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Assessment of life cycle patterns of Erebidae family moths and the impact of antibiotics on their life cycle : A Review

Omkar C. Yadav[a], Janhavi P. Kadam[a], Prasad C. Dhumal[a], Ganesh s. Jadhav, Vedant M. Potdar[a], Dr. Bandu S. Pawar[a*]

[a]Department of Microbiology, Yashavantrao Chavan Institute of Science Constituent College of Karmaveer Bhaurao Patil University, Satara 415 001, MH, India.

[b]Department of Zoology, Yashavantrao Chavan Institute of Science, Karmaveer Bhaurao Patil University, Satara 415 001, MH, India.

[*]Corresponding author: bspawar@ycis.ac.in

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Abstract

The gut microbiome of insects, especially lepidopteran pests like *Achaea janata* and *Spilosoma obliqua,* is essential for nutrition, digestion, detoxification, immunity, development, and reproduction. Chemical pesticides used in conventional control have caused resistance and ecological issues. As environmental contaminants, antibiotics inadvertently change the richness, function, and host physiology of insect gut microbial populations. Research demonstrates that exposure to antibiotics causes altered digestion, decreased growth, weakened immunity, and poor detoxification. Methods for gut microbiota analysis are highlighted in this review, including culture-based approaches and molecular methods like metagenomics and 16S rRNA sequencing. Innovative pest control techniques including microbial biopesticides and paratransgenesis are also covered. By lowering reliance on chemical pesticides, an understanding of antibiotic-microbiota interactions can aid in the creation of environmentally friendly, sustainable pest management strategies.

Introduction

Castor (*Ricinus communis* L.) is a highly valuable crop for both industrial and agricultural sectors. It is primarily cultivated for its non-edible oil, which is rich in ricinoleic acid, a compound widely utilized in the production of lubricants, polymers, coatings, cosmetics, pharmaceuticals, and biofuels. Owing to its adaptability to drought conditions and its ability to grow in marginal soils, castor plays a crucial role in sustaining agriculture in tropical and subtropical regions. Additionally, castor by-products such as castor cake are extensively used as organic fertilizers. India is the leading producer of castor globally, with

cultivation spanning approximately 9.90 lakh hectares, yielding about 12.70 lakh metric tonnes annually with an average productivity of 1419 kg per hectare [1]. As one of the oldest non-edible oilseed crops, castor holds significant economic importance due to its diverse industrial applications. Biofuel production from oilseed and starchy crops, including biodiesel and bioethanol, is increasingly recognized as a sustainable alternative that can reduce pressure on arable land used for food production [2].

Despite its importance, castor cultivation is severely affected by insect pests. Among them, *Achaea janata* (castor semilooper) is one of the most destructive species, causing extensive defoliation and, under severe infestation, damaging developing capsules, leading to substantial yield losses. The increasing resistance of pests to chemical pesticides has prompted the exploration of alternative pest management strategies [3]. It is estimated that insect pests contribute to yield losses of nearly 35–40% in castor crops. Although approximately 100 pest species are associated with castor, only a few are economically significant [4]. Among these, *Spodoptera litura* (tobacco caterpillar), *Achaea janata*, and *Spilosoma obliqua* are the most prevalent and damaging, often causing complete defoliation of plants [5,6]. The larval stages of *A. janata* predominantly feed on castor foliage during early growth stages, significantly affecting plant development.

Understanding insect gut microbiota is essential for elucidating host–microbe interactions. While most microbiome research has focused on vertebrates, particularly humans, insects also harbor diverse gut microbial communities that contribute to their survival and adaptation. These microbiotas play vital roles in digestion, nutrient assimilation, detoxification, immunity, growth, and reproduction [7]. The insect digestive system is generally divided into three regions: foregut, midgut, and hindgut, each providing distinct environments that influence microbial composition. Factors such as developmental stage, diet, and physicochemical conditions within the gut significantly affect microbial diversity [8,9].

The insect gut microbiome consists of a wide range of microorganisms, including bacteria, archaea, fungi, and protists. In some insects such as termites, protists dominate the hindgut microbial community, whereas both bacteria and archaea are commonly present across insect taxa [10]. Dietary habits play a critical role in shaping microbial diversity, with omnivorous insects typically hosting

more diverse microbial populations than strictly herbivorous or carnivorous species [11]. These microbial communities are actively involved in biochemical processes such as degradation, mineralization, and detoxification of organic compounds, which are particularly relevant in pest management strategies [12].

The alimentary canal of lepidopteran larvae comprises three main sections. The foregut and hindgut originate from the ectoderm and are lined with a chitinous layer, while the midgut is responsible for digestion and nutrient absorption [13]. The foregut, consisting of the oesophagus and crop, primarily functions in food storage and transport [14,15]. The midgut is the largest region and serves as the primary site for enzymatic digestion, producing enzymes such as proteases and carbohydrases. The hindgut, which includes the ileum, rectum, and posterior rectum, plays a key role in water and ion regulation, working in coordination with the Malpighian tubules for excretion [16,17]. Furthermore, physicochemical factors within the gut environment, including pH, oxygen levels, redox potential, ionic balance, and enzymatic activity, significantly influence the metabolic functions of gut microbiota [18].

