Review Article

OVERVIEW OF RICE LEAF FOLDER, *Cnaphalocrocis medinalis* AND UNDERSTANDING ITS MANAGEMENT THROUGH BIOLOGICAL, CHEMICAL AND GENETIC APPROACHES

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ABSTRACT

The rice leaf folder, *Cnaphalocrocis medinalis*, is a serious pest of rice causing economic losses worldwide. The larva spins a rice leaf longitudinally to feed inside the mesophyll tissues, affecting grain quality and lowering crop yield. Synthetic insecticide applications have traditionally controlled *C. medinalis*; however, over time, field populations resistant to different insecticides were reported, compromising chemical-based control measures. This review article covers different aspects related to the taxonomy and morphology, life history and biology, damage and economic impacts, distribution and ecology, and rearing methods of *C. medinalis*. It deals with current management approaches, including monitoring and forecasting, cultural and ecological control, biological control and host plant resistance, and synthetic and plant-derived pesticides. Furthermore, it also focuses on insecticide resistance and the latest advances in molecular biology, genomics, transcriptomic, RNA interference, and gut microbiome research, aiming to achieve sustainable control of *C. medinalis*. Nevertheless, many molecular mechanisms remain functionally unverified, and practical challenges associated with RNAi delivery and field application persist. Future research should focus on integrated pest management strategies combining biological, ecological, molecular, and chemical tools to achieve sustainable control. In addition, resistance monitoring, durable host plant resistance, functional genomics, artificial intelligence, remote sensing, and climate-based forecasting systems may contribute to the development of environmentally safe, economically feasible, and long-term integrated pest management programs.

Keywords: Rice leaf folder, molecular studies, integrated pest management, chemical control, biological control.

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INTRODUCTION

Rice is one of the world's most important cereal crops and a staple food for nearly half of the global population. It plays a critical role in food security, employment, economic growth, social stability worldwide (Maclean *et al.*, 2013). Major rice-producing countries include India, China, Bangladesh, Indonesia , Vietnam, Thailand, Philippines, Burma, Pakistan, and Brazil, with annual production ranging from 8.68 to 150 million tons USDA Production Data (https://www.fas.usda.gov/data/production/commodity/0422110) (Figure 1). Globally, rice provides more than 20% of dietary energy and supplies over 70% of daily caloric intake in several Asian countries (Yadav and Kumar, 2018). Numerous insect pests attack rice at different growth stages. Among them, the rice leaf folder, *Cnaphalocrocis medinalis* (Guenée) (Lepidoptera: Pyralidae), is one of the most destructive pest of rice. Larvae fold rice leaves and feed on mesophyll tissues within the rolled leaves, causing significant annual yield losses estimated at 63-80% worldwide (Horgan, 2017). Management of *C. medinalis* has traditionally relied on biological control, cultural practices, and particularly synthetic insecticides (Su *et al.*, 2003). However, effective control strategies face multiple challenges, including the pest's high reproductive capacity, migratory behavior, insecticide resistance; global climate changes induced alterations in its distribution, development, and reproduction (Bodlah *et al.*, 2017; Wang *et al.*, 2017; Hajjar *et al.*, 2023). This review summarizes relevant literature on the bioecology, geographical distribution, natural enemies, and management strategies and identifies future research priorities to address knowledge gaps and optimize integrated pest management strategies for *C. medinalis*.

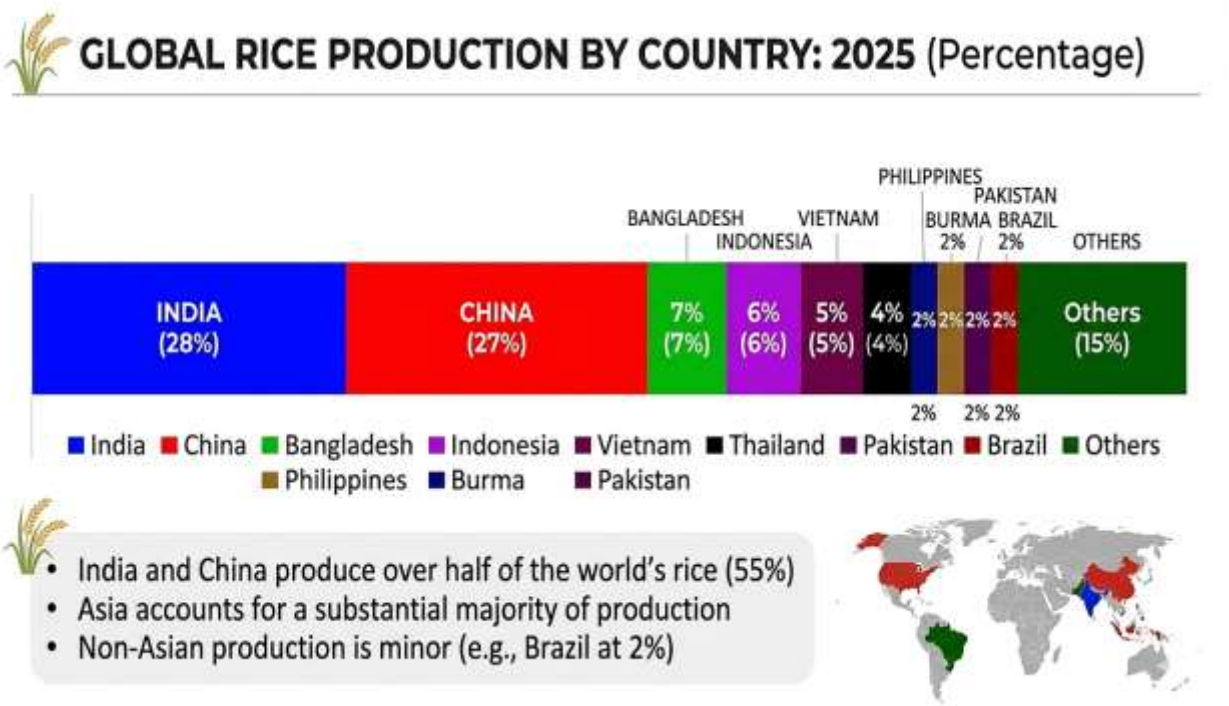

Figure 1. Percentage of rice production by country in 2025

A comprehensive literature search was conducted to collect and synthesize published information on the biology, ecology, host–pest interactions, monitoring, resistance mechanisms, and integrated management strategies of *C. medinalis*. The literature search was performed using reputable scientific databases, including Web of Science (WoS), Scopus, PubMed, Google Scholar, ScienceDirect, and SpringerLink. The search strategy employed combinations of the following keywords: "*Cnaphalocrocis medinalis*," "rice leaf folder," "rice leaf folder," "biology," "ecology," "population dynamics," "migration," "host plant resistance," "integrated pest management," "biological control," "entomopathogenic fungi," "entomopathogenic nematodes," "RNA interference," "*Bacillus thuringiensis*," "insecticide resistance," "gut microbiota," "monitoring," and "climate change." Publications from 1959 to 2025 were considered, search was restricted to peer-reviewed journal articles, books, book chapters, conference proceedings, and technical reports published in English. Approximately 450 publications were initially identified from all databases, with the majority retrieved from Web of Science and Scopus, while additional records were obtained from Google Scholar, PubMed, and reference lists of relevant publications. After removing duplicate records, the titles and abstracts were screened for relevance. Full-text articles were then evaluated according to predefined inclusion criteria, including studies focusing on the taxonomy, biology, ecology, behavior, migration, host plant interactions, insecticide resistance, molecular biology, genomics, RNA interference, biological control, ecological engineering, and integrated pest management of *C. medinalis*. Publications lacking sufficient methodological details, unrelated studies, duplicate records, non-peer-reviewed articles, and publications without accessible full texts were excluded. Following the screening and eligibility assessment, 220 publications were selected and included in this review to provide a comprehensive and up-to-date synthesis of current knowledge on *C. medinalis* and its sustainable management.

