

ICAR-NBAIR Advances Insect Genomics for Next-Generation Pest Management

Ongoing projects:

1. ICAR- CRP Genomics funded: Insect Genomics (CCPI: Dr. M. Mohan)
2. In-house (RPP) funded: Genome analysis & gene knockout studies using genomic tools in selected insect species (PI: Dr. M. Mohan)

ICAR–National Bureau of Agricultural Insect Resources (ICAR-NBAIR), Bengaluru, is strengthening India's capacity in **insect genomics and functional molecular biology** by generating high-quality genome resources for agriculturally important insect pests, beneficial insects and parasitoids. These efforts are creating a foundation for translating genomic information into **precision pest management, resistance monitoring, biological control and genome-enabled crop protection**.

ICAR-NBAIR has generated genome resources covering diverse insect groups, including major pests such as the **brinjal shoot and fruit borer (*Leucinodes orbonalis*)**, cotton leafhopper (*Amrasca biguttula*), legume pod borer (*Maruca vitrata*), root grub (*Holotrichia serrata*), fruit fly (*Bactrocera caryae*), as well as the chilli broad mite, (*Polyphagotarsonemus latus*). Importantly, **ICAR-NBAIR's genome sequencing efforts have advanced from conventional short-read draft assemblies to high-quality chromosome-scale genomes generated using long-read sequencing and Hi-C technologies**, enabling comprehensive characterization of insect genomes.

The genomic portfolio also encompasses organisms of direct importance to **biological control and sustainable agriculture**, including the green lacewing predator *Chrysoperla zastrowi sillemi* and the larval parasitoid *Goniozus nephantidis*. In addition, the chromosome-scale genome of the chilli broad mite *Polyphagotarsonemus latus* represents an important resource for understanding this highly polyphagous mite pest with its exceptionally small genome.

These genome resources provide a platform for identifying **genes and molecular pathways associated with insecticide resistance, host adaptation, virulence, development, reproduction and pest–host interactions**. In the longer term, such information can support the development of **molecular diagnostics, genomic surveillance tools, RNAi-based interventions, gene-editing strategies and improved biological control agents**. Comparative genomics can further facilitate identification of species-specific targets and markers for early detection and resistance management.

With genome datasets spanning **pests, natural enemies and agriculturally important insect groups**, ICAR-NBAIR is establishing a strategic genomic resource base for Indian agriculture. The initiative is expected to accelerate the transition from conventional pest management towards **data-driven, precision and environmentally sustainable crop protection**, while providing valuable resources for researchers, policy makers, biotechnology developers and future genome-enabled pest management programmes.

De novo Genome Sequencing and Annotation of Insects: Progress at ICAR-NBAIR

(As on Aug. 2026)

Sl. No.	Insect Species	Sequencing strategy	Genome assembly level	Genome features	Public Accession (NCBI Bioproject ID)	Publication
1	Brinjal shoot and fruit borer, <i>Leucinodes orbanalis</i> (Crambidae: Lepidoptera)	Short (Illumina), long read (PacBio) coupled with linked read sequencing	Scaffold level	Genome size: 855.6 Mb; 14,900 scaffolds; N50: 108 kb; repeat content: 35.38%; 27,857 genes annotated	PRJNA377400	Under progress
2	Cotton leafhopper, <i>Amrasca biguttula</i> (Cicadellidae: Hemiptera)	Short (Illumina), long read (PacBio) sequencing	Scaffold level	Genome size: 1.1 Gb; 23,645 scaffolds; N50: 83.3 kb; 15,448 genes annotated	PRJNA555157	Under progress
3	Chilli broad mite, <i>Polyphagotarsonemus latus</i> (Tarsonemidae: Acari)	Long read (PacBio)	Chromosome scale (Hi-C guided)	Genome size: 49.1 Mb; 2 chromosomes; N50: 30.9 Mb; repeat content: 49.4%; 9,286 genes annotated	PRJNA904956	Mohan M <i>et al.</i> , 2024. The miniature genome of broad mite, <i>Polyphagotarsonemus latus</i> (Tarsonemidae: Acari). <i>Sci Data</i> 11 , 748 (2024). https://doi.org/10.1038/s41597-024-03579-4
4	Green lacewing predator, <i>Chrysoperla zastrowi sillemi</i> (Chrysopidae: Neuroptera)	Short (Illumina), long read (PacBio) coupled with Hi-C	Chromosome scale (Hi-C guided)	Genome size: 597 Mb; 6 chromosomes; N50: 30.4 Mb; repeat content: 57.31%; 14,495 genes annotated	PRJNA905226	Mohan M <i>et al.</i> , 2025. High-quality genome assembly of a cosmopolitan insect predator, <i>Chrysoperla zastrowi sillemi</i> (Esben-Petersen). <i>Sci Data</i> 12 , 281 (2025). https://doi.org/10.1038/s41597-025-04571-2

