators. Building on these findings, GLV blends were formulated and tested for synergistic effects with sex pheromone. The best-performing blend was combined with the synthetic sex pheromone of *C. medinalis* to evaluate potential interactions. Behavioural assays, including an olfactometer, wind tunnel, and small-scale field bioassays, demonstrated that the GLV-pheromone combination significantly enhanced attraction, influencing insect orientation and landing behaviour. This research forms a foundation for further behavioural and molecular studies aimed at leveraging GLVs to manipulate pest behaviour in rice ecosystems effectively for devising semiochemical-based pest management strategies.

Keywords: behavioural assays; electroantennography; green leaf volatiles; olfactory response; semiochemical based pest management





Biofumigation: a safe way to manage red flour beetle in storage for ensuring food safety and biosecurity

**Rabbani Sab¹, Sushila Nadagouda^{1*}, A. Prabhuraj¹, Pramod Katti¹ and
Udaykumar Nidoni²**

¹Department of Agricultural Entomology, University of Agricultural Sciences, Raichur, India

²Department of Processing and Food Engineering, University of Agricultural Sciences, Raichur, India

*Correspondence: sushilanadagouda@gmail.com

Attempts have been made in recent years to reduce the use of synthetic pesticides and seek alternative and innovative methods for pest control in storage condition. Among different control measures, fumigation is still one of the most effective methods for the prevention of stored product losses from insect pests. The present investigation was done to study the role of bio fumigants in storage condition. In the present study, five important biofumigant plants namely *Lantana camara*, *Eucalyptus globulus*, *Ailanthus excelsa*, *Acorus calamus* and *Brassica juncea* were selected, the essential oil of five biofumigant plants was obtained by Supercritical fluid extraction method and analysed by GC-MS. Supercritical fluid extracts of bio fumigants were screened against Red flour beetle, *Tribolium castaneum* (Herbst) (Tenebrionidae) by using filter paper bioassay method. The results revealed that extracts of *L. camara* (0.5%) and *A. excelsa* (1.5%) was found to be best in causing maximum mortality against red flour beetle.

Keywords: *Ailanthus excelsa*; *Lantana camara*; safe extracts; *Tribolium castaneum*





Understanding the role of surface volatile compounds in modulating *Maruca vitrata* (Lepidoptera: Crambidae) oviposition behaviour on pigeon pea and its crop wild relatives

Dhanyakumar Onkarappa^{1,2*}, M. Murugan², J. Jaba¹ and K. Yogendra¹

¹International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, India

²Department of Entomology, Tamil Nadu Agricultural University, Coimbatore, India

*Correspondence: dhanyakumarento@gmail.com

The spotted pod borer, *Maruca vitrata*, is an emerging insect pest in legumes, which also feeds significantly on flowers and immature pods of pigeon pea (*Cajanus cajan*) which causes yield losses. Crop wild relatives (CWR) of pigeon pea, often more resilient due to their genetic diversity and evolved defense and antixenosis traits, including the production of volatile organic compounds that can influence oviposition behaviour. This study investigates the ovipositional behaviour *M. vitrata* on *C. cajan* lines of ICPL-87, ICP-332WR and its crop wild relatives from different gene pool level including *C. platycarpus* ICP-15669, *C. scarabaeoides* ICP-15712 and ICP-15716, *Rhynchosia densiflora* ICP-15826, *Rhynchosia suaveolens* ICP-15865, in modulating the ovipositional behaviour of *M. vitrata* in free-choice and no-choice condition. Among these, in free-choice condition, the highest number of eggs were noticed on ICPL-87 (203.67±31.85), ICPL-332WR (84.00±8.33) and the lowest was observed on ICP-15716 (27.67±14.15). In no-choice condition, the highest number of eggs on ICPL-87(221.00±14.19) and the lowest on ICP-15716 (52.67±8.45) and ICP-15867 (47.00±5.86). Moreover, using gas chromatography-mass spectrometry (GC-MS), we identified total surface volatiles emitted from the leaves and flowers of pigeon pea and its CWR were compared with total number of eggs laid on each genotype. These findings provide insights into the chemical cues for host plant selection and highlight the potential of wild relatives in breeding programmes aimed at enhancing pest resistance by reducing egg load on pigeon pea.

Keywords: crop wild relatives; *Maruca vitrata*; pigeonpea; surface volatile compounds





Nano-enabled effective approaches for diamondback moth control in cabbage cultivation

Pradeep Kumar^{1*}, S.R. Babu¹, Kinjal Mondal² and B.S. Tiwari³

¹Department of Entomology, Maharana Pratap University of Agriculture and Technology, Udaipur, India

²Department of Molecular Biology and Biotechnology, Maharana Pratap University of Agriculture and Technology, Udaipur, India

³Department of Entomology, Banda University of Agriculture and Technology, Banda, India

*Correspondence: rathourpradeepkumar1996@gmail.com

Leafy vegetables, particularly cabbage, are a staple of the human diet. They are high in minerals, dietary fiber, phytochemicals, and vitamins. Growers of cabbage incur significant losses annually as a result of their crop's vulnerability to insect infestation in the field. The diamondback moth (*Plutella xylostella*), among other contenders, is a common species in tropical and subtropical areas of several Asian nations. *Plutella xylostella* can cause yield losses ranging from 50% to 100%, dependent on the season and the extent of pest infestation. Conventional pesticides like tolfepryad 15%EC, emamectin benzoate 5%SG, flucamethamide 10%EC, difenthiuron 50% WP, etc. are readily accessible on the market to stop DBM infestation. However, contemporary studies indicate that DBM has developed pesticide resistance, and that continued insecticide usage, such as synthetic pyrethroids, demands the integration of cutting-edge techniques with traditional practices rather than entire dependence on conventional chemistry. In the long run, the use of nano-enabled functional pesticides is expected to be effective in DBM control. Nano pesticides are a new technical advancement in pesticide application that might provide a variety of benefits such as enhanced efficacy, durability, and a decrease in the amount of active chemicals required. NMs when applied on leaves and stem surface, get absorbed into the cuticle of the insects by physisorption and cause death of insects purely by physical means. Aside from the potential size benefits, they have no or little negative impacts on non-target species. As a result, nano pesticides can provide environmentally friendly and effective solutions for managing DBM infestation in cabbage agriculture. However, before they are widely adopted, NMs must undergo considerable testing.

Keywords: cabbage; nano pesticides; *Plutella xylostella*; synthetic pyrethroids





Bisexual attractants for managing brinjal shoot and fruit borer (*Leucinodes orbonalis* Guenee) (Lepidoptera: Crambidae) using sex pheromones and plant volatiles

S. Saravanan^{1,2}, Kesavan Subaharan^{2*}, Pagalahalli Sankaran Shanmugam^{1*}, Marimuthu Murugan¹, T.M. Vinay Kumar², C. Praveenkumar^{1,2}, Subrata Goswami^{2,4}, Ujjwal Vidyarthi³ and M. Eswaramoorthy³

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

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

³Jawaharlal Nehru Centre for Advanced Scientific Research, Bengaluru, India

⁴Department of Entomology and Agricultural Zoology, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India

*Correspondence: Kesavan.Subaharan@icar.gov.in, shanmugam.ps@tnau.ac.in

Leucinodes orbonalis Guenee (Lepidoptera: Crambidae) is a pest of concern on brinjal. Its cryptic nature complicates targeted pest management. A study was taken up to assess the electrophysiological and behavioural responses of *L. orbonalis* to different host plant volatiles and synthetic sex pheromones. Electrophysiological response employing the electroantennogram (EAG) revealed that the tested volatile compounds triggered antennal responses in both male and female moths. Mated females exhibited greater sensitivity to decanal, 1-heptanol, nonanal, octanal, and geraniol. Both sexes, mated and unmated, exhibited a strong response to (Z)-3-hexen-1-ol. In Y-tube olfactometer assays, male moths showed significant attraction to the sex pheromone, while both sexes were attracted to octanal and (Z)-3-hexen-1-ol, especially among mated individuals. A controlled-release nano matrix has been developed to deliver pheromones and host plant volatiles, enabling better spatiotemporal release. This composite triggers a strong electrical response in insect antennae, making it suitable for field evaluation. In field trials, traps with geraniol alone catches trapped higher number of moths, in addition to this octanal, and (Z)-3-hexen-1-ol when used in tandem with sex pheromones improved the number of adults trapped. The potential employing the pheromone, kairomone blend to be employed in management of BSFB will be discussed.

Keywords: brinjal; host plant volatiles; *Leucinodes orbonalis*; nano matrix; sex pheromones





Green synthesis of Ag-doped ZnO nanoparticles and prospects for novel application to enhance the shelf life of fruits and vegetables

U.S. Senapati^{1*}, T. Kataki² and H. Kalita²

¹Department of Physics, Handique Girls' College, Guwahati, India

²Advanced Level Institutional Biotech Hub, Handique Girls' College, Guwahati, India

*Correspondence: udaysankargu@gmail.com

In light of the shifting global environment, ensuring food and nutritional security of the world's growing population is a difficult and demanding task. Hence, cutting-edge technologies like biotechnology and nanotechnology are thought to be the ideal ways to handle this difficult task by boosting production and lowering post-harvest losses. ZnO is a promising antimicrobial agent due to its low cytotoxicity and Ag has been considered as the most favourable material for doping in order to increase the efficacy of ZnO due to its high stability. In the present work, Ag-doped ZnO nanoparticles was synthesised by a green synthesis route using *Datura metel* L. leaf extract. The Ag-doped ZnO nanoparticles were characterised using XRD, FESEM, EDAX, TEM, HRTEM, and FTIR. With an increase in extract volume, the XRD analysis revealed that the crystallite size of Ag-doped ZnO nanoparticles increased from 22 to 28 nm. The morphology of Ag-doped ZnO nanoparticles changed as the extract volume increased, as demonstrated by TEM and FESEM results. The biomolecules of *Datura metel* L. leaf extract functioned as reducing and capping agents during the green production of Ag doped ZnO nanoparticles, as demonstrated by FTIR analysis. Ag-doped ZnO nanoparticles showed outstanding antibacterial activity against both Gram-positive and Gram-negative bacteria that were isolated from locally available fruits and vegetables. The synthesised Ag-doped ZnO nanoparticles exhibited minimal cytotoxic impact on normal kidney cells HEK-293. Additionally, the green synthesised Ag-doped ZnO nanoparticles can be an effective preservative for improving fruits and vegetables shelf life and reducing food-borne illness.

Keywords: Ag-ZnO nanoparticles; antibacterial activity; cytotoxicity; shelf life; vegetables





**A controlled release nano dispenser to deliver the sex pheromone for the
management of *Plutella xylostella***

**T.M. Vinay Kumar^{1,2*}, K. Subaharan¹, R. Vani², M. Sowmya¹, S. Saravanan¹,
Subrata Goswami¹, C. Praveenkumar¹, M. Eswaramoorthy³ and Abhishek Garg³**

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Department of Zoology, Jain (Deemed-to-be University), Bengaluru, India

³Nanomaterials and Catalysis Laboratory, Jawaharlal Nehru Centre for Advanced Scientific, Research,
Bengaluru, India

*Correspondence: vinicool143@gmail.com

Considering the ease of adoption and availability, chemical insecticides are widely used for managing the diamondback moth, *Plutella xylostella* which is considered as the most destructive oligophagous insect pest of cruciferous crops. Exploiting the ethology of the pest is a clean and green method. The synthetic sex pheromone lures are available commercially, but the challenge in the use of pheromone technology is the volatile pheromone molecules loaded into a rubber/ silicone septa dispenser has a high release rate and warrants frequent replacement. This adds to the cost of labour and chemistry. Nanoporous materials offer a novel solution, providing a controlled release of pheromone to extend lure longevity. Dispensers made from mesoporous silica (SBA-15), with ordered pore channels, were developed for loading pheromone. Characterisation techniques, such as field scanning electron microscopy (FESEM) and X-ray diffraction (XRD), confirmed the nano matrix's pore structure. When loaded into the nano matrix, the pheromone showed delayed dissipation, as confirmed by Thermo gravimetric analysis (TGA), and Fourier transform infrared (FT-IR) measurements verified pheromone entrapment within the nano matrix. This nano matrix system provided a controlled pheromone release, resulting in a strong electrophysiological response from male moth antennae and a significant increase in insect capture in field tests compared to rubber septa. Additionally, nano matrix lures lasted 75–90 days, significantly longer than the traditional rubber septa, which required replacement within 20–30 days. Thus, nano matrix dispensers represent a cost-effective, sustainable advancement in managing *P. xylostella* infestations.

Keywords: mesoporous silica; nano matrix; pheromone; *Plutella xylostella*





**Synthesis and efficacy of chitosan nanoparticles encapsulating
Metarhizium anisopliae and *Beauveria bassiana* as biocontrol agents against the
banana aphid, *Pentalonia nigronervosa* Coquerel**

Ranjini Bhagwandas¹, Aiswarya Asokan¹, Suvetha Vasan¹ and Velavan Viswakethu^{2*}

¹Department of Biotechnology, School of Life-Science, Nehru Arts and Science College,
Bharathiar University, Coimbatore, India

²Department of Biotechnology, Bishop Heber College, Bharathidasan University, Tiruchirappalli, India

*Correspondence: velavan.sv@gmail.com

Pentalonia nigronervosa (Hemiptera: Aphididae) is an invasive pest originating from Belize. It serves as a vector for plant viruses such as BBMC and BBTv, making it one of the serious threats to banana. The aphid feeds on the phloem of banana plants, causing significant economic damage, primarily due to its role as vector for the banana bunchy top virus. In this study, we synthesise and characterised chitosan-nanoparticles incorporating the *M. anisopliae* and *B. bassiana*. Chitosan nanoparticles are being developed as next-generation green pest management solutions. Microbial-insect interactions can lead to the development of new chitosan nanoparticles, which were characterised using various techniques including UV-Vis spectroscopy, FTIR, SEM, and XRD analysis to confirm their structural properties. GC-MS analysis of VOCs for further confirmation by interactions between the insect and fungal pathogens. The results showed that, chitosan nanoparticles achieved significantly reduced the population rate in banana aphid for laboratory conditions. Encapsulation of EPF at various concentration showed high effective against aphid populations. The newly developed chitosan nanoparticles formulation exhibits potential biocontrol agents for banana aphids under laboratory conditions. These results suggested that chitosan nanoparticles incorporating *M. anisopliae* and *B. bassiana* could serve as effective biocontrol agents with potential application for nanoformulations. Furthermore, nano-formulations could be integrated into pest management programs for controlling *P. nigronervosa*.

Keywords: *Beauveria bassiana*; chitosan nanoparticles; *Metarhizium anisopliae*; *Pentalonia nigronervosa*





Session VII

Climate-Resilient Biocontrol Technologies



Climate shifts and biological control: balancing risks and opportunities

Ramasamy Srinivasan

World Vegetable Center, Tainan, Taiwan

Correspondence: srini.ramasamy@worldveg.org

Climate change profoundly affects agriculture, particularly by influencing crop productivity, the dynamics of pests and diseases, and the beneficial biodiversity within crop production systems. The ongoing and projected climate change impacts — such as elevated carbon dioxide concentrations (ECC), rising temperatures, drought and erratic rainfall patterns — affect plant growth and development in complex ways, which in turn directly influence pest biology, ecology and interactions with higher trophic levels, including biocontrol agents. Furthermore, these abiotic factors can independently affect the biology and ecology of both pests and their natural enemies. For example, climate change is expected to increase the population densities of *Helicoverpa armigera* and *Maruca vitrata* while facilitating their range expansion into temperate regions. Similarly, the South American tomato pinworm (*Phthorimaea absoluta*) may experience adverse impacts near the equator but positive effects in higher latitudes. Elevated carbon dioxide levels enhance leaf carbohydrate content while reducing nitrogen and protein levels, weakening plant defence mechanisms against insect pests by minimising the accumulation of defence-related hormones such as jasmonic acid. Studies have shown that ECC reduces tomato plant resistance to fruit worm *H. armigera*, with future climate scenarios predicting a 3–12% increase in the number of *H. armigera* generations. Although temperature, rainfall and ECC are critical factors affecting the pest's geographical range, population dynamics and migration patterns, limited research exists on how these factors influence the efficacy of its biocontrol agents. The diamondback moth (*Plutella xylostella*), a major pest of brassica crops worldwide, highlights the importance of biocontrol as an effective management tool, particularly due to its rapid development of resistance to chemical and biological pesticides. Introduced parasitoids such as *Diadegma semiclausum*, *Cotesia vestalis* and *Diadromus collaris* have proven effective, with *D. semiclausum* adapted to highland regions and *C. vestalis* thriving in lowland brassica systems. However, climate change threatens these biocontrol systems. Modelling studies in Australia indicate that rising temperatures may disproportionately reduce the distribution of *D. semiclausum* compared to its host, potentially excluding it from certain agricultural areas. Similarly, studies in East Africa suggest that warming conditions may enhance the reliability of *C. vestalis* in controlling *P. xylostella*. With gradual increases in minimum temperatures projected toward 2055, *C. vestalis* is likely to thrive in regions less favourable to temperature-sensitive *D. semiclausum*. Conversely, in Taiwan, a heat-tolerant strain of *D. semiclausum* collected from Syria has demonstrated adaptation





to lowland brassica production systems with average maximum air temperatures of 34 °C, indicating that natural enemies may also exhibit adaptive responses to changing climates. These findings underscore the complexity of climate change impacts on pests and their natural enemies, highlighting the need for context-specific analyses. Generalising results across regions and systems may lead to erroneous conclusions, and future research should focus on localised interactions to develop effective pest management strategies under changing climatic conditions.

Keywords: abiotic stress; heat-tolerance; insect pests; parasitoids





Climate-resilient biological control strategies for pest management

**S.N. Sushil*, Prabhulinga Tenguri, Omprakash Navik, Richa Varshney,
Gundappa Baradevanal and Kesavan Subaharan**

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

**Correspondence: director.nbair@icar.gov.in*

The increasing impact of changing weather patterns presents significant challenges to agricultural productivity, particularly in insect pest management. According to the FAO, pests (insects, diseases, nematodes, etc.) are responsible for approximately 40% of global crop losses, with climate change projected to exacerbate these losses by an additional 10–25%. Climate change directly influences pest composition, distribution and life cycles, as well as their interactions with natural enemies across agricultural, horticultural and forest ecosystems. Furthermore, the rising frequency of extreme weather events is expected to intensify these challenges. Changes in climatic conditions, combined with evolving land-use patterns, will significantly affect the future distribution and abundance of pests and their biological control agents. Key climatic drivers of these changes include rising temperatures, increased levels of carbon dioxide (CO₂), altered precipitation patterns and other greenhouse gases, all of which impact crops, pests and their natural enemies in various ways. Addressing these complex interactions requires targeted and innovative approaches to pest management. To ensure resilience under changing climatic conditions, pest management strategies must increasingly rely on biological control. Climate-smart pest control strategies provide sustainable solutions by integrating ecological principles and adapting practices to climate change impacts. Effective approaches include the use of climate-resilient natural enemies, such as temperature-tolerant parasitoids, predators, entomopathogenic fungi, bacteria, viruses, entomopathogenic nematodes, etc. Additionally, habitat management techniques, such as creating refuges and diverse cropping systems, play a crucial role in enhancing the survival and efficacy of beneficial organisms while suppressing pest populations. Furthermore, integrating decision-support tools powered by artificial intelligence and climate modelling enables precise timing and application of biological agents. Collaboration among researchers, policymakers and farmers is essential to facilitate knowledge sharing and adaptive management practices. Aligning biological pest control with climate-smart agricultural practices not only mitigates the adverse effects of climate change but also fosters a sustainable and resilient food system for the future.

Keywords: biological control; climate change; elevated CO₂; elevated temperature; greenhouse gases





Unravelling the potential of aphid hunter solitary wasp,
Carinostigmus costatus Krombein (Hymenoptera: Sphecidae),
in the natural regulation of phytophagous aphids

U. Amala*, H.S. Venu, A. Kandan, M. Arvind and T.M. Shivalingaswamy

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

*Correspondence: amala.uday@gmail.com

Aphid hunting wasp, *Carinostigmus costatus*, is a solitary wasp that constructs its nest in dried twigs and wood by chewing out the inner pith in the stem. The wasp hunts for aphids in different host plants for its brood provision in the nest. A study was conducted to study the aphid prey spectrum, prey foraging behaviour and nesting parameters of *C. costatus*. The predatory wasp, *C. costatus* foraged on six different host aphids, viz. *A. odinae* on *Anacardium occidentale*, *Aphis gossypii* on *Hibiscus rosasinensis*, *Aphis craccivora* on *Cajanus cajan* and *Vigna unguiculata*, *Hyadaphis coriandri* on fennel, *Rhopalosiphum maidis* on *Zea mays* and *Aphis nerii* on *Asclepias curassavica*. The wasp chewed up the soft pith of *C. pulcherrima* and constructed cells partitioned with chewed pith fibres. After chewing the pith of twigs, the wasp constructed the cells in 2.00 ± 0.70 days. On an average, the wasp constructed 6.20 ± 1.09 cells per twig and provisioned 17.80 ± 3.89 aphids per cell. The most abundant aphid prey species in the nests constructed by *C. costatus* were *H. coriandri* (28%), *A. craccivora* (24%) followed by *A. gossypii* (20%), *R. maidis* (16%), *A. odinae* (8%) and *A. nerii* (4%). The solitary wasp could be conserved by providing bundles of pithy stems in the crop bunds near the target crop infested with aphids to attract the wasps for nest construction. This study could be a fair lead to conservation biological control for natural regulation of phytophagous aphids.

Keywords: aphids; *Carinostigmus costatus*; natural regulation; solitary wasp





***Trichoderma* spp. for the management of plant health in tribal belt of
North Eastern Region of India**

Pranab Dutta^{1*} and Madhusmita Mahanta²

¹College of Agriculture, Kyrdemkulai, India

²College of Post-Graduate Studies in Agricultural Sciences,
Central Agricultural University (Imphal), Umiam, India

*Correspondence: pranabdutta74@gmail.com

Through a series of studies identified the potential strain of *Trichoderma* spp. for the management of soil-borne plant pathogens like *Rhizoctonia solani*, *Sclerotium rolfsii*, *Sclerotinia sclerotiorum*, *Fusarium solani*, etc. and root knot nematode. During the study competition, mycoparasitism, coiling, lysis, antibiosis, siderophore production, etc. were identified as the main modes of action of the potential biocontrol agent in suppressing the pathogens. We found that *Trichoderma* added directly to rhizosphere or as seed treatment protects plant against different biotic plant problems. The potential strain of *Trichoderma* showed compatible with commonly applied agrochemicals and fertiliser at certain concentration. The strain also showed tolerance to Al and Fe upto 70 ppm and 300 ppm respectively. Small-scale and large-scale field trial at different agro-ecological conditions of North East India also showed superiority of the liquid formulation supplemented with different additives. Through different programme awareness has been created among the farmers, extension personals, corporate sectors managers, SHG members of entire North East India etc. The bioformulation product prepared with native strain of *Trichoderma* has been commercialised through a biopesticides manufacturer, State Government of Nagaland, State Government of Meghalaya who is making available the products among the farmers. The technology may be utilised for development of small scale cottage industry or as a source of entrepreneurship in the region.

Keywords: biocontrol agent; entrepreneurship; mechanism; plant disease





**An improved and cost-effective package of practices for tomato cultivation:
impact on yield and pesticide maximum residue levels**

**Amaresh Hadimani¹, D.V. Pooja¹, Akash Bhargaw¹, H.G. Niranjana¹, S.K. Ghosh* and
Malvika Chaudhary²**

¹Multiplex R&D Laboratory, Bengaluru, India

²CABI, NASC Complex, New Delhi, India

*Correspondence: trainingmbt@multiplexgroup.com

This study by the Field and R&D Unit of Multiplex Private Limited, Bengaluru, evaluated the economic feasibility and efficacy of the Multiplex Package of Practices (POP) in tomato cultivation, focusing on its impact on pesticide residue levels. Conducted during the late rabi and kharif seasons of 2023–2024, the study hypothesised that optimal micro- and macronutrient applications improve crop health, reduce pest pressure, and minimise pesticide use, yielding high-value crops with low maximum residue levels (MRLs). Plots under the Multiplex POP achieved significantly higher yields, averaging 35 t/ha, compared to 15 t/ha in farmer-practiced plots. Pesticide residue analysis of the first harvest revealed cypermethrin (0.023 mg/kg), acetamiprid (0.104 mg/kg), tebuconazole (0.054 mg/kg) and profenofos (0.196 mg/kg) within MRLs specified by FSSAI and EU standards. The second harvest, conducted 50 days later, showed residues below quantification limits (BQL), confirming residue-free produce. The results highlight that Multiplex POP's balanced nutrient supply and judicious use of low-toxicity; short pre-harvest interval pesticides enhance yields and significantly reduce residues. This approach strengthens plant immunity, supports sustainable practices, and aligns with export standards, offering a competitive edge in global trade by ensuring MRL compliance. Mass media campaigns can help improve pesticide knowledge and change pesticide use behaviour among smallholder farmers. Awareness created can lead to increased adoption of safer alternatives to pesticides, including sustainable integrated pest management practices.

Keywords: global trade; maximum residue limit; pesticide risk reduction; pre-harvest interval





**Biocontrol of seed-infesting insect pests during storage:
do parasitoids have a justifiable role?**

Anjitha George^{1*}, R.S. Ramya², P. Ramya¹, G. Vanishree¹,
C.S. Shantharaja¹, Y.R. Aruna¹, S.S. Manjanagouda¹, A. Anandan¹ and Sanjay Kumar¹

¹ICAR–Indian Institute of Seed Science, Regional Station, Bengaluru, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: anjithakitty@gmail.com

Insect contamination in stored seeds is a significant issue for the seed industry. Seed samples, ranging from 0.5 to 1.0 kg, were collected from storage godowns and local farmers in Karnataka. Several parasitoids were identified, including the bethylid wasp *Cephalonomia tarsalis*, the braconid *Habrobracon hebetor*, and the pteromalids *Theocolax elegans* and *Anisopteromalus calandrae*. An egg parasitoid, *Uscana* sp., and the grain itch mite, *Pymotes tritici*, were also observed. The development of *A. calandrae* on late-instar pulse beetle grubs was completed in 18 ± 1.58 days, with developmental stages observed specifically on the fourth and fifth instar of the host. The highest parasitoid efficiency was observed with four mated female parasitoids, where only 53.89% of *Callosobruchus maculatus* adults emerged after a 48-hour release period. We performed molecular docking analysis to understand the molecular recognition mechanisms underlying plant volatile detection by insects. The results obtained using AutoDock Vina revealed strong binding affinities for (*Z*)-3-Hexenol, methyl salicylate, and linalool with both OBPs and ORs, indicated by binding energies lower than -6 kcal/mol. For OBP, the key interacting residues identified were Alanine (125 and 129) and Isoleucine (128). For OR, Threonine (220) and Cysteine (221) played significant roles in the interaction.

Keywords: biological control; molecular docking; olfactory receptors; parasitoid wasps; stored seeds





Evaluation of promising entomopathogenic fungi of ICAR–NBAIR against sucking pests of bhendi

A. Kandan*, E. Ashwini, U. Amala, C. Manjunatha, G. Sivakumar and
S.N. Sushil

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

*Correspondence: a.kandan@icar.gov.in

Aphis gossypii is a worldwide species that is extensively found in temperate, tropical, and subtropical regions of the world. It causes serious yield loss to variety of crops, particularly vegetable crops like bhendi. *Aphis gossypii* was tested against three entomopathogenic fungal strains, including *Lecanicillium fusisporum* NBAIR-VI8, *Metarhizium anisopliae* NBAIR-Ma4, and *Beauveria bassiana* NBAIR-Bb5a, under laboratory and field conditions. At the lowest spore concentration, *L. fusisporum* NBAIR-VI8 killed 50% of the aphids among the tested EPF strains. *L. fusisporum* NBAIR-VI8 had the lowest lethal time LT_{50} and LT_{90} . *A. gossypii* and hopper populations were much lower in bhendi plots treated with entomopathogenic fungi (VI8, Ma4, and Bb5a) than in untreated control plots, according to pooled data collected over a two-year period. Plots treated with the three EPF strains produced noticeably more bhendi yield than the untreated control. In both the EPF-treated and untreated control plots, the numbers of the predatory spiders, coccinellids, syrphids and green lacewings were statistically comparable, suggesting that the entomopathogenic fungi are safe for these natural enemies. In comparison to the control plot, the *L. fusisporum* NBAIR-VI8 treated plot had the highest cost-benefit ratio compared to other treatments. Images from the scanning electron microscope revealed spores and mycelial development of *L. fusisporum* NBAIR-VI8 on various *A. gossypii* components, indicating infection of this fungus. These findings suggest that *L. fusisporum* may be a useful biocontrol agent for hoppers and aphids.

Keywords: *Aphis gossypii*; bioassay; entomopathogenic fungi; field efficacy; yield





**Effect of pectinolytic and xylanolytic bacterial strains from termite gut for
retting and quality fibre production from jute**

**B.S. Manjunatha^{1,3*}, C. Bindushree³, B.S. Gotyal^{2,3}, Atul Singha¹,
Nilimesh Mridha¹, T. Nagesh Kumar¹, M. Pavan^{4,5}, Amit Das¹, Ruby Das¹,
Jayanta Mandal¹, D.B. Shakyawar¹ and Avijit Das¹**

¹ICAR–National Institute of Natural Fibre Engineering and Technology, Kolkata, India

²ICAR–Central Research Institute for Jute and Allied Fibres, Kolkata, India

³ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

⁴Punjab Agricultural University, Ludhiana, India

⁵NITTE School of Fashion Technology and Interior Design, Bengaluru, India

*Correspondence: manjubsuari@gmail.com

Jute is the golden fibre, second most important and affordable fibre next to cotton. In this study we optimised the bacterial retting protocol that can lower retting period and produce high quality fibre. Two bacterial strains with high pectinase and xylanase with minimal/ divide of cellulase activity used in jute retting. The 16S rDNA analysis revealed that the organisms were: *Bacillus cereus* TNA-2 and *B. cereus* TNA-15 which were screened for pectinase, xylanase and cellulase assay with individually and co-inoculation. *Bacillus cereus* TNA-2 individually showed pectinase (12.85±0.17 U/mg protein), xylanase (2.30±0.26 U/ mg protein) and cellulase (0.32±0.0112 U/mg protein) activity and *B. cereus* TNA-15 for pectinase (10.24±0.56 U/mg protein), xylanase (2.60±0.06 U/mg protein) and devoid of cellulase activity. These two bacterial strains in different combinations of consortia showed synergistic effect. The bacterial strains in different combinations of consortia reduced the retting period to 8 days as compared to 20 days in the control. These bacterial strains inoculations yielded the remarkable improvement in jute fibre strength (20.5–22.8g/tex), fineness (3.1–2.8 tex) and other parameters over control, produced high-quality fibre with a grade of TD2+75%↑. This improved retting technology can be adopted by jute growing farmers for industrial scale production of quality jute fibre in water scarcity areas.

Keywords: bacterial retting; fibre grading; fibre strength; fineness; pectinolytic; xylanolytic





Physiological host range and virulence of *Metarhizium pingshaense* against three key *Chilo* species, and temporal expression of virulence genes during infection of its original host, *Conogethes punctiferalis*

C.M. Senthil Kumar^{1*}, M. Samyuktha¹, M. Balaji Rajkumar²,
M. Punithavalli³, Sharon D'Silva¹, T.K. Jacob¹, S. Devasahayam¹ and
A.I. Bhat¹

¹ICAR–Indian Institute of Spices Research, Kozhikode, India

²ICAR–Indian Institute of Spices Research, Regional Station, Appangala, India

³ICAR–Sugarcane Breeding Institute, Coimbatore, India

*Correspondence: cmsenthil@gmail.com

The infectivity and virulence of *Metarhizium pingshaense* was tested against three major pests: *Chilo infuscatellus* (sugarcane early shoot borer), *C. sacchariphagus indicus* (sugarcane internode borer) and *C. partellus* (sorghum stem borer). Bioassay studies indicated high pathogenicity of this fungus against all the three species with the highest mortality recorded in *C. sacchariphagus indicus* (96%), followed by *C. infuscatellus* (93%) and *C. partellus* (83%). The median lethal concentrations of *M. pingshaense* against late-instar larvae were 4.6×10^5 , 1.7×10^5 , and 9.5×10^5 conidia/ml for *C. infuscatellus*, *C. sacchariphagus indicus* and *C. partellus*, respectively. Median survival times ranged from 5.3 to 6.9 days for *C. infuscatellus*, from 5.4 to 7.9 days for *C. sacchariphagus indicus* and from 6.9 to 8.3 days for *C. partellus*. Qualitative and quantitative analyses of cuticle-degrading enzymes by the fungus confirmed the production of chitinases and lipases. Genes encoding chitinase and protease were cloned, sequenced and were found to be closely related to those of *M. anisopliae*. Temporal expression of these genes in the fungus during infection of its original host, *Conogethes punctiferalis*, revealed a gradual upregulation over time. These findings highlight the potential of *M. pingshaense* as an effective biocontrol agent for a wide range of crambid pests, supporting its development as a broad-spectrum mycoinsecticide.