Taxonomy and morphology: *C. medinalis* was first described by Achille Guenée in 1854 and was previously reported under the synonyms *Salbia medinalis* Guenée and *Botys nurscialis* Walker (Walker, 1859). The genus *Cnaphalocrocis* comprises approximately 36 species distributed mainly across Asia, of which nearly eight species infest gramineous crops by folding or rolling leaves (Mashhoor *et al.*, 2019). However, only *Marasmia patnalis*, *M. exigua*, and *C. medinalis* are considered economically important pest (Liao *et al.*, 2017). Due to morphological similarities and comparable feeding habits, *C. medinalis* is often misidentified with *M. exigua* at different developmental stages (Barrion *et al.*, 1991). Nevertheless, adults can be distinguished based on coloration, body size, and wing patterns (Rani *et al.*, 2007). Larvae can be differentiated by coloration, size, subdorsal prothoracic spots, pronotum characteristics, and the presence of inverted M shaped markings on the head capsule (Rani *et al.*, 2007) (Figure 2).

Other morphological characteristics of *C. medinalis* are summarized below;

Egg: Eggs are oval, flattened, and approximately 1 mm long and 0.5 mm wide, with fine reticulations on the chorion surface. They are laid singly or in small groups, usually inside folded leaves (Pathak and Khan, 1994).

Larva: Larvae possess a light-brown head and a light yellow to green abdomen with distinct subdorsal spots on the prothoracic region. Mature larvae is 14-19 mm in length and become orange-red before pupation (Heong, 1993).

Pupa: Pupae are cylindrical, 7-10 mm long, and pointed at the posterior end. Newly formed pupae are light yellow but gradually turn reddish-brown to dark brown, with a darker dorsal region and lighter abdomen (Heong, 1993).

Adult: Adult moths are 7-9 mm long with a wingspan of 12-18 mm. The body and wings are yellowish brown and the wings are held obliquely while resting. The forewings possess three dark-brown transverse lines, of which the middle line is shorter and thicker. The hindwings contain two transverse lines; the inner line is short and does not extend to the trailing edge, whereas the outer line extends completely to the trailing edge (Dale, 1994).

Figure 2. Morphological characteristics of *Cnaphalocrocis medinalis* (Guénée)

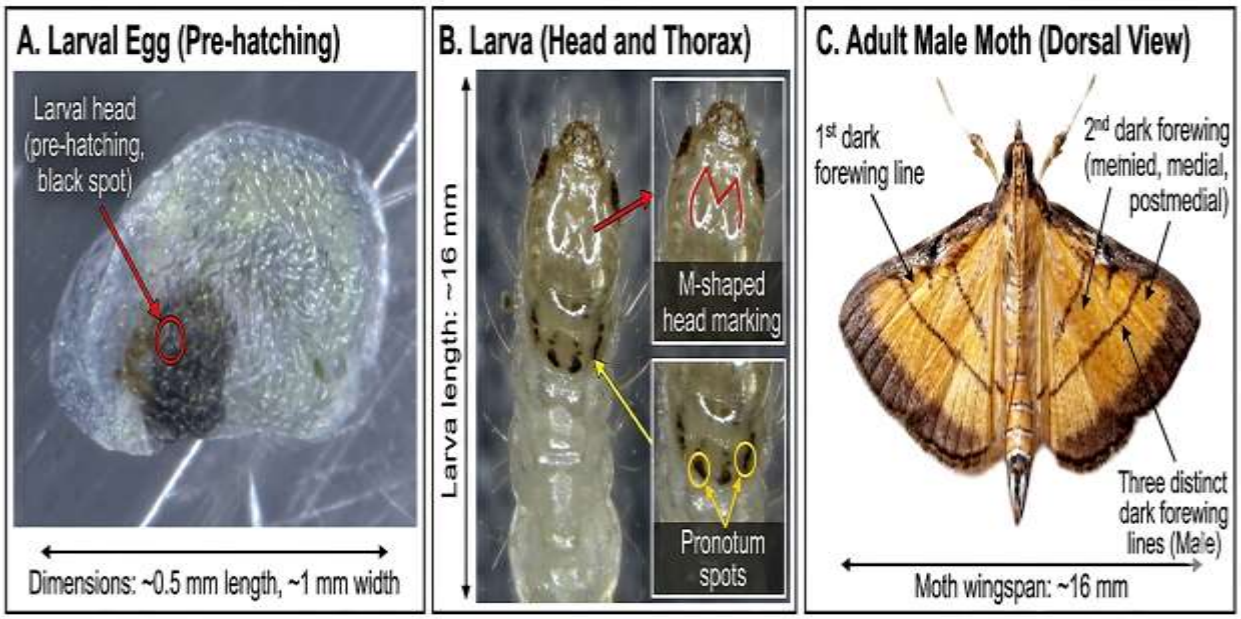

Figure 2. Morphology of *C. medinalis*

Life cycle and biology: The optimum temperature required for egg production is 25-26 °C (Lv *et al.*, 2021). A female lays approximately 50-300 eggs singly or in groups of 3-8 along the midrib of rice leaves (Pathak and Khan, 1994). Eggs hatch within about 5 days after oviposition. Newly emerged larvae are creamy white and later become yellow to yellowish green with a brownish head capsule. Neonate larvae feed gregariously on chlorophyll within unopened leaves (Fraenkel *et al.*, 1981). From the second instar onwards, larvae fold leaf blades using silken threads and feed internally by scraping the chlorophyll contents, producing characteristic longitudinal white streaks. In some cases, 2-3 leaves may be stitched together to form larger feeding shelters. Larval development is completed within 14–25 days through five instars (Gangwar, 2015). Prior to pupation, larvae become pinkish white and construct silken cocoons inside folded leaves by cutting and stitching leaf margins together and starts pupation (Elanchezhyan and Balakrishnan, 2020). Prior to pupation, larvae become pinkish white and construct silken cocoons inside folded leaves by cutting and stitching leaf margins together (Elanchezhyan and Balakrishnan, 2020). Pupation occurs within a single folded leaf. Newly formed pupae are light brown and gradually turn reddish brown within 6-10 days (Figure 3). Adults mostly emerge within an evening period (Heong, 1993). Oviposition generally begins 2-3 nights after mating and occurs mainly between dusk and midnight. Adults usually emerge during the evening. The pre-oviposition and oviposition periods last approximately 3 and 4 days, respectively. Adult females survive for 5-17 days, and the complete life cycle is completed within 23-40 days (Dale, 1994).