5	Legume pod borer, <i>Maruca vitrata</i> (Crambidae: Lepidoptera)	Short (Illumina), long read (PacBio) coupled with Hi-C and karyotype analysis	Chromosome scale (Hi-C guided, karyotype validated)	Genome size: 459.3 Mb; 21 chromosomes; N50: 15.6 Mb; repeat content: 36.67%; 21,586 genes annotated	PRJNA1281905	Mohan M et al., 2026. Hi-C guided genome assembly and karyotype analysis of the Indian population of <i>Maruca vitrata</i> (Lepidoptera: Crambidae) set the stage for structural and functional genomic insights. <i>BMC Genom Data</i> 27 , 48 (2026). https://doi.org/10.1186/s12863-026-01446-2
6	Larval parasitoid, <i>Goniozus nephantidis</i> (Bethyridae: Hymenoptera)	Short (Illumina), long read (PacBio) coupled with Hi-C	Chromosome scale (Hi-C guided)	Genome size: 49.1 Mb; 15 chromosomes; N50: 19 Mb; repeat content: 49.4%; 9,286 genes annotated	PRJNA1253398	Under progress
7	Root grub, <i>Holotrichia serrata</i> (Scarabaeidae: Coleoptera)	Short (Illumina), long read (PacBio) coupled with Hi-C	Chromosome scale (Hi-C guided)	Genome size: 942 Mb; 10 chromosomes; N50: 92.6 Mb; repeat content: 68.4%; 18,322 genes annotated	Under progress	Under progress
8	Fruit fly, <i>Bactrocera caryae</i> (Tephritidae: Diptera)	Short (Illumina), long read (PacBio) coupled with Hi-C	Chromosome scale (Hi-C guided)	Genome size: 582.83 Mb; 10 chromosomes; N50: 104.2 Mb; repeat content: 55.4%; 22,921 genes annotated	Under progress	Under progress

* All the genome annotations supported by RNA-seq data

CRISPR-Cas9 Mediated Genome Editing of Insect Pests - Progress at ICAR-NBAIR

Ongoing projects:

1. ICAR- EFC funded: Enhancing climate resilience and ensuring food security with genome editing tools (CCPI: Dr. M. Mohan)
2. In-house (RPP) funded: Genome analysis & gene knockout studies using genomic tools in selected insect species (PI: Dr. M. Mohan)
3. In-house (RPP) funded: CRISPR/Cas9 mediated gene editing in agriculturally important insect pests (PI: Dr. Sagar D.)
4. ANRF funded: Development of nanoformulated dsRNA and CRISPR-Cas9 based Biotechnological tools for the Sustainable Management of Invasive Fall Armyworm (*Spodoptera frugiperda*) (PI: Dr. G. Rajadurai / Mentor: Dr. M. Mohan)

ICAR-NBAIR is advancing in gene function validation through CRISPR-Cas9 **genome-editing technologies**. The CRISPR-Cas9 system provides a powerful platform for investigating gene function and understanding key biological processes governing **insect development, reproduction, fertility, host interaction and other traits of agricultural importance**.