Keywords: Crambidae; cuticle degrading enzymes; mycoinsecticide; pathogenicity; RT-qPCR





Endophytic microbes from rice landraces: a promising source for managing seed-borne diseases

**C.S. Shantharaja^{1*}, Ch. Rajeshwari², C. Manjunatha³, G. Vanishree¹,
Anjitha George¹, S. Aravindan¹, S.S. Manjanagouda¹, C. Gireesh¹ and
A. Anandan¹**

¹ICAR–Indian Institute of Seed Science, Regional Station, Bengaluru, India

²University of Agricultural Sciences, Bengaluru, India

³ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

Correspondence: shantharaja.cs@icar.gov.in

The management of seed-borne diseases has become increasingly difficult due to the development of resistance to chemical treatments. Recently, seed-borne endophytes have emerged as a promising area of research for managing such diseases. This study explores the evaluation of seed-borne endophytes from rice (*Oryza sativa* L.) landraces as a potential solution for managing blast (*Pyricularia oryzae*) and brown spot (*Bipolaris oryzae*). 10 endophytic fungal isolates L1, L8, L20-1, L31-2, L32, L33-2, L35, L38-1, L38-2, and L39-2 were isolated from seeds of rice land races and identified based on morphological and molecular characterisation as *Alternaria alternata*, *Phoma* sp., *Fusarium equiseti*, *Curvularia petarsonii*, *Fusarium* sp., *Aspergillus niger*, *Nigrospora sphaerica*, *Curvularia hawaiiensis*, *Talaromyces sayulitensis* and *Talaromyces verruculosus*, respectively. The antagonistic activities of isolates were evaluated using dual culture assays, which revealed that *A. niger* (L33-2) and *N. sphaerica* (L35) exhibited over 50% growth inhibition of both blast and brown spot pathogens. Volatilome assay also demonstrated that *A. niger* (L33-2) inhibited the growth of blast (62.87%) and brown spot (54.26%) pathogens, suggesting a possible role for volatiles in disease suppression. Additionally, the poison food technique showed that lipopeptide extracts from *A. niger* (L33-2) resulted in 87.10% inhibition of blast and 87.20% inhibition of brown spot pathogens. In pot experiments, bio-priming with *A. niger* (L33-2) recorded the lowest disease incidence (26.08%) and severity (16.67%) brown spot pathogen. These findings suggest that seed borne endophytic microbes from rice landraces have significant potential as a biocontrol agent against rice diseases.

Keywords: biocontrol; endophytes; landraces; seed-borne; seed-borne diseases



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Biosmart seed for managing seed- and soil-borne diseases in solanaceous crops

C. Vimalkumar^{1*}, Thukkaram Damodaran², Monalisha Ghosh¹ and
Dipak Nayak¹

¹ICAR–Central Institute for Subtropical Horticulture, Regional Research Station, Malda, India

²ICAR–Central Institute for Subtropical Horticulture, Lucknow, India

*Correspondence: vimalkumar.c@icar.gov.in

Tomato and brinjal are key vegetable crops in India and face numerous biotic stresses from seed- and soil-borne pathogens. Protecting seeds and seedlings at the earliest stage through eco-friendly methods is essential for achieving a healthy crop stand and optimal yield. The metabolite derived from *Trichoderma* species, in combination with adjuvants, demonstrated strong antagonistic activity against key pathogens of tomato and brinjal, such as *Fusarium oxysporum*, *Sclerotium rolfsii*, *Phomopsis vexans* and *Ralstonia solanacearum*, under *in vitro* conditions. As the concentration of the active ingredient increased, the zone of inhibition expanded accordingly. Even after autoclaving at 121°C (15 PSI for 20 minutes), the bioformulation remained relatively effective against these pathogens. This formulation was applied to tomato and brinjal seeds using a biopolymer coating to create biosmart seeds, which effectively managed *Sclerotium* wilt caused by *Sclerotium rolfsii* compared to both positive and negative controls under *in vivo* conditions. In the control, the cotyledons were macerated by mycelia, whereas in the biosmart seeds, the mycelia were unable to penetrate the coating. Even after the emergence of the radicle, the infection was significantly delayed compared to the positive control (carbendazim + mancozeb at 0.2%). The biosmart seeds had a disease incidence of only 18.4%, compared to 32% in the positive control and 73% in the negative control, at a high inoculum load (10 sclerotial bodies per treatment) on the 14 day after sowing. In addition to its fungicidal effect, it also promoted growth-stimulant activity, increasing growth by up to 15% compared to the controls.

Keywords: bioformulation; biosmart seed; *Sclerotium* wilt; seed- and soil-borne pathogens





Development of thermotolerant *Metarhizium anisopliae* strain and its virulence against brinjal mite *Tetranychus urticae*

E. Ashwini*, A. Kandan, U. Amala, C. Manjunatha, G. Sivakumar and S.N. Sushil

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

*Correspondence: ashwiniebpgowda@gmail.com

Tetranychus urticae Koch, the two-spotted spider mite, is one of the important pests that affect all variety of brinjal production in India. Tragically, *T. urticae* is well known for its quick development of chemical resistance. Its great fecundity, inbreeding, great reproduction, and extremely short life cycle results in numerous generations in short duration. High temperature acts as barrier for survival and penetration of entomopathogenic fungi in insect pests under field conditions. So, development of thermotolerant entomopathogenic fungi is urgently needed. Cereals and millets were used for the development of thermotolerant strain of *Metarhizium anisopliae* NBAIR-Ma4 at different temperature of exposure, ranging from (36°C–42°C) at different time intervals (2–8 hr). Variations in morphological and cultural characters were recorded in mother culture and thermotolerant culture of NBAIR-Ma4 grown on different millets and cereals. Significant difference of growth rate and survival was recorded in kodomillet and corn. Insecticidal enzyme activity was estimated in mother culture and thermotolerant culture of *M. anisopliae* at different days of incubation and significant difference in enzyme activity was observed. The bioefficacy and virulence of mother culture and thermotolerant culture of *M. anisopliae* NBAIR-Ma4 against two-spotted spider mite reveals that mortality percent ranging from 82.6% (mother culture) to 79.8% (thermotolerant). These studies revealed that thermotolerant *M. anisopliae* NBAIR-Ma4 strain can be further evaluated for the management of *T. urticae* under field conditions.

Keywords: bio-efficacy; entomopathogenic fungi; mite; mother culture; thermotolerant culture





**Resistance assessment of rice germplasm against the
brown planthopper, *Nilaparvata lugens***

Darshana Brahma^{1*}, Subhash Chander² and S. Rajna¹

¹ICAR–Indian Agricultural Research Institute, New Delhi, India

²ICAR–National Research Centre for Integrated Pest Management, New Delhi, India

*Correspondence: darshanabrahma1@gmail.com

The brown planthopper (*Nilaparvata lugens* Stal) (BPH), a major pest of rice (*Oryza sativa* L.), is responsible for severe crop losses by causing hopper burn and transmitting plant viruses. To mitigate this threat, host-plant resistance presents an effective, eco-friendly approach. This study assesses the resistance of various rice germplasms—RP 2068-18-3-5, RP bio-4918-230S, Salkathi, IRG-309, IRG-221, IRG-98, IR-64, and MTU-1010—against BPH, using PTB 33 as a resistant check and TN-1 as a susceptible control. Through evaluating antixenosis, antibiosis, and tolerance, the results identified RP 2068-18-3-5 and Salkathi as highly resistant, exhibiting minimal BPH damage, comparable to PTB 33. Resistance traits included elevated nymphal settlement and feeding marks, with increased unhatched egg counts, in contrast to higher honeydew excretion in susceptible varieties. Notably, IRG-98 showed reduced nymph emergence and elevated unhatched eggs, while IR-64 and MTU-1010 displayed higher nymphal survival rates and shorter developmental periods akin to TN-1. The study also observed a progressive increase in superoxide dismutase (SOD) activity with infestation duration, peaking in PTB 33, Salkathi, and RP 2068-18-3-5, while polyphenol oxidase (PPO) activity reached its highest levels in resistant germplasms around 72 hours post-infestation. Analysis indicated negative correlations between nymphal survival and honeydew production with SOD and PPO, highlighting a balance between defense mechanisms and BPH impacts.

Keywords: brown planthopper; host plant resistance; PPO; rice germplasm; SOD





Synergistic effects of the sterile insect technique and entomopathogenic fungi for managing *Spodoptera litura* in cabbage under protected cultivation

Deepak^{1*} and A.G. Sreenivas²

¹Directorate of Plant Protection Quarantine and Storage, Faridabad, India

²University of Agricultural Sciences, Raichur, India

*Correspondence: deepaksihimoge@gmail.com

In sustainable agriculture, managing pests like *Spodoptera litura* effectively is crucial. This study explores the combined use of the Sterile Insect Technique (SIT) and Entomopathogenic Fungi (EPF) for controlling *S. litura* larvae on cabbage, focusing on the synergetic effects of these methods. Conducted in the shade house of the Horticultural Garden, Main Agricultural Research Station, Raichur, the experiment included treatments such as the release of irradiated F₁ larvae, the release of healthy larvae combined with the application of a thermotolerant EPF strain, the combined use of irradiated F₁ larvae and EPF, the release of healthy larvae, and an untreated control. Treatments were applied at the cabbage head formation stage at the rate of one larva per square meter, with nylon nets restricting larval movement. Weekly recordings were made of surviving larvae, defoliation percentage, head damage, and yield potential. The combined release of irradiated F₁ larvae and EPF proved to be the most effective, showing a significant decrease of larvae in the third week and reduced cabbage head damage to 2%, resulting in a higher yield of 14.58 tons per hectare. Conversely, the release of healthy larvae led to higher larval counts (2.75 larvae), more head damage (17%), and lower yield (7.00 tons per hectare). The integration of SIT and EPF offers a promising approach for managing *S. litura* in cabbage, reducing pest damage, and increasing yield. Further research should focus on optimising this method for broader agricultural applications.

Keywords: cabbage; EPF; irradiation and F₁ larva; *Spodoptera litura*





Climate-resilient and thermotolerant strain of *Metarhizium anisopliae* as potential mycopesticide for the management of insect pests in tropical climates

K.B. Deepthy*, U.K. Sreelakshmi, Haseena Bhaskar, Mani Chellappan,
T. Nimisha and Sruthi

Kerala Agricultural University, Vellanikkara, India

*Correspondence: deepthy.kb@kau.in

Use of *Metarhizium anisopliae* as a biopesticide is hindered by the abiotic stress conditions viz., high temperature and low humidity. These restrictions would be exacerbated in the event of global warming and would lead to poor performance in the field conditions. Identifying thermotolerant *M. anisopliae* isolates is a possible strategy to overcome this problem. *Metarhizium* isolates, EKM2, CKD and M4 were collected from the Department of Agricultural Entomology repository and screened for their temperature tolerance. The isolate EKM2 had recorded higher mycelial weight and sporulation when compared to the other isolates at the highest temperature of 38°C. The isolates selected from the preliminary screening were continuously subjected to inducing temperature stress treatments starting from 35°C to 42°C. At the highest temperature of 41°C, the isolate, EKM2 recorded the highest mycelial weight, number of colonies, number of spores, etc. Hence EKM2 has been identified as the thermotolerant isolate. The thermotolerant isolate EKM2 was grown continuously for six successive generations at the same temperature level of 41°C in order to stabilise the stress tolerance. EKM2 also recorded higher levels of trehalose and virulence related enzymes viz. lipase, protease and chitinase. The isolate also showed the presence of heat shock proteins confirming its thermotolerance. *Metarhizium anisopliae* strains that are climate resilient and thermotolerant, especially EKM2, have the potential to elevate the usage of mycopesticides in tropical areas for controlling insect pests.

Keywords: *Metarhizium*; pest management; temperature tolerance; tropical climate





Identification of potential strains of actinobacteria for the management of lepidopteran and storage pests of pulses

R. Jagadeeswaran*, Revanasidda, G.K. Sujayanand, Neeraj Kumar Singh and Saksham Chaudhary

ICAR–Indian Institute of Pulses Research, Kanpur, India

*Correspondence: iari.nema@gmail.com

Bruchids belongs to the genus *Callosobruchus*, which is the most destructive storage pests of pulses. The infection starts from the field with egg laying and the grain damage occurs during storage leading to 60–100% grain losses in 2–3 months of storage time. Tobacco caterpillar is another important lepidopteran pest that infects leaves, pods of pulses in the field and causes severe yield losses. Because of the adverse effect of chemical insecticide use, researchers are searching for novel and ecofriendly molecules for insect management. actinobacteria is the well-known group of organisms that possess many primary and secondary metabolites (molecules) of medical and agricultural importance. In this study, we screened 20 strains of actinobacteria for their insecticidal efficacy on *Callosobruchus analis* and *Spodoptera litura*. The secreted metabolites were dissolved using the solvent, ethyl acetate in 1:1 ratio and the fraction was collected using separating funnel. The fraction of the strains was concentrated by using rotary evaporator, dried in petri dishes and dissolved with 90% ethanol and as such used for evaluation. Bioassay on *C. analis* was carried out for contact toxicity. Out of 20 strains, AIN32 showed 100% mortality followed by AIN 5,26 which showed 95% mortality and AIN 23 which showed 85% mortality in 48 hrs. Bio-assay on *S. litura* was carried out by diet contamination method for gut toxicity. Out of 20 strains, AIN-26 showed 100% mortality followed by AIN-27 which showed 90% mortality and AIN-28 which showed 80% mortality on the 5th day after treatment.

Key words: actinobacteria; *Callosobruchus analis*; ethyl acetate fraction; novel insecticide molecule; *Spodoptera litura*





Effect of biopesticides on larval, pupal and adult duration of *Chrysoperla zastrowi sillemi* (Esben-Peterson) in subsequent generation

Moirangthem Monalisa Devi^{1*}, Khumukcham Ibohal Singh¹ and S.K. Mukherjee²

¹College of Agriculture, Central Agricultural University, Imphal, India

²College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, India

*Correspondence: monalisa.mdevi@gmail.com

Efficacy of biopesticides, *Bacillus thuringiensis*, *Lecanicillium lecanii*, *Beauveria bassiana*, *Metarhizium anisopliae*, Azadirachtin and synthetic insecticide Fipronil (check) were recorded on the larval, pupal and adult duration of *Chrysoperla zastrowi sillemi* in the subsequent generations after one round treatment of larvae in the previous generation by diet contamination method under laboratory conditions. The larval and pupal duration varied from 8.70 to 9.85 days and 6.07 to 6.61 days respectively, in which maximum duration was observed in *L. lecanii* treatment and minimum duration was observed in Fipronil treatment followed by Azadirachtin treatment in both the life stages, i.e., larval and pupal stages. In case of adult, duration of female varies from 33.66 to 37.80 days, while duration of male varies from 26.84 to 30.47 days. In both adult male and female, maximum duration was observed in *L. lecanii* treatment followed by *M. anisopliae* treatment and minimum was observed in Fipronil treatment followed by Azadirachtin treatment in both the cases. The results derived from the experiment showed that the microbial pesticides have little or no effect on the duration of larva, pupa and adult of *C. zastrowi sillemi* in the subsequent generation concluding that these biopesticides can go hand in hand with the biocontrol agent, *C. zastrowi sillemi* in IPM packages.

Keywords: adult duration; biopesticides; *Chrysoperla zastrowi sillemi*; larval duration; pupal duration





**Characterisation and quantification of peptaibol produced by novel
Trichoderma spp.: harnessing the potential of these isolates to mitigate
moisture stress through enhanced biochemical and physiological responses in
black pepper (*Piper nigrum* L.)**

**R. Praveena*, K.V. Vijayasanthi, Titty Anna Thomas, Priya George, N.K. Leela, K. Anees,
K.S. Krishnamurthy and R. Dinesh**

ICAR–Indian Institute of Spices Research, Calicut, India

*Correspondence: praveenaravindran55@gmail.com

Trichoderma spp. is primarily applied to manage biotic stresses in plants; however, it can also mitigate abiotic stresses by stimulating antioxidative protective mechanisms and enhanced synthesis of secondary metabolites. The study optimised the conditions to enhance peptaibol production by novel *Trichoderma* spp, characterised and quantified peptaibol- alamethicin using HPLC and LC-MS/MS. Also investigated the efficacy of these isolates in enhancing growth and the associated physio-biochemical changes in black pepper plants under moisture stress. Under *in vitro* conditions, out of 51 isolates studied, six isolates viz., *Trichoderma asperellum* (IISRNAIMCC0049), *Trichoderma erinaceum* (IISRAPT1), *Trichoderma harzianum* (IISRAPT2), *T. harzianum* (IISR KL3), *Trichoderma lixii* (IISR KA15) and *T. asperellum* (IISR TN3) showed tolerance to low moisture levels (5, 10 and 20%) and higher temperatures (35 and 40°C). In vivo evaluation on black pepper plants maintained under four different moisture levels (Field capacity [FC]; 75%, 50%, and 25%) showed that the plants inoculated with *Trichoderma* accumulated greater quantities of secondary metabolites viz., proline, phenols, MDA and soluble proteins at low moisture levels (50 and 25% FC). In the present study, plants inoculated with *T. asperellum* and *T. harzianum* showed significantly increased growth compared to uninoculated plants. The shortlisted *Trichoderma* isolates exhibited differences in peptaibol production and indicated that the peptide might be the key factor for their efficiency as biocontrol agents. The present study demonstrated that the isolates *T. asperellum* and *T. harzianum* enhanced the drought tolerance of black pepper by promoting plant growth and increasing secondary metabolite production.

Keywords: drought; peptaibol; phenols; proline; *Trichoderma* spp.





Efficacy of biorationals for the management of citrus thrips in acid lime

L. Ranjith Kumar^{1*} and K. Sireesha²

¹Citrus Research Station, Dr Y.S.R. Horticultural University, Tirupati, India

²Horticultural Research Station, Guntur, India

*Correspondence: ranjithento27@gmail.com

Citrus thrips, *Scirtothrips dorsalis*, is an important pest of citrus causing silvery scars on the rind leading to deformity in fruit shape which downgrades reducing fruit quality in local and export quality fruit. There is lack of biorational approaches for the management apart from insecticides among citrus growers of Nellore and Tirupati districts. In this view, the experiment was conducted during 2022-24 at Citrus Research Station, Petlur, Tirupati, Andhra Pradesh to evaluate the efficacy of biorationals against citrus thrips in RCBD with seven treatments and two sprays were carried out at petal fall and pea size of crop growth. Among the treatments, T₆, T₁ and T₃ recorded lowest incidence of thrips at 3, 7 and 14 DAS and were on par with each other, and differed with rest of the treatments, i.e., T₆-HMO (Horticultural Mineral Oil) @ 10 ml/lit followed by Spinosad 45 SC @ 0.25 ml/lit (4.50, 3.18 and 1.74 thrips/ shoot) and T₁-Azadirachtin (10,000 ppm) @ 2ml/lit followed by Spinosad 45 SC @ 0.25 ml/lit (4.64, 3.24 and 1.86 thrips/shoot) and T₃-HMO @ 10 ml/lit followed by HMO (4.70, 3.30 and 1.98 thrips/ shoot) at 3, 7 and 14 DAS. Similarly, the lowest fruit infestation of 3.80 per cent and 4.05 per cent and highest yield of 22.40 t/ha and 21.90 t/ha was recorded in Treatments T₆ and T₁ which were on par with each other and differed significantly with rest of the treatments. So, biorationals help in reducing input cost with environmental sustainability.

Keywords: acid lime; azadirachtin; biorationals; horticultural mineral oil; thrips





**Pathogenicity characteristics of the entomopathogenic fungus
Metarhizium anisopliae to *Leucinodes orbonalis***

K. Rupa*, A. Kandan and S.N. Sushil

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

*Correspondence: kundurupa73@gmail.com

Leucinodes orbonalis (Lepidoptera: Crambidae) is a serious invasive pest in global brinjal (eggplant) production, known for developing high levels of pesticide resistance. Environmentally sustainable control strategies, such as entomopathogenic fungi (EPF), offer a promising alternative. However, genetic variation among EPF strains due to geographic and climatic factors influences their pathogenicity, making localised strain screening crucial. In this study we assessed the pathogenic potential and insecticidal enzymatic activities of *Metarhizium anisopliae* isolates against *L. orbonalis*. A total of forty indigenous *Metarhizium* strains were isolated from various geographic soil types and ten isolates were short listed based on their Biological Efficiency Index (BEI). These isolates (1×10^8 spores/ml) caused 65% to 80% mortality against third-instar larvae of *L. orbonalis*. Ma-83 exhibited the highest mortality (more than 80%) with Lethal Time (LT_{50}) values ranging from less than 5 days at the lowest spore concentration (1×10^4 spores/ml). Lethal Concentration (LC_{50}) values ranged from $1.5 - 5.3 \times 10^4$ spores/ml. Insecticidal enzymatic activity studies showed Ma-83 strain had the highest chitinase, lipase, esterase and protease levels. These *invitro* findings suggest that *M. anisopliae* isolates, especially Ma-83, possessed strong potential insecticidal activities and further field evaluation studies are in progress.

Keywords: biological control; entomopathogenic fungi; *Leucinodes orbonalis*; *Metarhizium anisopliae*; pest management





**Population growth parameters and life history traits of native
Trichogramma sp. parasitising eggs of *Corcyra cephalonica* (Stainton)
reared on various cereal substrates**

Adarsh Sharma*, P.L. Sharma and Nikshubha Sharma

Dr Y.S. Parmar University of Horticulture and Forestry, Solan, India

*Correspondence: adarshsharma7487@gmail.com

The successful proliferation of superior parasitoids relies fundamentally on mass production of high-quality factitious hosts, viz. *Corcyra cephalonica* (Stainton) eggs with its exceptional suitability and efficacy in rearing *Trichogramma* spp. The fitness of *Trichogramma* spp. is intricately linked to nutritional quality of host eggs (interior-development of egg-parasitoid's immature stages), which is significantly influenced by type of cereal substrates used to rear *C. cephalonica*. Therefore, the study aimed to evaluate effect of *C. cephalonica* eggs reared on four cereal substrates on life-history traits and population growth parameters of *Trichogramma chilonis* Ishii and *Trichogramma achaeae* Nagaraja and Nagarkatti, with the goal of identifying optimal substrate for rearing *C. cephalonica* and subsequently *Trichogramma* spp. The fastest pre-adult development of *T. chilonis* and *T. achaeae* was observed on *C. cephalonica* eggs reared on jowar (7.76 and 8.18 days, respectively), followed by maize-reared eggs (8.21 and 8.40 days). Moreover, fecundity oscillated between 43.90 to 50.76 eggs/female in *T. chilonis* and 41.16 to 49.12 eggs/female in *T. achaeae*, with oviposition periods of 4.05 to 4.46 and 3.89 to 4.29 days/female, respectively, showing no significant differences. Significant differences were noted in growth parameters for both *T. chilonis* and *T. achaeae*, with higher net-reproductive rate, intrinsic-rate of increase, and finite-rate of increase on jowar-reared *Corcyra* eggs, followed by maize-reared eggs. Additionally, mean generation and doubling time were lower on jowar-reared *C. cephalonica* eggs followed by maize-reared eggs. In conclusion, *C. cephalonica* eggs reared on jowar and maize proved efficient and superior host substrates to mass-produce *Trichogramma* spp.

Keywords: *Corcyra cephalonica*; intrinsic rate of increase; life history traits; population growth parameters; *Trichogramma* spp.





Effect of low temperature storage on biology and demographic parameters of the predatory mite *Neoseiulus longispinosus* (Evans)

Nikshubha Sharma*, P.L. Sharma and Adarsh Sharma

Dr. Y.S. Parmar University of Horticulture and Forestry, Solan, India

*Correspondence: nikshubhasharma761@gmail.com

The two-spotted spider mite (*Tetranychus urticae*) is a major agricultural pest responsible for significant crop damage. Chemical control methods have led to resistance and environmental concerns. In contrast, predatory mites such as *Neoseiulus longispinosus* (Evans) provides an eco-friendly alternative and have been successfully mass-produced for biological control in India. However, their short shelf life limits their long-term availability, increasing production costs. While low-temperature storage has been effective in extending the viability of parasitoids, it has been less explored for predators like *N. longispinosus*. Low-temperature storage can synchronise the release of these predators with pest outbreaks, but challenges like reduced survival, reproduction and altered behaviour must be addressed. In this experiment, mated adult females of *N. longispinosus* stored at $6 \pm 2^\circ\text{C}$ for 7 and 10 days showed survival rates of 90% and 50%, respectively. Cold storage also reduced fecundity, with egg production per female declining from 48.4 for the control group (0 days) to 22.8 and 12.6 for females stored for 7 and 10 days, respectively. Despite these changes, the progeny's developmental biology, population growth, feeding potential and functional response were largely unaffected by maternal cold storage for up to 10 days. Based on these findings, mated females of *N. longispinosus* can be cold-stored for 7 and 10 days and used for field releases with slightly higher release rates. However, further studies are needed to standardise these release rates to ensure the most effective biological control strategies.

Keywords: biological control; ecofriendly agriculture; low-temperature storage; predatory mite





**Development of an integrated management module for whitefly,
Bemisia tabaci (Hemiptera: Aleyrodidae), infesting bitter gourd**

B.D. Shinde*, A.S. Dhane, D.B. Ingole and S.N. Kale

Dr Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, India

*Correspondence: bdshinde@rediffmail.com

Bitter gourd (*Momordica charantia* L.) is a widely cultivated cucurbit in all districts of Konkan, where whitefly (*Bemisia tabaci* Gennadius) is a major pest causing significant crop loss. A three-year field experiment (2017–2020) was conducted at the Agricultural Research Station, Palghar, on the bitter gourd variety Konkan Tara, to evaluate the efficacy of various pest management modules against whitefly. The experiment followed a randomised block design with five treatments and four replications, including a control. All tested modules were more effective than the control in reducing whitefly infestations. Among them, Module I, which included the use of yellow sticky traps (25 traps/ha), silver plastic mulch, and a spray combination of castor and neem oil (1:2 ratio, 5ml/l), followed by a second spray of Acetamiprid (0.5% @ 5g/10L) during the vegetative growth stage, proved most effective. This module recorded the lowest whitefly count, the highest marketable yield (13.38 t/ha), and the best incremental cost-benefit ratio (ICBR) of 1:7.47. The results indicated that Module I provides an effective and economically viable strategy for managing whiteflies in bitter gourd cultivation, offering promising implications for reducing crop losses and improving farmer income.

Keywords: biological control; bitter gourd; module; whitefly





Ecological characterisation of *Steinernema shori* (Nematoda: Steinernematidae), a warm-adapted entomopathogenic nematode from India

Sonia Soni^{1*}, Jagadeesh Patil², Jayalaxmi Ganguli¹ and R.N. Ganguli¹

¹Indira Gandhi Krishi Vishwavidyalaya, Raipur, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: soniasoni0203@gmail.com

Entomopathogenic nematodes (EPNs) from the *Heterorhabditis* and *Steinernema* genera serve as efficient biological control agents against insect pests. EPNs are highly sensitive to environmental conditions, including temperature, humidity, and soil type. The study describes the basic ecological characteristics of the entomopathogenic nematode *Steinernema shori*, including its response to temperature and moisture. Isolated from Chhattisgarh state of India, which experiences a tropical climate with hot and humid summers, the nematode showed remarkable tolerance to high temperatures, exhibiting 97.7% survival at 41°C (after 48h of exposure). The effect of temperature and soil moisture on the infectivity of *S. shori* to *Galleria* larvae was determined. *S. shori* was infective to larvae of *Galleria* at a temperature range of 20–39°C and reproduced within *Galleria* cadaver at a temperature range of 25–37°C, with 30°C being the most optimum temperature for survival, infectivity, and reproduction. This nematode species isolated from a warm region of India exhibited warm-adapted temperature characteristics. The optimum soil moisture content of the soil for *S. shori* to infect the host was 7%, resulting in 100% mortality of *Galleria* larvae.

Key words: biological control; ecological characteristics; entomopathogenic nematodes; *Steinernema shori*; temperature





Enhancing photostability of *B. thuringiensis* strains: phytopigments as alternatives to synthetic UV protectants

Ashish Tiwari^{1,2}, G.K. Sujayanand^{1*}, Anup Chandra¹ and G.P. Dixit¹

¹ ICAR–Indian Institute of Pulses Research, Kanpur, India

² Chaudhary Charan Singh University, Meerut, India

*Correspondence: sujayanand.gk@icar.gov.in ; sujayanand_agri@yahoo.co.in

The global warming has resulted in increased amount of Ultra Violet (UV) radiations entering into troposphere in recent years. Developing adjuvant for enhancing the microbial bio-control agents is need of the hour. Among the various microbial bio-control agents *Bacillus thuringiensis* (*Bt*) is most popular and widely used for lepidopteran pest management. The efficiency of *Bt* and baculoviruses are impacted by UV radiations. The UV radiations impact endospores viability and toxin integrity thereby reduces the efficiency of *Bt* spore crystal mixtures (SCM). Researchers had identified many synthetic photoprotectants like para amino benzoic acid (PABA), benzaldehyde, congo red, malachite green, etc., depending on its compatibility with the microbial biocontrol agent. In order to minimise the environmental pollution and global warming natural pigments derived from plants were screened for their suitability as UV protectant for *Bt* SCM. In the present investigation, phytopigments derived from three different plant source viz., P1 (*Moringa* leaf powder), P2 (*Bougainvillea* flower powder) and P3 (*Cockscomb* flower powder) were screened with 3 *Bt* strains (F8.IIPR, F1.IIPR and HD1). Their UV-A protectant efficiency was compared with PABA against pod borer, *Helicoverpa armigera* Hubner larva. The results showed that P1 and P2 as promising UV protectants. Hence the 2 treatments were evaluated in field condition on green gram with 2 different time points of spraying. During both time of spraying, P2 has recorded higher mortality of pod borer, *H. armigera*. Thus, it is concluded that bougainvillea flower powder can be deployed as an alternative to synthetic UV protectant for enhancing the *Bt* efficiency.

Keywords: endotoxin; microbial pest management; photostabiliser; phytoprotectant; UV protectant





Characterisation and biological control of emerging fungal diseases of vegetable crops

A.N. Tripathi*, Kirti Tiwari, Tripti Dubey, A.N. Singh and N. Rai

ICAR–Indian Institute of Vegetable Research, Varanasi, India

*Correspondence: Atma.Tripathi@icar.gov.in

Every year, emerging fungal diseases cause losses up to 40-60 % in vegetable crops. Fungal pathogens from chilli, brinjal, tomato, French bean, bottle gourd and water spinach were isolated and pure cultures were established on PDA. These cultures were sub-cultured in PDA slants for further experimentation. Pathogen isolates were used to test the Koch's postulate for pathogenicity. Pure cultures were morphologically and molecularly characterised and genetic sequences were submitted to NCBI to obtain accession numbers. Further, isolates were identified as *Colletotrichum truncatum* (PP716496, PP716518) on chilli; *Diaporthe vexans* (PP716500) on brinjal; *Alternaria alternata* (PP716498) and *Corynespora cassiicola* (PP716497) on tomato; *Sclerotinia sclerotiorum* (PP716499) on French bean, *Fusarium solani* (PP716501) on bottle gourd and *Diaporthe batata* (PP716500) on water spinach. Apart from this, talc based formulation of bioagents, *Bacillus subtilis* (IIVR-CRB7, 2.5×10^{11} cfu/g), *Trichoderma asperellum* (IIVR-strain, 2×10^7 cfu/g), IIVR-TGV (1.5×10^7), IIVR-TCV (1.6×10^8), *Actinomyces* N 1.2 (5.30×10^6 cfu/g) and Kashi Jaivshakti (10×10^{12} cfu/g) were applied as seed treatment @ 4 g/kg and soil application with bioagents fortified vermicompost (1:150) @ 600g/m² in tomato (Kashi Aman), cabbage (Golden Acre) and cauliflower (Pusa Snowball) against fungal diseases. Among treatments, *T. asperellum* was found most effective against damping off (2%) in tomato, however *B. subtilis* was found most effective against *Rhizoctonia* root rot (2%) in cabbage and cauliflower in comparison to control. Characterisation of vegetable pathogens (diseases) are essential for better understanding of pathogens as well as formulation of safe disease management strategy of vegetable crops.

Keywords: biological control; characterisation; disease; pathogen; vegetable crops





Session VIII

Genomics in Biological Control of Crop Pests and Diseases



RNA interference as next-gen biocontrol tool for innovative and sustainable management of invasive species

Amol Ghodke¹, Biko Muita², Tess James¹, Ben Hoffmann³, John Roberts², Ian Greaves⁴,
Ming-Bo Wang⁴ and Nagalingam Kumaran^{1*}

¹CSIRO Health and Biosecurity, Dutton Park, Australia

²CSIRO Health and Biosecurity, Canberra, Australia

³CSIRO Health and Biosecurity, Winnellie, Australia

⁴CSIRO Agriculture and Food, Canberra, Australia

*Correspondence: kumaran.nagalingam@csiro.au

Gene technologies offer promising avenues for developing innovative genetics-based biocontrol tools for the sustainable management of pests, weeds and diseases. These innovations aim to reduce reliance on synthetic chemicals and mitigate the risks posed by broad-spectrum pesticides to non-target organisms. Notably, RNA interference (RNAi) *sensu stricto* is a promising tool that can effectively silence genes that are critical for essential functions (e.g., growth, reproduction, resistance) in pest organisms. While RNAi-based pesticides are now available on the market, using RNAi for managing invasive pests remains a relatively new approach facing challenges in empirical validation, regulatory frameworks and social acceptance. For example, the effectiveness of RNAi can vary across different target systems, influenced by factors such as the stability and cellular delivery of gene-silencing molecules and the target organisms' responses to RNAi-based treatments. Recent advancements have sought to address some of these challenges, such as using 'nano clay' to protect RNAi molecules and developing more stable double-stranded RNA to enhance RNAi efficacy. In this presentation, we will discuss the challenges associated with RNAi-based pest control and explore emerging strategies to overcome them. We will also share our progress in developing RNAi-based tools for managing key invasive pests, including the red imported fire ant (*Solenopsis invicta*), wild radish (*Raphanus raphanistrum*), and bee pests like the varroa mite (*Varroa destructor*). Although RNAi-based approaches may disrupt traditional biological pest management methods, embracing these innovations is essential for developing pest management tools that align with the One Health framework.