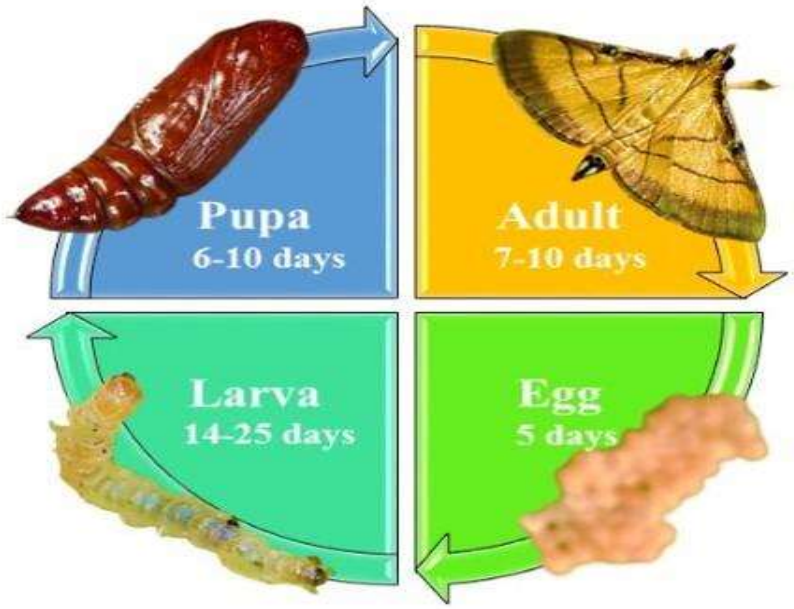

Figure 3. The life cycle of *C. medinalis*

Damage and economic impact: *C. medinalis* damages the rice plants exclusively during the larval stage (Liu *et al.,* 2021). Continuous feeding removes chlorophyll, causing leaves to become whitish, papery, and eventually desiccated (Tiwari *et al.,* 2021). Larval feeding reduces photosynthetic activity, weakens plant vigor, and may result in 20-30% grains yield loss (Litsinger *et al.,* 2005). Although damage during the vegetative stage is often recoverable, infestations during the reproductive stage severely reduce the grain filling and yield. Under heavy infestations, extensive leaf destruction may completely devastate rice fields, resulting in substantial economic losses (Padmavathi *et al.,* 2013). Due to its severe impact, *C. medinalis* was included in the Class I Crop Diseases and Insect Pests list by the Ministry of Agriculture and Rural Affairs of China in 2023. Between 2013 and 2022, this pest affected an average of 14 million hectares annually in China, causing estimated yearly grain losses of 350,700 t, while mitigated losses reached 3.67 million t (Fuyan *et al.,* 2024).

Distribution and ecology: *C. medinalis* is widely distributed in tropical and subtropical rice-growing areas, active year-round, with peak activity typically occurring during the rainy season (Ali *et al.,* 2019). In colder regions, this pest is primarily active from May to October, completing approximately 4-5 generations per year (Junaid and Khan, 2023). *C. medinalis* is commonly found in dark, over-fertilized rice paddies, multiple rice cultivation, increased irrigated areas, and pesticide overuse have all led to population *C. medinalis* (Roseli *et al.,* 2021). Climatic factors, particularly temperature, humidity and rainfall significantly influence the occurrence, development, behavior, distribution, and population size of the *C. medinalis* (Morshed *et al.,* 2020; Morshed *et al.,* 2023). Historically, *C. medinalis* was considered a minor pest before the 1920s; however, its economic importance gradually increased in the late 1980s due to the intensification of rice cultivation and modern agricultural practices (Ranasinghe, 1992). The first serious outbreaks were reported in India during (Litsinger, 1994), followed by widespread outbreaks in China, Japan, and Korea between 1967 and 1981 (Heinrichs, 1985; Lee, 1992). Migration is an important ecological adaptation of *C. medinalis* and contributes significantly to its seasonal distribution and outbreak dynamics. Annual migration generally occurs from tropical to temperate rice-growing regions, with adults initiating migratory flights mainly during the evening (Chatterjee *et al.,* 2023). Migrating adults typically fly at altitudes below 500 m and are capable of sustaining flight for up to nine consecutive nights (Wang *et al.,* 2010). Unlike many migratory insects, mating and feeding do not significantly reduce migratory ability, and females can continue ovarian development and egg maturation during migration (Chang *et al.,* 1980). Trap survey conducted between period 2003 and 2013 revealed migration periods ranging from 72 to 122 days, with a higher proportion of mated females captured during June and July, indicating that migration is not constrained by oogenesis-flight syndrome (Fu *et al.,* 2014). Based on cumulative flight duration, *C. medinalis* populations are categorized as residence (AFD < 40 min), migratory (40–130 min min), and strong migratory (AFD>130 min), with average cumulative flight durations of 11, 82, and 232 min, respectively (Chapman *et al.,* 2010; Zhang *et al.,* 2015). In addition, *C. medinalis* exhibits strong remigration ability, with more than 90% of individuals capable of a first remigration and over 70% capable of a second remigration (Guo *et al.,* 2019).

Insect rearing: *C. medinalis* is polyphagous and have several gramineous hosts, including millet, sorghum, wheat, maize, oats, sugarcane, and other wild grasses (Gao *et al.*, 2023). Extensive studies have been conducted on laboratory rearing of *C. medinalis* using rice seedlings, corn seedlings, and artificial diets (Waldbauer and Marciano, 1981). Early studies demonstrated that neonate larvae perform best when initially reared on rice seedlings before transfer to artificial diet (Shono and Hirano, 1989; Baik, 2006). Subsequent research optimized artificial diets supplemented with rice or corn leaf powder and essential nutrients to support larval growth and development (Guo *et al.*, 2013; Xu *et al.*, 2013). Optimized diets containing wheat germ (8 g), rice leaf powder (3 g), corn powder (4 g), yeast (4 g), and casein (4 g) enabled completion of larval and pupal development within approximately 27 days (Wang *et al.*, 2013). Later formulations further improved diet composition by incorporating distilled water (100 g), agar (1.50 g), wheat germs (6 g), soybean powder (8 g), casein (2 g), methylparaben (0.10 g), sorbic acid (0.10 g), yeast (4 g), natamycin (0.03 g), antibiotics (0.03 g), ascorbic acid (0.10 g), and vitamin mix (0.10 g) reducing the developmental period to approximately 21 days (Wang *et al.*, 2014).

Transcriptomic, genomic, and microbiome Studies: *C. medinalis* has been extensively investigated for its toxicology, ecology, and physiology insecticide resistance, population dynamics, and migration behavior (Alvi *et al.*, 2003). However, molecular studies on this pest have expanded only recently. The transcriptomic analysis generated over 23 million sequencing reads assembled into 44,941 unigenes of which 56.8% matched known proteins in the NCBI database (Li *et al.*, 2012). Subsequent de novo transcriptome sequencing of *C. medinalis* generated 29,367,797 reads assembled into 63,174 unigenes with an average length of 753 bp. Among these, 31,810 unigenes were annotated against the NCBI Nr database and 10,043 were mapped to 285 KEGG pathways. The analysis identified 360 genes potentially associated with insecticide resistance and 16 genes involved in chitin metabolism of *C. medinalis* (Yu *et al.*, 2015). Later, transcriptome sequencing using Illumina HiSeqTM2000/MiSeq technology from antennae, protarsus, and reproductive organs identified 102 chemoreception-related genes, including 29 odorant receptors (ORs), 15 ionotropic receptors (IRs), 30 odorant-binding proteins (OBPs), 26 chemosensory proteins (CSPs), and 2 sensory neuron membrane proteins (SNMPs) (Zeng *et al.*, 2015). Similarly, RNA-Seq analysis of adult antennae identified 90 olfactory-related genes comprising 46 ORs, 15 IRs, 12 OBPs, 15 CSPs, and 2 SNMPs (Liu *et al.*, 2017). Further transcriptomic analysis in 2020 generated 191,974 unigenes with an average length of 791 bp and 289,127 transcripts with an average length of 1,040 bp from, leading to the identification of several genes associated with larval heat acclimation and thermal adaptation (Quan *et al.*, 2020). *C. medinalis* mitochondrial genome is 15,388 bp long and contains 37 genes arranged similarly to those of other lepidopteran insects (Chai *et al.*, 2012). Earlier transcriptomic assemblies were highly fragmented, limiting comprehensive understanding of the pest's biology and ecology. However, advances in long-read sequencing technologies, particularly Illumina, PacBio, and Hi-C platforms, enabled chromosome-level genome assembly of *C. medinalis*. The assembled genome size was approximately 528.5 Mb with 31 chromosomes, 3,248 scaffolds, 4,671 contigs, 38.5% GC content, and 330× chromosomal coverage, leading to the annotation of 15,045 protein-coding genes (Zhao *et al.*, 2021). These genomic advances provide an important foundation for future functional genomics and molecular ecology studies.