At ICAR-NBAIR, genome-editing research is being pursued across diverse and economically important pest groups, including **fruit flies, bollworms, *Spodoptera* species, maize stem borer and potato tuber moth**. The programme currently encompasses multiple target genes and involves different stages of the genome-editing pipeline, ranging from **target selection and sgRNA design to in-vitro validation, embryo microinjection, mutant screening and molecular confirmation of edited individuals**.

A key strength of the programme is the progressive development and optimisation of **species-specific genome-editing platforms**, including embryo microinjection and molecular screening systems. Successful generation and confirmation of homozygous mutants in *Bactrocera zonata* represents an important milestone, while several additional targets in other major pests are currently under editing and validation.

CRISPR-Cas9 Genome Editing in Agriculturally Important Insect Pests - Progress at ICAR-NBAIR

(As on Aug. 2026)

Sl. No.	Insect pest	Target gene(s)	No. of sgRNAs designed and validated	No. of embryos injected	Current status / progress
1	Fruit fly, <i>Bactrocera zonata</i>	<i>white / scarlet</i>	2	~5000	Homozygous mutants confirmed (G5)
		<i>Tektin</i>	2	Under progress	Invitro-cleavage assay is done and microinjection in progress
2	Cotton pink bollworm, <i>Pectinophora gossypiella</i>	<i>Vitellogenin</i>	2	Under progress	Injection and screening in progress
		<i>CYP6AE</i>	3	Under progress	Invitro-cleavage assay in progress
3.	Cotton leafworm, <i>Spodoptera litura</i>	<i>NPC1b</i>	2	Under progress	Injection and screening in progress
		<i>abdA</i>	2	>3500	Injection and screening in progress
4	Fall armyworm, <i>Spodoptera frugiperda</i>	<i>abdA</i>	4	2520	Cloning and Sanger sequencing in progress (G0)
		<i>Vitellogenin</i>	2	3430	Cloning and Sanger sequencing in progress (G2)
		<i>white</i>	Under progress	Under progress	Under progress
		<i>vermilion</i>	Under progress	Under progress	Under progress
		<i>Sfsxl</i>	Under progress	Under progress	Under progress
5	Cotton bollworm, <i>Helicoverpa armigera</i>	<i>Transformer</i>	Under progress	Under progress	Under progress
6.	Maize stem borer, <i>Sesamia inferens</i>	<i>Dsx</i>	Under progress	Under progress	Under progress

7.	Fruit fly, <i>Zeugodacus tau</i>	<i>white / scarlet</i>	Under progress	Under progress	Under progress
8.	Fruit fly, <i>Bactrocera caryae</i>	<i>Scarlet & Transformer</i>	Under progress	Under progress	Under progress
9.	Potato tuber moth, <i>Phthorimaea operculella</i>	<i>Tryptophan oxygenase (To) & Tssk</i>	6	Under progress	Under progress

The genomic resources generated through ICAR-NBAIR's genome sequencing initiatives provide an important foundation for this work. Integration of **genome-scale information, CRISPR-Cas9 editing and functional validation** will enable systematic investigation of genes associated with economically important insect traits. In the longer term, these efforts are expected to contribute to the development of **innovative pest-management technologies, functional genomics resources and precision strategies for insect population management**, while strengthening India's capability in insect genome engineering and biotechnology.



Progressive accumulation of eye colour from the mid pupal stage in normal unedited *B. zonata*



Wild type *B. zonata*



scarlet gene edited *B. zonata*

Scarlet gene editing in fruit fly *Bactrocera zonata*



Abdominal A (*abdA*) gene editing in *Spodoptera frugiperda*: Larvae and pupae showing fused abdominal segments (marked with arrows)