Keywords: biological control; biological pest management; biosecurity; gene silencing





Genomic and metabolomic characterisation of *Beauveria bassiana* isolates for biological control of cassava mites

M. Chaithra^{1,2*}, Deeba Kamil², T. Prameeladevi², S.N. Bhagyasree³,
L. Prasad² and T.N. Madhu⁴

¹ICAR–Central Plantation Crop Research Institute, Research Centre, Kahikuchi, India

²ICAR–Indian Agricultural Research Institute, New Delhi, India

³ICAR–Indian Institute of Horticultural Research, Bengaluru, India

⁴ICAR–Central Plantation Crop Research Institute, Vittal, India

*Correspondence: chaithram06@gmail.com

Beauveria bassiana isolates from diverse ecosystems were identified using morphological and molecular approaches, including phylogenetic analysis of three loci: ITS, EF-1 α , and Chitinase 1. Maximum likelihood analysis revealed distinct phylogenetic clustering, indicating high population diversity among isolates. Mating types were determined using MAT1 and MAT2 primers, with 11 isolates showing amplification, mostly for MAT1. Pathogenicity against the cassava mite *Tetranychus truncatus*, was assessed using leaf disc and potted plant bioassays, where isolates Bb6, Bb12, and Bb15 exhibited high mite mortality rates of 97.73%, 96.73%, and 94.50%, respectively, outperforming other isolates, including a commercial formulation. Bb6, Bb12, and Bb15 strains showed pathogenicity against *T. truncatus* with LC₅₀ values of 1.4×10^6 , 1.7×10^6 , and 1.4×10^6 , and LC₉₀ values of 7.3×10^7 , 1.4×10^8 , and 4.2×10^8 , respectively, at 3 days after inoculation, and were considered potential strains for mite control. Metabolomic analysis of volatile and non-volatile metabolites using GC-MS and UPLC-Q-TOF-MS highlighted significant levels of acaricidal and insecticidal compounds, including bis (dimethylethyl)-phenol, n-Hexadecanoic acid and nonadecene, correlating with higher pathogenicity. Unique metabolites like brassinolide and beauvericin, crucial for virulence, were found only in the most potent strains. These findings demonstrate that the bioactive metabolome profiles of Bb6, Bb12, and Bb15 isolates make them a viable alternative to chemical pesticides for effective mite management.

Keywords: acaricidal compound; bioassay; biopesticide; insecticidal activity; mortality





**Deciphering genomic resistance in contrasting rice varieties: a case study on
brown planthopper**

**Guru-Pirasanna-Pandi Govindharaj*, Rudra Madhab Panda,
Mridul Chakraborti, Meera Kumari Kar, G. Basana-Gowda and
S.D. Mohapatra**

ICAR–National Rice Research Institute, Cuttack, India

**Correspondence: guru.g@iacr.gov.in; guruagri@gmail.com*

Rice production is significantly impacted by biotic and abiotic stresses, with the brown planthopper (BPH) being a major biotic factor affecting yield. Present study aimed to elucidate the mechanisms underlying BPH resistance in rice. This study reports on the resistance of the rice variety CR Dhan 805, developed from crosses between the BPH-resistant genotype Salkathi and the susceptible genotype Naveen. Phenotyping and transcriptome analysis were conducted on two resistant genotypes, Salkathi and CR Dhan 805 (Naveen-NIL), and one susceptible genotype (Naveen), under both control and BPH-infested conditions. High-throughput sequencing generated 409 million quality-filtered reads, of which 344 million were successfully aligned to the rice genome. These aligned reads were used for differential gene expression analysis. A total of 7,941 differentially expressed genes (DEGs) were identified under stress conditions across the genotypes. Out of these, 3,288 DEGs were functionally annotated, with distribution across biological Process (2,417 genes), cellular Component (2,045 genes), and molecular Function (2,593 genes). These common DEGs were enriched in pathways associated with defense response, phytohormone signaling, and transcription factors. Notably, several genes were involved in the signaling pathways of jasmonic acid (JA), salicylic acid (SA), and ethylene (ET). Additionally, important transcription factors such as WRKY and NAC were significantly modulated. This indicates that these signaling molecules and transcription factors play crucial roles in the plant's defense mechanisms against brown planthopper infestation.

Keywords: cereals; gene expression; hoppers; resistance; transcriptome analysis





**Cracking the case: decoding *Bactrocera dorsalis* (Hendel) (Diptera: Tephritidae)
CRISPR/Cas9 white and odorant binding protein-13 gene mutants**

**Ashok Karuppannasamy^{1,2*}, Bhargava C. Nagaraja^{1,3} and
Asokan Ramasamy¹**

¹ICAR–Indian Institute of Horticultural Research, Bengaluru, India

²Tata Institute for Genetics and Society, Bengaluru, India

³CrisprBits Private Limited, Bengaluru, India

*Correspondence: ashokg3s@gmail.com

The Oriental fruit fly, *Bactrocera dorsalis* is a highly invasive pest of quarantine importance affecting the global fruit trade. The sterile insect technique is the method of choice for a chemical-free, long-term suppression of *B. dorsalis*, followed in many countries across the globe. The non-specific mutations caused by irradiation affect the overall fitness of flies, thus requiring a more precise method for a heritable, fitness-not-compromising approach. In this study, CRISPR/Cas9 mediated genome editing enabled the creation of mutations at the precise genomic location/s through RNA-guided dsDNA cleavage of *white* and *OBP* genes. Lately, DNA-free editing employing the ribonucleoprotein complex (RNP) has been preferred to validate the target genes at G0 stage embryos in insects. It requires characterising genomic edits from adults after completing their life cycle, which may entail a few months, depending on longevity. The present employed sgRNA targeting *white* and *OBP* genes to generate marker phenotypes and methyl eugenol non-receptive flies. Additionally, edit characterisation is required from each individual, as edits are unique. To overcome this impediment, we pre-determine the genomic edits from the pupal cases, to maintain only edited individuals. In this study, we have shown the utility of pupal cases from males and females of *B. dorsalis* to pre-determine the genomic edits, which corroborated the edits from the respective adults. The present study is the first of its kind for the non-invasive sampling protocol to screen the mutant individuals.

Keywords: CRISPR/Cas9; genomic edits; *OBP13*; pupal cases; *white*





**Bioefficacy and genomic landscape of Shatpada Armour: a highly effective
Bacillus thuringiensis var. *tolworthi* strain NBAIR Bt 25 for combatting fall
armyworm in India**

C. Manjunatha*, K. Aditya, R. Rangeshwaran, R.S. Ramya,
K.T. Shivakumara, A. Kandan, G. Sivakumar and S.N. Sushil

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

*Correspondence: manjuc.nbair@gmail.com

The fall armyworm, *Spodoptera frugiperda* of maize is a major invasive pest in India since 2018, causing yield losses of 21-53%, affecting 90% of maize-growing regions. Biological control is the most sustainable approach for the management of invasive pests. *Bacillus thuringiensis* is an extensively used biological control agent against various insect pests due to its strain-specific toxicity. In this study, the *B. thuringiensis* strain NBAIR-Bt 25 was isolated from naturally infected *S. frugiperda* cadavers collected from maize fields. Microscopic analysis, including SEM, revealed various crystal protein shapes such as bipyramidal, cuboidal, and triangular. Whole-genome sequencing using Illumina and Oxford Nanopore identified 15 insecticidal toxin-related genes, including *cry* and *vip* genes and two novel *cry* proteins (*cry70Aa1* and *cry8Aa1*). Genome annotation predicted 6,980 genes, including 6,756 protein-coding sequences, 16 rRNAs, and 7 tRNAs, and close phylogenetic relatedness to *B. thuringiensis* var. *tolworthi*. *In vitro* bioassays demonstrated 92% larval mortality at 96 h, with an LC_{50} of 42.92 $\mu\text{g/mL}$. Field trials conducted over two kharif seasons from three agroclimatic zones demonstrated consistent reductions in *S. frugiperda* populations accounting for 55.13, 61.22, and 58.02% at three respective locations. This study highlights entomopathogenic properties of NBAIR-Bt25 elucidating the molecular mechanisms responsible for its insecticidal activities, and underscores its potential as a sustainable alternative to chemical insecticides for the management of *S. frugiperda* in maize.

Keywords: annotation; biocontrol; genomics; maize; hybrid assembly





**High-quality genome assembly of a cosmopolitan insect predator
Chrysoperla zastrowi sillemi (Esben-Petersen) (Neuroptera: Chrysopidae)**

**M. Mohan*, T. Venkatesan, S. Selva Babu, P.J. Aneesha, K. Ashok,
R.G. Gracy and S.N. Sushil**

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

*Correspondence: Mohan.M@icar.gov.in

Indian green lacewing, *Chrysoperla zastrowi sillemi*, is an extensively employed biocontrol agent for managing a wide range of insect pests across crop ecosystems. However, the lack of genomic information hinders understanding of the molecular basis of its adaptive evolution and predator-prey interaction for enhancing its predatory potential. Here, we presented a high contiguity, chromosome-level genome assembly of *C. zastrowi sillemi* using short and long-read sequencing platforms (Illumina and PacBio) coupled with Hi-C. The highly homozygous genome assembly has 597 mega bases in span. The assembly got scaffolded into six chromosomal pseudomolecules, occupying 84% of the genome. The size of the six pseudomolecules ranged from 29.36 to 170.05 Mb. We further compared the genome of 11 insects representing various orders and found a major phylogenetic split between Coleoptera and Neuroptera during Devonian era. The evolution of gene family analysis revealed a convergent expansion of 212 gene families. Genome annotation using Refseq, EggNOG, SwissProt and Eukaryotic Orthologous Groups (KOG) database has identified 14,495 protein coding genes. The mitochondrial genome is 16 Kb in length with 13 protein-coding genes, 22 tRNAs and three rRNA genes without any gene rearrangements. The genomic information furnished herein could be useful in choosing heritable traits into a selective breeding for improving its biocontrol potential.

Keywords: chromosome-level genome assembly; green lacewing; predator





**Quick and precise molecular diagnostics of melon fruit fly
Zeugodacus cucurbitae: a pest of quarantine importance**

Srinivasa Narayana* and Varun Arya

Banaras Hindu University, Varanasi, India

**Correspondence: srinivasa@bhu.ac.in*

Melon fruit fly, *Zeugodacus cucurbitae* is a major pest of cucurbits, widely distributed in Southeastern Asia, the Mediterranean region, parts of Australia, Africa, and the Hawaiian Islands. The maggot stage is the primary source of damage, feeding internally on the fruit and causing significant economic losses in cucurbit production. The discrimination of *Z. cucurbitae* from other species of fruit flies especially at immature stages is often difficult due to lack of taxonomic characters. DNA barcoding has proved to be more reliable alternative in some cases, but its high cost and time-consuming nature make it inaccessible for many laboratories. To address this limitation, the present study aimed to develop PCR-based species-specific primers for *Z. cucurbitae*, coupled with a rapid DNA extraction technique. This streamlined protocol has the potential to significantly reduce processing time and can be highly beneficial for plant protection and quarantine centers. We have developed species specific primer, that identifies the species (*Z. cucurbitae*) accurately without any cross amplification in other species of fruit flies. Further, the primers have sensitivity to detect target species DNA down to 1 pg/μl. The specific primers also validated on different developmental stages and geographic population of *Z. cucurbitae* and it has shown 100% accuracy. The cross-specificity was further validated by real time PCR by comparing the critical threshold (Ct) values and by analysing melting curve. The developed protocol significantly plays an important role in detection and management of *Z. cucurbitae*.

Keywords: quarantine pest; quick detection technique; rapid DNA extraction; real-time PCR; species-specific primers





**Expression analysis of defense-related markers in the tri-trophic interaction
between *Trichoderma harzianum* TIND02, *Pseudopestalotiopsis theae*
and tea plant**

Abhay K. Pandey*, Shivanand Yadav and Harshit K. Sharma

Tea Research Association, Jalpaiguri, India

*Correspondence: abhaykumarpandey.ku@gmail.com

The gray blight caused by *Pseudopestalotiopsis theae* is a prevalent disease affecting tea cultivation, and managing it with *Trichoderma* spp. is an alternative to synthetic fungicides. In the present study, dual culture test revealed isolate TIND02 as the most potential candidate with 74.6% inhibitory activity against *P. theae*. Scanning electron microscopic study showed the mycoparasitic nature of *T. harzianum* TIND02 (TH-TIND02) to *P. theae*. The ethyl acetate extract of TH-TIND02 at 100 and 200 µg/mL showed potential inhibitory activity (>69.9%), confirmed the presence of volatile metabolites. Gas chromatography–Mass spectrometry study revealed that ethyl acetate extract of TH-TIND02 showed acetamide, 2, 2, 2-trifluoro-N, N-bis trimethylsilyl-C (94.74%) as a major component. Nursery experiments revealed that 2% and 5% doses (2×10^6 CFU/mL) of TH-TIND02 significantly reduced respective 65.0% and 70.0% disease severity over control with improved plant growth. Besides, expressions of defence-related enzymes (chitinase, phenolics, peroxidase, phenylalanine ammonia lyase, β -1, 3-glucanase, and polyphenol oxidase) and pathogenesis-related genes (*chitinase* and β -1, 3-glucanase) due to TH-TIND02 were determined. The secretion of defence-related enzymes was highly upregulated in plants applied with TH-TIND02 followed by *P. theae* inoculation compared to controls. The RT-qPCR analysis showed that the expression of both genes in co-inoculated plants was two-fold higher than in control after 21-day post incubation. These results suggest that TH-TIND02 application reduced gray blight severity by elevated enzyme activity and overexpressed pathogenesis-related genes in tea.

Keywords: beta glucanase; chitinase; foliar spray; tea plant





**miR-X regulates egg fertilisation through ribogenesis in the invasive fall
armyworm, *Spodoptera frugiperda***

**Jyoti Pathak, Selva Babu Selvamani, Subhi Srivastava, Ashwitha Gopal, T.C. Suman,
Gandhi R. Gracy, Venkatesan Thiruvengadam*, M. Mohan and Satya N. Sushil**

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

**Correspondence: Venkatesan.T@icar.gov.in*

Understanding reproduction's epigenetic molecular mechanisms is crucial for developing advanced and targeted control strategies for the invasive fall armyworm, *Spodoptera frugiperda*. Differential expression analysis revealed 11 known miRNAs with varying expression levels, including nine upregulated and two downregulated miRNAs, in virgin females compared with males. The predictive analysis identified 426 target genes for these miRNAs, with ribogenesis highlighted as a key process in oogenesis and egg fertilisation. This study also investigated the expression of miRNAs in both virgin and mated male and female *S. frugiperda*, with a focus on their roles in reproduction. A strong negative correlation was observed between miRNA expression levels and their target hub genes, confirming the transcriptional regulation by miRNAs. Additionally, the protein-protein interaction network identified the gene GENE-X, as a central hub, and was also predicted to be the target of miR-X in *S. frugiperda*, involved in the maturation of large ribosomal RNA subunits. This study further provided experimental evidence that either the depletion of miR-X in virgin females or the knockdown of GENE-X in virgin males led to post-mating infertile egg production. These findings validate the regulatory role of the miR-X - GENE-X interaction and underscore its importance in oogenesis and fertilisation.

Keywords: microRNAs; reproduction; transcriptional regulation





**The tale of two genes and sex determination in
Maconellicoccus hirsutus: exploration for pest management via RNAi**

**R. Gandhi Gracy*, Nikita Negi, Selva Babu Selvamani,
Airneni Sunny Rao, Thiruvengadam Venkatesan, M. Mohan and
S.N. Sushil**

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

**Correspondence: gandhi.gracyr@icar.gov.in*

The developmental phenomenon that determines if an embryo is male or female is termed as “sex determination.” The mechanisms that determine sex in insects are similar to any other genetic pathways that lead to the particular traits. As a matter of fact, in insect group exhibits varied mechanism to determine the sex viz., haplo-diploid in Hymenoptera, varied chromosomes or difference in chromosome numbers. However, in few insects, a set of two genes regulating the expression of male and female specific transcripts, as in the case *Maconellicoccus hirsutus*. In this study, we mined around seven genes associated with the sex-determination pathway from the *de novo* transcriptome assembly and characterised the genes. The domain prediction of all these genes revealed the presence of key domains in the genes. The stage specific gene expression analysis using qRT-PCR of sex determining genes in male vs female revealed the significant downregulation of key genes: *sex lethal*, *doublesex*, *fruitless*, and *transformer-2*, with fold change values of (-13.56), (-93.10), (-17.97), and (-24.86) respectively in males. Further the female specific transcript was silenced using RNAi via dsRNA administration, showed the potential of RNAi can be explored for mitigating the pest menace in an efficient ecofriendly manner.

Keywords: dsRNA; *Maconellicoccus hirsutus*; RNAi; sex-determination





**Anchoring accuracy: identifying stable reference genes for
Chrysoperla zastrowi sillemi gene expression studies**

R.S. Ramya^{1*}, D. Sagar¹, P. Bhavitha¹, R.L. Vinodhini¹, Neenu Augustine²,
C. Manjunatha¹, K.T. Shivakumara¹, T. Venkatesan¹, C. Divya¹, M.H. Kavya¹ and
S.N. Sushil¹

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Vellore Institute of Technology, Vellore, India

*Correspondence: ramya.ento@gmail.com

Housekeeping genes are widely utilised as reference genes in Quantitative real-time (qRT-PCR) due to their involvement in fundamental biological processes and presumed uniform expression. However, their stability can vary under different experimental conditions, such as tissue type, developmental stages, biotic, and abiotic stresses. This study evaluates 12 candidate reference genes in *Chrysoperla zastrowi sillemi*, an important biological control agent, under diverse experimental conditions including temperature stress, insecticide treatment, starvation, and developmental stages. The expression stability of genes was assessed using algorithms such as NormFinder, BestKeeper, geNorm, and RefFinder. The results highlight *Actin* and *ARF2* as the most stable reference genes under temperature stress, while *ARF2* and *RAB1A* were optimal for developmental stage studies. *TBP* and *Actin* showed stability under starvation conditions, and *CS6* with *GAPDH* were identified as robust for insecticide treatments. Primer efficiency analysis, melt curve verification, and amplification efficiencies ranging from 92% to 105.5% confirmed the quality of selected primers. These findings provide a validated set of reference genes for reliable normalisation in qRT-PCR studies of *C. zastrowi sillemi*, ensuring precise gene expression analysis under varying biotic and abiotic stress conditions. This study supports the development of molecular tools to further understand the adaptive mechanisms in biological control agents.

Keywords: gene expression analysis; gene stability; reference gene validation; stress responses





**Decoding the genome of a pan-tropical leguminous insect pest,
Maruca vitrata Fabricius (Lepidoptera: Crambidae)**

**D. Sagar^{1*}, M. Mohan¹, P.J. Aneesha¹, S. Selva Babu¹, K. Ashok¹,
T.C. Suman¹, R.J. Suresh¹, N. Vijayakumari¹, C.R. Chandana¹,
R. Gandhi Gracy¹, T. Venkatesan¹, S.N. Sushil¹ and R. Srinivasan²**

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²World Vegetable Centre, Tainan, Taiwan

*Correspondence: garuda344@gmail.com

The spotted or legume pod borer *Maruca vitrata*, is a global insect pest predominantly found in tropical and subtropical areas. It causes severe crop damage and consequently reduce the grain yield of many economically important cultivated legumes. Though it reportedly originated from the Indo-Malayan region, it has split into numerous cryptic species or host races, each of which has its genetic variety and has demonstrated distinct responses to male-released pheromones, host plants, and management tactics. Understanding its evolution to the creation of many cryptic species and their varying responses to pheromones and pesticides is difficult because of the absence of its genomic information. Using PacBio HiFi sequencing and proximity ligation technique (Hi-C), we provide here a high-quality chromosome-scale genome assembly for *M. vitrata*. The 459 Mb genome got assembled into 31 pseudochromosomes and 14 scaffolds with a scaffold N50 of 15.6 Mb. The genome has a repeat content of 36.5% and 23,310 protein-coding genes. The genome completeness analysis using BUSCO with the Insecta lineage captured 98.6% of the complete BUSCO's in which 98.2% of the genes were single copies. This genome-scale data helps to develop genomic-assisted pest management strategies in the future.

Keywords: chromosome-level genome assembly; genome sequencing; *Maruca vitrata*; spotted pod borer





Morphological identification and molecular characterisation of indigenous strains of entomopathogenic fungi isolated from soils of major groundnut growing districts of Andhra Pradesh, India

S. Harika¹, D.V. Sai Ram Kumar^{1*}, Jagdish Jaba², B. Sree Lakshmi³ and S. Gopalakrishnan²

¹Agricultural College, Acharya N.G. Ranga Agricultural University, Bapatla, India

²International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, India

³Acharya N.G. Ranga Agricultural University, Guntur, India

*Correspondence: dv.sairamkumar@angrau.ac.in

The study aimed at identifying and characterising the isolated entomopathogenic fungi from different soils of groundnut growing districts of Andhra Pradesh, India. The identification of the fungi at genus level was carried out by using macroscopic and microscopic examination depending on the colony morphology, shape of conidia and conidiophore. The species level identification of the fungi was carried out by molecular identification. For the molecular characterisation, the extracted fungal genomic DNA was amplified by PCR using ITS 1 and ITS 4. The PCR products were sequenced and compared with the other related sequences in GenBank (NCBI) for the detection of homology. Finally, three fungal Genera were identified i.e., *Beauveria bassiana*, *Lecanicillium lecanii*, *Metarhizium flavoviridae*. The genetic diversity studies among the isolates were carried by using MEGA-X software.

Keywords: *Beauveria bassiana*; genomic studies; *Lecanicillium lecanii*; *Metarhizium flavoviridae*; morphology





**Molecular and biochemical characterisation of symbiotic bacteria
Photorhabdus / *Xenorhabdus* spp.: insecticidal activity against *Galleria
mellonella* and *Holotrichia serrata*, and purification of insecticidal
metabolites**

**C. Sankaranarayanan^{1*}, K.P. Salin¹, K. Hari¹, B. Singaravelu¹, U. Sivakumar²,
S. Karthikeyan² and M. Rajeshkumar¹**

¹ICAR–Sugarcane Breeding Institute, Coimbatore, India

²Tamil Nadu Agricultural University, Coimbatore, India

*Correspondence: chellappasankar@gmail.com

Photorhabdus and *Xenorhabdus* spp. are gram-negative symbiotic bacteria having relationship with entomopathogenic nematodes, *Heterorhabditis* spp. and *Steinernema* spp., respectively. They are known to produce several toxins, antibiotic with antifungal and antibacterial compounds. Twenty-two symbiotic bacteria *Photorhabdus* and *Xenorhabdus* were isolated from *Heterorhabditis* spp. and *Steinernema* spp. maintained in the culture collection of ICAR–SBI, Coimbatore. Molecular characterisation of the symbiotic bacteria isolated was carried out using 16SrDNA specific primers. Eight *P. luminescens* sub sp. *akhurstii* and five *P. luminescens* sub sp. *laumondii*; eight *X. stockiae* and one *X. poinarii* identified. The 16SrDNA sequences were submitted to Genbank. Biochemical characterisation with 27 tests were carried out for all bacterial isolates to identify the gram-negative bacteria. Insecticidal activity of cell and cell free culture of bacterial strains against *G. mellonella* larvae and first instar white grub *Holotrichia serrata* revealed mortality (20–100%) of the tested insects. Purification and identification of insecticidal metabolites from *P. luminescence akhurstii* (SBIPLATND78) was done using GCMS analysis. The total ion chromatogram (TIC) showed presence of 40 compounds and the GCMS profile showed the presence of anti-helminthic and bioactive compounds such as piperazinedione, pyrolol, phenol, hepta oxa cyclo heneicosanone and other compounds. Volatile substance had insecticidal activity (23.3%) against *G. mellonella*.

Keywords: *Galleria mellonella*; *Holotrichia serrata*; insecticidal toxins; symbiotic bacteria



Metabolomics from rhizospheric fluorescent pseudomonads and their potential against bacterial wilt disease of tomato

V. Shanmugaiah*, P. Suresh and V. Vimala Devi

Madurai Kamaraj University, Madurai, India

*Correspondence: shanmugaiah.biological@mkuniversity.ac.in

Tomato production has been dramatically reduced worldwide as a result of bacterial wilt caused by *Ralstonia solanacearum*. In light of this, *Pseudomonas* sp. VSMKU3054 was chosen due to its outstanding biocontrol activity as a potential antibacterial and antifungal agent. *Pseudomonas fluorescens* VSMKU3054 was identified as the chosen isolate using morphological, physiological, biochemical and 16s rDNA investigations. The promising isolate produced remarkable amounts of hydrolytic enzymes including as amylase, protease, cellulase, and chitinase. *P. fluorescens* produces numerous antibacterial and plant growth-promoting compounds, including HCN, siderophores, phosphate solubilisation, and IAA. Using a specific primer and PCR with 629 bp, the essential antimicrobial encoding gene, DAPG was identified. *P. fluorescens* VSMKU3054 exhibited the highest growth and antibacterial activity in King's B medium, as tested at pH 7.0, 35°C, and 36 h. The antimicrobial isolate from *P. fluorescens* VSMKU3054 was characterised using thin-layer chromatography, UV-Vis, FT-IR, GC-MS, and NMR. When compared to a control, the cell viability assay of DAPG against *R. solanacearum* revealed a decrease in the proportion of viable cells and a buildup of reactive oxygen species (ROS), which reduced the pathogen's ability to damage the cell membrane and induce DNA damage. When the biocontrol efficiency of *P. fluorescens* VSMKU3054 and DAPG in greenhouse conditions was assessed, the results revealed a significant decrease in the incidence of bacterial wilt (46.66% and 47.61%) when compared to other treatments. Furthermore, it was observed that *P. fluorescens* VSMKU3054 had a great growth-promoting effect on tomato seedlings. Native pseudomonads have been identified as a superior biological control agent for tomato bacterial wilt disease due to their robust antagonistic action against bacterial and fungal pathogens.

Keywords: antagonistic effect; antibiotic encoding gene; DAPG; wilt disease; tomato rhizosphere





Novel *Bacillus thuringiensis* Berliner crystal toxin gene *Cry8Sa1* for resistance against the white grub *Holotrichia serrata* F. in sugarcane

B. Singaravelu^{1*}, G.S. Suresha¹, C. Appunu¹, N. Crickmore², C. Shu³, J. Zhang³, J. Srikanth¹, K. Hari¹, C. Sankaranarayanan¹, P. Mahesh¹ and R. Nirmala¹

¹ICAR–Sugarcane Breeding Institute, Coimbatore, India

²School of Life Sciences, University of Sussex, Brighton, United Kingdom

³State Key Laboratory for Biology of Plant Diseases and Insect Pests, Chinese Academy of Agricultural Sciences, Beijing, People's Republic of China

*Correspondence: singaravelu.b@icar.gov.in

Bacillus thuringiensis (Bt) is a gram-positive bacterium which produces several toxins that are toxic to several insect orders and other phyla. The genes producing these toxins are widely used in the development of insect resistant transgenic crops. Lepidopteran active *cry1* genes are widely used but *cry* genes for the Coleopteran insects are very limited. Among the toxins synthesised by Bt, *cry8* gene toxin subfamily is found specifically toxic to the members of the Coleopteran family Scarabaeidae. The scarabid *Holotrichia serrata*, is a very important pest in sugarcane causing economic damage to the tune of 100%. In the absence of resistant genotypes for breeding resistant varieties and to circumvent the problems faced in white grub control with available methods, scarabid active Bt crystal toxin genes can be used in the development of transgenic sugarcane that can offer innate resistance much like host plant resistance. To identify and isolate a candidate Bt crystal toxin gene for *H. serrata*, we prospected soils samples in India and isolated a novel Bt isolate Bt 62. Among the two *cry8* genes identified from this isolate and expressed in Bt shuttle vector for bioassay against *H. serrata* grubs, *cry8Sa1* was identified as a candidate gene for construction of *H. serrata* resistant transgenic crops.

Keywords: *Bacillus thuringiensis*; *cry8Sa1*; *Holotrichia serrata*; Scarabaeidae; sugarcane transgenics





Whole microbiome and metatranscriptome analysis of detritivorous insects, white grub and rhinoceros beetle

Mahesh S. Yandigeri^{1*} and Sampada N¹

¹ICAR–National Bureau of Agricultural Insect Resources (NBAIR), Bengaluru, India

*Correspondence: Mahesh.Yandigeri@icar.gov.in

White grub (*Holotrichia serrata* F.) (WG) and rhinoceros beetle (*Oryctes rhinoceros* L.) (RB) are known for their scavenging activity principally engaged in decomposition of plant material and decaying organic matter apart from their pestiferous nature to the crops. With the goal of understanding these two insects focusing on symbionts and digestive enzymes next generation sequencing study was carried out through metagenomic and metatranscriptomic approaches for microbial community and gene expressions, respectively. DNA Shotgun sequencing was used for comparative analysis of WG and RB using Illumina HiSeq 2500. Metagenomic approach for taxonomic classification using Kaiju tool yielded high-coverage draft genomes of abundant and active microorganisms belonging to the phyla Firmicutes, Actinobacteriota, Pseudomonadota and Bacteroidota where *Bacillus* species being the abundant ones in both the insect species. Microbial diversity was found high in RB compared to WG according to DNA Shannon and Simpson diversity indices. A total of 325 bacteria-16S rRNA genes were predicted using Metaerg. Meta-transcriptomic approach linked many of these expressed genes with the coding sequences (CDS) identified from the draft genomes. Comparative distribution of CDS across groups inferred 3864 in RB and 28568 in WG and 118 were common in both insects. Significantly expressed transcripts were identified with p (0.05) value of 9. Enzymes such as α -amylase (carbohydrate metabolism), cellulase (galactose metabolism), protease (tyrosine metabolism) and many other degradative enzymes were evident. This approach yielded a comprehensive image of functional microbes and genes and their related activities from diverse microbial community between the gut of both the insects.

Keywords: meta-transcriptome; microbiome; organic waste degradation; rhinoceros beetle; white grub





Genomic insights into an indigenous *Bacillus thuringiensis* strain with antifungal activity against *Sclerotium rolfsii*

K. Aditya^{1,2}, A.S. Kotasthane², C. Manjunatha^{1*}, S. Ruqiya¹, S.M. Lavanya¹, C. Divya¹,
S. Raksha¹, G. Sivakumar¹ and S.N. Sushil¹

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Indira Gandhi Krishi Vishwavidyalaya, Raipur, India

*Correspondence: manjuc.nbair@gmail.com

Bacillus thuringiensis Berliner is a Gram-positive, rod-shaped bacterium known for its ability to produce endospores and is recognised as a leading biopesticide, due to its benefits, including ease of use, accessibility, proven virulence, and ecofriendly nature. While much research has focused on its insecticidal properties, the bacterium also produces secondary metabolites such as lipopeptides, which show potential against phytopathogens. However, comprehensive studies on the antagonistic effects of *B. thuringiensis* lipopeptides against plant pathogens are scarce. In this study, a novel strain of *B. thuringiensis* BtAr was isolated from a naturally infected cadaver of *Anomala ruficapilla*. The strain was characterised using light and scanning electron microscopy, revealing bipyrnidal, cuboidal, and spherical parasporal crystals. The crude lipopeptide of the strain was extracted and tested for its antifungal activity against *Sclerotium rolfsii* *in vitro*, where it demonstrated complete inhibition of the pathogen at a concentration of 50 µL/mL potato dextrose agar. Hybrid *de novo* whole genome sequencing revealed a circular chromosome of 5,379,913 bp and a plasmid of 175,362 bp, with a GC content of 36.06%. Phylogenetic analysis classified the strain as the *Konkukian* serovar. Genome analysis identified gene clusters related to secondary metabolites with 100%, 85%, 40%, and 35% similarity to petrobactin, bacillibactin, fengycin and paenilamicin, along with novel biosynthetic clusters for zwittermicin A and chitinase. This study is the first to report antifungal activity against *S. rolfsii* in an indigenous *B. thuringiensis* strain, which in the future may offer broad-spectrum capabilities for sustainable crop protection.

Keywords: antagonistic potential; biosynthetic gene clusters; fengycin; hybrid genome assembly; poison food technique





Genomic basis of host selection in *Goniozus nephantidis* (Muesebeck) (Hymenoptera: Bethyridae)

P.J. Aneesha^{1,2*}, M. Mohan^{1*}, T. Venkatesan¹, R. Gandhi Gracy¹, R.S. Ramya¹, D. Sagar¹
and Richa Varshney¹

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Jain University, Bengaluru, India

*Correspondence: anuneena1998@gmail.com; Mohan.M@icar.gov.in

The larval parasitoid *Goniozus nephantidis* (Muesebeck) (Hymenoptera: Bethyridae) regularly attains high levels of parasitism and contributes substantially to biological management of black headed caterpillar, *Opisina arenosella* Walker (Lepidoptera: Xyloryctidae) in coconut ecosystem. This gregarious ectoparasitoid is the dominant species in India and the extent of its parasitism reaches nearly 48% under field conditions, especially in southern India. The behavioural response elicited in *G. nephantidis* in response to various olfactory cues emanated from the opposite sex of the parasitoid, its insect host and host plant is essentially driven to achieve feeding, reproduction and habitat selection. To enhance the parasitism efficiency, it is essential to decipher the role of the genes and genes families involved in olfaction and gustation. In the present study we constructed chromosome-level genome assembly of *G. nephantidis* by sequencing its genome by short and long-read sequencing platforms (Illumina and PacBio) coupled with Hi-C. The genome spanned of 163 Mb in size consisting of 15 scaffolds with the N50 size of 19 Mb. The BUSCO reveals 99.6% of genome completeness under insecta_db10 database. A number of genes involved in chemoreception such as olfaction and gustation were mined and identified from the genomic resource.

Keywords: chemosensory system; genome; *Goniozus nephantidis*; larval ectoparasitoid





Identification and expression analysis of potential effector genes in the cotton mealybug (*Phenacoccus solenopsis*) to understand pest-plant interactions

Anand Bahadur^{1,2}, Shatrughan Shiva³, Manisha Singh^{2,4}, Shalini Srivastava¹ and
Praveen C. Verma^{2,4*}

¹Department of Botany, University of Lucknow, India

²CSIR–National Botanical Research Institute, Lucknow, India

³Department of Entomology, Michigan State University, USA

⁴Academy of Scientific and Innovative Research, Ghaziabad, India

*Correspondence: praveencverma@nbri.res.in

The cotton mealybug (*Phenacoccus solenopsis*) is a major pest affecting cotton crops by feeding on plant sap and significantly reducing yields. When feeding, mealybugs inject saliva into the plant, which may contain molecules known as effectors—proteinaceous or protein-conjugate molecules that manipulate the host plant's cellular processes. These effectors can weaken the plant's defence mechanisms, making it more susceptible to viral and fungal pathogens. In this study, we identified potential effector genes in *P. solenopsis* by analysing expressed sequence tags (ESTs) from related insect pests, *Myzus persicae* and *Acyrtosiphon pisum*. Through bioinformatics analysis, we pinpointed ten candidate effector genes, with eight showing high expression in the mealybug's gut and salivary glands, the primary feeding organs. RNA was isolated from different mealybug tissues—gut, salivary glands, head, thorax, and whole body—and sent for transcriptomic analysis. Our results indicate that these eight genes are predominantly expressed in the gut and salivary glands. To confirm expression patterns, we used quantitative real-time PCR (qRT-PCR), normalising the data with β -*tubulin* as the most stable reference gene across tissues. Our findings highlighted the critical role of these effector genes in potentially subverting plant defenses, allowing the pest to thrive on cotton plants. This research provides insights into pest-plant interactions, with implications for developing pest management strategies targeting mealybug effectors to enhance crop resilience.