The insect gut plays an important role in nutrient digestion, absorption, immunity, communication, and host defense, while also providing a favorable environment for diverse microbiota, including bacteria, fungi, archaea, protozoa, and viruses (Dillon and Dillon, 2004; Douglas, 2007; Rajagopal, 2009; Engel and Moran, 2013; Gurung *et al.*, 2019). Gut microbiota contribute to food digestion, nutrient metabolism, protection against pathogens and predators, and regulation of reproduction and behavior (Engel and Moran, 2013). Subsequently, Illumina MiSeq sequencing identified dominant bacterial phyla such as Actinobacteria, Proteobacteria, Acidobacteria, Firmicutes, and Chloroflexi in fourth-instar larvae (Liu *et al.*, 2016). Further studies across different life stages revealed 22 bacterial phyla, 42 classes, 100 orders, 179 families, 350 genera, and 395 species, with Actinobacteria, Proteobacteria, and Acidobacteria as the predominant groups (Yang *et al.*, 2020). Feeding studies using rice and maize diets demonstrated that host diet significantly influences gut microbial diversity and composition (Yang *et al.*, 2022). Metagenomic analyses further revealed dominance of Firmicutes, particularly Enterococcus spp., including *E. gallinarum* and *E. casseliflavus*, accounting for approximately 96% of gut bacteria in different feeding groups (Li *et al.*, 2022).

Management Strategies

Monitoring and forecasting: The identification of the correct *C. medinalis* is needed. In adults, the sexual features and patterns of the forewings are required to identify and separate different *Cnaphalocrocis* species (Islam and Karim, 1997). Conventional visual assessments methods are labor-intensive, time-consuming, and dependent on farmers' expertise (Martinelli *et al.*, 2015). Consequently, remote sensing (RS) hyperspectral imaging technologies have been increasingly adopted to detect pest-induced changes in crop physiology, canopy structure, pigment composition, and water content over large areas (Huang *et al.*, 2012; Mahlein *et al.*, 2013; Liang *et al.*, 2021). Additional approaches, including soil moisture and crop growth analyses, have also been used to characterize pest habitats (Calderón *et al.*, 2013). Recent studies

combined traditional assessment methods with digital tools such as CompuEye and ImageJ program, and leaf symptom analysis software to improve the accuracy of leaf damage estimation caused by *C. medinalis* (Adhikari *et al.,* 2023).

C. medinalis monitoring has traditionally relied on searchlight traps, moth-repellent methods, and sex pheromone traps (Wu *et al.,* 2013). However, searchlight traps are often ineffective because *C. medinalis* adults exhibit weak phototactic responses and urban lights interferes with trap performance traps (Sun *et al.,* 2022; Gao *et al.,* 2023). The disturb-and-count method (DCM) has therefore been widely adopted in Asian countries, although it remains labor-intensive and costly (Yao *et al.,* 2011). The study was also carried out in other countries to confirm that (Z)-13-octadecenyl acetate and (Z)-11-hexadecenyl acetate, while additional compounds have been reported in Japanese populations (Ramachandran *et al.,* 1990). The study was also carried out in other countries to confirm that (Z)-13-octadecenyl acetate and (Z)-11-hexadecenyl acetate, while additional compounds have been reported in Japanese populations (Ramachandran *et al.,* 1990; Wu *et al.,* 2013). Although pheromone traps effectively monitor adult population, they are less reliable for predicting larval density and female fecundity (Zeng *et al.,* 2018). Food attractants such as methyl salicylate, benzaldehyde, valeraldehyde, and phenylacetaldehyde have also shown strong attraction to both male and female moths (Eigenbrode *et al.,* 2016). Integrating food attractants with pheromone-based trapping systems may therefore improve the monitoring and forecasting accuracy of *C. medinalis* populations (Zeng *et al.,* 2021).

Cultural control and ecological engineering: Cultural practices are important components of integrated management strategies for *C. medinalis*. These approaches are environmentally safe cost-effective, and more sustainable than chemical control when implemented on a community-wide scale (Yadav *et al.,* 2012). Recommended practices include crop rotation, destruction of ratoon crops, plowing and flooding after harvest, weed removal, optimum planting time, proper seedbed leveling, balanced plant density, water management, and judicious nitrogen fertilizer application (Devi *et al.,* 2023). Excessive nitrogen fertilization favors *C. medinalis* outbreaks; therefore, split fertilizer applications at recommended levels are advised (Lella and Jagadeesh, 2023). Although cultural practices alone may not provide complete control, they are highly effective when integrated with other pest management strategies.

Ecological engineering has emerged as an important approach for sustainable rice pest management. This concept involves enhancing biodiversity and strengthening natural biological control by regulating agricultural ecosystems (Odum, 1962; Mitsch, 2012). In rice ecosystems, ecological engineering focuses on protecting natural enemies and reducing reliance on pesticides by designing field habitats that favor beneficial arthropods (Gurr *et al.,* 2012). Excessive pesticide application in rice paddies often disrupts predators and parasitic natural enemies, including spiders and parasitic wasps, thereby undermining natural pest control mechanisms (Ngin *et al.,* 2017). Early application of pesticides is particularly harmful because it reduces the effectiveness of late-stage biological control (Ali *et al.,* 2019). Therefore, to protect natural enemies that play a role early in the crop, a "no-spraying-early" strategy is recommended, which avoids pesticide use within the first 30-40 days after sowing or transplanting (Way and Heong, 1994). In addition, maintaining flowering plants along the edges of rice paddies can provide nectar, shelter, and alternative hosts for parasitic wasps and predators, thereby enhancing their effectiveness against *C. medinalis* and other rice pests (Schoenly *et al.,* 1996).

Biological control: Numerous predators, including hymenopterans, hemipterans, coleopterans, neuropterans, dipterans, spiders, dragonflies, damselflies, coccinellids, carabids, earwigs, and rove beetles, contribute to natural regulation of *C. medinalis* populations (Parasappa, 2017). Among them, Spiders, ground beetles, and ladybugs have the highest predation potential, especially during the vegetative growth stage of rice; while mirid bugs and rove beetles are more common during the reproductive growth stage (Bhattacharyya *et al.,* 2006; Rautaray *et al.,* 2019). Dermaptera and Coleoptera insects are particularly effective against the eggs and larvae of *C. medinalis* (Meng *et al.,* 2016). In contrast, dragonflies primarily feed on adults and therefore contribute less directly to reducing leaf damage. Many species of predators are useful against *C. medinalis* throughout the crop-growing period. For instance, predators such as coccinellids, mirid bugs, dragons and damselflies, and carabids could be found throughout the rice crop season. However, coccinellids, spiders, dragonflies, and damselflies were more prominent during the vegetative stage of the rice crop, while Cerambycidae, mirids, and Staphylinids were dominant during the reproductive stage (Rautaray *et al.,* 2019).