Keywords: cotton; effectors; *Phenacoccus solenopsis*; plant defense



Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources



**Impact of CRISPR/Cas9 genome editing on gossypol distribution in cotton:
enhanced seeds for human consumption while retaining insecticidal properties**

Punam Chakraborty^{1,2} and Praveen C Verma^{1,2*}

¹Academy of Scientific and Innovative Research, Ghaziabad, India

²CSIR–National Botanical Research Institute, Lucknow, India

*Correspondence: praveencverma@nbri.res.in

Cotton is the most important textile crop and is also a significant food crop. According to previous research, cotton seed is recognised as an excellent source of high-quality protein for animal and human diets. Cotton seed is rich in many nutrients like proteins, oil, sugars, cellulose, and nutrients. The use of cotton seed protein in food processing is widespread, and it is thought to be a healthy dietary additive and protein-rich feed. However, the presence of the toxic substance known as “gossypol” restricts the production of edible protein products and oil from cottonseed. A polyphenolic substance named gossypol is found in the pigmented gland of cotton plants. Gossypol produces food discoloration and is harmful to monogastric animals like humans. These compounds defend the plant from insect herbivory, pathogens and parasitic organisms. Several effective approaches have been established to get free of the gossypol content in cotton seeds, like developing commercial varieties of gossypol-free cotton by introducing the glandless trait. Later, in the year 2019, Rathore’s group developed a genetically stable transgenic RNAi cotton line driven by a seed-specific promoter, with extremely poor gossypol in cotton seeds but gossypol level was normal in other parts of the plants to prevent susceptibility to insect pests. Considering the positive relationship between gossypol glands, we have identified crucial gossypol synthesising gene (δ -cadinene) through transcriptome analysis and also identified pigmented gland forming genes. We aim to develop a novel “genome edited” cotton variety having glanded leaves with glandless seeds by using CRISPR/Cas9 so that seeds can be directly used as food source and oil. Our genome edited plant contains gossypol in vegetative organs thus retains their insecticidal property but simultaneously reduced level of gossypol in seeds for human consumption.

Keywords: cadinene synthase; cotton; gland forming gene; gossypol; reduced susceptibility to insect pests





Insights into the core RNAi machinery genes in Indian green lacewing predator, *Chrysoperla zastrowi sillemi*

V.S. Chinnu^{1,2*}, M. Mohan¹, P.J. Aneesha¹, R. Manjunatha³ and T.C. Suman^{1,2}

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Gandhi Krishi Vigyana Kendra, University of Agricultural Sciences, Bengaluru, India

³College of Sericulture, Chintamani, India

*Correspondence: chinnuvikramannair@gmail.com

The Indian green lacewing predator, *Chrysoperla zastrowi sillemi* (Esben-Petersen) (Neuroptera: Chrysopidae), commonly known as aphid lion, comprises an eminent group of predators with great potential for biological control of many insect pests. RNA interference (RNAi) is a natural regulatory gene silencing mechanism present in eukaryotes. RNAi technology is based on the introduction of dsRNA which, after processing by the RNAi machinery genes, binds to the mRNA transcript of the target gene causing its knockdown. This technology offers great potential in insect pest management. Their sequence-guided mode of action facilitates a high species-selectivity, preventing harm on non-target organisms. RNAi in insects and studies have shown that adverse effects in non-target insects such as *C. zastrowi sillemi* cannot always be ruled out since no published literature is available. Hence, the core machinery genes facilitating the RNAi pathway were mined from the genomic datasets of *C. zastrowi sillemi* (NCBI Project ID: PRJNA905226) and identified through various bioinformatics tools like tBLASTn and hmmsearch. Core machinery genes like Argonaute2 (*Ago2*) and Dicer2 (*Dcr2*) of siRNA pathway and Dicer1 (*Dcr1*), Drosha, Pasha (DGCR8) and Loquacious (*Loqs*) of miRNA pathway were identified. Further, the transmembrane dsRNA transporter protein, systemic RNA interference deficient-1 (*Sid1*) gene responsible for systemic RNAi was also identified. The expression patterns of the core RNAi machinery were evaluated using RT-PCR.

Keywords: *Chrysoperla zastrowi sillemi*; core machinery genes; RNAi





**Decoding the genetic landscape of *Cnaphalocrocis medinalis*:
evidence from ITS2 gene studies**

Soumya Shephalika Dash^{1,2*}, Prasanthi Golive^{2*}, C. Parameswaran², Sucharita Mohapatra², Partha Sarathi Tripathy³, Prakash Chandra Rath², Hirak Chatterjee¹, Arup Kumar Mukherjee² and Shyamaranjan Das Mohapatra²

¹Institute of Agriculture, Visva-Bharati, Sriniketan, India

²ICAR–National Rice Research Institute, Cuttack, India

³College of Fisheries, Rani Lakshmi Bai Central Agricultural University, Jhansi, India

*Correspondence: soumyadashshephalika@gmail.com; prasanthigolivi@gmail.com

Cnaphalocrocis medinalis, a major rice pest in Asia, poses significant threats to agricultural productivity. Understanding its genetic diversity and population structure is essential for developing targeted pest management strategies. This study focused on the nuclear internal transcribed spacer 2 (ITS2) gene, analysing 63 sequences from India, China, and South Korea. This included 21 newly generated sequences from *C. medinalis* specimens collected from major rice-growing regions of India. The study revealed high nucleotide diversity ($\pi = 0.72087$) and haplotype diversity ($H_d = 1$) in Indian populations compared to lower diversity outside India. Shared haplotypes like Hap_1 spanned all regions, indicating ancestral gene flow, while localised haplotypes reflected regional adaptations. AMOVA attributed 43.86% of genetic variation to differences among populations and 56.14% to within-population variation. Phylogenetic analysis identified polyphyletic patterns in Indian populations and monophyletic clades in China and South Korea, showcasing complex evolutionary dynamics. Neutrality tests supported evidence of population expansion in Indian populations, whereas populations outside India displayed stability. Motif analysis of ITS2 sequences further supported regional adaptations, with conserved motifs across all populations and unique motifs confined to specific regions. These findings provide critical insights into the evolutionary dynamics and genetic structure of *C. medinalis*, informing pest management strategies tailored to specific regions.

Keywords: genetic diversity; haplotype; ITS2; leaf folder; phylogenetics





**Metabolomic profiling and genome-wide analysis of *Bacillus subtilis*
NBAIR-BSWG1 reveals cyclic lipopeptides as key antagonists**

C. Divya, K. Aditya, S. Ruqiya, S. Raksha, S.M. Lavanya, G. Sivakumar, A. Kandan,
C. Manjunatha* and S.N. Sushil

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

*Correspondence: manjuc.nbair@gmail.com

Understanding bacterial genetics and metabolism is vital for developing biopesticides. This study investigates *Bacillus subtilis* NBAIR-BSWG1, a strain well known for its antagonistic potential. Crude lipopeptides extracted from the strain were evaluated for *in vitro* activity, showing complete inhibition of *Rhizoctonia solani* at a concentration of 50µL/mL potato dextrose agar. To delve deeper into its antagonistic mechanisms, we conducted whole-genome sequencing of NBAIR-BSWG1 using Illumina NextSeq500. Subsequent analysis with the BlastX diamond tool revealed 19 key biosurfactant genes, including surfactin (*srfAA*, *srfAC*, *srfAD*, *srfP*), fengycin (*ppsE*, *ppsD*, *ppsC*, *ppsB*), and putisolvin (*dnaK*), which were further confirmed by PCR using specific primers. Meanwhile, antiSMASH analysis revealed gene clusters with 100% similarity to those responsible for the synthesis of fengycin, bacilaene, bacillibactin, subtilosin A, and bacilysin, as well as clusters with 82% similarity to surfactin synthesis genes. Additionally, liquid chromatography-mass spectrometry was performed to analyze the cell-free extract produced by NBAIR-BSWG1, revealing the presence of various cyclic lipopeptides, including multiple peaks corresponding to surfactin, fengycin, iturin, and several novel lipopeptide compounds. This study highlights *B. subtilis* NBAIR-BSWG1 cyclic lipopeptides as a key to broad-spectrum bio-control and establishing the strain as highly potent.

Keywords: biocontrol; biosynthetic gene clusters; LC-MS; poison food technique; *Rhizoctonia solani*





**Genome editing of detoxification gene inventories in insects using CRISPR:
a systematic review and meta-analysis**

Vinithashri Gautam* and M. Mohan

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

**Correspondence: vinithashri1994@gmail.com*

Decoding the molecular mechanisms of insect resistance to insecticides and host plant adaptation is inevitable for effective and sustainable Insecticide Resistance Management (IRM). Use of reverse genetics approaches for deciphering the “Target Site Resistance” helps to control the targeted pest alone rather than affecting the non-target insects including biocontrol agents and pollinators. Understanding the role of mutations in xenobiotic resistance helps us in judicious use of pesticides. CRISPR tool-based genome editing aids in creating mutations in these detoxification genes and reveals their role in insect resistance development. The current review presents a comprehensive information on CRISPR mediated genome editing of detoxification genes in insects and their role in resistance development. Knock-out/-in and point mutations in- ABCs, CCEs, CYPs, GSTs, nAChRs, RyRs, UGTs and other genes related to target site resistance either made insects resistant or susceptible to xenobiotics. PRISMA protocol was followed in collection and inclusion of articles for this review. The quality of the included articles was validated by a risk of bias analysis. This systematic review and meta-analysis provide insight into present scenario and future possibilities for studying detoxification genes of insects with CRISPR tool.

Keywords: CRISPR; genome editing; insect detoxification genes; insecticide resistance; systematic review





**Unveiling epigenetic dynamics in insect–pathogen interactions:
implications for pest control**

Ayushi Gupta^{1*} and Ramcharan Bhattacharya¹

¹ICAR–National Institute for Plant Biotechnology, New Delhi, India

*Correspondence: ayushi.gupta3220@gmail.com

Epigenetic mechanisms drive diverse biological phenomena in insects. Studies have demonstrated how epigenetic reprogramming enhances genetic flexibility, aiding insect adaptation. However, we believe the significance of epigenetic modifications goes beyond this and influences insect-pathogen dynamics and coevolution. Insects serve both as a vector and the host for critical viral diseases in plants and animals. Studies have shown that they undergo massive phenotypic shifts upon encountering viral pathogens. This rapid insect-pathogen co-adaptation challenges the exclusive role of genetic changes. In which case, epigenetic modifications can serve as an additional source of rapid and reversible phenotypic variation, shaped by insect and pathogen selection pressures. With this view, we are using a combination of methylation inhibitors, advanced sequencing techniques, and computational analyses to investigate the role of epigenetics role in shaping insect-pathogen interactions. Our study focuses on unravelling the epigenetic underpinnings of viral acquisition, persistence, and transmission in the whitefly (*Bemisia tabaci*), a major agricultural pest and a well-known vector of various economically devastating Begomoviruses. We believe that understanding the dynamic interplay between epigenetic modifications and insect-pathogen interactions offers a compelling avenue for understanding rapid phenotypic adaptation and co-evolution. By bridging the fields of epigenetics, entomology, and plant pathology, this research highlights the potential of epigenetic insights in developing innovative biological control strategies to mitigate crop losses. Moreover, this research aligns with national and global priorities of sustainable agriculture and food security, offering transformative solutions to counter the growing challenges of insect-borne diseases.

Keywords: epigenetic epidemiology; host-pathogen interactions; pest management; phenotypic plasticity; viral epigenetics



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Introgression of susceptible alleles: a novel strategy towards *Bt* resistance management in cotton pink bollworm, *Pectinophora gossypiella*

Suresh R. Jambagi^{1,2*}, M. Mohan¹, K. Muralimohan² and T. Venkatesan¹

¹ ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

² University of Agricultural Sciences, Bengaluru, India

*Correspondence: jambagisuru@gmail.com

Genetically modified (GM) *Bacillus thuringiensis* (Bt) cotton was developed and introduced primarily to manage cotton bollworm pests. Although it has been effective against target pests, the pink bollworm, *Pectinophora gossypiella* (Gelechiidae: Lepidoptera), has evolved significant resistance to both Cry1Ac and Cry2Ab toxins, complicating its control in India. To address this challenge, a strategy was employed to introgress Cry toxin-susceptible alleles into resistant field populations by releasing large numbers of laboratory-reared, homozygous Bt-susceptible male moths. A dose-response bioassay conducted on susceptible and field-collected resistant populations revealed LC₅₀ values of 0.011 ppm ($\chi^2 = 0.829$; df=3; h= 0.414) for the susceptible population and 0.931 ppm ($\chi^2 = 5.334$; df=3; h= 1.781) for the resistant population with a resistance ratio (RR) of 84.64 for Bollgard® II Bt cotton. The introgression of susceptible moths into the resistant population demonstrated a non-sex-linked transfer of genes conferring resistance to Cry toxins (Cry1Ac and Cry2Ab). LC₅₀ values for the crossed population were 0.135 ppm ($\chi^2 = 2.910$; df=3; h= 0.970; RR= 12.27) and 0.144 ppm ($\chi^2 = 1.729$; df=3; h= 0.576; RR= 13.09) for male and female moths infused, respectively. Successive generations of release of susceptible moths led to a measurable dilution in Bt Cry toxin resistance levels. The dose-response patterns of the resistant, susceptible, and their crossed populations indicated that the resistance alleles are autosomal and homozygous recessive. This approach shows potential as a para-biological strategy for diluting Bt resistance in pink bollworm under field conditions.

Keywords: Bt cotton; cry toxins; *Pectinophora gossypiella*; resistance dilution; susceptible alleles





Genomic characterisation of entomopathogenic fungus associated with natural mycosis of sugarcane leaf hopper

Janaki Prasad^{1*}, P. Kishore Varma², N. Kamakshi², A. Bavana Keerthi¹ and Hameeda Bee³

¹Agricultural College, Bapatla, India

²Regional Agricultural Research Station, Lam, India.

³Osmania university, Hyderabad, India

*Correspondence: janakiprasad24@gmail.com

Pyrilla perpusilla, commonly referred to as the sugarcane leaf or plant hopper, is a significant pest affecting sugarcane and sorghum crops in Asia. In February 2023, natural mycosis was observed on both adult and nymph stages of *P. perpusilla* in China Ogirala village, Krishna district. The infected specimens were collected, and an entomopathogenic fungus was isolated. Morphological and molecular analysis, specifically ITS sequence homology, identified the fungus as *Metarhizium koreanum*, designated strain PCO1. BLAST analysis revealed that the *M. koreanum* sequence aligned with several *Metarhizium* species, necessitating further genomic clarification. To address this, *de novo* next-generation sequencing (NGS) was performed using the Illumina platform. This approach aimed to distinguish *M. koreanum* PCO1 from closely related species like *M. anisopliae* and to gain a deeper understanding of its genetic makeup for biological control applications. Microscopic examination showed extensive parasitism of *P. perpusilla* by *M. koreanum*. Contigs shorter than 200 base pairs were excluded from the genome assembly, which was evaluated using QUAST v5.0.2. Genome completeness was assessed with BUSCO v5.3.2, and functional annotations, CRISPR-Cas genes, and secondary metabolites were identified using ANTIMASH and GC-MS. Light microscopy revealed dense mycelial growth and sparser growth on the forewings, legs, and snout. *In vitro* pathogenicity tests confirmed the PCO1 strain's effectiveness. This comprehensive analysis underscores the potential of *M. koreanum* PCO1 as a promising biological control agent for *P. perpusilla*, requiring further field evaluations to validate its efficacy and impact on other hosts.

Keywords: *Metarhizium anisopliae*; *Metarhizium koreanum*; *Pyrilla perpusilla*; secondary metabolites; whole genome





**Insights into transcriptional changes in male accessory glands of
Spodoptera litura (Fabricius) (Lepidoptera: Noctuidae) under heat stress**

Hemant Kumar^{1*}, D. Sagar², Sweta Verma¹ and S. Subramanian¹

¹ICAR–Indian Agricultural Research Institute, New Delhi, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: hksahu.iari@gmail.com

The destructive insect pest, tobacco cutworm (*Spodoptera litura*), infesting more than 100 crops, is leaving a trail of destruction that continues to threaten food security and livelihood that sparkles an urgent requirement of its management. Its high reproductive potential, rapid insecticide resistance development and mobility make it more challenging to manage. However, the greatest challenge lies in the impact of rising temperature, driven by global climate change, which significantly influences its development, survival, and population dynamics. To examine the impact of heat stress on accessory gland proteins (ACPs), male accessory glands (MAGs) were dissected out from fresh male moths emerged from larvae exposed to heat stress (44 °C) and control (27 °C). Subsequently, RNA sequencing and bioinformatic analysis were carried out which revealed that a total of 15,783 unigenes exhibited differential expression, out of which 345 genes were downregulated and 229 genes were significantly upregulated. Our study report that genes like carboxypeptidase, JHEPH, JHAMT, serine proteases, circadian controlled clock, lipase, glucose dehydrogenase, chymotrypsin and odorant receptors got downregulated. However, genes like odorant binding proteins, acyl co-A desaturase, insulin like growth factor, doublesex and mab-3-related transcription factor, Nose resistant to fluoxetine protein 6, Elongation of very long chain fatty acids protein and juvenile hormone-suppressible protein 2 got upregulated. Overall, these gene networks working in a cumulative and collective manner offset heat stress effects, preserving the biology like oxidative stress, sperm, female, hormonal, photoperiod, adaptation and reproductive efficiency under challenging environmental conditions. Current findings will help in developing pest management strategies against this voracious pest.

Keywords: ACPs; heat stress; RNA seq; *Spodoptera litura*; temperature





Molecular characterisation of biocontrol potential and plant growth promoting *Bacillus thuringiensis* strains isolated from the Western Ghats of India

S.M. Lavanya^{1,2}, R. Muthuraju², A. Kandan¹, R.S. Ramya¹, C. Divya¹, S. Raksha¹,
K. Aditya¹, S.N. Sushil¹ and C. Manjunatha^{1*}

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²University of Agricultural Sciences, Bengaluru, India

*Correspondence: manjuc.nbair@gmail.com

Western Ghats is one of India's richest biodiversity hotspots and is home to diverse microbial communities of significant agricultural importance. *Bacillus thuringiensis* is widely recognised for its pesticidal properties however, limited exploration has been done for its plant growth-promoting activities. In this study, 100 *B. thuringiensis* strains were isolated and characterised from the Western ghats of India. Crystal protein production displayed diverse morphologies including bipyrmidal, spherical, and cuboidal forms. Molecular characterisation through 16S rRNA sequencing confirmed 99–100% homology with reference *B. thuringiensis* strains. Biochemical assays revealed various enzymatic activities crucial for biocontrol, with protease activity detected in 89 strains, lipase in 87, lecithinase in 64, and chitinase in 27 strains. These enzymes play essential roles in degrading proteins, lipids, and chitinous materials in pests and phytopathogens, thereby enhancing the biocontrol potential of *B. thuringiensis* strains. Furthermore, the production of indole-3-acetic acid and ammonia by all 100 strains was confirmed through *in vitro* studies, highlighting their role in promoting plant growth. Phosphate solubilisation was observed in 81 isolates, while siderophore production was detected in 35 strains, indicating the ability of *B. thuringiensis* strains to enhance nutrient availability and improve soil fertility. Thus, this study highlights the dual functionality of *B. thuringiensis* as both a potent biocontrol agent and a plant growth promoter, offering promising eco-friendly alternatives to chemical pesticides and fertilisers. The findings further emphasise the Western Ghats as a valuable reservoir of beneficial microbes, providing critical insights into the potential application of *B. thuringiensis* in integrated pest and disease management for sustainable agriculture.

Keywords: biocontrol; chitinase; lecithinase; plant growth promotion; siderophore production





Gene expression dynamics in rice challenged with *Magnaporthe oryzae* and biocontrol agents

Sucharita Mohapatra^{1*}, S.R. Prabhukarthikeyan², Gayatri Biswal¹, U. Keerthana² and Soumya Shephalika Dash²

¹Odisha University of Agriculture and Technology, Bhubaneswar, India

²ICAR–National Rice Research Institute, Cuttack, India

*Correspondence: sucharitamohapatra450@gmail.com

Rice blast, caused by the fungus *Magnaporthe oryzae* (anamorph *Pyricularia oryzae* Cava), is one of the most destructive diseases affecting rice cultivation. Biocontrol agents such as *Streptomyces* spp. offer a sustainable and eco-friendly alternative for managing plant diseases. This study focused on isolation of various *Streptomyces* spp. from rice rhizosphere soils of Odisha and evaluation of their effectiveness against *M. oryzae*. Among the isolates, *Streptomyces caeruleatus* S14 demonstrated the highest efficacy, reducing the mycelial growth of *M. oryzae* by 74.7%. Quantitative RT-PCR analysis was performed to assess the expression levels of defense-related genes such as peroxidase (Prx), polyphenol oxidase (PPO), phenylalanine ammonia lyase (PAL), superoxide dismutase (SOD), and catalase (CAT) in the rice variety Tapaswini following inoculation with *M. oryzae* (RLB 06) and treatment with different *Streptomyces* isolates at intervals of 0, 24, 48, 72, 96, and 120 hours. Significant differences were observed in the expression of peroxidase, polyphenol oxidase, phenylalanine ammonia lyase, superoxide dismutase, and catalase genes among treatments compared to the control, with the liquid formulation of S14 inducing the highest relative fold changes of 70.63, 73.56, 83.6, 69.95, and 72.35, respectively. In contrast, gene expression levels in healthy control plants remained significantly lower. The study highlights the potential of *S. caeruleatus* S14 as an eco-friendly biocontrol agent for mitigating rice blast by enhancing the plant's defense mechanisms, emphasising its importance for sustainable agriculture.

Keywords: catalase; peroxidase; phenylalanine ammonia lyase; polyphenol oxidase; superoxide dismutase





Decoding the halloween genes: RNAi-based functional analysis of *shade* and *shadow* in *Maconellicoccus hirsutus* (Green)

Nikita Negi^{1,2}, R.G. Gracy^{1*}, Selva Babu Selvamani¹, Ashok Karuppannasamy³,
A. Sunny Rao^{1,2}, T. Venkatesan¹, M. Mohan¹ and Vinod Kumar Dubey²

¹ ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

² Indira Gandhi Krishi Vishwavidyalaya, Raipur, India

³ TATA institute for Genetics and Society, Bengaluru, India

*Correspondence: gandhi_gracy@yahoo.co.in

Ecdysteroids, a class of steroid hormones, are pivotal for moulting cascade during insect growth and development. The “Halloween genes” - a collection of genes residing within the mitochondrial and clan 2 of CYP450 families regulate the biosynthesis of 20 hydroxyecdysone (20E), an active moulting hormone from dietary cholesterol. Genes namely *neverland* (*nvd*), *shroud* (*sro*), *spook* (*spo*; CYP307A1), *phantom* (CYP306A1), *disembodied* (CYP302A1), *shadow* (CYP315A1), and *shade* (CYP314A1) are the prominent members of this Halloween ensemble. Among these, Spook has two paralogs, *spookier* (CYP307A2) and *spookiest* (CYP307B1). *Shadow* (*sad*) regulates the crucial conversion of 2-deoxyecdysone into ecdysone, while *shade* (*shd*) catalyses the final step of this pathway, transforming ecdysone into the active hormone, 20E. The current study delineated the significance of *shd* and *sad* genes, in insect development through functional characterisation and expression studies by utilising qRT-PCR. Furthermore, this study employed RNA interference (RNAi) to investigate the functional consequences of gene knockdown for these two genes. Our findings unveiled that RNAi-mediated knockdown of MhCYP315A1 (*sad*) and MhCYP314A1 (*shd*) significantly reduced their expression levels by 85% in 24h followed by 51% at 48 h (*sad*) and 40% at 48h (*shd*). Concomitantly, we observed significant delays in molting, accompanied by the development of deformed phenotypes. These findings underscore the critical roles of *shd* and *sad* in regulating ecdysteroid biosynthesis. This study provides valuable insights into the molecular mechanisms underlying insect metamorphosis and creates avenues for developing innovative RNAi-based strategies for the sustainable management of *M. hirsutus*.

Keywords: halloween genes; *Maconellicoccus hirsutus*; RNAi; *shade*; *shadow*





**Identification and expression analysis of Cytochrome P450 genes in
Phenacoccus manihoti Matile-Ferrero (Hemiptera: Pseudococcidae)**

**K.M. Nived^{1,2}, R.G. Gracy^{1*}, Selva Babu Selvamani¹, Nikita Negi^{1,3}, A. Sunny Rao^{1,3},
N. Veeramanikanta Reddy¹ and T. Venkatesan¹**

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²University of Agricultural Sciences, Bengaluru, India

³Indira Gandhi Krishi Vishwavidyalaya, Raipur, India

*Correspondence: gandhi_gracy@yahoo.co.in

Phenacoccus manihoti is a highly destructive pest of cassava globally. While comprehensive biological and ecological investigations of *P. manihoti* have been conducted in its native and introduced regions, the paucity of genetic data has impeded our understanding, especially regarding the molecular underpinnings of its growth and development. Cytochrome P450 (CYP450) genes represent one of the most diverse gene families found across numerous insect species and play a crucial role in various physiological processes like the synthesis and degradation of ecdysteroid and juvenile hormones, as well as the metabolism of xenobiotic compounds. This study employs the construction of *de novo* transcriptome from crawler and adult stages of *P. manihoti*, followed by identification, nomenclature and phylogenetic classification of CYPome. 55 proteins were identified as CYP450 genes through a comparative analysis of predicted protein sequences across various databases. Phylogenetic analysis categorised the identified CYP450 genes of *P. manihoti* into four major CYP clans: the mitochondrial clan, clan 2, clan 3 and clan 4. These genes were further classified into 15 families and 23 subfamilies, revealing four new subfamilies (CYP7IGU, CYP87M CYP7064L and CYP706AM). Furthermore, quantitative real-time PCR analysis of ten selected CYP450 genes revealed notable variations in their expression between the crawler and adult stages. This study of CYP450 expression profile lays the groundwork for future functional studies to elucidate the roles of these genes in the growth, development and adaptability of this important agricultural pest.

Keywords: Cytochrome P450; expression analysis; *Phenacoccus manihoti*; phylogenetic classification; quantitative real-time PCR





Deciphering limb regeneration potential in ladybird beetles: a potent biocontrol against aphids

S. Pandita^{1,2}, G. Mishra² and P.C. Verma^{1,3*}

¹CSIR–National Botanical Research Institute, Lucknow, India

²University of Lucknow, Lucknow, India

³Academy of Scientific and Innovative Research, Ghaziabad, India

*Correspondence: praveencverma@nbri.res.in

Crops are constantly subjected to biotic stress, resulting in physiological damage and alterations to their metabolism, lowering their yield. Aphids feed on crops by sucking sap from the upper leaves. The infected leaves become covered in honeydew, which makes the plant sticky and results in its wilting. This impairs photosynthesis, which can have an impact on crop yield. Ladybirds are gaining much scientific attention due to their biocontrol properties as they feed on aphids and protect crops against their infestation. Unraveling the genes and pathways involved in limb regeneration in the prospective biocontrol agent, *Cheilomenes sexmaculata* is the main objective of this study. For this, the RNA-Seq platform was used to execute *de novo* transcriptome assembly and differential gene expression profiling of beetles at different time intervals post-amputation. For accurate normalisation of the target genes, the stability of five housekeeping genes was investigated and gene expression profiles were analysed by geNorm, normFinder, and refFinder. *Actin* turned out to be the most stable reference gene followed by *elongation factor-2* and *glyceraldehyde-3-phosphate dehydrogenase* and were taken as internal controls for validation of the transcriptomics results. Additionally, RNA interference (RNAi) technology was employed to validate target genes involved in regeneration. Several genes from the *Hedgehog* (*Hh*), *Wnt*, and *JAK-STAT* pathways were found to be crucial for the regeneration process. This study lays the foundation for an in-depth omics dissection in this emerging biocontrol agent and also paves the way for various research on the evolution of limb regeneration.

Keywords: biotic stress; ladybird; reference gene; RNA interference; transcriptome





Molecular phylogenetics of bacterial endosymbiont *Wolbachia* associated with *Tuta absoluta* populations

Arpit Prashar¹, Ashok B. Hadapad¹, Vikas¹, Basavaraj S. Kalmath² and Ramesh S. Hire^{1*}

¹Bhabha Atomic Research Centre, Mumbai, India

²University of Agricultural Sciences, Bengaluru, India

*Correspondence: rshire@barc.gov.in

The tomato leaf miner, *Tuta absoluta*, is a significant and invasive insect pest that affects tomatoes and other solanaceous plants. To study its interactions with reproductive endosymbiotic bacteria, *T. absoluta* samples were collected from 10 different locations across India. The presence of symbionts such as *Arsenophonus*, *Cardinium*, *Spiroplasma* and *Wolbachia* was assessed in both wild and laboratory-reared populations. PCR assay results revealed no infections by *Arsenophonus*, *Cardinium* or *Spiroplasma* in any of the populations. However, *Wolbachia* infections were detected in 42.8% to 91.6% of field-collected samples. Further genotyping of *Wolbachia*-positive samples using multi-locus sequence typing (MLST) and WSP analyses showed that a dominant strain, ST41, was present in most populations, except for samples from southern India, which harboured two strains-ST41 and ST367. Phylogenetic analysis using Bayesian inference clustered *Wolbachia*-positive samples into two supergroups (A and B) based on 16S rRNA and concatenated MLST/WSP sequences. Strain ST41 belonged to supergroup B, while strain ST367 was classified under supergroup A. The high prevalence of *Wolbachia* and its low genetic diversity in natural *T. absoluta* populations highlight the potential for developing *Wolbachia*-based pest management strategies.

Keywords: phylogeny; reproductive parasite; tomato leaf miner; *Wolbachia*





Unveiling the genomic landscape of NBAIR BSWG1, a potential *Bacillus subtilis* strain

S. Raksha, K. Aditya, C. Divya, S. Ruqiya, S.M. Lavanya, G. Sivakumar,
A. Kandan, S.N. Sushil and C. Manjunatha*

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

*Correspondence: manjuc.nbair@gmail.com

Bacillus subtilis NBAIR BSWG1 is an efficient indigenous strain with broad-spectrum antagonistic activity. In this study, whole genome sequencing (WGS) of NBAIR BSWG1 was performed to explore the genomic characteristics responsible for its effectiveness. WGS produced 17,107,973 paired-end reads with 42.61% GC content and a genome size of 4.1 MB. Gene prediction identified 4,313 genes, 57 tRNAs, and 4,153 coding sequences. Gene ontology revealed 1,106 genes linked to biological processes, 1,197 to molecular function, and 934 to cellular components. Antimicrobial resistance studies showed that many genes, including *mphK*, *tmrB*, *vanT*, *vanG*, *vmlR*, *ykkC*, *ykkD*, *qacJ*, and *qacG*, code to produce antibiotics. All the NBAIR BSWG1 protein-coding genes were grouped into 9,899 gene clusters by comparative genomic analysis, of which 466 genes make up the core genome. Four new zwittermicin A biosynthesis gene clusters with antibacterial properties were identified in the NBAIR BSWG1 genome by the Bt_toxin_digger analysis. PHASTER analysis of NBAIR BSWG1 identified two phage sequences of evolutionary significance: PHAGE_Brevib_Jimmer2, a fully intact and complete phage, and PHAGE_Aeriba, a partial and non-functional phage. Variant calling analysis revealed 32,456 SNPs, predominantly located in genic regions, along with six indels identified in intergenic regions. Overall, WGS revealed detailed insights into the genetic characteristics of the NBAIR BSWG1 strain, emphasising its potential as a useful biocontrol agent with broad-spectrum antimicrobial activities.

Keywords: antimicrobial resistance; KEGG pathway; SNP; whole genome; zwittermicin





**Effect of *lambda* cyhalothrin on redox potential of *Trichogramma chilonis* —
molecular basis of combat assessment**

K. Roopa¹, Richa Varshney², T. Venkatesan² and P. Niranjana^{1*}

¹Kuvempu University, Shankaraghatta, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: bpniru@gmail.com

Indiscriminate use of pesticides has resulted in the development of resistance in many lepidopteran insect pests, with more emphasis laid on the inclusion of natural enemies in pest management programs in agriculture. The efficiency of biocontrol agents in the ecosystem is highly hindered by various factors like pesticide application by the farmers and is very much susceptible to insecticides. Egg parasitoids have fascinated many biological control practitioners, and they control the pest damage in the initial stage itself by parasitising the host egg. *Trichogramma chilonis* has been a widely used biocontrol agent for the management of agricultural pests belonging to Lepidoptera. Reactive oxygen species are produced as endogenous products of cellular metabolism. There exists a regulatory equilibrium between their synthesis and scavenging. The use of insecticides disrupts the homeostasis as they cause overproduction of ROS in insects, including natural enemies, which can lead to oxidative stress and a variety of negative effects. In the present study, *Trichogramma chilonis* was subjected to sublethal concentration of *lambda* cyhalothrin. Oxidative stress markers were assessed in terms of protein oxidation (measured as Advanced Oxidation Protein Products, AOPP), lipid peroxidation (quantified as Malondialdehyde), sialic acid levels, total thiol content and antioxidant capacity by Cupric Ion-Reducing Antioxidant Capacity (CUPRAC), and 2,2'-azino-bis (3-ethylbenzothiazoli-6-sulfonic acid) (ABTS) cation radical scavenging activity. The activity of Superoxide Dismutase (SOD) and Catalase was investigated. By using in-house transcriptome of *T. chilonis*, SOD and Catalase-specific primer pairs were designed, and their expression levels were assessed by performing qPCR.

Keywords: antioxidant capacity; catalase; oxidative stress markers; qPCR; superoxide dismutase





Multilocus sequence typing and development of a species-specific PCR marker for specific identification of *Lysinibacillus sphaericus*

S. Ruqiya^{1,2}, N. Nagaraju², D. Biplab¹, K. Aditya¹, K.T. Shivakumara¹, R.S. Ramya¹,
A. Kandan¹, C. Manjunatha^{1*} and S.N. Sushil¹

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²University of Agricultural Sciences, Bengaluru, India

*Correspondence: manjuc.nbair@gmail.com

Lysinibacillus sphaericus is an entomopathogenic bacterium that targets mosquitoes, particularly *Culex pipiens*, and agricultural pests like *Spodoptera litura*. It also exhibits antagonistic activity against fungi such as *Alternaria alternata*, *Aspergillus* spp. and *Sclerotinia* spp., providing an eco-friendly alternative to chemical insecticides and fungicides. However, limited studies have been carried out to understand its genetic diversity and a species-specific molecular diagnostic assay for its precise detection is yet to be developed. Multi-Locus Sequence Typing (MLST) is a rapid technique to study the genetic diversity and evolutionary relationships within and between bacterial species. Hence, in this study, MLST was employed to assess the genetic diversity of *L. sphaericus* using 12 housekeeping genes, including 16S *rRNA*, *glpF*, *gmk*, *ilvD*, *pta*, *pur*, *pycA*, *tpi*, *clpC*, *gdpD*, *panC* and *dinB*. The results revealed significant nucleotide variability among *Lysinibacillus* species, with the *panC* gene showing the highest variability (43.28%), followed by *dinB* (42.48%), *gdpD* (32.36%), and *pur* (31.30%). A phylogenetic tree based on the *panC* gene demonstrated a distinct separation between *Lysinibacillus* sp. and *Bacillus* sp. Hence, *pantothenate synthetase (panC)* gene was chosen to develop a species-specific PCR marker due to its higher polymorphic sites. A PCR-based species-specific marker developed using the *panC* region showed a specific amplicon of 776 bp in *L. sphaericus* and no amplification was found in other related bacterial species used in the study. The PCR-based species-specific detection assay developed in the study offers early and accurate identification of *L. sphaericus* in bioformulations, ensuring quality control in commercial products.

Keywords: biocontrol; bioformulations; detection; genetic diversity; pantothenate synthetase





Micro RNAs (miRNAs) — prospective targets for insect pest management

C. Sabitha^{1*}, D.V. Sai Ram Kumar¹, R.G. Gracy², V. Prasanna Kumari¹ and
B.S. Manjunatha²

¹Acharya N.G. Ranga Agricultural University, Bapatla, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: sabithachellem@gmail.com

MicroRNAs (miRNAs) are endogenous regulatory RNA molecules, 21-24 nucleotides in length, that modulate gene expression post-transcriptionally by base pairing with target sites within messenger RNAs (mRNAs), typically binding complementary seed match sites in the 3' untranslated region. These non-coding RNAs regulate vital biological processes, including development, reproduction, metamorphosis, immunity, and insecticide resistance. Discovered first in *Caenorhabditis elegans*, miRNAs are now identified across diverse species, including insects, using computational tools like PicTar, TargetScan and RNAhybrid. MicroRNA biogenesis begins with the transcription of pri- miRNAs, processed by an RNase III enzyme in the nucleus into pre-miRNAs. These are exported to the cytoplasm and further processed in to miRNA-miRNA* duplexes, which load into the RNA-induced silencing complex (RISC) to inhibit translation or degrade mRNAs. miRNAs are named using “mir” for the gene locus and precursor miRNA, while the mature product is “miR,” with numbers and letters distinguishing closely related miRNAs. In insects, miRNAs regulate molting, insecticide tolerance, caste differentiation and many other vital functions. For instance, miR-173 in *Nilaparvata lugens* controls molting by targeting 20E signaling genes, in *Spodoptera frugiperda* four microRNAs, miR- 13b-3p, miR-278-5p, miR-10483-5p and miR-10485-5p mediate insecticide tolerance while in *Apis mellifera* and *Bombus terrestris*, miRNAs influence caste determination. This review discusses that research on pest species, facilitated by high-throughput sequencing, highlights the potential of miRNAs for environmentally friendly pest control strategies by targeting genes vital to survival, reproduction or development. Future advancements in understanding miRNA stability and interactions will enhance their application in pest management.

Keywords: microRNA; pest management; regulatory role





The long-term effects of population bottleneck during biocontrol introduction: from a population genomics perspective

Ranjit Kumar Sahoo

CSIR–Centre for Cellular and Molecular Biology, Hyderabad, India

Correspondence: sahoo_rk@outlook.com

Utilising genomics to understand the ecology and adaptability of target species presents a promising approach to improve the effectiveness and sustainability of biocontrol programs. For example, having a reference genome and re-sequencing data from multiple individuals of a biocontrol agent allows us to characterise its genomic diversity in the introduced landscape. This knowledge is vital for identifying inbreeding depression and understanding local adaptation, if any, during the post-release period. This is particularly important when the founding population consists of only a few individuals, often leading to a bottleneck effect in the introduced population. My research on the beetle *Zygogramma bicolorata*, introduced to India as a biocontrol agent, examined the influence of historical bottleneck on its contemporary population. With the help of genome re-sequencing data from 72 individuals from climatically different regions in India, my analyses showed a distinct population structure of the beetle species within the introduced landscape. Despite the recent introduction/founding event, I found signatures for one of the sub-populations, from the desert-like region, being genetically divergent from the others, indicating the plausibility of local adaptation. Comparative measures of genetic variation across the sub-populations further revealed the potential effect of inbreeding on the population's genetic diversity. These results, along with the reconstruction of population demographics, provide insights into the processes that have shaped the genetic composition of the study species in the introduced landscape.

Keywords: founding effect; inbreeding; local adaptation; population genomics; *Zygogramma bicolorata*



Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources



**Bacterial diversity across developmental stages of the litchi stink bug
(*Tessaratoma javanica*): insights from 16S rRNA sequencing**

Ipsita Samal^{1*}, Jaipal Singh Choudhary², Ansh Raj¹ and Vinod Kumar¹

¹ICAR–National Research Centre on Litchi, Muzaffarpur, India

²ICAR–Research Complex for Eastern Region, Farming System Research Centre for Hill and Plateau Region,
Ranchi, India

*Correspondence: ipsita.saml@icar.gov.in

The litchi stink bug, *Tessaratoma javanica* (Thunberg), poses a significant threat to litchi cultivation, particularly during the critical development stages. This hemipteran pest inflicts substantial damage by feeding on the sap of floral buds and young fruits, leading to reduced yields and compromised fruit quality. Recent outbreaks have highlighted its increasing prevalence and impact on litchi production in diverse litchi growing regions of India. While research has primarily focused on the pest's biology and control measures, there is a notable gap in understanding the microbial communities associated with *T. javanica*. Current study aims to explore the diversity of microbiota throughout the developmental stages of this pest using 16S rRNA amplicon sequencing. These findings underscore the variability in microbial communities associated with different developmental phases of the litchi stink bug, suggesting that as the nymphs mature, their gut microbiota becomes more diverse and potentially more specialised. The results elucidated the role of symbiotic bacteria in the insect's growth, reproduction, immunity, and adaptability, thereby contributing to a comprehensive understanding of its ecological dynamics. Proteobacteria and Firmicutes were identified in all embryonic stages and considered crucial to the ecological characteristics of *T. javanica*. Insights gained from this research could inform effective Integrated Pest Management (IPM) strategies, enhancing the resilience of litchi farming against this emerging threat. Ultimately, understanding the intricate interactions between *T. javanica* and its microbiota will provide valuable information for farmers and policymakers, promoting sustainable agricultural practices in litchi cultivation.

Keywords: bacterial diversity; ecological dynamics; gut microbiota; litchi stink bug; *Tessaratoma javanica*





Unveiling pheromone perception: molecular insights into pheromone reception in *Leucinodes orbonalis*

Selva Babu Selvamani, Jyoti Pathak, T.C. Suman, Nishtha Nayyar, Manikanta Nalimala,
R.G. Gracy, T. Venkatesan*, M. Mohan and Kesavan Subaharan

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

*Correspondence: Venkatesan.T@icar.gov.in

Pheromone perception is a cornerstone of insect mating behaviour. By manipulating this process, we can effectively disrupt mating and control pest populations. In this study, we delved into the molecular mechanisms underlying pheromone perception in *Leucinodes orbonalis*. Through transcriptome analysis, we identified a comprehensive repertoire of genes involved in olfactory perception, including OBPs, PBPs, ORs, IRs, CSPs, and SNMPs. We focused on four PBP proteins and constructed their 3D models. Docking studies revealed a strong hydrogen bond between Ser52 of PBP1 and the pheromone molecule, suggesting its crucial role in pheromone binding. Expression analysis demonstrated sex-biased expression patterns for PBPs, with PBP1, PBP2, and PBP3 predominantly expressed in males and PBP4 in females. To validate the functional significance of PBP1, we employed RNA interference (RNAi) to silence its expression. EAG studies conducted post-RNAi induction revealed a significant reduction in pheromone response, confirming the role of PBP1 in pheromone perception. Our findings provide valuable insights into the molecular mechanisms underlying pheromone perception in *L. orbonalis* and offer potential targets for developing novel pest control strategies.

Keywords: EAG; *Leucinodes orbonalis*; pest management; pheromone binding protein; RNAi





Detection and molecular phylogeny of soft scale insect, *Megapulvinaria maxima* (Hemiptera: Coccidae): a major pest of Madhunashini, *Gymnema sylvestre*

K.T. Shivakumara^{1,2*}, Sunil Joshi¹, A.C. Polaiah², T. Venkatesan¹, M.C. Keerthi³,
S.S. Udikeri⁴, C. Divya¹, C. Manjunatha¹, R.S. Ramya¹ and B.S. Gotyal¹

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²ICAR–Directorate of Medicinal and Aromatic Plants Research, Anand, India

³ICAR–Indian Institute of Horticultural Research, Bengaluru, India

⁴University of Agricultural Science, Dharwad, India

*Correspondence: shiva.kt@icar.gov.in

The soft scale, *Megapulvinaria maxima* (Green, 1904) (Hemiptera: Coccidae), has emerged as a serious pest infesting *Gymnema sylvestre* in India. A random survey indicated infestations on leaves, stems, and fruits caused by nymphs and adults extracting plant sap and secreting excess honeydew. This honeydew adversely impacts leaf quality which is critical for essential for bio-molecule extraction. Early pest detection is crucial for effective control, but the precise morphological identification of scale insects is challenging. Using morphological keys and the *Cytochrome c oxidase subunit I* (COI) gene (GenBank No. OR602704), we identified the scale insects as *M. maxima*. Evolutionary divergence investigations and phylogenetic analysis revealed no divergence with the Republic of Korea isolate (MK543913), while the isolate with the accession number MW450949 showed the greatest evolutionary divergence (0.72%). The isolates from China (KP189890) and (KP189893) demonstrated a lesser association with the study isolate. The severity of incidence peaked during the 48th and 45th standard meteorological weeks (SMW) in 2019–20 and 2020–21, with severity levels of 3.67 and 3.56, respectively. The morning relative humidity correlated considerably positively in both the years ($r=0.152$ and 0.364^*). These findings are useful for early pest detection and designing effective management strategies. To our knowledge, this is the first report of *M. maxima* affecting the therapeutic herb, *G. sylvestre* in India.

Keywords: anti-diabetic; cytochrome c oxidase subunit I; *Gymnema sylvestre*; *Megapulvinaria maxima*; phylogenetic analysis





Identification of suitable reference genes for normalising gene expression of qPCR studies in the peach fruit fly (*Bactrocera zonata*)

T.C. Suman^{1,2}, Selva Babu Selvamani¹, K. Ashok³, R.G. Gracy¹, M. Mohan¹, D. Sagar¹,
R.S. Ramya¹, Anitha Peter² and T. Venkatesan^{1*}

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²University of Agricultural Sciences, Bengaluru, India

³Tata Institute for Genetics and Society, Bengaluru, India

*Correspondence: tvenkat12@gmail.com

Bactrocera zonata, the peach fruit fly, is indigenous to South and Southeast Asia and attacks a wide variety of soft fruits, especially mango, guava, and peach. Now, it is found in more than 20 countries in Asia and Africa. Being a polyphagous species with high biotic potential, high reproduction rate, and quick dispersion, it may readily adapt and spread. Studying gene expression is essential for understanding insect biology and behaviour, insect vector-virus relationships, developing pest-resistant crops, and monitoring insecticide resistance. The most accurate and sensitive method for quantifying gene expression is qPCR, which measures RNA levels. For gene expression studies to be accurate, dependable, and reproducible, normalisation of gene expression using reference genes is essential. In the current study, we have assessed the stability of eight potential genes (*G3PDH*, *G6PDH*, α -*Tub*, β -*Tub*, *RPL19*, *EF1*, *SOD*, *V-ATPaseA*) across a range of experimental conditions. Five distinct statistical algorithms, including delta CT, BestKeeper, NormFinder, geNorm, and RefFinder, were used to assess the stability of the candidate genes. A comprehensive stability analysis found that α -*Tub* and β -*Tub* genes were most stable across developmental stages, whereas *RPL19* and β -*Tub* were most stable in adult males and females and across insect tissues. Our results improve the robustness of experimental results and fortify the interpretation of gene expression data by assisting in the precise and trustworthy normalisation of gene expression data by taking biological and technical variability into account.

Keywords: *Bactrocera zonata*; gene expression; qPCR; reference genes





**de novo transcriptome and gene expression analysis of cassava mealybug,
Phenacoccus manihoti Matile-Ferrero (Hemiptera: Pseudococcidae),
across two developmental stages**

**Sunny Rao^{1,2}, R.G. Gracy^{1*}, N. Veeramanikanta Reddy¹, Nikita Negi^{1,2},
K.M. Nived^{1,3}, D.K. Rana², M. Sampathkumar¹ and T. Venkatesan¹**

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Indira Gandhi Krishi Vishwavidyalaya, Raipur, India

³University of Agricultural Sciences, Bengaluru, India

*Correspondence: gandhi_gracy@yahoo.co.in

Cassava mealybug (CMB), *Phenacoccus manihoti*, is one of the most serious insect pests of cassava inflicting yield loss to the extent of 80%. The present study constructed a de novo transcriptome assembly for CMB for developmental stages (crawlers and adults) using the Illumina NovaSeq-6000 platform. The assembly statistics revealed that the total number of contigs generated is 258,482 with an N50 value of 2,080bp. The transcriptome completeness as determined by BUSCO is 99.6%, and the percentage of reads that were correctly mapped to the assembled transcripts ranged from 93.88% to 94.81%. A total of 6,204 (up-regulated) and 8,569 (down-regulated) gene isoforms showed differential expression (DE) of 2log-fold change between crawlers and adults. The Clusters of Orthologous Groups (COG), used for functional annotation, revealed 21 clusters, the largest being a cluster with an unknown function followed by the signal transduction mechanisms. The Gene Ontology (GO) enrichment plots for DE transcripts revealed that those involved in organonitrogen compound biosynthetic processes were enriched for up-regulated transcripts, while, in down-regulated transcripts protein metabolic processes were enriched. The KEGG enrichment plots revealed that the metabolic and oxidative phosphorylation pathways as the most upregulated and downregulated, respectively. The transcriptome was validated by randomly selected DEGs using qPCR analysis and the expression profile was found to correlate with the RNA-Seq data. Furthermore, the genes involved in these pathways can be taken up for RNAi-based gene silencing, for pest suppression.

Keywords: cassava mealybug; differential expression; Illumina; qPCR; transcriptome





Non-destructive DNA extraction for whitefly and their natural enemies

J. Vasundhara*, G.A. Kavya Yadav, K. Selvaraj and T. Venkatesan

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

**Correspondence: vasundharajagan1710@gmail.com*

DNA extraction methods often cause significant damage to specimens, rendering them unsuitable for subsequent taxonomic studies and morphological analysis. Non-destructive DNA extraction methods offer a solution by preserving the structural integrity of specimens, allowing for combined molecular and morphological research. A comparative study was done with rugose spiraling whitefly, *Aleurodicus rugioperculatus* and parasitoid, *Encarsia cubensis* using both destructive and non-destructive methods with the QIAGEN DNeasy Blood & Tissue kit, employing single specimens for each. Amplification and sequencing of both the *COI* and *ITS2* gene fragments yielded high-quality, accurate sequencing results across all samples. Specifically, *ITS2* primers were employed for the parasitoid DNA, and *COI* primers were used for whitefly DNA. Non-destructive method showed several advantages over the destructive approach. It allowed the preservation of the entire specimen, making it available for further morphological examination and contributing to long-term reference collections. Despite its specimen-preserving advantage, the time required for non-destructive DNA extraction was comparable to the traditional destructive method, ensuring no significant delays in research workflows. Both methods produced sufficient DNA for successful PCR amplification and sequencing of the target gene regions. This approach highlights the versatility of the QIAGEN DNeasy Blood & Tissue kit in extracting DNA from whiteflies and their associated parasitoids using both destructive and non-destructive methods. By facilitating accurate molecular identification alongside morphological preservation, the non-destructive method proves to be an effective tool for integrative taxonomic research and holds significant potential for application in other insect taxa.

Keywords: *COI*; destructive; *ITS2* gene; molecular; non-destructive





Developmental expression study and silencing of nuclear receptor *E75A* in brinjal shoot and fruit borer, *Leucinodes orbonalis* Guenee

N. Veeramanikanta Reddy^{1,2}, T.C. Suman¹, R.G. Gracy¹, Y.K. Yadu² and T. Venkatesan^{1*}

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Indira Gandhi Krishi Vishwavidyalaya, Raipur, India

*Correspondence: tvenkat12@gmail.com

Brinjal shoot and fruit borer (BSFB), *Leucinodes orbonalis* (Lepidoptera: Crambidae), is a major limiting biotic factor in brinjal production causing yield losses to an extent of 90%. The development of insecticide resistance by BSFB and raised consumer demand for chemical residue-free food created an urge for new modes of crop health management. dsRNA based silencing of important genes for insect survival can be an ecofriendly and sustainable management strategy. The ecdysone inducible protein *E75A* is one of the early genes of ecdysone pathway belonging to nuclear receptors with ligand binding domains, induced by ecdysone in the insects during moulting process. The stage-specific expression studies revealed that, the third and fifth instar larvae had higher expression, whereas in adult, the expression peaked at 48 h post emergence in both the sexes and later declined. The third instar larva fed with dsRNA designed for *E75A*, showed significant down regulation at 48 h post treatment with 56 % (P=0.009) reduction in transcript abundance in comparison with control (dsGUS). There was 62% (P=0.009) cumulative mortality 10 days post feeding with dsRNA specific for gene at a concentration 2 µg of dsRNA overlaid on diet for three days. Moreover, the phenotypic deformities and larval-pupal intermediates have been observed post treatment with dsRNA targeting *E75A*. The results show that, this gene has a crucial role in the growth, development and survival of *L. orbonalis*. Furthermore, this gene could be an efficient target for dsRNA-based management of *L. orbonalis*.

Keywords: dsRNA; *E75A*; ecdysone; gene expression; *L. orbonalis*





Designing and validation of species-specific primers in stored grain pests

K.M. Venugopala, T. Venkatesan*, K. Subaharan, Selva Babu and A. Raghavendra

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

**Correspondence: tvenkat12@gmail.com*

Stored grains are important source of food during the offseason. But they are infested by many insect pests, leading to spoilage and post harvest damage, finally leading to economic losses. So, it is very important for correct identification of the pest for its management. But, it is difficult to rapidly identify adult and other stages based on external morphological characteristics. So, there is need for molecular techniques for the rapid and accurate identification of different stored grain pests, particularly for pest monitoring. Here, we collected five economically important stored grain pests, viz. *Sitophilus oryzae*, *Tribolium castaneum*, *Callosobruchus maculatus*, *Corcyra cephalonica* and *Rhyzopertha dominica*. The primers were designed by employing orthologos analysis and multiple sequence alignment. Unique regions were identified and subsequently primers were designed for species-specific amplification. Nine pairs of species-specific primers based on the mitochondrial DNA cytochrome oxidase subunit I (COI) were developed for their species-specific identification, viz. So1, So2, So3, MTSO1, TC1, TC2, TC3, Cchi1 and Cor1. These primers were tested in all possible combinations through PCR, to check the cross amplification among the stored grain pests. Results have shown that, among the primers, all have shown species specificity except MTSO1. So, all the other primers can be used as a species-specific primer for the correct identification of stored grain pests and it also led to the development of an identification method using the mitochondrial cytochrome oxidase subunit I gene.

Keywords: mitochondrial cytochrome oxidase subunit I gene; orthologos analysis; PCR; species specific primer; stored grains pests





Identification and molecular validation of cytochrome P450 genes involved in insecticide resistance in *Maruca vitrata* (Lepidoptera: Crambidae) and scope for RNAi-mediated management

N. Vijayakumari N^{1,2*}, M. Mohan^{1*}, M. Shanthi², M. Murugan² and R.G. Gracy¹

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Tamil Nadu Agricultural University, Coimbatore, India

*Correspondence: nviji216@gmail.com; mohan_ari@yahoo.com

Maruca vitrata (Lepidoptera: Crambidae), commonly known as legume pod borer, is a highly destructive pest that primarily affects food legumes in tropical Asia and sub-Saharan Africa. However, over-reliance on insecticides has led to the emergence of insecticide resistance, a growing challenge for sustainable pest management in *M. vitrata*. Cytochrome P 450 (CYP) genes play a crucial role in insecticide resistance by encoding enzymes that metabolise and detoxify insecticides, reducing their efficacy. Understanding the expression pattern of cytochrome P450 genes in resistant and susceptible strains of *M. vitrata* is critical for devising genome assisted resistance management strategies and ensuring long-term efficacy of insecticides. Transcriptome mining for the identification of putative genes coding cytochrome P450 monooxygenases revealed 136 transcripts with 63 unigenes of CYP genes. MviCYP064-6AGP1 was found to be a new three letter subfamily under CYP clan 3, which is a detoxification gene, significantly over-expressed. Other CYP genes which are involved in detoxification were validated by qPCR and RNAi.

Keywords: cytochrome P450 monooxygenases (CYPs); detoxification; *Maruca vitrata*





Enhancing biotic resistance and shelf-life of tomato through ethylene biosynthesis downregulation using CRISPR/Cas9 gene editing

S. Yadav Rajkumar^{1,2} and Praveen C. Verma^{1,2*}

¹Academy of Scientific and Innovative Research, Ghaziabad, India

²CSIR–National Botanical Research Institute, Lucknow, India

*Correspondence: praveencverma@nbri.res.in

Tomato (*Solanum lycopersicum*) is one of the most economically important crops globally but faces significant yield losses due to pests and pathogens. Ethylene, a key phytohormone, plays a dual role in plant defence, often contributing to both resistance and susceptibility depending on the stress context. This study explores the potential of downregulating ethylene biosynthesis as a strategy to enhance the shelf life and biotic resistance in tomatoes using CRISPR/Cas9 gene-editing technology. Targeting critical genes in the ethylene biosynthesis pathway, such as *1-aminocyclopropane-1-carboxylic acid synthase* (ACS) and *1-aminocyclopropane-1-carboxylic acid oxidase* (ACO), we designed guide RNAs (gRNAs) to achieve precise and stable gene knockouts. Advanced bioinformatics tools facilitated the identification of target sites and ensured that off-target effects were minimised. Transcriptomic analyses revealed reduced ethylene production, which reprogrammed plant defence signalling pathways, enhancing resistance to major biotic stresses, including *Helicoverpa armigera* and other insect pests' infestation. Real-time PCR validated the downregulation of ethylene biosynthesis genes, while insect and pathogen bioassays demonstrated improved pest and disease resistance. The integration of CRISPR technology with molecular breeding offers a sustainable approach to reduce the reliance on chemical pesticides while improving crop productivity. This work highlights the potential of ethylene biosynthesis downregulation strategy for delayed fruit ripening, enhancing shelf life and biotic stress resistance in tomatoes, contributing to sustainable agriculture and food security.

Keywords: 1-aminocyclopropane-1-carboxylic acid synthase; biotic resistance; CRISPR-Cas9; ethylene; tomato





Session IX

**Satellite Symposium on Chemoecological
Innovations in Modern Pest Management**



S09-LS-01

**Exploring livestock pathogens and vector interaction to manage
vector-borne diseases**

Merid Getahun

International Centre of Insect Physiology and Ecology, Nairobi, Kenya

Correspondence: mgetahun@icipe.org

Livestock offer high-quality, affordable, nutritious food and play a crucial role in the ecosystem by enhancing belowground microbial diversity, soil health, functionality, fertility and crop productivity. It is estimated that over a billion individuals worldwide earn their livelihoods in the livestock business across several value chains. Nevertheless, the resilience of livestock to climate shocks and productivity is strongly impacted by vector-borne diseases. This presentation will examine the interaction between livestock and vectors, as well as the influence of infection on modulating this interaction. We investigate the mechanism of the interaction to develop tools that disrupt livestock vector interaction to block vector-borne disease transmission. Additionally, we investigate how infections alter metabolites to facilitate the diagnosis of animal diseases.

Keywords: animal disease; livestock pathogens; vectors

Lead Speech



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



From local farms to global fields: the transformative impact of CREMIT pheromone technologies

Markandeya Gorantla

ATGC Biotech Private Limited, Genome Valley, Hyderabad, India

Correspondence: mg@atgc.in

The CREMIT Pheromone Delivery Platform, developed by ATGC Biotech in collaboration with leading research institutions such as ICAR–NBAIR, JNCASR, and NCL, has redefined sustainable pest management through its innovative and ecofriendly technologies. Leveraging advanced delivery systems, including glue dispensers, solid tablets, and sprayable formulations, CREMIT effectively targets a wide range of pests using sex pheromones (SCLPs), aggregation pheromones, anti-aggregation compounds, attractants and oviposition deterrents. Field studies and deployments demonstrate CREMIT's global impact in managing critical pests such as pink bollworm, brinjal fruit and shoot borer, fruit fly, diamondback moth, gypsy moth, tomato pinworm, rice yellow stem borer and fall armyworm. The platform has also been integral to implementing mating disruption and male annihilation technique strategies, providing a sustainable alternative to chemical pesticides while promoting environmental and human health. Through collaborations with ICAR–NBAIR for applied pest control strategies, JNCASR for molecular and chemical ecology insights, and NCL for cutting-edge formulation technologies, ATGC has built a robust foundation for the CREMIT platform's success. These partnerships have enabled the development and global adoption of this technology across millions of hectares, benefiting farmers and advancing high-value horticultural and essential row crops. This presentation will explore CREMIT's innovations, highlighting global success stories and the platform's adaptability in pest management. By addressing challenges like pest resistance, rising input costs and environmental degradation, CREMIT exemplifies ATGC Biotech's dedication to sustainable agriculture and its vision of a greener and more productive future.

Keywords: male annihilation technique; mating disruption; sex pheromones





Leveraging chemical ecology for Indian agriculture: decoding the science of signals for sustainable pest management

P.D. Kamala Jayanthi

ICAR–Indian Institute of Horticultural Research, Bengaluru, India

Correspondence: jaiinsect@gmail.com

As insects mainly depend on odour-mediated strategies to perceive their environment, chemical ecological studies mainly revolve around isolating and identifying these potent infochemical cues that play a role in crucial decision-making behaviours of phytophagous insects like host location, mate location and oviposition site selection. Learning the chemical language of host plants, insect pests and their natural enemies in an agro-ecosystem helps us to elucidate the role and origin of critical infochemicals that play a crucial role in insect–plant interactions and to locate the trophic level. Phyto-semiochemicals, viz. kairomones and pheromones, remain underexploited in integrated pest management (IPM) programmes. Our studies at ICAR–IIHR on phyto-semiochemicals in insect–plant interactions of major horticultural pests led to the identification of potential cues that elicit behaviour modification in polyphagous pests such as fruit flies: *Bactrocera dorsalis*, *B. correcta* and *B. cucurbitae*. The impetus to identify chemical cues that are involved in host location, oviposition site selection and mate location across the pests and host plants will help us to bring out viable behavioural cues that will aid in the formulation of end-to-end pest management programmes. The ‘push–pull’ strategy uses a combination of behaviour-modifying stimuli to manipulate the distribution and abundance of insect pests and/or natural enemies. To formulate successful ‘push–pull’ strategies for insect pests across the horticultural crops, we must have more appropriate behavioural inputs. Considering the potential merits of chemical ecological studies, a collaborative effort among the research fraternity involving entomologists, biochemists and molecular biologists is paramount.

Keywords: chemical cues; infochemicals; phyto-semiochemicals; push–pull strategy



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Chemical ecology of multitrophic interactions: a goldmine of biopesticides

Sagar Pandit

Indian Institute of Science Education and Research, Pune, India

Correspondence: sagar@iiserpune.ac.in

Plants constantly interact with different biotic and abiotic factors in their environment. Herbivore insects are one of the common biotic interactors. Since insect herbivores cause damage, plants use defence strategies against these herbivores. In response, the insect herbivores evolve counter-defence strategies. This race towards one-upmanship is constantly on in the nature, so it is popularly called an ‘evolutionary arms race’. Since most of these defence and counter-defence are chemically based, they are also considered to be a part of the ‘biochemical warfare’ between plants and insects. Insect herbivore’s natural enemies like parasitoids, predators, pathogens, etc., add another dimension to this interaction and make it ‘tritrophic’. In ecological terms, plants exert a bottom-up force by using defence chemicals, natural enemies exert a top-down force on the insect herbivores. From the agricultural viewpoint, herbivores are pests, plants’ defence chemicals are biopesticides, and the natural enemies are the biocontrol agents. Therefore, integration of the classical ecological and modern omics such as genomics, transcriptomics and metabolomics to study these interactions, and finding agriculturally important solutions is the key. Such integration will help us understand the natural biochemical warfare strategies and provide new approaches for pest management.

Keywords: biochemical warfare; evolutionary arms race; plant defence strategies; tritrophic interactions





Session X

**Integration of Macrobiotics and
Microbiotics in Organic Farming**



S10-LS-01

**The use of *Cydia pomonella* granulovirus in organic apple
production — overcoming the threat of virus resistance
in codling moth**

**Johannes A. Jehle*, Karin Undorf-Spahn, Eva Fritsch, Jiangbin Fan,
Jörg T. Wennmann, Shili Yang, Lina Dammel and Sarah Biganski**

Institute for Biological Control, Julius Kühn Institute, Dossenheim, Germany

**Correspondence: Johannes.jehle@julius-kuehn.de*

The codling moth granulovirus (CpGV) is a highly efficient agent for biological control of the codling moth (*Cydia pomonella*). CpGV products have been registered in nearly all apple-growing countries worldwide wherever codling moth is a major pest. During the last 20 years, numerous organic apple plantations with codling moth populations showing low susceptibility to commercial CpGV products have been identified in Germany and other countries. Genetic analyses and susceptibility testing revealed at least three different types of resistance (types I–III). On the other hand, by exploiting the genetic diversity of CpGV and registering novel isolates as plant protection agents, it was possible to overcome resistance and to provide growers efficient tools in their continuing efforts to control codling moth. To sustain the successful use of CpGV, resistance monitoring and resistance management measures are of crucial importance. We report results from laboratory and field observations on the efficacy of different CpGV isolates belonging to different phylogenetic lineages of CpGV. Laboratory selection experiments using different regimes of virus application provided a mixed picture on the efficiency of resistance selection but proved that application of a single CpGV genome type may increase the likelihood of resistance development. For resistance management it will be important to further exploit the natural genetic diversity of wild-type CpGVs and those to be used in commercial products, and to combine CpGV sprays with other control tools, such as mating disruption.

Key words: Baculoviridae; biological control; *Cydia pomonella*; resistance management; virus selection

Lead Speech



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Inundative releases of biological control agents reduce *Pontederia crassipes* (Pontederiaceae) invasions in South Africa

Samella Ngxande-Koza^{1*} and Julie Coetzee^{1,2}

¹Centre for Biological Control, Department of Zoology and Entomology,
Rhodes University, Makhanda, South Africa

²South African Institute for Aquatic Biodiversity, National Research Foundation,
Makhanda, South Africa

*Correspondence: s.ngxande-koza@ru.ac.za

Pontederia crassipes Mart. (Pontederiaceae) (water hyacinth) is one of the worst weeds globally and is widespread, occurring on every continent except Antarctica. It is native to the Amazon Basin, South America, and was first documented in South Africa in the early 1900s. Biological control against water hyacinth was initiated in South Africa in 1974, and it is the longest-running programme against water weeds. Since then, eight species of biocontrol agents have been released against it, yet it remains the most difficult aquatic weed to control due to cold winters in temperate regions, eutrophic water bodies and inconsiderate application of herbicides. In an attempt to improve prospects for control, the Centre for Biological Control (CBC) at Rhodes University transitioned from classical biological control to augmentative biological control through frequent inundative releases of large numbers of the most recently released agent, *Megamelus scutellaris*, as it is easily reared and is highly damaging. This was made possible through the CBC's biocontrol agent mass-rearing facility that was initiated in 2008, as well as community-based satellite rearing stations at invaded sites. More than one million agents have been released from these rearing stations, at key times in the plant's invasion trajectory, viz. in spring following regeneration from seed banks, and after flooding events. This has allowed rapid build-up of *M. scutellaris* populations, resulting in faster control. Key to this programme is community engagement which has bridged the research–implementation boundary, and strengthened biocontrol efforts, enabling a more sustainable approach to the management of water hyacinth in South Africa.