Many species of parasitoids are used as an important biocontrol tool against *C. medinalis* in China, Pakistan, India, Malaysia, Philippines, Vietnam, Japan, Korea, Sri Lanka, Thailand, Indonesia, Myanmar, Laos, and Nepal (Gurr *et al.,* 2012). There were ninety-one species of hymenopteran parasitoids and fourteen species of dipteran parasitoids have been reported to infect *C. medinalis* (Joshi *et al.,* 1987). Since then, many species of parasitoids have been discovered in other countries (Hemachandra and Perera, 2016; Zhu *et al.,* 2022). Significant parasitoid efficiency has been reported in different parts of the world, with most studies focusing on rice-growing regions such as 5–61% in rain-fed regions, 9–13% in dry a regions, and 7–33% in irrigated regions (Litsinger *et al.,* 1987). Among the many parasitic wasps, the efficiency of *Trichogramma* spp. has been documented in details (Mishra and Kamlesh, 2009; Huang *et al.,* 2012). Among its species, *T. chilonis* is considered an effective egg parasitoid of *C. medinalis* after undative releases it ranging from 33 to 89.5 kg/acre of paddy fields.(Khan *et al.,* 2005). The augmentative release of *T. chilonis* @ 100,000 in the paddy fields of

Punjab has been found effective for the significant suppression of *C. medinalis* (Kaur and Brar, 2008). Release of *T. chilonis* @ 100,000/ha, after the application of 1% azadirachtin reduced damage by 41.68 to 98.60% and resulted in an increase of production by 25.79 to 45.13% as compared with the insecticide-treated field (Jena *et al.*, 2012). A field trial revealed the effective dose of *T. chilonis* among different doses of 50,000, 75,000, 100,000, 125,000, and 150,000 parasitoid eggs /ha, and the results showed that maximum control was achieved at 150,000 parasitized eggs (Zhang *et al.*, 2020). For example, combining the *T. chilonis* with neem-based products or *Bacillus thuringiensis* (*Bt*) can improve the control efficacy against the *C. medinalis* (Karthikeyan *et al.*, 2007). These combinations are generally more effective because selective biopesticides suppress pest populations while causing relatively little damage to parasitic wasp and predatory natural enemy communities (Jena *et al.*, 2012). In contrast, broad-spectrum insecticides such as monocrotophos and endosulfan, while potentially providing short-term suppression, negatively affect parasitic wasp survival, emergence, and field colonization, thus reducing long-term biocontrol efficiency (Zhang *et al.*, 2020). Despite the promising results achieved by parasitic wasps in controlling the *C. medinalis*, their large-scale field application remains limited by several practical factors. Large-scale production and storage of high-quality parasitic wasps require specialized facilities and stringent quality control measures to maintain their emergence rate, sex ratio, and field survival rate (Parker *et al.*, 2021). Environmental factors such as temperature, humidity, rainfall, and wind significantly affect the survival rate, dispersal, and field colonization of parasitic wasps after release (Gurr *et al.*, 2012). Furthermore, asynchronous release timing, excessive insecticide applications, and low farmer awareness frequently reduce parasitoid persistence and effectiveness in rice ecosystems (Jena *et al.*, 2012). Consequently, although *T. chilonis* is an effective component of integrated pest management programs, its long-term success depends on proper release timing, compatibility with selective pesticides, conservation of natural enemies, and coordinated field-level implementation (Karthikeyan *et al.*, 2007; Gurr *et al.*, 2012).

Entomopathogenic nematodes are important biological control agents against many soil-associated insect pests and are widely distributed worldwide (Kaya and Gaugler, 1993). More than 3,100 natural associations between nematodes and insects involving 23 insect orders and 11 nematode orders have been documented (Kamminga *et al.*, 2012). Several entomopathogenic nematodes species have demonstrated strong pathogenicity against *C. medinalis* under laboratory conditions such as *Steinernema carpocapsae* caused up to 98% mortality in fifth-instar larvae of *C. medinalis* through rapid multiplication within the host (Srinivas and Prasad, 1993). Similarly, *Heterorhabditis indica* achieved nearly 100% mortality within 18 to 20 h of exposure (Prasad *et al.*, 2006); while *Steinernema asiaticum* also showed high virulence against all larval stages under laboratory assays (Padmakumari *et al.*, 2008). Combined inoculation of *S. asiaticum* and *H. indica*, increased larval mortality and produced large numbers of infective juveniles, indicating their potential for population persistence and recycling in the field (Sankar *et al.*, 2009). Overall, members of the families Heterorhabditidae and Steinernematidae are considered effective biological control agents against *C. medinalis* (Devi, 2020). Differences in efficacy among Entomopathogenic nematodes species are mainly associated with their host-seeking behavior, virulence, reproductive capacity, symbiotic bacteria, and tolerance to environmental stress. For example, *H. indica* is generally more effective because its symbiotic bacteria rapidly kill the host and promote rapid nematode reproduction, while the infectivity and host-finding ability of Steinernemacan vary depending on environmental conditions (Kaya and Gaugler, 1993). Furthermore, the survival rate of infective larvae is strongly influenced by factors such as soil moisture, temperature, ultraviolet radiation, and air humidity, which significantly affect the results of field trials. Despite during laboratory findings, several practical limitations restrict the large-scale application of entomopathogenic nematodes in the control of *C. medinalis*. Mass production and formulation of infective juveniles require specialized fermentation or in vivo rearing systems, which may increase production costs and reduce commercial feasibility (Shapiro *et al.*, 2012). Their field effectiveness is also highly dependent on proper application timing, particularly during early larval stages and under favorable moisture conditions. Furthermore, exposure to broad-spectrum insecticides and adverse environmental conditions may reduce nematode survival and persistence after application (Naidoo, 2025).

Entomopathogenic fungi are ubiquitous and have the ability to grow and enter insect bodies after breaching the lining of insect cuticles, thereby contributing to the biological control of both sucking and chewing insect pests in agricultural ecosystems. Although synthetic insecticides are commercially available and widely used, they are not considered permanent solutions because of residue persistence, environmental and health risks, and the development of insecticide resistance (Kalyabina *et al.*, 2021). Consequently, researchers have increasingly focused on biocontrol control agents, including entomopathogenic fungi such as *Beauveria bassiana* and *Metarhizium anisopliae*, for the management of *C. medinalis* (Ullah *et al.*, 2018). In vitro and Greenhouse assay of *B. bassiana* and *M. anisopliae* against *C. medinalis* have demonstrated promising results, with larval mortality reaching up to 70% under laboratory conditions and approximately 50% under greenhouse conditions (Rizwan *et al.*, 2019). A study reported that *B. bassiana* could serve as an important biological control agent against *C. medinalis* larvae (Abdullah *et al.*, 2021). Furthermore, the feeding preference of *C. medinalis* was significantly reduced when plant growth-promoting rhizobacteria were combined with *B. bassiana* (Karthiba *et al.*, 2010). Studies have also documented the compatibility of entomopathogenic fungi with selected insecticides against *C. medinalis* (Sahoo and Dangar, 2014). For example, *B. bassiana* applied at a concentration of 10^{10}

spores ml^{-1} performed effectively when combined with acephate, chlorantraniliprole, malathion, and thiamethoxam (Sankaranarayanan and Askary, 2017). In addition, a bioassay revealed that two protein elicitors Hrip 1 and PebB, extracted from *Alternaria tenuissima* and *B. bassiana*, respectively, negatively affected the survival, developmental duration, and fecundity of *C. medinalis* (Basit *et al.*, 2021). Despite these encouraging findings, the efficacy of entomopathogenic fungi varies considerably among fungal species, isolates, and environmental conditions. *Beauveria bassiana* is often considered more effective than *M. anisopliae* against foliar-feeding insects such as *C. medinalis* because it exhibits superior adhesion and penetration abilities on soft-bodied larval cuticles and performs well under humid rice field conditions (Shakeel *et al.*, 2024). In contrast, *M. anisopliae* exhibit relatively low persistence on plant leaves when exposed to ultraviolet radiation and temperature fluctuation (Alviti *et al.*, 2025). The virulence of entomopathogenic fungi greatly depends on other factors including, enzymatic activity, spore germination rate, tolerant to environmental stress and host specificity (Alviti *et al.*, 2025). Therefore, these factors restrict the field application of entomopathogenic fungi at large-scale in rice fields. Large-scale formulation of fungal spores technically demanding and remain costly, especially in maintaining shelf life and high spore viability during storage and transportation (Mascarin *et al.*, 2024). Entomopathogenic fungi release timing is important, as it is more effective at early stage of *C. medinalis* larvae, while the older larvae produce thicker cuticles that may exhibit greater toleration and enhanced immune responses (Rizwan *et al.*, 2019). Furthermore, while some insecticides are compatible with entomopathogenic fungi, overuse can inhibit fungal growth, reduce spore germination rates, and negatively affect field persistence (Sahoo and Dangar, 2014).