Keywords: aquatic weeds; augmentative control; biocontrol agents; inundative releases; mass-rearing





**Microbial and botanical based biopesticides for management of pod borer,
Maruca vitrata (Pyralidae: Lepidoptera) in cowpea**

**M.H. Kodandaram*, Nagaratna Wangi, P.R. Sabale, B. Manu and
B. Revanappa**

ICAR–Indian Institute of Pulses Research, Regional Research Station, Dharwad, India

*Correspondence: kodandaram75@gmail.com

Cowpea is an important nutritious legume crop grown in India and South East Asia. Pod borer, *Maruca vitrata* Geyer is a major constraint in production of cowpea and causes yield loss of 20–60 per cent. Presently, the control of this pest relies on the use of chemical insecticides, which leads to residues, resistance and environmental pollution. There is a need to identify and evaluate effective microbial and botanical biopesticides for the control of *M. vitrata* in the cowpea. A field experiment was conducted during 2021–2022 and 2022–2023 to evaluate different microbial and botanical biopesticides against pod borer *M. vitrata* in cowpea at ICAR–IIPR, Dharwad, Karnataka. Cowpea cultivar DC 15 was sown in randomised complete block design with 10 treatments and three replications. First spray was given at the 50% flowering and subsequent spray at 10 days interval. The percent pod damage was recorded at harvest and data was statistically analysed. The results indicated that all the treatments were found to be significantly superior over the control in terms of pest reduction. The pooled analysis of two-year data indicated that *B. bassiana* was effective with lowest per cent pod damage (9.99) followed by *B. thuringiensis* (13.85) resulted 67.06 and 54.32 per cent reduction over control, respectively. Neem soap was best botanical biopesticide with 13.75 per cent pod damage and 54.64 per cent reduction over control. Highest grain yield of 1,277.84 kg/ha was observed in *B. bassiana* treatment with higher benefit–cost ratio (1: 2.32). Thus, the biopesticides *B. bassiana*, *B. thuringiensis* and neem soap could be utilised in ecofriendly management of legume pod borer in cowpea.

Keywords: biopesticides; botanical; cowpea; microbial; pod borer





Banana weevil killer: a bioformulation for the management of banana pseudostem weevil, *Odoiporus longicollis* (Olivier)

A. Mohanasundaram*, N. Baskar, M. Loganathan, R. Thanigairaj and
R. Selvarajan

ICAR–National Research Centre for Banana, Tiruchirappalli, India

*Correspondence: entosundaram@gmail.com

Banana faces significant yield losses due to the pseudostem weevil (*Odoiporus longicollis*) in India. Infestation by this weevil can result in yield losses to the tune of 10–90%, depending on the timing of infestation and the management practices applied. Given the drawbacks of chemical control methods, an eco-friendly approach using entomopathogenic fungal formulations have been explored as an alternative pest management strategy. Seven indigenous fungal strains, isolated from naturally infected insects like *Basilepta subcostata* and *O. longicollis* across India, were identified both morphologically and molecularly. The fungal strains identified were *Metarhizium anisopliae*, *Beauveria brongniartii* and *B. bassiana*. In *in-vitro* trials, *B. brongniartii* strain EPF 27 showed a significant mortality rate (26–42%) between 4 and 8 days after inoculation, while strains of *B. bassiana* EPF 22 and *M. anisopliae* EPF 50 resulted in even higher mortality (66–78%) from the 5th to the 11th day. Further tests on *B. bassiana* EPF 22 demonstrated high efficacy against *O. longicollis* with LC_{50} values of 2×10^4 conidia/ml and LC_{90} values of 6×10^9 conidia/ml in the sheath dipping method, and a similar trend was seen in the insect spray method. The strains of *B. bassiana* EPF 22 and *M. anisopliae* EPF 50 attracted more weevils and resulted in increased mortality when applied to disc-on-stump traps. Based on these findings, the bioformulation Banana Weevil Killer®, developed using *B. bassiana* EPF 22, was found effectively targeting all life stages of the pest. When compared with the commercial formulation Beauverilin®, Banana Weevil Killer® showed superior efficacy, achieving 100% mortality at all dosages in laboratory tests, while Beauverilin® ranged from 24% to 76% mortality on the 7th day. Banana Weevil Killer® is currently being validated at multiple locations under the All-India Coordinated Research Project on Banana.

Keywords: banana; *Beauveria bassiana*; entomopathogenic fungi; *Odoiporus longicollis*





**Identification of potential *Metarhizium* spp. for the ash weevil
Myloccerus subfasciatus (Curculionidae: Coleoptera) management**

**U. Monisha¹, P.S. Shanmugam^{1*}, R. Yamini¹, M. Murugan¹, S. Jeyarani¹,
T. Srinivasan¹, K. Indhumathi² and R. Ragu¹**

¹Tamil Nadu Agricultural University, Coimbatore, India

²ICAR–Krishi Vigyan Kendra, Dharmapuri, India

*Correspondence: shanmugam.ps@tnau.ac.in

The isolation and evaluation of fungal strains hold significant potential for sustainable agricultural practices, particularly pest and disease management. The ash weevil *Myloccerus subfasciatus* (Curculionidae: Coleoptera) causes a significant loss of brinjal. Under uncontrolled conditions, this pest has the potential to cause complete yield loss. Fungal strains were isolated from the soils of diverse ecological niches under field conditions to assess their effectiveness as biocontrol agents. Eleven *Metarhizium* spp. were isolated, purified and identified based on their morphological and molecular characteristics. Preliminary screening was performed under laboratory conditions against second-instar *M. subfasciatus*. The TNAU ENTMA TDM 8 strain was found to be superior under laboratory conditions and was used for field evaluation. The potential strain was compared with the commercial *Metarhizium* formulations (Green Meta, Katayani) and with insecticide fipronil 0.3 GR and rynaxypyr 0.4 GR. The results from the field trials demonstrated that after the chemicals, TNAU ENTMA TDM 8 was more promising than the commercial strains available in the market. The efficacy of the different treatments was as follows: rynaxypyr 0.4 GR > fipronil 0.3 GR > TNAU ENTMA TDM 8 talc formulation > commercial formulation II > commercial formulation I. The efficacy of EPF can be increased by standardising the crop stage in which its application should be enacted.

Keywords: ash weevil; brinjal; insecticides; *Metarhizium*





Recruitment of egg parasitoid *Trichogramma chilonis* Ishii for managing the fall armyworm in maize: insight from a field study

Omprakash Navik*, Jagadeesh Patil and T. Prabhulinga

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

*Correspondence: navik.samodhi@icar.gov.in

The fall armyworm (FAW), *Spodoptera frugiperda*, is a highly destructive pest of maize in India. Managing FAW is challenging due to its ability to develop resistance to chemical pesticides. In this context, biological control offers a safe alternative for its management. Among various biological control strategies, the use of egg parasitoids is particularly beneficial, as it targets the pest at the egg stage, preventing damage before it occurs. To identify potential egg parasitoids, a survey was conducted across 12 Indian states. The emerged trichogrammatid species were identified and reared on a factitious host for laboratory, cage and field evaluations. In total, thirty strains of *Trichogramma chilonis* were collected and assessed. Among these, the strain of *T. chilonis* (TC184) collected from Karnataka produced higher parasitism and superior biological attributes. The potential strain was further tested alongside widely used species such as *T. pretiosum* and *T. mwanzai* which have been reported effective in FAW control in the Americas and Africa, respectively. The native strain of *T. chilonis* (TC184) performed better in both laboratory and cage conditions. Based on these results, *T. chilonis* (TC184) was selected for field release in maize. Field evaluation of *T. chilonis* was conducted over two years, resulting in 45–73% egg mass parasitism and 35–57% egg parasitism. This study suggests that the field release of the native species, *T. chilonis* was effective and could be incorporated into integrated pest management programmes for FAW management in maize.

Keywords: biological control; field efficacy; egg parasitoids; *Spodoptera frugiperda*





**Genomic insights into *Phytophthora* pod rot and bioefficacy of
Trichoderma reesei in pod rot disease management**

**B. Neeraja^{1*}, V. Prasanna Kumari², K. Gopal³, V. Govardhan Rao¹ and
N.B.V. Chalapathi Rao¹**

¹Horticultural Research Station, Dr Y.S.R. Horticultural University, Ambajipeta, India

²Acharya N.G. Ranga Agricultural University, Bapatla, India

³Dr Y.S.R. Horticultural University, Venkataramannagudem, India

*Correspondence: neeru.boddepalli@gmail.com

This study aimed to characterise the pathogen responsible for black pod rot in cocoa, incited by *Phytophthora palmivora* (E.J. Butler), a hemibiotrophic oomycete capable of infecting over 200 plant species, including the economically important cash crop *Theobroma cacao* L., commonly known as cocoa. *P. palmivora* infects multiple parts of the cocoa plant, particularly the pods, leading to black pod rot disease. Molecular analyses of nuclear ribosomal DNA (rDNA-ITS region), mitochondrial cytochrome oxidase-II (COX-II), and β -tubulin genes, followed by phylogenetic construction, confirmed *P. palmivora* as the primary pathogen associated with black pod rot in cocoa. Field evaluation of *Trichoderma reesei* (Drysru1) as foliar and soil applications demonstrated its potential for biological control; a foliar spray at 2×10^6 cfu/ml significantly reduced the mean disease incidence to 25.04%, followed by soil application of 50 g *T. reesei* along with 5 kg neem cake, which reduced disease incidence to 17.03%. These findings highlighted that *T. reesei* as a promising biocontrol agent for sustainable management of black pod rot disease in cocoa.

Keywords: cocoa; COX-II; ITS; pod rot; β -tubulin





**Efficacy of entomopathogenic nematodes and *Bacillus thuringiensis*
combinations against the invasive pest *Spodoptera frugiperda*
in maize**

**Jagadeesh Patil^{1*}, Aarthi Nekkanti¹, Manjunatha T. Gowda² and
R. Rangeshwaran¹**

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²ICAR–Indian Institute of Vegetable Research, Varanasi, India

*Correspondence: patiljaggi@gmail.com

Entomopathogenic nematodes (EPNs) serve as significant biological agents for the management of various insect pests and can be applied together with various biocontrol agents and insecticides. The aim of this study was to assess the survival of infective juveniles (IJs) from three indigenous EPN species, *Heterorhabditis indica* and *Steinernema carpocapsae*, as well as *S. abbasi*, following exposure to *Bacillus thuringiensis* Bt25. The effectiveness of these nematodes, both individually and in combination with Bt25 at varying concentrations, was evaluated for controlling the maize fall armyworm (FAW), *Spodoptera frugiperda*, in both laboratory and maize fields. Laboratory results indicated that Bt25, at various concentrations, had minimal to no impact on the survival of the nematode species. The combinations of nematodes and Bt25 exhibited either a synergistic or additive effect on the third-instar larvae of FAW, resulting in a more rapid mortality rate compared to the use of a single EPN species or Bt25 alone. Notably, the combination of *H. indica* with Bt25 and *S. carpocapsae* with Bt25 significantly enhanced both mortality and the speed of kill, although the establishment of the nematodes was not adversely affected by these combinations. The nature of the interaction varied by nematode species in both laboratory and field conditions, demonstrating synergistic effects for *H. indica*–Bt25, *S. abbasi*–Bt25 and *S. carpocapsae*–Bt25 against FAW larvae. The performance of these nematode–Bt25 combinations was comparable to that of emamectin benzoate treatment.

Keywords: compatibility; entomopathogenic bacteria; entomopathogenic nematodes; maize



Macrobiotics for rice pest management: successes and challenges

Chitra Shanker

ICAR–Indian Institute of Rice Research, Hyderabad, India

Correspondence: chitrashanker@gmail.com

Rice faces significant pest pressure from various insect species, and while a variety of natural enemies are present in rice ecosystems, the number of predators and parasitoids suitable for applied/ augmentative biological control remains limited. *Trichogramma* spp., particularly for managing lepidopteran pests, has been used since the 1960s and remains the most widely utilised parasitoid in rice integrated pest management systems. However, laboratory studies have shown that *Trichogramma* results in relatively low egg parasitisation rates within an egg mass. *Tetrastichus schoenobii*, a eulophid parasitoid, has shown greater potential, with the ability to achieve 100% parasitism of stem borer eggs. Despite its effectiveness, mass production of *T. schoenobii* has faced challenges, primarily due to difficulties in producing its host insect. Among predators, various asopine pentatomids such as *Andrallus spinidens*, *Amyotea malabarica*, *Zicrona caerulea*, and reduviids like *Rhynocoris fuscipes* and *R. marginatus* have shown promise in laboratory evaluations. However, as generalist predators, they are more suited for conservation biological control. The green mirid, *Cyrtorhinus lividipennis*, is particularly effective as an egg predator of rice leaf and planthoppers, and its in-situ rearing and conservation have been successful in some regions. In recent developments, standardised mass production of anthocorid predators like *Amphiareus constrictus* has opened new avenues for augmentative biological control. Cage experiments have demonstrated that *A. constrictus* can significantly reduce the population of brown planthopper, with up to 90% mortality across various predator–prey ratios.

Keywords: biological control; rice IPM; *Tetrastichus schoenobii*; *Trichogramma* spp.





Characterisation and field evaluation of indigenous nucleopolyhedrovirus infecting rice oriental armyworm, *Mythimna separata*

G. Sivakumar^{1*}, P. Ram Kumar¹, M. Kannan², M. Mohan¹, T. Venkatesan¹, A. Kandan¹,
C. Manjunatha¹, K. Subaharan¹ and M.S. Yandigeri¹

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Tamil Nadu Agricultural University, Coimbatore, India

* Correspondence: sivakumarg.nbair@gmail.com

Oriental armyworm, *Mythimna separata*, is a major pest of rice, maize, wheat, sugarcane and millets. An indigenous isolate of *Mythimna separata* nucleopolyhedrovirus (MyseNPV) was isolated from the diseased larvae collected from rice fields of Kalpetta, Wayanad district, Kerala, India. The extracted occlusion bodies of MyseNPV were examined under an electron microscope. Scanning electron photo micrograph revealed the irregular, tetrahedral and triangular shaped occlusion bodies. The size of the occlusion bodies ranged from 1.313–1.700 μm with an average size of 1.52 μm . Transmission electron photo micrograph showed the tetrahedral and triangular shaped OBs. PCR amplification for detection of viral DNA in *M. separata* NPV was done by using polyhedrin gene (*polh*) specific primers. The amplicon of 374 bp was amplified, sequenced and NCBI GenBank accession number was obtained (PP156667). Bioassay studies with MyseNPV against second, third and fourth instar larvae of *M. separata* revealed that the second instar larvae were highly susceptible to MyseNPV. Second instar larvae recorded much lower LC_{50} (2.01×10^3 OBs/ml) than third instar (2.95×10^3 OBs/ml) and fourth instar (3.23×10^3 OBs/ml) larvae. MyseNPV did not infect other insect pests tested in this present study. Field trial results revealed that there was 84.32 and 80.84% reduction of rice oriental armyworm and 47.95% and 56.78% increase in yield in the field plots treated with MyseNPV NBAIR1, during 2019 and 2020, respectively. Based on the field experiments data, it was concluded that MyseNPV NBAIR1 is a potential isolate to manage the rice oriental armyworm.

Key words: India; *Mythimna separata*; nucleopolyhedrovirus; oriental armyworm; rice



Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources



**A comprehensive year-round approach centring on *Hirsutella thompsonii*
[ICAR–NBAIR–MF(Ag)66] for broad mite control in mulberry**

**Prakya Sreerama Kumar*, Nanjundaiah Sheela and
Chikkalingaiah Bindushree**

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

**Correspondence: psreeramakumar@yahoo.co.in*

No other pest poses as severe a threat to mulberry cultivation in southern India as the broad mite, *Polyphagotarsonemus latus*, due to its unceasing attacks. The absence of effective and silkworm-safe synthetic pesticides has led farmers to resort to inappropriate or questionable substitutes in an attempt to control this pest, which also affects several other economically significant crops. Our research has been focussed on biological control as a viable alternative to chemicals in this unprecedented situation. Since August 2019, we have conducted over thirty field trials in the states of Karnataka and Tamil Nadu, demonstrating the efficacy of the acaropathogenic fungus *Hirsutella thompsonii* [ICAR–NBAIR–MF(Ag)66]. This ophiocordycipitaceous fungus has shown promise both as a standalone treatment and as a component of an integrated pest management strategy for broad mite control in mulberry. Favourable results were obtained when the predatory mite *Typhlodromus* (*Anthoseius*) *transvaalensis* and the botanical biopesticide azadirachtin were included in sequences with the mycelial–conidial liquid formulation of the fungus. A comprehensive year-round application approach centring on the fungus is ready to be shared with mulberry growers. To provide farmers with greater flexibility in biocontrol use, it is essential to also address the threats posed by other common mulberry pests, such as several mealybug species, a leaf roller and multiple thrips species, particularly *Pseudodendrothrips darci*.

Keywords: biocontrol; *Hirsutella thompsonii*; integrated pest management; mulberry; *Polyphagotarsonemus latus*





Evaluation of biointensive pest and disease management modules in small cardamom in Idukki district, Kerala, India

S. Sudhakar^{1*}, Ajay Kumar Kaurav², D. Kalaivanan³ and Bharat Singh⁴

¹ICAR–Krishi Vigyan Kendra, Idukki, India

²Sun Rise University, Alwar, India

³ICAR– Indian Institute of Horticultural Research, Bengaluru, India

⁴ICAR–Krishi Vigyan Kendra, Gurugram, India

*Correspondence: sudhakarsonda@gmail.com

Small cardamom (*Elettaria cardamomum*), the queen of spices, enjoys a unique position in the international spice market. A study has been conducted to assess the effect of three biointensive pest management (BIPM) modules on pests and diseases of cardamom in Idukki district of Kerala during 2021–2024. The BIPM modules evaluated against pests and diseases of small cardamom were BIPM module-1 (soil application of EPN ICAR-NBAIR @ 5 kg/ha, spray of *Lecanicillium psalliotae* ICAR-IISR @ 5 mL/L, application of *Bacillus thuringiensis* ICAR-NBAIR @ 2 mL/L, soil application of *Paecilomyces lilacinus* ICAR-IIHR, and spray of bacterial consortium containing *Pseudomonas fluorescens* ICAR-NBAIR and *Bacillus subtilis* ICAR-NBAIR, spray of pink-pigmented facultative methylotrophs @ 3 mL/L. BIPM module -2 (Soil application of *Metarhizium anisopliae* ICAR-NBAIR @ 2%, spray of *Beauveria bassiana* ICAR-NBAIR @ 20 g/L, soil application of organic manures and neem cake twice a year @ 250-1000 g per plant, basal application of *T. harzianum* ICAR-NBAIR and *Pseudomonas fluorescens* ICAR-NBAIR, BIPM module -3 (spray of 0.2% poneem, spray of spinosad 0.0135%, soil application of bacterial consortium containing *Pseudomonas fluorescens* ICAR-NBAIR and *Bacillus subtilis* ICAR-NBAIR, farmers practice and untreated control. Results revealed that BIPM module-1 was found significantly superior in reducing both pests and diseases and increasing yield of cardamom as compared to other BIPM modules, farmers' practice and control. Significantly larger number of parasitoids and predators were recorded from the filed plots treated with BIPM module.

Keywords: *Bacillus thuringiensis*; *Metarhizium anisopliae*; *Pseudomonas fluorescens*; *Trichoderma harzianum*





Exploring *Blaptostethus pallescens* and its interactions with entomopathogens as a potential solution for thrips management

Richa Varshney*, A. Kandan, T. Prabhulinga, K. Subaharan and S.N. Sushil

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

*Correspondence: richavarshney84@gmail.com

Predatory bugs play an important role in managing thrips and other insect pests in both open and protected cultivation. The current study focusses on the role of *Blaptostethus pallescens* in managing thrips species in different crops. This predatory bug has shown its efficiency against different densities of *Frankliniella schultzei*, *Scirtothrips dorsalis* and *Thrips parvispinus*. There are microbial biopesticides which are found effective against thrips. It would be interesting to study how these two biocontrol agents could be used together to curtail thrips menace. The effect of *Lecanicillium fusisporum* (VI-8) treated *F. schultzei* larvae was studied on biological parameters of *B. pallescens* and results exhibited the higher nymphal duration (25.25 ± 0.13 days) when treated thrips larvae was fed by nymphs of *B. pallescens*. The VI-8 strain did not show any negative effect on hatchability of eggs (83% hatchability in treatment; 86% in control). The rate of daily feeding potential of bugs on treated thrips was less (7.29 ± 0.15) than the untreated thrips (12.54 ± 0.1) throughout their lifetime. Moreover, when the F1 generation from both parents line fed on treated and untreated thrips allowed to feed on *Corcyra cephalonica* eggs, it did not show any difference in terms of nymphal duration which revealed that the fungi did not affect the F1 generation. In mango, release of *B. pallescens* @ 50 adults per plant alone exhibited significant reduction in *S. dorsalis* population. Similarly, tailored strategies involving the release of *B. pallescens* alongside *Beauveria bassiana* in chilli resulted in a reduction in *Thrips parvispinus* population. These studies highlight the potential of *B. pallescens* in managing thrips populations and its compatibility with entomopathogens.

Keywords: *Blaptostethus pallescens*; chilli; entomopathogens; protected cultivation; thrips





**Base-line susceptibility of cotton pink bollworm, *Pectinophora gossypiella*
against *Bacillus thuringiensis* Cry1Fa1 toxin**

**M. Mohan¹, J. Thawfeeq Ahamed^{1*}, M. Saravanakumar², K.S. Mohan², M. Dinesh² and
R.G. Gracy¹**

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Rasi Seeds Private Limited, Salem, India

*Correspondence: thawfeeq25599@gmail.com

The susceptibility of six populations of cotton pink bollworm, *Pectinophora gossypiella*, collected from major cotton growing states of India to the insecticidal protein Cry1Fa1 from *Bacillus thuringiensis* was determined through dose-response bioassays. Probit estimates of LC₅₀, LC₉₀, MIC₅₀, MIC₉₀, IC₅₀, IC₉₀, EC₅₀, and EC₉₀ were computed. The LC₅₀ and MIC₅₀ values with field-sourced geographical populations of *P. gossypiella* when assayed with Cry1Fa1 ranged from 1.52 to 3.21 (mean 2.25, SD 0.49) and 0.61 to 1.47 ppm (mean 1.04, SD 0.26), respectively. All the five populations of *P. gossypiella* were sourced from cotton growing areas with reported resistance to Bollgard II™ cotton. A single laboratory-bred population of *P. gossypiella* showed LC₅₀ and MIC₅₀ values of 1.47 (SD 0.38) and 1.10 (SD 0.22) ppm, respectively, which were similar to the probit estimates of *P. gossypiella* populations sourced from Bollgard II™ cotton fields. The LC₉₀, MIC₉₀, IC₉₀, and EC₉₀ probit estimates were also calculated for all the populations. The probit estimates of multiple geographical populations of *P. gossypiella* to Cry1Fa1, reported here, could serve as benchmark values, useful in the future monitoring of resistance in case of commercialisation of Bt cotton expressing Cry1Fa1 gene in future.

Keywords: *Bacillus thuringiensis*; base-line susceptibility; Bt cotton; Cry1Fa1; *Pectinophora gossypiella*





**Cow dung-based formulations and organic amendments: shaping soil microflora
and mesofauna dynamics for effective pest control in paddy**

C. Bindushree^{1*} and M.C. Nagaraju²

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²ICAR– KVK, West Tripura

*Correspondence: shreebindu12.bs@gmail.com

A comparative study was conducted to examine the variations in soil mesofauna populations and pest management effectiveness in rice ecosystem. The study was carried out during the Kharif seasons of 2020, 2021 and 2022 at ZARS, Mandya. The pooled data over three years revealed that organic farming practices supported the highest population of soil mesofauna per 500g of soil, followed by the organic + natural farming combination and natural farming treatments. The lowest mesofauna populations were recorded in chemical practices. Additionally, the study assessed the incidence of insect pests, particularly the yellow stem borer, and their management using both botanical and chemical insecticides. The impact of these pest management methods on beneficial soil mesofauna was also evaluated. Among the various treatments, natural farming with hand weeding resulted in the lowest white ear incidence (14.64%), followed by the recommended dose of fertiliser practices (14.73%). Organic farming showed a moderate incidence (16.10%), while conventional farming practices exhibited the highest incidence (22.17%). The absolute control treatment had the highest white ear incidence at 38.61%. Over four seasons, organic farming practices consistently supported the highest arthropod population (26.20 arthropods per 400g of soil). The findings highlighted that eco-friendly farming practices, particularly organic farming and Zero Budget Natural Farming (ZBNF), are effective in managing yellow stem borer populations and fostering beneficial soil mesofauna, suggesting their potential for sustainable pest control in rice ecosystems.

Keywords: arthropod; natural farming; organic farming; soil mesofauna





Potential of phytoseiid mites (Acari: Phytoseiidae) as biocontrol agents in the biointensive integrated pest management of terrestrial arthropods

Shubhadeep Biswas* and Krishna Karmakar

¹*Department of Agricultural Entomology, Bidhan Chandra Krishi Viswavidyalaya, Nadia, India*

**Correspondence: shubhadeep81096@gmail.com*

The intensification of agriculture to meet global food demands has led to increased reliance on synthetic chemical pesticides, resulting in ecological disruptions, pesticide resistance, and harmful environmental effects. To address these issues, biointensive integrated pest management has emerged as a sustainable approach, focusing on ecological harmony and long-term pest control by utilising natural predators. Among these, phytoseiid mites have proven to be highly effective biocontrol agents, capable of managing soft-bodied arthropods such as spider mites, thrips, and whiteflies. Their exceptional predatory efficiency, adaptability to diverse agroecosystems, high searching capabilities, and rapid multiplication make them indispensable in reducing pesticide dependence. It delves into advanced methods for mass-rearing, strategies to conserve and promote their populations in farming landscapes, and presents global case studies showcasing their successful integration into pest management systems. Key challenges, such as predator-prey dynamics and interspecific competition, are discussed alongside the influence of abiotic factors like temperature, humidity, and pesticide residues on their performance. Faunistic studies on Indian Phytoseiidae began in 1960s, with the current documented species count reaching 309. Genera *Neoseiulus* and *Typhlodromalus* are generalist predators that feed on multiple pest species, increasing their utility in mixed pest infestations. By leveraging the predatory potential of phytoseiid mites, farmers can achieve sustainable pest management solutions, reducing dependence on chemical pesticides fostering healthier agroecosystems. These mites play pivotal role in environmentally sound pest control and contribute significantly to global food security.

Keywords: agroecosystem; biological control; biointensive integrated pest management ; natural enemies; Phytoseiidae



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Bioprospecting microbiocidal and insecticidal activities of symbiotic bacterial extract, *Xenorhabdus indica* identified from *Steinernema pakistanense* isolated from the semi-arid regions of Rajasthan

Parul Chauhan* and Istkhhar

Banasthali Vidyapeeth, Tonk, India

*Correspondence: parulchauhan9929@gmail.com

Xenorhabdus are group of bacteria belonging to family *Enterobacteriaceae*, which are symbiotically associated with entomopathogenic nematodes of *Steinernema* genus. In this study, molecular analysis of bacteria isolated from *Steinernema pakistanense* from Tonk district of Rajasthan, using 16S rRNA gene sequencing indicates the phylogenetic position of *Xenorhabdus indica* (BSBT_S11). Further, organic fraction of ethyl acetate of *Xenorhabdus indica*, was characterised using FTIR (Fourier Transform Infrared Spectroscopy) method, and screening for their antibacterial activity by disk diffusion method and insecticidal activities on *Galleria mellonella* using 12-well plates were performed. FTIR analysis of the crude ethyl acetate extract of *Xenorhabdus indica* (BSBT_S11) showed the peak values of functional groups having antibacterial and insecticidal activities. Therefore, present study shows that the symbiotic bacteria of entomopathogenic nematodes can produce a wide range of secondary metabolites with potent biological activities. Due to these bioactive compounds, symbiotic bacteria can be explored for their use in pharmaceuticals, agricultural applications as well as in biological pest control.

Keywords: antibacterial activities; biological pest control; entomopathogenic nematodes; insecticidal activities; *Xenorhabdus indica*





Investigation of biocontrol mechanism of different *Trichoderma* sp. against fungal phytopathogens

Navjot Kaur and Samiksha Gupta*

Plaksha University, Mohali, India

*Correspondence: samiksha.gupta@plaksha.edu.in

Agricultural crops are constantly under the threat of biotic stresses, particularly fungal phytopathogens. Currently, chemical pesticides are used to control these pathogens, but their excessive and constant use is worsening environmental and human health problems. In India, pesticide use has increased more than 100X, from 154 MT in 1953–1954 to 57,000 MT in 2016–17. Globally, over 385 million people are affected by acute pesticide poisonings annually. Therefore, eco-friendly solutions like Biological Control Agents (BCAs) are required to manage phytopathogens. Beneficial microbes (fungi, bacteria, viruses) form a significant class of BCAs that suppress pathogens and enhance crop yield. *Trichoderma* spp. is widely used to control a range of soil and air-borne phytopathogens. While being commercially available, their large-scale adoption is limited due to weaker performance compared to chemical pesticides. This study aimed to assess the baseline biocontrol activity of three widely studied *Trichoderma* spp. (*Trichoderma harzianum*, *Trichoderma viride*, *Trichoderma asperellum*) obtained from natural environments in India against *Fusarium oxysporum* f. sp. *lycopersici* (Fol), a pathogen causing significant yield losses (30–40%) in tomato plant. The experimental design included a pathogenicity test and dual culture assays to understand plant-pathogen-microbe interaction and *Trichoderma* biocontrol efficiency, respectively. Findings highlighted that *T. viride* and *T. asperellum* are the most efficient antagonists for Fol. To validate the findings, a greenhouse-based dual culture assay was performed replicating natural conditions. Filtrate assays for secondary metabolites, sandwich test for VOC detection, enzymatic and mycoparasitism assays will also be conducted for identification of predominant antagonistic pathways involved.

Keywords: biological control agents; chemical pesticides; fungal phytopathogens; *Fusarium oxysporum* f. sp. *lycopersici*; *Trichoderma* spp.





Assessing natural mortality factors of *Helicoverpa armigera* Hubn (Lepidoptera: Noctuidae) in menthol mint (*Mentha arvensis*) in India

Santosh C. Kedar^{1*} and Omprakash Navik²

CSIR–Central Institute of Medicinal and Aromatic Plants, Lucknow, India

² ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

**Correspondence: santoshkedar56@yahoo.com*

Menthol mint (*Mentha arvensis*) is an important aromatic and medicinal crop in India, contributing significantly to the economy. However, its cultivation faces severe challenges from *Helicoverpa armigera*, a highly destructive and polyphagous pest that causes considerable yield losses across various crops, including menthol mint. Effective management of this pest requires an in-depth understanding of its natural mortality factors, particularly natural enemies that regulate pest populations. This study assessed the diversity and abundance of natural enemies associated with *H. armigera* in menthol mint agroecosystems across Uttar Pradesh and Uttarakhand from 2020 to 2024. Field surveys revealed 23 natural enemies, including 18 predators (78.3%) and 5 parasitoids (21.7%). Parasitoids were dominated by Hymenoptera (e.g., *Trichogramma chilonis*, *Campoletus chloridae*, and *Cotesia* sp.) and Diptera (tachinid flies), with larval and egg parasitoids being the most prevalent. Predators represented a wide range of taxa, with coleopteran and hemipteran predators being dominant, followed by members of Neuroptera, Dermaptera, Hymenoptera, and Arachnida. These findings provide valuable insights into the natural enemies of *H. armigera* in menthol mint ecosystems, offering opportunities to develop sustainable pest management strategies. Conservation and enhancement of these natural enemies, combined with integrated pest management approaches, can effectively reduce *H. armigera* populations while minimising dependency on synthetic pesticides. This study highlighted the potential of natural enemy-based solutions for environment friendly pest management in menthol mint cultivation.

Keywords: *Helicoverpa armigera*; menthol mint; natural enemies; parasitoids; predators





Entomopathogenic endophytes as a sustainable tool in organic farming for the management of sucking pests of capsicum

K. Logeswaran^{1*}, D.N. Kambrekar², P.U. Krishnaraj², C.P. Mallapur² and M.S. Biradar²

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²University of Agricultural Sciences, Dharwad, India

*Correspondence: waranlogesh105@gmail.com

Endophytic microorganisms, a diverse group of microorganisms such as fungi, bacteria actinobacteria, etc. residing within the internal tissues of plants, have garnered considerable attention in recent years. In this study, after the initial screening of 10 endophytic fungi and one actinobacterium from three botanical plants such as *Azadirachta indica*, *Pongamia pinnata* and *Ocimum santum* at four different concentrations (20, 30, 40 and 50 ml/l), three of most effective entomopathogenic endophytes, *Phomopsis asparagi*, *Diaporthe pseudomangiferae* and *Phomopsis* sp. were further investigated for bio-efficacy against sucking pests such as nymphs of *Thrips parvispinus*, *Polyphagotarsonemus latus* and *Aphis gossypii* and adults of *Bemisia tabaci* under laboratory conditions. When tested at different concentrations of endophytic fermented extracts, 50ml/l exhibited the highest mortality and increased significantly in a dose-dependent manner. The laboratory bioassay studies revealed that *Phomopsis* sp., *P. asparagus*, *Diaporthe pseudomangiferae* and *P. asparagus* were found to be effective against *T. parvispinus*, *P. latus*, *A. gossypii* and *B. tabaci* and exhibited the mortalities of 73.30, 66.60, 73.30 and 70.00 percent at 72 hours after application. The results of this present study could help develop endophytes-based commercial bio-insecticides, and incorporating these beneficial microorganisms into pest management strategies holds significant potential for reducing the environmental impact of conventional pesticides while maintaining crop productivity and sustainability.

Keywords: *Azadirachta indica*; endophytic fungi; *Phomopsis asparagi*; *Polyphagotarsonemus latus*; *Thrips parvispinus*





Production of *Bacillus thuringiensis* biopesticide on industrial by-products and its evaluation against white grub *Holotrichia serrata* in sugarcane

P. Mahesh*, B. Singaravelu, J. Srikanth, K. Hari, C. Sankaranarayanan, K.P. Salin, C. Appunu, G. Suresha, R. Nirmala and B. Ishwarya

ICAR–Sugarcane Breeding Institute, Coimbatore, India

Correspondence: agrimahesh@gmail.com

In the present study, we standardised the production technology for a biopesticide containing a scarabaeid-specific isolate (*Bt-62*) of *Bacillus thuringiensis* harbouring the novel coleopteran-specific crystal toxin Cry8Sa1 on low-cost industrial by-products and evaluated it for the control of white grub, *Holotrichia serrata* in sugarcane. We used sugar-industry products and by-products such as jaggery, trash, juice, bagasse and molasses, and agro-industry by-products including wheat bran, rice bran, groundnut cake, castor cake, neem cake and cotton cake in shake-flask cultures. Selected media from these preliminary studies were evaluated for *Bt-62* production in 20 litre lab-scale fermenter developed for this study. Among these media material tested in the fermenter, wheat bran and jaggery produced the highest bacterial CFU ml⁻¹ whereas neem cake and cotton cake produced the lowest. When cell protectants were added as preservatives to the best liquid formulations and their shelf-life was examined, dimethyl sulfoxide 0.5% and PVP 0.5% sustained maximum number of colonies for about two years of storage at room temperature. Laboratory bioassays against *H. serrata* with biopesticide produced on selected media illustrated its efficacy. In white grub endemic sugarcane fields, soil application of the formulation produced on standard media reduced grub numbers significantly. The studies demonstrated that *Bt-62* can be mass-produced and used for the control of *H. serrata* in sugarcane.

Keywords: *Bacillus thuringiensis*; biopesticide; *Holotrichia serrata*; industrial by-products; management; white grub





Evaluation of the different plant protection modules against *Spodoptera litura* in soybean [*Glycine max* (L.) Merrill]

Manoj Kumar Mahla^{1*} and H. Swami²

¹Maharana Pratap University of Agriculture and Technology, Udaipur, India

*Correspondence: mkmahla2@gmail.com

The investigations were carried out to evaluate the different plant protection modules against major insect pests of soybean [*Glycine max* (L.) Merrill] at Entomology farm, Rajasthan College of Agriculture, Department of Entomology, MPUAT, Udaipur during *Kharif*, 2023. The observation on the effect of different plant protection modules revealed that the chemical module was the most promising module in recording the minimum larval population of lepidopteran pests like *Spodoptera litura*. The next best module after the chemical module was bio-control module which performed better against lepidopteran pests. The remaining modules were found comparatively less effective. The observations recorded on the larval population of tobacco caterpillar revealed that all the plant protection modules recorded significantly superior results over untreated control. The chemical module including spray of spinosad 45 SC @ 0.4 g per litre at 30 DAS, spray of emamectin benzoate 5 SG @ 0.4g litre⁻¹ at 45 DAS and spray of indoxacarb 15.80 % EC at 60 DAS exhibited the lowest larval population of *S. litura*, with a count of 1.74 per mrl, followed by the bio-control module (1.99 per mrl) which includes the seed treatment with *Trichoderma viride* @ 6g kg⁻¹ seeds, installation of pheromone traps @ 12 ha⁻¹, azadirachtin spray 1500 ppm @ 2.50 L per ha at 15 DAS, release of *Trichogramma* @ 1.0 lakh ha⁻¹ at 30 DAS, application of *Metarhizium anisopliae* (2 kg ha⁻¹) + *Bacillus thuringiensis* (Bt) (1 kg ha⁻¹) at 55 DAS; the IPM module (2.12 per mrl) and the organic module (2.13 per mrl), and all these four modules were found statistically at par with each other. The data on the average number of natural enemies i.e., lady bird beetle and spider per mrl revealed that the bio-control module recorded the maximum population of lady bird beetle and found most safer to natural enemy fauna whereas in spider, maximum population was in IPM module. Grain yield of soybean was highest in bio-control module and followed by chemical module. This shows that these modules were most effective in increasing yield. The highest ICBR was registered in the bio-control module and observed as the most economically viable plant protection module followed by the IPM module.

Keywords: *Bacillus thuringiensis*; ICBR; indoxacarb; plant protection modules; soybean





**Deploying *Typhlodromus (Anthoseius) transvaalensis* against
Polyphagotarsonemus latus and *Pseudodendrothrips darci* in mulberry**

Rupanagudi Maruthi Mehanth, Prakya Sreerama Kumar* and Nanjundaiah Sheela

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

*Correspondence: psreeramakumar@yahoo.co.in

The thrips *Pseudodendrothrips darci* (Thysanoptera: Thripidae) poses a threat as severe as that of the broad mite, *Polyphagotarsonemus latus* (Acari: Tarsonemidae), across many mulberry-growing districts in southern India. Total crop losses on one hand and the inefficacy of chemical pesticides, coupled with their rejection by farmers, have created opportunities for biological control of these pests in mulberry cultivation. In a series of field trials conducted in four districts of Karnataka, the predatory mite *Typhlodromus (Anthoseius) transvaalensis* (Acari: Phytoseiidae) successfully controlled these pests in mulberry infested by either the broad mite or the thrips. For example, at Chakkalurdoddi in Ramanagara district, the predatory mite (60 adults per plant) reduced the broad mite population by 89.1%, and at Mattur in Raichur district, it suppressed the thrips by 76%. In areas with high broad mite incidence, the predatory mite proved to be an effective complement to the acaropathogenic fungus, *Hirsutella thompsonii* [ICAR–NBAIR–MF(Ag)66] and other control measures. A simple, cost-effective mass production and application technology ('Shatpada Treat') has been developed for this Type III generalist predatory mite at ICAR–NBAIR. As it is safe for the silkworm, *Bombyx mori* (Lepidoptera: Bombycidae), its use is expected to bolster biological control methods in mulberry cultivation. Nonetheless, achieving significant results hinges on precise timing.

Keywords: biological control; mulberry; *Polyphagotarsonemus latus*; *Pseudodendrothrips darci*; *Typhlodromus (Anthoseius) transvaalensis*





**Toxicity of indigenous *Bacillus thuringiensis* (Berliner) isolates against
Spodoptera litura (Fabricius) (Lepidoptera: Noctuidae)**

Vasanta Mutalikdesai^{1,2*}, M. Mohan² and C. Manjunatha²

¹ ICAR–Indian Institute of Horticultural Research, Bengaluru

² ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: vasantadesai90@gmail.com

Spodoptera litura (Fabricius) (Lepidoptera: Noctuidae) is a serious polyphagous and cosmopolitan pest that affect more than 80 species of host plants including potatoes, sugarcane, maize, cabbage, tomatoes, and coffee. Historically, control measures for these pests have predominantly depended on chemical insecticides. However, the indiscriminate application of these insecticides has resulted in the development of resistance among pest populations and raised substantial environmental concerns. In the current study, screening of native *B. thuringiensis* isolates and their toxicity bioassay were tested against the 1st instar larvae of *Spodoptera litura* under laboratory condition. Preliminary bioassay was conducted using diet incorporation method and treated with spore crystal lysates prepared from the native *Bacillus thuringiensis* isolates. Upon screening, *B. thuringiensis* isolates exhibited mortality ranging from 0% to 46.73% at a concentration of 1 ppm and from 0% to 83.11% at a concentration of 10 ppm after 7 days of exposure. Among the eighty isolates tested, Bt 83 and Bt 147 demonstrated the highest mortality rates of 80.80% and 83.11%, respectively, at the 10 ppm concentration after 7 days of exposure. The study will help to identify the most effective Bt isolates that can be utilised for the management of *S. litura*.

Key words: *Bacillus thuringiensis*; indigenous strains; *Spodoptera litura*; toxicity bioassay





Insecticidal potential of native actinobacterial extracts against lepidopteran pests: a sustainable approach for ecofriendly pest management

V. Naveen^{1*}, D.N. Kambrekar¹, P.U. Krishnaraj¹, C.P. Mallapur¹, Y.P. Arun², S.M. Pralhad¹,
P. Harikrishnan¹, S.M. Puthani¹ and P. Suma¹

¹University of Agricultural Sciences, Dharwad, India

²ICAR–National Institute of Veterinary Epidemiology and Disease Informatics, Bengaluru, India

*Correspondence: nv.insecta@gmail.com

Microbial pesticides, derived from organisms such as bacteria, fungi, and viruses, are environmentally friendly alternatives for crop protection and pest suppression. Among these, actinobacteria are widely recognised for their ability to produce bioactive compounds and antibiotics, yet they remain underexplored in pest management applications. This study evaluates the insecticidal potential of native actinobacterial extracts against major lepidopteran pests, including *Plutella xylostella*, *Spodoptera litura*, and *Spodoptera frugiperda*. Screening of 27 actinobacterial extracts revealed that isolates DBT-80, DBT-64, and DBT-59 demonstrated the highest efficacy, with larval mortalities of 80.75%, 78.85%, and 79.50%, respectively, at 72 hours post-treatment. Under greenhouse conditions, DBT-80 achieved larval population reductions of 84.00% in *P. xylostella*, 82.75% in *S. litura*, and 80.50% in *S. frugiperda* within 96 hours, while DBT-64 and DBT-59 also exhibited substantial activity. Molecular characterisation through 16S rDNA sequencing identified DBT-64 as *Streptomyces hyderabadensis* (99% homology), DBT-80 as *Streptomyces xiaminensis* (98% homology), and DBT-59 as *Streptomyces racemochromogenes* (99% homology). Secondary metabolites with insecticidal properties were identified, including linoleic acid, cis-trans-farnesyl acetate, and oleanane in DBT-64; delsemine A, huperzine A, and sulphur compounds in DBT-80; and tris(2-chloroethyl) phosphate, 9-octadecenamide, and sulphur compounds in DBT-59. These findings demonstrate the promise of native actinobacterial extracts as eco-friendly alternatives to chemical insecticides. By effectively suppressing pest populations with minimal environmental impact, they provide a sustainable and innovative solution for integrated pest management in agriculture. Furthermore, these actinobacterial isolates can be integrated into organic farming as a key component.

Keywords: actinobacterial extracts; integrated pest management; lepidopteran pests; organic farming secondary metabolites





Indigenous entomopathogenic nematodes (Heterorhabditidae and Steinernematidae): efficient biological control agents against the cutworm, *Agrotis ipsilon* (Hufnagel) (Lepidoptera: Noctuidae), in potato cultivation

Aarthi Nekkanti^{1*}, Jagadeesh Patil¹, B.S. Gotyal¹, Manjunatha T. Gowda² and S.N. Sushil¹

¹ICAR–National Bureau of Agricultural Insect Resources, Karnataka, India

²ICAR–Indian Institute of Vegetable Research, Uttar Pradesh, India

*Correspondence: aarthinekkanti@gmail.com

Agrotis ipsilon (Hufnagel) (Lepidoptera: Noctuidae) is a cosmopolitan and polyphagous pest that is known to attack around 30 cultivated plant species and is observed to cause the most significant damage to potatoes and other vegetable crops. The single concentration bioassay against larvae and pupae of *A. ipsilon* was carried out with ten EPN species. The bioassay results showed that only five EPN species caused more than 50% mortality in third instar larvae and pupae. Therefore, further studies used only those EPN species that caused more than 50% mortality. In laboratory assays, *Heterorhabditis indica* NBAIIH38 caused significantly greater mortality (47.5-100%) than *Heterorhabditis bacteriophora* NBAIRH75 (17.5-67.5%) against second instars, and *H. indica* caused 40-100% mortality in fourth instar larvae, while *H. bacteriophora* caused 10-60% mortality. *H. indica* caused 72.5% mortality in pupal stages, whereas *H. bacteriophora* caused only 47.5%. Temperature- and moisture-dependent bioassays showed that, among the EPN species tested, *H. indica* caused the highest mortality (95%) at 28°C, followed by 90% mortality at 25°C, and *H. indica* caused more than 50% mortality at all the moisture levels tested in this study except at the 5% moisture level. Field trial data showed that ten days after application of the treatments, the percentage reduction in *A. ipsilon* larval population was significantly higher (85.73%) using *H. indica* at 2.5×10^8 IJs ha⁻¹ than *Steinernema carpocapsae* NBAIRS59 (68.60%).

Keywords: biocontrol; cutworm; lepidopteran pests; potato; virulence



Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources



Showcasing the effectiveness of *Metarhizium anisopliae* for the sustainable management of mango hoppers through large-scale validation

B.L. Raghunandan*, N.B. Patel and Neha M. Patel

Anand Agricultural University, Anand, India

*Correspondence: rbl@aaau.in

Mango (*Mangifera indica* L.), known as the 'king of fruits' is an important tropical crop in India. It faces threats from various insect pests and diseases, particularly hoppers, which can lead to yield losses of up to 60%. Among these pests, *Amritodus atkinsoni* primarily infests the trunk and new vegetative growth, while two species of *Idioscopus*, *I. clypealis* and *I. nitidulus*, target the trees during the flowering season. Growing concerns about environmental safety and the demand for pesticide-free food have increased interest in ecofriendly pest management strategies. A continuous field experiment conducted from 2011–2012 to 2013–2014, and again in 2018–2019, prompted us to validate this technology on a larger scale. Demonstrations were carried out in 2020–2021 and 2021–2022 across five locations in Gujarat. The biointensive pest management (BIPM) module included a single spray of *Metarhizium anisopliae* NBAIR Ma-4 1% WP (2×10^8 cfu/g) @ 50 g/10 litres of water on the tree trunk in November, followed by three sprays on the foliage during the flowering season, each at 15 day intervals, starting with the initiation of pest. In all five locations, varying populations of mango hoppers were observed during the off-season and flowering period. Nakhtrana recorded the highest population of mango hoppers at 9.68 per sweep, while Dhangdhra had the lowest at 6.58 per sweep. The BIPM module showed significantly lower populations in Dhangdhra (5.31 per twig), Talala (6.79 per twig), and Valsad (6.95 per twig). In Nakhtrana, the chemical module also showed a significantly lower population (5.80 per twig), while Navsari recorded a non-significantly lower population in the chemical module (6.90 per twig). The results from the large-scale demonstration clearly demonstrate the effectiveness of biointensive management of mango hoppers using the microbial biopesticide *Metarhizium anisopliae* (NBAIR Ma-4) 1% WP.

Keywords: BIPM; demonstration; Gujarat; mango hoppers; *Metarhizium anisopliae*





Biocontrol potential of *Trichoderma* spp. and *Bacillus* spp. isolated from tomato rhizosphere against important soil-borne fungal plant pathogens

R. Rajeshwari^{1*}, K.R. Abhinandana¹ and C.G. Sangeeta²

¹College of Horticulture, GKV Campus, Bengaluru, India

²College of Horticulture, Kolar, India

*Correspondence: pdrcraji@yahoo.co.in

Tomato (*Solanum lycopersicum* L.) is consumed globally as a fresh vegetable due to its high nutritional value and antioxidant properties. However, soil-borne diseases can severely limit tomato production. Using agrochemicals to combat these diseases can lead to pesticide resistance and environmental pollution. Henceforth, the use of biological control agents as opposed to synthetic agrochemicals to control plant pathogens has gained momentum, considering their numerous advantages. In the present study, the naturally associated rhizospheric microorganisms specifically *Trichoderma* spp. and *Bacillus* spp. were evaluated for their antimicrobial potential against soil borne fungal pathogens viz., *Fusarium oxysporum*, *Sclerotium rolfsii*, *Ceratocystis fimbriata* and *Stagnosporopsis cucurbitacearum*. A total of twenty-four *Bacillus* spp. and ten *Trichoderma* spp. were isolated from the rhizospheric soil of tomato. *Trichoderma* isolate-UHSBF1 exhibited maximum per cent inhibition of pathogen *F. oxysporum* (88.23%), *C. fimbriata* (100%) and *S. cucurbitacearum* (79%). Among *Bacillus* isolates, UHSBB4 inhibited growth of *F. oxysporum* by 41.37%, *C. fimbriata* by 16.38% and *S. cucurbitacearum* by 62.34%. Subsequently, the efficient isolates were subjected to various biocontrol assays viz., dual petri dish assay, biomass assay, siderophore production and HCN production. All the efficient isolates produced significant amount of siderophore. Furthermore, GC-MS analysis of the crude extract of UHSBF1 and UHSBF5 has revealed the presence of many volatile compounds that may have bioactive properties. These promising isolates were later subjected to molecular characterisation. The BLAST searching results indicated that UHSBF1 showed 99.45% similarity with *Trichoderma asperellum* and UHSBB4 showed 97.98% similarity with *Bacillus subtilis*. These identified efficient isolates having antagonistic property could be used as a biocontrol agents against various phytopathogenic fungi for the benefit of several types of crops and the environment.

Keyword: *Bacillus*; biocontrol; *Trichoderma*; soil borne pathogens





White grubs (*Holotrichia serrata*) gut microflora in organic waste degradation

N. Sampada*, Mahesh S. Yandigeri, Gundappa and B.S. Manjunatha

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

*Correspondence: sampada823@gmail.com

Holotrichia serrata (Scarabaeidae) though a severe pest of agricultural and horticultural crops it is considered as a detritus insect whose gut houses various beneficial microorganisms which converts complicated plant polysaccharides into simpler molecules with the help of digestive enzymes. Disintegration of photosynthetically produced organic matter is aided by the gut and also associated native microflora which proceeds through multiple enzymatic reactions through oxidative process. The current investigation yielded 42 isolates from the gut of *Holotrichia serrata* which were characterised using culture dependent approach in which *Bacillus* being the dominating genera. These bacteria were tested for degradative enzymes qualitatively, which revealed most of the bacteria could degrade polysaccharides like starch, cellulose, protein, lipid, pectin and gelatin. Among these four isolates namely *Bacillus subtilis* (WG 25), *Chryseobacterium* (WGHS19), *Bacillus subtilis* (WGM1) and *Bacillus cereus* (WGM4) proved to be the promising degraders. Further the quantification of enzymes from these potent organisms revealed *Bacillus subtilis* (WGM1) to have high enzyme activity producing 3.97 U/ml of amylase, 0.53 U/ml of cellulase, 3.14 U/ml of lipase, 3.77 U/ml of pectinase, 2.49 U/ml of protease and also 4.75 U/ml of gelatinase. Pot trial resulted in significant change of pH and EC, gradual increase in NPK content, and decrease in C:N to 31:1 by 30th day after inoculation of microbial culture. This study inferred that, successive catabolic reactions by these beneficial bacteria aided in faster degradation of organic matter which mineralises into soil essential constituents, and most effective sources of macro- and micronutrients for the soil fertility.

Keywords: enzyme activity; gut microbes; organic waste degradation; soil fertility; white grubs





Investigation on effect of *Metarhizium anisopliae* on mirid bug, *Dortus primarius*, a predator of *Phthorimaea absoluta* in tomato

K. Sundaravalli^{1,2}, Richa Varshney^{1*} and A. Kandan¹

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Department of Research, MAHER, Chennai, India

*Correspondence: richavarshney84@gmail.com

The integration of macrobial and microbial agents in organic farming provides a sustainable alternative for pest management, particularly for crops like tomato, which is vulnerable to many insect pests. This study investigates the interactions between entomopathogenic fungi (EPF), *Metarhizium anisopliae* (ICAR Ma-4 strain) and predatory bug, *Dortus primarius*, of *Phthorimaea absoluta* (tomato leaf miner) in tomato. In previous studies, *D. primarius* was found feeding on *P. absoluta* eggs, and on 1st instar larvae of *P. absoluta*. In the present study, the biology of *D. primarius* was studied on *P. absoluta* eggs infected with Ma-4 to evaluate its survival and assess the impacts on predator's biology. *Dortus primarius* reared on Ma-4 infected *P. absoluta* eggs exhibited a longer total nymphal period (16.63 vs. 14.28 days) and reduced hatchability (76% vs. 85%) compared to those fed on uninfected eggs. Longevity and fecundity differences were minimal. A nymph could consume an average of 150.44 ± 5.26 Ma-4 infected *P. absoluta* eggs during nymphal duration which is significantly less than uninfected *P. absoluta* eggs consumption (271.94 ± 5.31) by a nymph. In choice tests, *D. primarius* showed a preference for uninfected *P. absoluta* eggs over infected ones, as indicated by the Manley index at different stages like adult female *D. primarius* ($\beta=0.67$), 2nd instar ($\beta=0.64$), 5th instar ($\beta=0.63$) and 4th instar ($\beta=0.60$). To manage *P. absoluta*, we need to have multiple options including macrobiotics and biopesticides. These studies showed that both *D. primarius* and Ma-4 could be used together to curtail *P. absoluta* as they target different stages of the pest. Further research is needed to optimise application techniques and evaluate the long-term impacts on pest populations and crop health in diverse agricultural settings.

Keywords: invasive pests; macrobial agents; microbial agents; pest management; sustainable agriculture





Development of microbial consortium for the management of fall armyworm and stalk rot of maize

P. Vaishnavi¹, P. Ram Kumar¹, G. Sivakumar^{1*} and Diptimayee Dash²

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Indira Gandhi Krishi Vishwavidyalaya, COA, Raipur, India

*Correspondence: sivakumarg.nbaii@gmail.com

Maize or corn is the third most important cereal crop after rice and wheat for India. Globally it is highly valued for its multifarious use as food, feed, fodder and raw material for large number of industrial products. India remained among the top 10 producers of maize in the world since 1961 and presently ranks 6th with annual output of 31.65 million MT. An invasive insect pest, fall armyworm, *Spodoptera frugiperda* and stalk rot disease are the major production constraints in maize in India, which can cause substantial yield losses in maize if uncontrolled. Currently, the management of FAW and stalk rot disease in maize in India is carried out using chemical insecticide and fungicide respectively. Management of FAW and stalk rot disease using microbial pesticides is a viable alternative and long-term sustainable management strategy that pre-serves the environment and human health. Natural occurrences of native entomopathogens on FAW larvae such as *Metarhizium rileyi*, *Beauveria bassiana*, nucleopolyhedrovirus and *Bacillus thuringiensis* (Bt) from the maize-growing areas of India were reported. In addition to these microbes such as *Pseudomonas fluorescens* and *Bacillus subtilis* have been found effective against FAW and stalk rot of maize. Currently, the use of individual microbes is in practice for the management of crop pests and diseases. In order to get faster outcomes and a higher output over time, combining microorganisms as a new biocontrol approach may show to be more important. This present study developed a bacterial consortium consisting of *P. fluorescens*, *B. thuringiensis* and *B. subtilis* which was found effective in suppressing FAW larvae and soil borne pathogens of maize such as *Fusarium verticillioides*, *Macrophomina phaseolina* *in vitro*. Further the evaluation of the efficacy of this bacterial consortium under *in vivo* condition is in progress.

Keywords: fall armyworm; maize; management; microbial consortium; stalk rot of maize





Session XI

**Information and Communication
Technology in Biological Control:
Artificial Intelligence, Internet of Things,
Mobile Apps, Drones and Robotics**



Enhancing bioprotection adoption: a digital campaign for managing Southeast Asian thrips with CABI digital tools

**Malvika Chaudhary^{1*}, Madhu Manjari¹, H.M. Mahesh¹, Kritika Khanna¹,
Tamsin Davis², Laura Hollis² and Vinod Pandit¹**

¹CABI South Asia, NASC Complex, Pusa, New Delhi, India

²CABI UK, Wallingford, Oxfordshire, UK

*Correspondence: m.chaudhary@cabi.org

The outbreak of *Thrips parvispinus*, commonly known as the chilli black thrips or Southeast Asian thrips, is posing significant losses ranging from 40–80% for smallholder farmers in India, especially those dependent on chilli crops for their livelihoods. Farmers face lack of real-time information to facilitate adoption of sustainable pest management practices, such as the use of BioProtection products. In recent years, digital tools have proven to be effective in disseminating rural farm advisory services, optimising outreach to farmers and enabling them to make informed decisions. However, the success of these digital interventions depends on their accessibility and hyper local content to ensure the information reaches farmers and is well understood for adoption. CABI (CAB International), in collaboration with its partners globally, has been using digital tools to increase knowledge and promote sustainable pest management among smallholder farmers. This has led to over 765,000 users, both men and women, interacting with CABI's digital tools, according to data from Google Analytics. The effectiveness of these tools was evident during the campaign in October and December 2024, when CABI and its partners launched communication campaigns to tackle the threat of *T. parvispinus* to chilli crops in the Indian states of Karnataka, Andhra Pradesh and Tamil Nadu. Google Analytics data also revealed that during this period, the usage of CABI's digital tools rose by an impressive 83%. This significant rise in usage during the campaign underscores the potential of digital tools in enhancing pest management awareness and the adoption of sustainable farming practices among smallholder farmers.

Keywords: bioprotection; digital tools; mass extension campaign; Southeast Asian thrips



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Utilising UAVs (drones) for application of biopesticides and granular insecticide formulations: opportunities and challenges

**N. Rama Gopala Varma*, T. Kiran Babu, K. Supriya and
K. Bhargavi Reddy**

Professor Jayashankar Telangana Agricultural University, Hyderabad, India

**Correspondence: varmanrgv@gmail.com*

The fusion of cutting-edge technologies with ecofriendly pest management solutions stands as a beacon of hope for modern agriculture. Currently, unmanned aerial vehicles (UAVs/ drones) are being developed extensively to assist the practice of precision agriculture as overuse of agricultural chemicals is being avoided via reducing and optimising the inputs. In most cases, drones are used preferably by farmers for application of chemical pesticides. With rising awareness and concern about health among people, demand for organic food is increasing. Even some organic growers are coming forward to use drones for the application of biopesticide formulations. Even though the standard operating procedures (SOPs) for chemical pesticide application through drones are available, information on application of biopesticides and granular insecticide formulations through drones is negligible and the studies are meagre. To address these issues, a series of studies were conducted during 2022–2024 at PJTAU and developed SOPs for application of biopesticides and granular formulations using drones. This paper briefly narrates the journey in deploying drones for biopesticides and granular formulations along with the opportunities and challenges.

Keywords: biopesticides; challenges; drones; granular formulations; opportunities



X-ray based fruit fly screening for gherkins

**Shekhar Basavanna^{1*}, M.B. Arbaz¹, Samarth Moodithaya¹, M.A. Rashmi² and
Abraham Verghese²**

¹Wide Mobility Mechatronics Private Limited, Hubballi, India

²Rashvee International Phytosanitary Research and Services, Bengaluru, India

*Correspondence: shekhar@widemobility.com

Gherkin is a 100% export crop grown in Karnataka, Tamil Nadu and Telangana. India holds the title of the largest exporter of gherkins in the world, but gherkins face a significant challenge: fruit fly infestations. The fruit fly species *Zeugodacus cucurbitae* and occasionally *Dacus ciliatus* pose a major threat in harvested gherkins where detection of infestation is difficult. Exporters are vulnerable to customer claims, complaints and container rejection. To add to this, bans imposed are a big threat to the industry and its ecosystem as a whole. Although tremendous effort is put in containing the issue at the field, but the industry needs a plan Z that can effectively remove the infested gherkins from the incoming lot. Non-destructive imaging techniques offers plenty of opportunities to detect infested gherkins. However, considering daily working of a gherkin pickling industry, its schedule and targets, we need to find techniques that meet the quality and production needs of factory. Given the pros and cons of available technologies, X-ray imaging is the most promising of all, and economical as well. X-ray imaging can see through the given object and represent density variation in the form of varying pixel values in the image captured. This paper discusses the approach to use X-ray imaging to detect infestation. It also discusses the accuracy, performance and limitation of this technique by mapping the defect to time since infested. The paper concludes with the potential application that can benefit from this technology for mango and potato inspection.

Keywords: *Bactrocera cucurbitae*; fruitfly; gherkins; melonfly; radiography; x-ray imaging





Modern machine learning techniques for the detection and classification of pests and natural enemies in tomato crop

**M. Pratheepa^{1*}, K. Selvaraj¹, B. Gundappa¹, R.G. Gracy¹, T. Venkatesan¹ and
V.M.J. Zinnith²**

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

²Sathyabama Institute of Science and Technology, Chennai, India

*Correspondence: mpratheepa.nbair@gmail.com

Detection and classification of insect pests and its natural enemies is a crucial task in agriculture for effective pest management. Creation of awareness about the beneficial insects, viz. predators and parasitoids, is essential to the farming community. To address this problem, modern machine learning techniques can be used for automatic detection and classification of insect pests and their natural enemies. There are various insect image datasets used in machine learning for the automation of insect detection. In the proposed research work, the image data set has been created for the pests and its natural enemies in tomato crop. The image data set contains around 1,500 images with various tomato pests, viz. *Phthorimaea absoluta*, *Helicoverpa armigera*, *Liriomyza trifolii*, *Bemisia tabaci*, *Spodoptera litura* and their natural enemies. The image dataset includes adult, larva and nymphal stages of pests and adult stages of natural enemies. The state-of-the-art machine learning method convolutional neural network, has been used for the detection of pest and natural enemies in tomato crop. This application can be integrated with mobile application for easy and automated detection of pest and natural enemies in tomato field. Hence, this application is useful to differentiate the pest and natural enemies in the tomato field and to promote the biological control for pest management.

Keywords: artificial intelligence; biological control; machine learning; natural enemy detection; pest detection





Smart delivery systems for *Cordyceps* (= *Isaria*) *fumosorosea* for management of invasive whiteflies in coconut

K. Selvaraj*, B.V. Sumalatha, A. Kandan and B. Gundappa

¹ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: selvaentomo@gmail.com

The dissemination and transmission of entomopathogenic fungi are important factors for determining their potential as microbial control agents of pests in agro-ecosystems. The conidia present on an insect can be transferred to the same or different species of insects by horizontal transmission and they can develop new infection cycles and natural epizootics in the field. On the other hand, smart agricultural drones for crop spraying which offer targeted delivery of natural enemies and biopesticides, improving efficiency and reducing reliance on chemical pesticides. Despite their potential, adopting drone technology in agriculture faces regulatory challenges, such as the need for standard operating procedures (SOPs). Therefore, we developed SOP such as flight height (m), swath width, wind speed and suitable time of spray were standardised for foliar spray of oil-based formulation of *Cordyceps* (= *Isaria*) *fumosorosea* (ICAR–NBAIR Pfu-5) against invasive whiteflies in coconut. Data on bioefficacy, phytotoxicity, height of the drone spray above crop canopy (4 m), swath width (2 m), droplet settlement, wind spread, crop canopy temperature and suitable time of spray (after 4 pm) for biopesticide developed. Moreover, drone spraying leads to uniform biopesticide application, maximum penetration of active ingredient into the dense canopy and high application efficiency and bioefficacy leading to maximum control of target pests. Further, about 30 biopesticide spraying demonstrations were conducted to create farmers' awareness, which benefitted 1,000 progressive farmers and other stakeholders. Horizontal transmission of *C. fumosorosea* is caused considerable mortality on rugose spiralling whitefly which may contribute to the overall performance of microbial control in coconut.

Keywords: *Cordyceps fumosorosea*; drone; oil formulation; whiteflies





***Leucinodes orbonalis* database: a genomic and transcriptomics
web data resource**

**Anu Sharma^{1*}, M. Mohan², R. Gandhi Gracy², Dwijesh Chandra Mishra¹,
Sudhir Srivastava¹, Priyanka Balley¹, T. Venkatesan², S. Selva Babu² and
Girish Kumar Jha¹**

¹ICAR–Indian Agricultural Statistics Research Institute, New Delhi, India

²ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India

*Correspondence: anu.sharma@icar.gov.in

Brinjal crop is damaged by 53 important insect pests, among which, the shoot and fruit borer, *Leucinodes orbonalis* (Lepidoptera: Crambidae) is the most destructive and cosmopolitan in distribution. Studies reporting high level of insecticide resistance development in *L. orbonalis* might be attributed to the long-term indiscriminate use of various insecticides on brinjal. In light of the availability of genome and transcriptome information generated under CRP Genomics Platform at ICAR–NBAIR on *L. orbonalis*, a comprehensive database is highly desirable for sharing these resources. Here, we present (<http://webapp.cabgrid.res.in/lodb/index.php>), a web-based database of genomic and transcriptomic data of *L. orbonalis* developed using HTML, CSS and JavaScript for the front-end user interface, PHP for server-side scripting and MySQL as the back-end. This database contains 14,900 scaffolds of *L. orbonalis* and 30,879 genes identified using GenMark and Augustus along with their structural and functional annotations using GO, COG, eggNOG, KEGG and Interproscan. It also contains transcriptomics data information of unigenes, SNPs, InDels and SSRs. Web services such as BLAST and JBrowse 2 are provided for searching and visualising. This is a valuable platform for entomologists and researchers in light of the availability of genome and transcriptome information. It is now possible to pinpoint the genes and regulatory elements involved in insect growth and development, behaviour and metabolism of xenobiotics.

Keywords: database; genome; transcriptome



National pest surveillance system: transforming pest management with AI in India

**Niranjan Singh, Manoj Choudhary, Mukesh Kumar Khokhar, Anoop Kumar and
S.M. Haldhar**

ICAR–National Research Institute for Integrated Pest Management, New Delhi, India

**Correspondence: attri.ns@gmail.com*

India's diverse agro-climatic conditions present significant challenges in managing agricultural productivity due to various biotic and abiotic stresses. Farmers' over-reliance on pesticide dealers often results in excessive and irrational pesticide use, posing risks to health and the environment. To address this, the National Pest Surveillance System (NPSS) was developed, leveraging AI, smartphones and web-based tools to provide timely pest management advisories. The NPSS focusses on all agricultural and horticultural crops such as rice, cotton, maize, mango and chilies, and comprises three components: a mobile app, a cloud-hosted database and a web portal. The mobile app employs deep learning models for pest detection, capturing field data and images. The web portal provides visualisation tools for expert analysis, while the database securely stores surveillance data. Since its launch on 15 August 2024, NPSS has recorded 5,117 surveillance entries and 89,624 pest images, resulting in 61 expert advisories. Covering all 31 states/UTs in India and 61 crops, the system has identified 781 pests through AI models. Available in multiple languages, NPSS enhances farmers' access to sustainable IPM solutions.

Keywords: AI-based surveillance; integrated pest management; mobile app; pest detection



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Feeding the Future: startups and incubation in the world of insect science

Swetha Kumari Koduru

Department of Biosciences and Sericulture, Sri Padmavati Mahila Visvavidyalayam, Tirupati, India

Correspondence: drksk2015@gmail.com

Insect science is at the forefront of revolutionary changes in industries ranging from agriculture and food production to biotechnology and environmental sustainability. Startups working in insect science are developing innovative solutions to global challenges like food security, waste management, and sustainable agriculture. Incubation centres are playing a critical role in nurturing these startups, providing the necessary infrastructure, mentorship, and funding to scale their innovations. In recent years, insect-based startups have gained considerable attention for their potential to solve some of the world's most pressing issues which led to the rise of Insect-Based Startups. For startups in insect science, incubation centres offer critical support by providing access to specialised facilities, funding opportunities, and strategic mentorship. These centres are crucial in helping these early-stage companies navigate technical, regulatory, and market challenges. As climate change, population growth, and resource scarcity become more pronounced, the importance of sustainable solutions like those offered by insect science startups will continue to grow. Incubation centres will play a pivotal role in scaling these innovations and helping them reach global markets. Further, advancements in the fields of insect-based food products, bioplastics, and biomaterials, alongside the continued development of genetically engineered insects for environmental management and health purposes could be anticipated. With the right support, insect science startups have the potential to transform industries, feed the future, and contribute significantly to global sustainability efforts.