Crystal *parasporal* proteins (Cry) of the gram-positive bacterium *B. thuringiensis* have been widely used as a foliar spray against agricultural pests worldwide. Cry proteins exhibit insecticidal activity after enzymatic digestion (Heckel, 2020). After ingestion by insects, the Cry protein is activated in the alkaline environment of the midgut, producing toxic fragments. These fragments bind to brush border membrane vesicle receptors, insert into the epithelial cell membrane, leading to ion leakage and cell death (Gurr *et al.*, 2012; Guo *et al.*, 2015). Transgenic rice containing the *Bt* Cry gene significantly reduced damage caused by lepidopteran pests while also reducing pesticide use (Huang *et al.*, 2005). Studies have shown that *Bt* rice production can exceed that of non-*Bt* rice by more than 60% under severe pest pressure (Wang *et al.*, 2010). Furthermore, reduced insecticide use in *Bt* rice cultivation may improve farmers' health and decrease environmental contamination (Huang *et al.*, 2015). Several *Bt* rice lines and Cry proteins, including KMD, *Bt* Shanyou 63, and Huahui 1 developed through collaborations between Chinese universities and the International Rice Research Institute, have been evaluated for the control of *C. medinalis* (Chen *et al.*, 2006). Transgenic *Bt* rice plants with toxicity reduced the suitability for *C. medinalis*, although resistance and tolerance to Bt toxins have been reported in both laboratory and field populations (Xu *et al.*, 2016; Gassmann *et al.*, 2020; Gothandaraman *et al.*, 2023). A report suggested that *C. medinalis* has developed resistance to low concentrations of Cry proteins, and that Cry1Aa, Cry1Ac, and Cry1C proteins can be degraded by enzymes present in the insect midgut, thereby reducing toxin efficacy (Yang *et al.*, 2023) (Figure 4). The effectiveness of Cry proteins varies depending on receptor-binding affinity, toxin stability, expression levels in rice tissues, and target insect susceptibility, with Cry1C and Cry2A generally providing broader and stronger toxicity against lepidopteran pests (Bravo *et al.*, 2011). In contrast, some Cry proteins lose efficacy when insects evolve altered midgut receptors or enhanced detoxification mechanisms, leading to reduced toxin activation and increased resistance development (Heckel, 2020). Additionally, the level and tissue-specific expression of *Bt* toxins in transgenic rice lines strongly influence pest suppression (Chen *et al.*, 2006). Despite the success of *Bt* rice, several practical constraints limit its large-scale adoption and long-term sustainability. One major challenge is the rapid evolution of insect resistance due to continuous exposure to single Cry toxins, particularly when refuge strategies are not properly implemented (Xu *et al.*, 2016; Gassmann *et al.*, 2020).

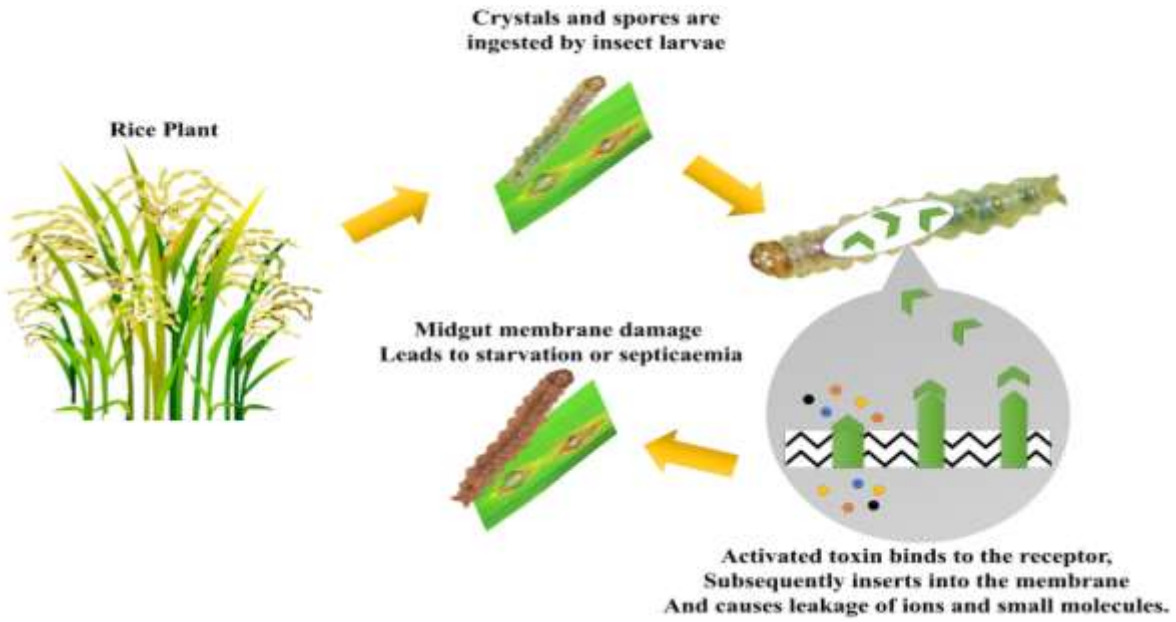

Figure 4. The schematic representation shows how *Bt* toxin affects *C. medinalis* larvae.

Host plant resistance: Host plant resistance is an important component of integrated pest management programs for the control of *C. medinalis*. During the 1990s, extensive efforts were made to evaluate rice germplasm for resistance rice against *C. medinalis* under both laboratory and field conditions (Heinrichs *et al.,* 1985; Dakshayani *et al.,* 1993). Several resistant rice cultivars and breeding lines were subsequently identified (Khan and Joshi, 1990). By the early 2000s, approximately 271 rice genotypes had been reported to possess resistance against different developmental stages of *C. medinalis* (Ram *et al.,* 2001). Studies further demonstrated that rice cultivars such as Guanglingxiangjing, Changyou 1, Nanjing 44, Huidao 9, and Huidao 10 exhibited greater resistance than Yangjing 9538, Line 91SP, and TN1 (Xu *et al.,* 2010). Similarly, mutant rice lines MSM 139 and MSM 127 showed significantly higher resistance compared with TN1(Javvaji *et al.,* 2021). Under field conditions, 20 resistant rice germplasm lines were identified among 66 evaluated genotypes, while wild and traditional rice genotypes such as Oryza rhizomatis, TKM 6, Ptb 33, and Oryza minuta also showed resistance by reducing the leaf-folding efficiency of *C. medinalis* larvae (Punithavalli *et al.,* 2011). In addition, BRRI rice 87 and BRRI rice 72 were identified as resistant cultivars under Kharif-II conditions (Das *et al.,* 2022). Resistance in rice varieties is associated with several biochemical and morphological traits, including higher silica and wax contents, volatile compounds, trichome density, leaf toughness, and plant architecture characteristics such as tiller number and leaf dimensions (Wang *et al.,* 2008). These traits may reduce feeding efficiency, larval establishment, and oviposition preference of *C. medinalis*, making host plant resistance a cost-effective and environmentally safe strategy, although its effectiveness may vary across environments and pest populations due to genetic variability and adaptation this pest (Punithavalli *et al.,* 2013; Liao *et al.,* 2017). In addition, some resistant cultivars may possess undesirable agronomic traits, such as lower yield potential or poor grain quality, limiting their adoption by farmers. Continuous cultivation of resistant varieties may also impose selection pressure on pest populations, potentially leading to the breakdown of resistance over time (Das *et al.,* 2022).

Chemical control and plant-based insecticides: Heavy damage to rice crops and extensive applications of insecticides against *C. medinalis* have been widely reported in Pakistan and India (Wakil *et al.,* 2001). Between 1980 to 2000, farmers relied heavily on insecticides such as carbofuron, pyrethroids, chlorpyrifos, malathion, monocrotophos, deltamethrin, diazinon, dimethoate, fenthion, fenitrothion, cypermethrin, endosulfan, methamidophos, carbaryl, and phorate for *C. medinalis* management (Shaki *et al.,* 2020; Zala and Sipai, 2021). Currently, commonly used insecticides against *C. medinalis* include abamectin benzoate, cartap, spinosyns, insect growth regulators, fipronil, neonicotinoids, diamides, and neem oil extracts (Shaki *et al.,* 2020). Among them, fipronil and cartap hydrochloride have been extensively used under both laboratory and field conditions because of their strong larvicidal activity (Kumar and Singh, 2013). However, prolonged use of fipronil has reduced its field effectiveness over time, indicating possible resistance development and declining efficacy under outdoor conditions (Supawan and Chongrattanameteekul, 2017). The effectiveness of these insecticides varies depending on application method, dosage, timing, and environmental conditions (Zala and Sipai, 2021). Neonicotinoid insecticides, particularly imidacloprid at 25 g active ingredient per hectare (a. i. ha^{-1}) became widely

adopted because of their systemic action and high toxicity against *C. medinalis* (Krishnaiah *et al.,* 2002). Field reports from southern India indicate an increase in *C. medinalis* infestations in paddy fields treated with imidacloprid. This suggests that the pesticide-induced pest rebound is related to increased pest reproductive capacity, shortened larval stages, and reduced toxicity to eggs, all of which contribute to rapid population growth (Chintalapati *et al.,* 2016). Similarly, novel diamide insecticides, such as flubendiamide and chlorantraniliprole, initially showed good control efficacy against lepidopteran pests due to their selective action on insect ryanoalkaloid receptor channels (Lahm *et al.,* 2007). Chlorantraniliprole, particularly in combination with thiamethoxam (Virtako), effectively reduced *C. medinalis* population while conserving predator abundance in paddy ecosystems (Zala and Sipai, 2021). However, the development of resistance to diamide insecticides in *C. medinalis* populations has raised concerns about their long-term sustainability (Isman, 2020). While chemical insecticides can rapidly and effectively suppress *C. medinalis,* overuse and repeated use have led to a range of ecological and managerial problems, including insecticide resistance, pest recurrence, environmental pollution, and adverse effects on natural enemies (Chintalapati *et al.,* 2016).

Plant-derived insecticides are considered ideal alternatives to synthetic insecticides because they are generally safer for non-target organisms and possess multiple mechanisms of action, including repellency, toxicity, antifeedant activity, and growth regulation, making them suitable for controlling agricultural pests (Isman, 2020). Studies have shown that several plant-derived products have significant insecticidal activity against the *C. medinalis* (Nathan *et al.,* 2005). Several plant-derived insecticides, including commercial formulations and locally available plant extracts, have been evaluated for the control of the *C. medinalis* (Gopalakrishnan *et al.,* 2014). For example, extracts from *Jatropha curcas* and *Ipomoea carnea* have dual antifeedant and larval-killing effects against the rice *C. medinalis* (Pandey *et al.,* 2017). Similarly, application of *Azadirachta indica* (neem seed kernel extract) and *Vitex negundo* (Nirgundi leaf extract), alone, or in combination with *Bt*, significantly affected the nutritional indicators and feeding behavior of *C. medinalis* larvae (Gopalakrishnan *et al.,* 2014). Compared with traditional synthetic insecticides, plant-derived insecticides are less likely to cause environmental pollution, pest recurrence, or severe toxicity to beneficial arthropods (Pandey *et al.,* 2017). However, the field efficacy of plant-derived insecticides is generally less stable than that of synthetic chemicals because their activity is affected by plant source, extraction method, environmental conditions, and degradation by sunlight and rainwater (Rajpoot *et al.,* 2021).

Insecticide resistance: Resistance of insects to different synthetic insecticides is an ongoing challenge in pest management worldwide (Sparks *et al.,* 2021). Resistance to insecticides typically involves several detoxifying enzymes that increase detoxification capabilities, to make the insecticide molecules less toxic and more easily eliminated from the body as well as reduce the target site sensitivity (Hilliou *et al.,* 2021). Insecticide resistance in insect pests is a complex process and can be broadly categorized into different types including metabolic resistance, target site resistance, and behavioral resistance (Sparks and Nauen, 2015). Recent research development has been made in identifying resistance genes against different insecticides and their target site mutations affecting their functions (Hawkins *et al.,* 2019). The metabolic resistance occurs through the upregulation of different enzymes such as Cytochrome P450s, Glutathione S-transferases, and Carboxylesterases (Carvalho *et al.,* 2018). Target site resistance of insect-pest occurs due to the mutations in the insecticide target sites that prevent the insecticide molecule from binding, thus ultimately reducing their toxic effects (Renault *et al.,* 2023). Insecticide resistance in *C. medinalis* was first reported by Rajamma and Das, India in 1969 (Rajamma and Das, 1969). In 1975, resistance to bromophos-ethyl was documented following repeated field applications (Gangwar, 2015). Subsequent studies in Japan revealed increasing resistance ratios against diazinon, Chlorpyrifos-methyl, dimethylvinophos, tetrachlorvinphos between 1988 and 1991 (Endo, 1993). From 1994 to 2017, *C. medinalis* populations developed resistance to several insecticide classes under both laboratory and field conditions (Endo *et al.,* 1993; Su *et al.,* 2004; Misra, 2008; Zheng *et al.,* 2011; Zhang *et al.,* 2014; Nayak *et al.,* 2017) (Figure 5).

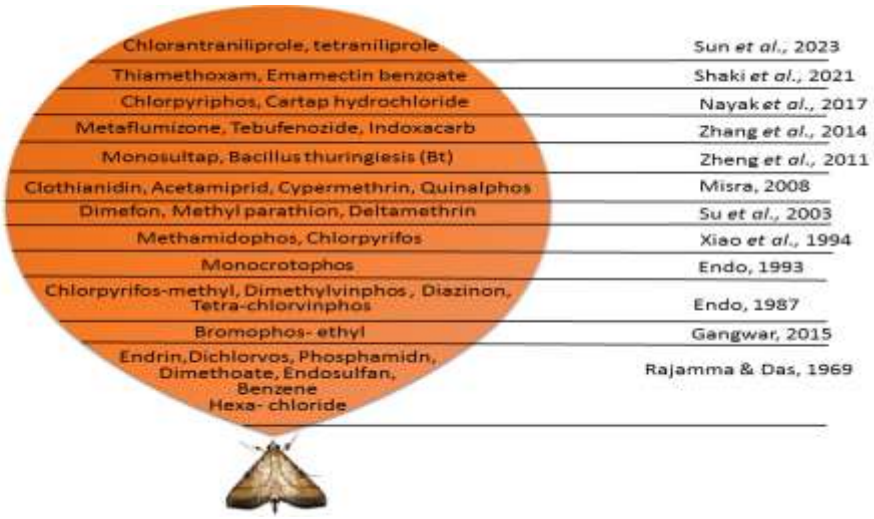

Figure 5. Timelines on resistance development in *C. medinalis* to different insecticides.