Keywords: agri-startups; biocontrol entrepreneurship; innovation in insect science; skill development in entomology



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Artificial intelligence based large language model for mobile phone alerts to enhance biocontrol methods

V.M.J. Zinnith^{1*}, J. Cruz Antony¹, B. Sandhiya¹ and M. Pratheepa²

¹*Sathyabama Institute of Science and Technology, Chennai, India*

²*ICAR–National Bureau of Agricultural Insect Resources, Bengaluru, India*

**Correspondence: zinnithvmj@gmail.com*

A mobile application is a novel Information and Communication Technology (ICT) tool designed to run on a mobile device such as phone, tablet which helps to disseminate the knowledge in an easy and fast manner. Mobile application makes the user to feel an interactive way because of its ability to convey the information in multimedia mode. In the current scenario, mobile phones are being used as a best communication device and it is very handy. Farming advisory system is required for effective pest management. Biological control method is safe to the environment and human health. Dissemination of biological control methods and timely advisory system to the farmers is needed now-a-days to take up the proper control measures in time. Artificial intelligence based Large Language Model (LLM) has been developed to send the alerts to the farmers' mobile phones. This model is mainly designed to understand the pest problems in the crop field and to advise about biological control methods. The proposed model performs various types of Natural Language Processing (NLP) task and LLM Chat Bots and helps in clarifying queries from the various types users, viz. researchers, students and farmers about the pest management. Presently, this model contains large amount of text data of biocontrol methods especially for tomato pests and its natural enemies. This application can be integrated with mobile applications for prompt alert to the farmers which helps to increase the crop productivity and for safer environment.

Keywords: Artificial Intelligence; biological control; Large Language Model; mobile phone alerts; tomato



**Society for Biocontrol Advancement &
ICAR–National Bureau of Agricultural Insect Resources**



Author Index

A
Aarthi, K. 141
Abhinandana, K.R. 272
Adak, Totan 92, 145
Adhikari, Debraj 116
Aditya, K. 191, 204, 210, 216, 222, 224
Ahamed, Thawfeeq J. 258
Ajaykumara, K.M. 76
Alam, Shahela 134
Amala, U. 103, 127, 160, 164, 169
Amarendra, B. 25
Anandan, A. 163, 167
Anees, K. 175
Aneesha, P.J. 192, 198, 205, 208
Anes, K.M. 102
Anitha, G. 105
Anoop Krishnan, K. 123
Anoosha, V. 67
Ansh Raj 227
Antony, Cruz J. 287
Appunu, C. 202, 265
Aravindan, S. 167
Arbaz, M.B. 281
Arun, Y.P. 269
Aruna, Y.R. 163
Arvind, M. 160
Arya, Varun 193
Ashok, K. 61, 190, 192, 198, 218, 230
Ashoka, K.S. 94
Ashwini, E. 164, 169
Asokan, Aiswarya 154
Asokan, R. 59, 190
Austin, Hans K.H. 39, 47
Azam, M.M. 136
B
Babu, Kiran T. 280
Babu, Merin 102
Babu, Nagendra B. 140
Babu, Ramakrishna A. 80
Babu, Ramesh S. 27, 54
Babu, S.R. 150
Bahadur, Anand 206
Balakrishnan, Rohini 17
Balley, Priyanka 284

Bandyopadhyay, Pritha 33
Banerjee, A. 53
Banne, S.N. 111
Basavanna, Shekhar 281
Baskar, N. 248
Bawaskar, D.M. 129
Bee, Hameeda 214
Bhagat, Deepa 135
Bhagwandas, Ranjini 154
Bhagyashree, S.N. 93
Bhamare, V.K. 19
Bhargaw, Akash 162
Bhaskar, Haseena 38, 117, 172
Bhat, A.I. 166
Bhattacharya, Ramcharan 212
Bhavani, B. 106
Bhavitha, P. 197
Biganski, Sarah 245
Biko, Muita 187
Bindushree, C. 165, 255, 259
Biplab, D. 224
Biradar, A.P. 109
Biradar, M.S. 264
Biswal, Gayatri 217
Biswas, Shubhadeep 260
C
Chaithra, M. 188
Chakraborti, Mridul 189
Chakraborty, Punam 207
Chandana, C.R. 144, 198
Chandel, R.S. 104, 107, 113
Chandel, V.G.S. 104, 107, 113
Chander, Subash 122, 137, 170
Chandra, Anup 182
Chandrakumara, K. 110
Chatterjee, Hirak 209
Chaudhary, Malvika 71, 162, 279
Chaudhary, Saksham 173
Chauhan, Nikita 113
Chauhan, Parul 261
Chavadal, Narayana 31
Chellappan, Mani 172
Chinnu, V.S. 208
Chintalapati, Padmavathi 136, 147

Choudhary, Jaipal Singh 227
Choudhary, Manoj 108, 285
Chowdary, N.B. 37
Coetzee, Julie 246
Correya, Judith Corolin 34
Crickmore, N. 202
D
D'Silva, Sharon 166
Dammel, Lina 245
Damodaran, Thukkaram 168
Dara, Surendra, K. 89
Darshana Brahma 170
Das, Amit 165
Das, Avijit 165
Das, Madhab Chandra 134
Das, Ruby 165
Dash, Diptimayee 275
Dash, Soumya Shephalika 209, 217
Dash, Swetapadma 50
David, K. J. 21, 48, 55, 139
Davis, Tamsin 279
Day, M.D. 66
Deeksha, Mudagadde, G. 68
Deepak 171
Deepthy, K.B. 172
Devasahayam, S. 166
Devi, Moirangthem Monalisa 174
Devi, Romila 35
Devi, Vimala V. 201
Devika, Sharma 74
Dey, Nilanjan 133
Dey, Debjani 110
Dhakar, Divya Kumari 27, 54
Dhane, A.S. 180
Dhinesh, R. 77
Dhoj, Yubak G.C. 116
Dinesh, M. 258
Dinesh, R. 175
Divya, C. 197, 204, 210, 216, 222, 229
Dixit, G.P. 182
Dubey, Tripti 183
Dubey, Vinod Kumar 218
Durán, Álvaro 96
Dutta, Pranab 161

Dutta, Suvasri 145
Dyamanagouda, P. 36, 41
E
Edward, Johnson Thangaraj Y.S. 51
Eswaramoorthy, M. 142, 146, 151, 153
F
Fan, Jiangbin 245
Fand, Babasaheb B. 24
Fasna Sherin, K. 82
Fritsch, Eva 245
G
Gadad, H.S. 129
Gadad, Hanamant 37
Gaddi, G.M. 79
Gadekar, Manish 146
Gagana, S. 121
Ganguli, Jayalaxmi 181
Ganguli, R.N. 181
Ganiger, Prabhu C. 20, 120, 126
Garg, Abhishek 153
Gautam, Vinithashri 211,
Gayathri, S.R. 27, 54
George, Anjitha 163, 167
George, Priya 175
Getahun, Merid 239
Ghante, Vijayakumar 69
Gharde, Yogita 68
Ghodke, Amol 187
Ghosh, S.K. 162
Ghosh, Monalisha 168
Gireesh, C. 167
Goergen, Georg 72
Golive, Prasanthi 209
Gopal, SurendraK. 117
Gopal, Ashwitha 195
Gopal, K. 251
Gopalakrishnan, S. 199
Gorantla, Markandeya 134, 240
Goswami, Subrata 146, 151, 153
Gotyal, B.S. 21, 93, 165, 229, 270
Gouthami, Desavath 38
Govardhan Rao, V. 67, 251
Gowda, Manjunatha T. 252, 270
Gowda, Basana G. 92, 189

Gowda, Chinnamade C. 36, 41, 43
Grace, Nike H. Br.S. 96
Gracy, G.R. 22, 48, 52, 61, 127, 192, 195, 196, 198, 205, 218, 219, 225, 228, 230, 231, 233, 235, 258, 282, 284
Greaves, Ian 187
Gundappa 93, 139, 159, 273, 282, 283
Gupta, Ankita 22, 26, 72
Gupta, Ayushi 212
Gupta, Samiksha 262
Guru PirasannaPandiGovindharaj 92, 189
H
Hadapad, Ashok 94, 221
Hadimani, Basavaraj N. 110
Hadimani, Amaresh 162
Haldhar, S.M. 285
Haldhar, Shravan M. 125
Hancock, D.L. 48
Hari, K. 200, 202, 265
Harika, S. 199
Harikrishnan, P. 269
Harish, M.N. 40
Harshitha, K.N. 77
Haveri, Rachappa 94
Hegde, R.V. 124
Heide, Hessel van der 70
Hemalatha, G. 141
Hingole, D.G. 111
Hire, Ramesh S. 94, 221
Hiremath, Renuka 36, 41, 43
Hiremath, Varun 76
Hoffmann, Ben 187
Hollis, Laura 279
Hosamani, Arunkumar 69
I
Ika Feronika, L.S. 96
Indhumathi, K. 249
Ingole, D.B. 180
Irma Yunara, Br.G. 96
Ishwarya, B. 265
Istkhar 28, 261
J
Jaba, J. 149, 199
Jacob, T.K. 166

Jagadeeswaran, R. 173
Jalgaonkar, V.N. 44
Jambagi, Suresh R. 213
James, Tess 187
Janaki Prasad, A. 214
Jat, S.L. 73
Jayanthi, Kamala P.D. 241
Jayasekhar, S. 72
Jayashree, S. 30, 42
Jehle, Johannes, A. 3, 245
Jeyarani, S. 249
Jha, Girish Kumar 284
Jones, Jeffrey B. 108
Jose, Anna 36, 41, 43
Josephrajakumar, A. 102, 138
Joshi, Sunil 38, 72, 229
Jyoshna, E. 78, 83
Jyoti, P. 51, 127, 195, 228
K
Kadam, D.R. 84
Kadam, S.S. 111
Kalaivanan, D. 256
Kale, S.N. 44, 180
Kalita, H. 152
Kalita, Surajit 144
Kalleshwaraswamy, C.M. 46
Kalmath, Basavaraj S. 94, 221
Kalyani, M.B. 147
Kamakshi, N. 214
Kamal, Ashish 112
Kambrekar, D.N. 264, 269
Kamil, Deeba 188
Kandan, A. 75, 160, 164, 169, 177, 191, 210, 216, 222, 224, 254, 257, 274, 283
Kannan, M. 254
Kar, Angshuman 47
Kar, MeeraKumari 189
Kar, Payel 45
Kariyanna, B. 140
Karmakar, Krishna 33, 45, 260
Karmarkar, M.S. 44
Karthik, C.M. 46
Karthik, R.S. 101
Karthikeyan, S. 200

Kataki, T. 152
Katti, Gururaj 23
Katti, Pramod 148
Kaundal, Shashank 113
Kaur, Harpreet 114
Kaur, Navjot 262
Kaur, Rabinder 114
Kaur, Sahilpreet 115
Kaurav, Ajay Kumar 256
Kaushik, Snata 39, 47
Kavya, M.H. 197
Kedar, Santosh C. 263
Keerthana, U. 217
Keerthi, Bavana A. 214
Keerthi, M.C. 77, 78, 229
Kennedy, Ningthoujam 76
Khanna, Kritika 279
Khedkar, Pratiksha B. 19
Khemrajji, Hatwar Nikhil 48
Khokhar, M.K. 95, 285
Kireeti, A. 67
Kodandarama, M.H. 247
Koduru, Swetha Kumari 286
Kolesik, Peter 21
Kotasthane, A.S. 204
Krishnamurthy, K.S. 175
Krishnaraj, P.U. 264, 269
Kumar, Anoop 95, 97, 285
Kumar, Dileep N. T. 109
Kumar, Hemant 215
Kumar, Mukesh 49
Kumar, N. 73
Kumar, Nagesh T. 165
Kumar, Niranjan 98
Kumar, Nirmal B.J. 99
Kumar, Pawan 35
Kumar, Pradeep 150
Kumar, Ram P. 254, 275
Kumar, Ranjith L . 176
Kumar, Sai Ram D.V. 199, 225
Kumar, Sameer C.V. 78
Kumar, Sanjay 163
Kumar, Vinay 142, 146, 151, 153
Kumar, Vinod 227

Kumaran, N. 187
Kumari, Prasanna, V. 225, 251
L
Latha, H. 32
Lavanya, S.M. 204, 210, 216, 222
Leela, N.K. 175
Loganathan, M. 248
Logeswaran, K. 264
Lokesh, K. 147
M
Madhu, T.N. 99, 188
Magar, S.J. 111
Mahanta, Madhusmita 161
Mahesh, H.M. 116, 279
Mahesh, P. 202, 265
Mahla, M.K. 128, 266
Mallapur, C.P. 264, 269
Mamatha, M. 69
Manda, Raghavendra Reddy 70
Mandal, Jayanta 165
Manjari, Madhu 279
Manjunatha, B.S. 165, 225, 273
Manjunatha, C. 127, 164, 167, 169, 191, 197, 204, 210, 216, 222, 224, 229, 254, 268
Manjunatha, Ramakrishnappa 122
Manu, B. 247
Marantika, Hengki, P. 96
Masudur Rahman, M.D. 134
Mathew, Manju 47
Mazumdar, S.M. 37, 129
Meghashree, M.C. 121
Mehanth, RupanagudiMaruthi 267
Mehra, Keshav 49
Menon, Athira G. 117
Menon, Gopalakrishnan 127
Messelink, Gerben 70
Mishra, Om Prakash 125
Mishra, Dwijesh Chandra 284
Mishra, G. 220
Mittal, Vishal 37
Mohan, M. 61, 72, 192, 195, 196, 198, 205, 208, 211, 213, 218, 228, 230, 235, 254, 258, 268, 284
Mohan, K.S. 258
Mohan, Murali, K. 79, 213

Mohanasundaram, A. 248
Mohanprasad, G. 20, 120, 126
Mohapatra, S.D. 189
Mohapatra, Shyamaranjan Das 92, 209
Mohapatra, Sucharita 209, 217
Mondal, Kinjal 150
Mondal, Rahul 50
Monisha, U. 249
Moodithaya, Samarth 281
More, S.A. 118
Mridha, Nilimesh 165
Mukherjee S.K. 174
Mukherjee, Abhishek 145
Mukherjee, Arup Kumar 209
Mule, R.S. 44
Mulimani, Vidya 36, 41, 43
Muniappan, Rangaswamy 134
Murugan, Marimuthu 151
Murugan, M. 149, 235, 249
Mutalikdesai, Vasanta 268
Muthuraju, R. 216
N
Nadaf, H. 129
Nadagouda, Sushila 148
Nagaraja, Bhargava C. 190
Nagaraju, M.C. 259
Nagaraju, N. 224
Nagaraju, T. 140
Nagpal, Akanksha 71
Naidu, G.K. 124
Naik, Chinna Babu 136
Naik, Santhosh 29
Nalimala, Manikanta 228
Narayana, Srinivasa 48, 193
Naveen, V. 269
Naveena, K. 141
Naveena, P. 20, 120, 126
Navi, Shivaray 112
Navik, Omprakash 24, 51, 159, 250, 263
Nayak, Dipak 168
Nayyer, Nishtha 228
Nebapure, Suresh M. 137
Neenu, A. 197
Neeraja, B. 67, 251

Negi, Nikita 196, 218, 219, 231
Nekkanti, Aarthi 252, 270
Ngxande-Koza, Samella 246
Nidhi, C.N. 125
Nidoni, Udaykumar 148
Nimisha, T. 172
Niranjana, H.G. 162
Niranjana, P. 121, 223
Nived, K.M. 219, 231
Noor, N.R. 55
O
Onkarappa, Dhanyakumar 149
P
Padala, Vinod K. 81, 137
Pal, Amartya 50
Palli, Subba Reddy 9, 60
Panda, Rudra Madhab 189
Pandey, Abhay K. 194
Pandian, Thava Prakasa R. 99
Pandit, Sagar 242
Pandit, Vinod 71, 116, 279
Pandita, S. 220
Papireddy, Maddireddy 122
Parameswaran, C. 209
Paret, Mathews L. 108
Pashupat, V. D. 73
Patel, N.B. 100, 271
Patel, Neha M. 100, 271
Pathak, Mahesh 76
Patil, Jagadeesh 52, 181, 250, 252, 270
Patil, Naveenkumar B. 92
Patil, Sachin R. 32
Pattar, Rohit 22
Pavan, M. 165
Pavana, J.K. 55
Peter, Anitha 230
Polaiah, A.C. 229
Pooja, D.V. 162
Poon, Aashiq V.S. 29
Prabhu, B. 51
Prabhu, S.T. 124
Prabhukarthikeyan, S.R. 217
Prabhulinga, T. 24, 159, 250, 257
Prabhuraj, A. 148

Pradeep, S. 51, 55
Prakash, K.N. 79
Pralhad, S.M. 269
Prameeladevi, T. 188
Prasad, L. 188
Prasannakumar, N.R. 77
Prashar, Arpit 221
Pratheepa, M. 282, 287
Prathibha, P.S. 102, 138
Praveena, R. 175
Praveenkumar, C. 52, 151, 153
Punithavalli, M. 166
Puthani, S.M. 269
R
Rachana, R.R. 25, 52
Raghavendra, A. 234
Raghavendra, K.V. 122
Raghu, S. 4
Raghunandan, B.L. 100, 271
Raghuraman, M. 146
Raghuraman, Mahadevan 48
Ragu, R. 249
Rai, N. 183
Raj, Neethu G. 123
Rajashekar, B. 78, 83
Rajashekhar, M. 78, 83
Rajashekharappa, K. 36
Rajeshkumar, M. 200
Rajeshwari, Ch. 167
Rajeshwari, R 272
Rajgopal, N.N. 26
Rajkhowa, Denisha 76
Rajkumar, Balaji M. 166
Rajkumar, Yadav S. 236
Rajna, S. 137, 170
Raksha, S. 204, 210, 216, 222
Rakshitha, T.N. 124
Ramakrishna, K. 78, 83
Raman, Anantanarayanan 65
Rameshkumar, A. 38, 85
Ramya, N. 81
Ramya, P. 163
Ramya, R.S. 21, 61, 81, 163, 191, 197, 205, 216, 224, 229, 230

Rana, D.K. 231
Rangeshwaran, R. 191, 252
Ranjith, M. 39, 47
Rao, Chalapathi N.B.V.
Rao, Sanjeeva, D. 67, 251
Rao, Sunny A. 196, 218, 219, 231
Rashmi, M.A. 139, 281
Rath, Prakash Chandra 209
Raut, A.A. 40
Ray, Aishwarya 92
Ray, Sabyasachi 53
Reager, M.L. 49
Reddy, Thirupam B. 37, 129
Reddy, Bhargavi K. 280
Reddy, D.S. 21
Reddy, Karthik, M. 29
Reddy, Nagabhushana 20, 120, 126
Reddy, Prabhakar T. 83
Reddy, Subba B.V. 140
Reddy, T.P. 78
Reddy, Veeramanikanta N. 219, 231, 233
Reji Rani, O.P. 101
Rekha, Balodi 122
Revanappa B. 247
Revanasidda 173
Revi, Smitha 82
Roberts, John 187
Roopa, K. 223
Roy, Pranita 125
Ruqiya, S. 204, 210, 222, 224
S
Sab, Rabbani 148
Sabale, P.R. 247
Sabitha, C. 225
Sagar, D. 21, 61, 81, 197, 198, 205, 215, 230
Sahoo, Kishore C. 29
Sahoo, Ranjit Kumar 226
Sainath, G. 140
Saini, Khushi 27, 54
Sai Teja, K. S. 120
Sajan, Jilu V. 102, 138
Salin, K.P. 200, 265
Samal, Ipsita 227
Saminathan, V.R. 52

Sampada, N. 203
Sampathkumar, M. 32, 72
Samyuktha, M. 166
Sandhiya, B. 287
Sangeeta, C.G. 272
Sangha, K.S. 114, 115
Sangma, Shannon N. 98
Sankaran, K.V. 5, 66
Sankaranarayanan, C. 200, 202, 265
Sannagoudar, Manjanagouda S. 79, 163, 167
Santhoshkumar, T. 123
Saravanakumar, M. 258
Saravanan, S. 52, 146, 151, 153
Sathyapala, Shiroma 10
Savithri, Shravya K. 20, 120, 126
Sehgal, Mukesh 95, 97, 122
Sekhar, J. C. 73
Selva Babu, S. 127, 192, 195, 196, 198, 218, 219, 228, 230, 234, 284
Selvakumar, T. 129
Selvaraj, C. 129
Selvaraj, K. 85, 232, 282, 283
Selvarajan, R. 248
Semwal, Anshuman 104, 107, 113
Senapati, U.S. 152
Senthil Kumar, C. M. 166
Shaila, O. 78, 83
Shakyawar, D.B. 165
Shankar, A. 78
Shankar, Adhi 83
Shanker, Chitra 23, 147, 253
Shanmugaiah, V. 201
Shanmugam, P.S. 249
Shanmugam, PagalahalliSankaran 151
Shantharaja, C. S. 163, 167
Shanthi, M. 141, 235
Sharma, Nikshubha 178, 179
Sharma, Adarsh 178, 179
Sharma, Anu 284
Sharma, Harshit K. 194
Sharma, Nikita 107
Sharma, P.L. 104, 107, 113, 178, 179
Sharma, Pankaj 107
Sharma, Simran 113

Sharma, Vibhuti 104
Shashank, P.R. 29
Sheeba, Jenifer J. 127
Sheela, N. 112, 119, 255, 267
Sheppard, Andy 5
Shera, P.S. 114
Shinde, B.D. 44, 180
Shiva, Shatrughan 206
Shivakumara, K.T. 21, 191, 197, 224, 229
Shivalingaswamy, T.M. 160
Shreyansh 37
Shruthi, K. K. 27
Shu, C. 202
Shubha, G.M. 121
Shukla, Shantanu P. 18
Shylesha, A.N. 40, 68, 72
Siddamma 20, 120, 126
Siddayya 79
Singaravelu, B. 200, 202, 265
Singh, A.N. 183
Singh, Beerendra 27, 54
Singh, Bharat 256
Singh, Chander 104, 107, 113
Singh, Jitendra 37
Singh, Khumukcham Ibohal 174
Singh, Manisha 206
Singh, Neeraj Kumar 173
Singh, Niranjana 98, 285
Singh, S.R.K. 40
Singh, Veer 49
Singha, Atul 165
Sireesha, K. 176
Sivakumar, U. 200
Sivakumar, G. 127, 164, 169, 191, 204, 210, 222, 254, 275
Skanda, H. 99
Smitha, M. S. 117
Soni, Sonia 181
Sood, A. K. 74
Soujanya, P.L. 73
Sowmya, E. 69
Sowmya, M. 153
Sreedevi, K. 30, 34, 42
Sreekumar, K.M. 39

Sree Lakshmi, B. 199
Sreelakshmi, U.K. 172
Sreelatha, D. 95
Sreenivas, A. G. 171
Sreerama Kumar, Prakya 66, 119, 255, 267
Sridhar, V. 77
Srikanth, J. 202, 265
Srikumar Koda Kkadan 96
Srinivasa, N. 41
Srinivasan Ramasamy 90, 157, 198
Srinivasan, G. 141
Srinivasan, T. 249
Srivastava, Shalini 206
Srivastava, Subhi 195
Srivastava, Sudhir 284
Sruthi 172
Sruthi, K.K. 54
Subaharan, K. 52, 138, 142, 146, 151, 153, 159, 228, 234, 254, 257
Subramanian Sevgan 91
Subramanian, Madhu 82
Subramanian, Sabtharishi 127
Suby, S.B. 73, 95
Sudhakar, S. 256
Sudharshan, K. R. 39
Sujayanand, G.K. 173, 182
Suma, P. 269
Sumalatha, B.V. 283
Suman, T.C. 195, 198, 208, 228, 230, 233
Sundaram, R.M. 136
Sundaravalli, K. 274
Sunitha, N.D. 31
Supriya, K. 280
Suresh, P. 201
Suresha, G.S. 202
Surjeet, Kumar 74
Sushil, S.N. 25, 26, 30, 72, 93, 127, 159, 164, 169, 177, 191, 192, 195, 196, 197, 198, 204, 210, 216, 222, 224, 257, 270
Sushmita 113
Swami, H. 266
Swami, Hemant 128
T
Tamgond, Sushma 118

Tamò, Manuele 90
Tarigan, Marthin 96
Thakur, Manju 71
Thanigairaj, R. 248
Thomas, Titty Anna 175
Thube, Shivaji H. 24
Tippannavar, P.S. 124
Tiwari, Ashish 182
Tiwari, B.S. 150
Tiwari, Kirti 183
Tripathi, A.N. 183
Tripathy, Partha Sarathi 209
U
Udikeri, S.S. 32, 229
Ugale, M.V. 84
Ullah, Hedyiet 134
Undorf-Spahn, Karin 245
V
Vaishnavi, P. 275
Vani Sree, K. 80
Vani, R. 153
Vanishree, G. 163, 167
Varma, Kishore P. 75, 214
Varma, Rama Gopala, N. 280
Varshney, R. 24, 68, 95, 114, 146, 159, 205, 223, 257, 274
Vasan, Suvetha 154
Vasundhara, J. 85, 232
Veena, K. 69
Vellaikumar, S. 141
Venkataramana, M.N. 79
Venkatesan, Radhika 143
Venkatesan, T. 51, 61, 72, 127, 192, 195, 196, 197, 198, 205, 213, 218, 219, 223, 228, 229, 230, 231, 232, 233, 234, 254, 282, 284
Venkateshaiah, Abhishek 55
Venu, H.S. 103, 160
Venugopala, K.M. 51, 234
Verghese, Abraham 139, 281
Verma, P.C. 220
Verma, Praveen C. 206, 207, 236
Verma, S.C. 104, 107, 113
Verma, Sweta 215
Vidya, C.V. 82

Vidyarthi, Ujjwal 146, 151
Vijayakumari, N. 198, 235
Vijayasanthi, K.V. 175
Vikas 221
Vimalkumar, C. 168
Vinodhini, R.L. 197
Visalakshi, M. 75, 106
Vishaka, G.V. 129
Viswakethu, Velavan 154
W
Wang, Ming-Bo 187
Wangi, Nagaratna 247
Waykule, P.K. 84
Wennmann, Jörg T. 245
Y
Yadav, Kavya G.A. 85, 232
Yadav, Ramawtar 49
Yadav, Shivanand 194
Yadu, Y. K. 233
Yamini, R. 249
Yandigeri, Mahesh 93, 203, 254, 273
Yang, Shili 245
Yogendra, K. 149
Z
Zhang, J. 202
Zinnith, V.M.J. 282



Conference Sponsors

Conference Sponsors
Platinum
Dhanuka Agritech Limited, Gurugram
UPL Limited, Mumbai
Gold
Tropical Agrosystem (India) Private Limited, Chennai
Silver
ATGC Biotech Private Limited, Hyderabad
Bengaluru International Airport Limited, Bengaluru
CAB International, New Delhi
Corteva Agriscience, Hyderabad
HIL (India) Limited, New Delhi
Jain irrigation systems Limited, Jalgaon
PI Industries Limited, Gurugram
Syngenta India Private Limited, Pune
T. Stanes and Company Limited, Coimbatore
Bronze
Bannari Amman Sugars Limited, Coimbatore
Bayer, Thane
Bharat Certis Agriscience Limited, New Delhi
Bionivid Technology Private Limited, Bengaluru
Biostadt India Limited, Mumbai
Eppendorf India Private Limited, Chennai
IPL Biologicals Limited, Gurugram
Mankind Agritech Limited, New Delhi
Microplex, Nagpur
Multiplex Group of Companies, Bengaluru
National Bank for Agriculture and Rural Development, Mumbai
P.J. Margo Private Limited, Bengaluru
Rasi seeds (Private) Limited, Coimbatore
Others
Agricultural Microorganisms Manufacturers & Farmers Association, Nashik
Vasa Scientific Company, Bengaluru



India Ka Pranam[®] Har Kisan Ke Naam



The dedicated hardworking farmer of India deserves recognition.

For more than four decades, *Dhanuka Agritech Limited* is working with farmers and moving forward together.

During this journey, Dhanuka took a pledge to bring prosperity in the lives of these farmers using advanced tools and technology. Dhanuka's trained field force is empowering farmers with new age ways of increasing farm yields and crop production.

At Dhanuka, we believe every citizen of India will salute the farmers for their dedication, determination and grit.

**DHANUKA SALUTES ALL THE FARMERS
OF INDIA FOR THEIR UNMATCHED
CONTRIBUTION IN NATION BUILDING**



Dhanuka Agritech Limited

Global Gateway Towers, Near Guru Dronacharya Metro Station, MG Road, Gurugram - 122002, Haryana, Tel.: +91-124-434 5000, E-mail: headoffice@dhanuka.com.

Toll free no.: 1800-102-1022 | Log on to: www.dhanuka.com or follow us on:   

NPP

Natural Plant
Protection by UPL



Reimagining Sustainability

for farmers, food systems
and our global future.



Find out more
at upl-ltd.com

Ushering in the New Age Integrated Crop Management Solutions for Maximising Productivity



We Manufacture:

- INSECTICIDES
- FUNGICIDES
- ACARICIDES
- HERBICIDES
- PGRs
- BIOLOGICAL PESTICIDES
- BIO-FERTILIZERS
- BIOSTIMULANTS
- ORGANIC NUTRIENTS
- SEED TREATMENT PRODUCTS



TROPICAL AGRO
PROTECTING FARMERS GLOBALLY

TROPICAL AGROSYSTEM (INDIA) PVT. LTD.

AN ISO 9001:2008 COMPANY

Old No.195, New No.82, St. Mary's Road, Alwarpet, Chennai-600 018.

Tel.: 044-2858 7841 / 7874 / 7880, Fax : +91-044-2854 8938

website: www.tropicalagro.in



Kempegowda
INTERNATIONAL
AIRPORT
BENGALURU

FRIENDS OF THE EARTH



- BIO PESTICIDES
- ORGANIC FERTILIZER
- BIO FERTILIZER
- BIO STIMULANTS

T. STANES AND COMPANY LIMITED

8/23-24, Race Course Road, Coimbatore-641018, INDIA.

Tel: +91-422-2221514, 2223515-18.

E-mail: info@t-stanes.com, Web: www.tstanes.com

(A MEMBER OF THE AMALGAMATIONS GROUP)

How do we feed a growing world population?

■ Farm new land

■ Get more from existing farmland

syngenta

The world needs more food. By 2050, there will be another 2 billion people on our planet. How do we provide enough high-quality food and preserve our environment? At Syngenta, we believe the answer lies in the boundless potential of plants. We develop new, higher yielding seeds and better ways to protect crops from insects, weeds and disease. So farmers can get more from existing farmland and take less new land into cultivation. It's just one way in which we're helping growers around the world to meet the challenge of the future: to grow more from less. To find out more, please visit us at www.growmorefromless.com

© 2015 Syngenta International AG, Basel, Switzerland. All rights reserved.
The Syngenta logo, wordmark and SHIELDING PLANT POTENTIAL TO LIFE
are registered trademarks of a Syngenta Group Company. www.syngenta.com

Bringing plant potential to life

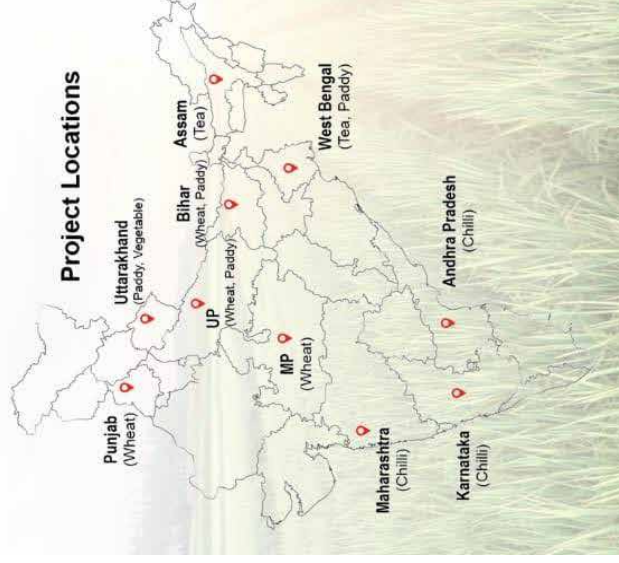


HIL's initiatives Promoting Sustainable Farming Practices Under FARM Project

Project Objective:

- 1) Phase out POPs and reducing HHPs.
- 2) Imparting knowledge for promotion of IPM practices and shifting of farming practices from conventional pesticides to the eco-friendly crop protection solutions.
- 3) Converting 1.45 million hectare agriculture land to safer alternatives.
- 4) To protect 1.45 million farmers from the exposure of chemical pesticides.
- 5) Commercializing eco friendly crop protection agents.

Project Locations



Commercialization of ICAR Technologies

Products:

- 1) *Bacillus thuringiensis kurstaki* - ICAR - NBARI
- 2) *Trichoderma* spp. - ICAR/TNAU
- 3) *Pseudomonas* spp. - TNAU
- 4) *Beauveria bassiana* - ICAR
- 5) *Verticillium lecanii* - ICAR
- 6) Neem formulations



Imparting training on

"Safe and Judicious Use of Pesticides and IPM Practices"



Reimagining a **HEALTHIER** Planet

Sustainable
Value Creation for
People and Planet



PI Industries Ltd

www.piindustries.com | info@piindustries.com

TM
CREMIT
PBW

Award winning technology for
Eco-friendly management of
Pink Bollworm in Cotton

Pheromone based slow release
mating disruption technology



Temperature resistant & Rainfast



Akarsh ME

Your secret weapon against

Oriental fruit fly in

Mango, Guava, Custard Apple, Papaya,
Banana, Dragon fruit & Kinnow etc.,

Now, Protect your Fruits, Naturally!



TOLL-FREE
1800 121 2842

sales@atgc.in www.atgc.in

Buy online @
www.growvera.app

**THE BEST THING YOU
CAN DO FOR THE FUTURE
IS GROW TODAY.**

KEEP GROWING.

© Trademark of Corteva Agriscience and its affiliated companies. © 2024 Corteva.



CORTEVA
agriscience

www.corteva.in

Conference Sponsors