In Tamil Nadu, resistance frequencies were particularly high for chlorpyrifos (53.34–80.00%), cartap hydrochloride (51.8–63.34%), and profenophos (43.34–61.34%), while relatively lower resistance levels were observed for chlorantraniliprole (10.66–26.67%) (Shaki *et al.*, 2020) (Figure 6A and B). Moderate resistance levels were also reported for abamectin, spinetoram, and emamectin benzoate (Sun *et al.*, 2023).

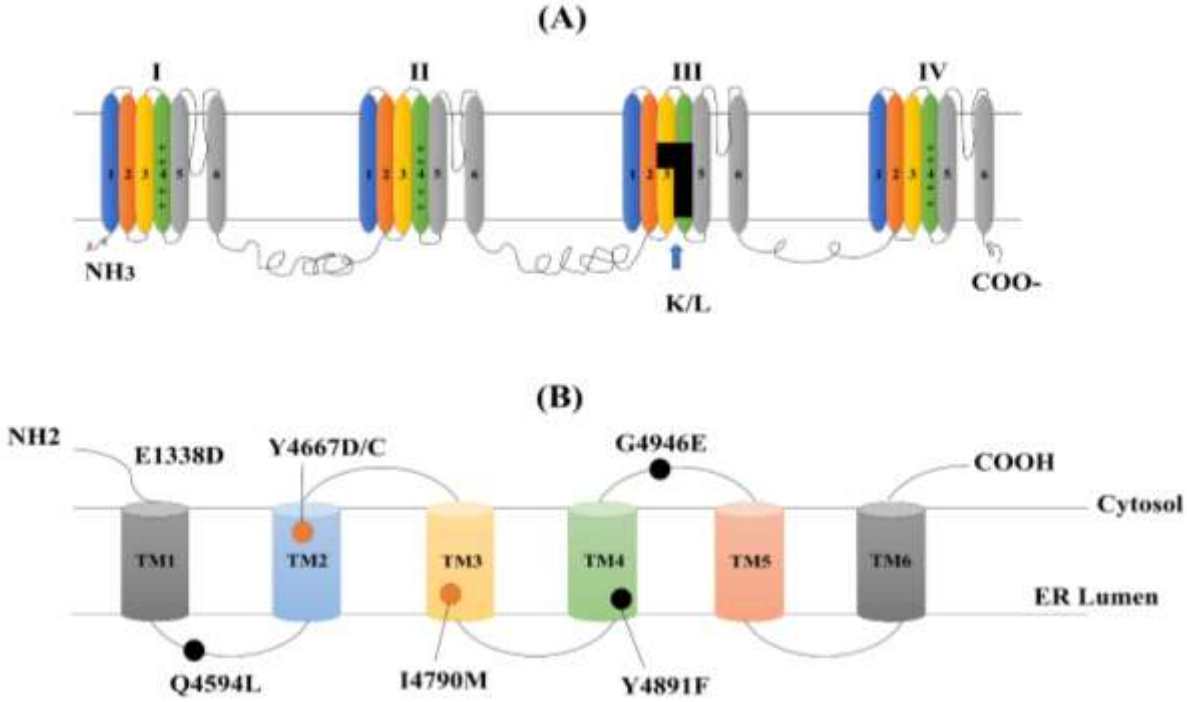

Figure 6. Schematic diagram of the *C. medinalis* Para –orthologous sodium channel representing kdr-associated mutations. Four (I-IV) homologous domains and six (S1-6) transmembrane segments and kdr-associated mutation (K/L) are shown in (A). Schematic representation with red and black dots represents mutation sites identified in *C. medinalis*, where cylinders show the transmembrane domains are shown in (B).

Genetic and molecular tools: RNA interference (RNAi) has emerged as a promising molecular approach for the management of *C. medinalis*. In this mechanism, double-stranded RNA (dsRNA) is processed into small interfering RNAs (siRNAs), which bind to complementary mRNA sequences and induce gene silencing (Ma, 2006). Silencing of certain desired genes may induce insect body deformities, inhibit the chitin metabolism, morbidity, or even cause death (Zhang and Yao, 2017). A study reported that the injection of dsRNA to the larval stage of *C. medinalis* decreased the *CmHK*

mRNA level, and that can cause larval and pupal mortality, structural deformities, reduction of average body weight loss, reduced female fecundity, and significant variation in the sex ratio (Shakeel *et al.*, 2020). A study investigated the dsRNA injection knockdown of the target gene (*CmCHSB)* that is essential for the growth and development of *C. medinalis* (Zhang *et al.*, 2021). Knockdown of *CmUAP* by injection of dsRNA causes stunted growth, reduced feeding and excretion, body weight loss of larvae, and several other developmental disorders (Zhou *et al.*, 2021). A study reveals that the *CmdsRNase* can degrade the dsRNA and consequently reduce the efficacy of RNAi in *C. medinalis*; however, co-silencing of *CmdsRNase* and *CmCHS* genes can cause adverse effects on the growth and development of *C. medinalis* and ultimately improve the RNAi efficiency (Li *et al.*, 2022).

Conclusion: The management of *C. medinalis* remains challenging due to different factors such as operational constrains, variability, insecticide resistance, and inconsistent field effectiveness. While cultural and biological control, ecological engineering, host plant resistance, and molecular control methods such as RNAi are ecofriendly alternatives, however, their large-scale implantation is limited by issues with long-term stability, implementation difficulty, and with effectiveness. Furthermore, over-reliance on chemical pesticides accelerates resistance development and exacerbates ecological damage. In conclusion, sustainable management of *C. medinalis* requires an integrated pest control strategy that combines biological, ecological, molecular, and chemical control methods while minimizing environmental risks and resistance development.

Future Research Directions: Future research work on *C. medinalis* should prioritize climate-adaptive control strategies to reduce reliance on chemical pesticides. The development of predictive models and long term ecological studies are needed to study the pest distribution, outbreaks, and migration under different environmental conditions. The molecular studies such as transcriptomic, genomics, microbiome research, RNAi, should be further utilized to validate different genes associated with heat adaptation, pesticide resistance, reproduction, host selection, and migration. Future biological control such as, predators, parasitoids, entomopathogenic fungi, bacteria, and nematodes research should emphasize field assessments under different agroecological conditions. Ecological engineering approaches, including habitat diversification and pesticide reduction, should also be optimized to protect natural enemies and enhance ecosystem stability. Continuous monitoring of pest adaptation and resistance loss is crucial for maintaining long-term effectiveness. Pesticide resistance management should remain a top priority through research on resistance evolution, cross-resistance, adaptation costs, and molecular markers. Greater emphasis should also be placed on botanical insecticides, pheromone-based systems, remote sensing, hyperspectral imaging, artificial intelligence, and precision agriculture as environmentally safer alternatives to conventional chemical control. Overall, multidisciplinary approaches integrating entomology, molecular biology, ecology, climatology, agronomy, biotechnology, and precision agriculture will be essential for developing sustainable and long-term integrated pest management strategies against *C. medinalis*.

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