Gut microbiota of the Erebidae family insects

Eudocima, a fruit-piercing moth belonging to the family Erebidae, is recognized as a highly polyphagous and economically important pest. This species was first reported in India by Lefroy and Howlett in 1909. Studies conducted in Chennai have demonstrated the isolation and functional characterization of gut microorganisms from different instars of *Bombyx mori*. These microbial communities are known to produce digestive enzymes that facilitate the degradation of complex polysaccharides [19]. Enzymatic investigations have further confirmed the significant roles of both aerobic and anaerobic bacteria in supporting digestion and nutritional processes in *Samia ricini*. In addition, metagenomic analyses have revealed a diverse composition of both culturable and unculturable bacterial populations distributed across different gut regions, along with variations in their abundance [20].

Paniagua Voirol et al. conducted a comprehensive study on 30 lepidopteran species and reported that bacterial families such as *Enterobacteriaceae*, *Pseudomonadaceae*, and *Bacillaceae* are commonly dominant within their gut microbiota [21]. For example, the larval gut of *Acronicta major* was found to harbor genera including *Enterobacter*, *Pantoea*, *Pseudomonas*, and *Acinetobacter*

[22]. In contrast, *Diaphania pyloalis* exhibited comparatively lower microbial diversity, with *Wolbachia* constituting approximately 40.60% of the bacterial community [22]. Furthermore, high-throughput sequencing techniques applied to *Bombyx mori* larvae have identified major bacterial phyla such as Proteobacteria, Firmicutes, Actinobacteria, and Bacteroidetes as predominant components of the gut microbiome [22].

Life cycle of the Erebidae family of insects

The family Erebidae represents one of the largest and most diverse groups of moths, encompassing several agriculturally significant pests such as fruit-piercing moths and semiloopers. Species within this family, including *Achaea janata*, *Spilosoma obliqua*, and *Eudocima materna*, exhibit distinct oviposition behaviors influenced by their life cycle characteristics and the availability of suitable host plants. Insects of the Erebidae family undergo complete metamorphosis, a developmental process involving distinct stages from egg to larva, pupa, and adult (as shown in Table 1). This transformation is characterized by significant morphological and physiological changes driven by cellular growth, differentiation, and reorganization, resulting in the formation of a structurally and functionally distinct adult organism.

Table 1: Comparative Life Cycle Characteristics of Erebidae Family Insects

Stage	***Achaea janata***	***Spilosoma obliqua***	***Eudocima materna***
Egg	Eggs are laid singly; hatching occurs within 2–5 days.	Eggs are laid in clusters (130–250 per batch); incubation period ranges from 4–8 days.	Females lay approximately 500–800 eggs on host plants; hatching occurs within 3–4 days.
Larva	Undergoes 5–6 instars; larval duration is about 11–15 days.	Passes through 6 instars; larval stage prolonged, lasting 20–28 days.	Completes 5–6 instars; larval period lasts approximately 15–20 days.
Pupa	Pupal stage lasts around 10–14 days.	Duration of pupal stage is 8–13 days.	Pupal stage extends for about 12–15 days.
Adult	Adult lifespan is approximately 7–8	Adults survive for about 3–9 days.	Adults are relatively long-lived, often surviving more

	days.		than 30 days.
Total Life Cycle	Entire life cycle is completed in approximately 45 days.	Life cycle duration ranges between 35–47 days.	Total life cycle spans approximately 45–60 days.

The eggs of *Achaea janata* (castor semilooper) are hemispherical in shape with distinct ridges and vary in colour from light to dark green. They are typically deposited singly on the underside of host plant leaves. The fully developed larva is greyish-brown, characterized by a black head, a prominent red marking on the looping region, and red anal tubercles. The pupal stage is reddish-brown and usually enclosed within a cocoon. The adult moth is medium-sized, exhibiting brownish-grey forewings and hindwings marked with black and white spots.

In *Spilosoma obliqua*, the eggs are greenish-white and are laid on the lower surface of leaves. Early instar larvae feed gregariously, scraping chlorophyll from leaf surfaces. As they mature, the larvae develop dense, elongated hairs ranging in colour from orange to black. Pupation occurs within a silken cocoon incorporating body hairs. The adult moth is predominantly white with distinct black spots on the wings.

The eggs of *Eudocima materna* are light yellow and are laid in groups on host plants. The larvae are smooth, green, and lack body hairs, with a rounded head capsule. The adult moth is relatively large, possessing dark brown forewings and vividly coloured orange to yellow hindwings. Species of *Eudocima* are generally nocturnal in nature. The adults are characterized by cryptic forewings, brightly coloured hindwings, and a specialized piercing proboscis adapted for feeding on fruits, which is why they are commonly referred to as fruit-piercing moths. Fig. 1 shows developmental stages of selected Erebidae Moths from egg to adult.




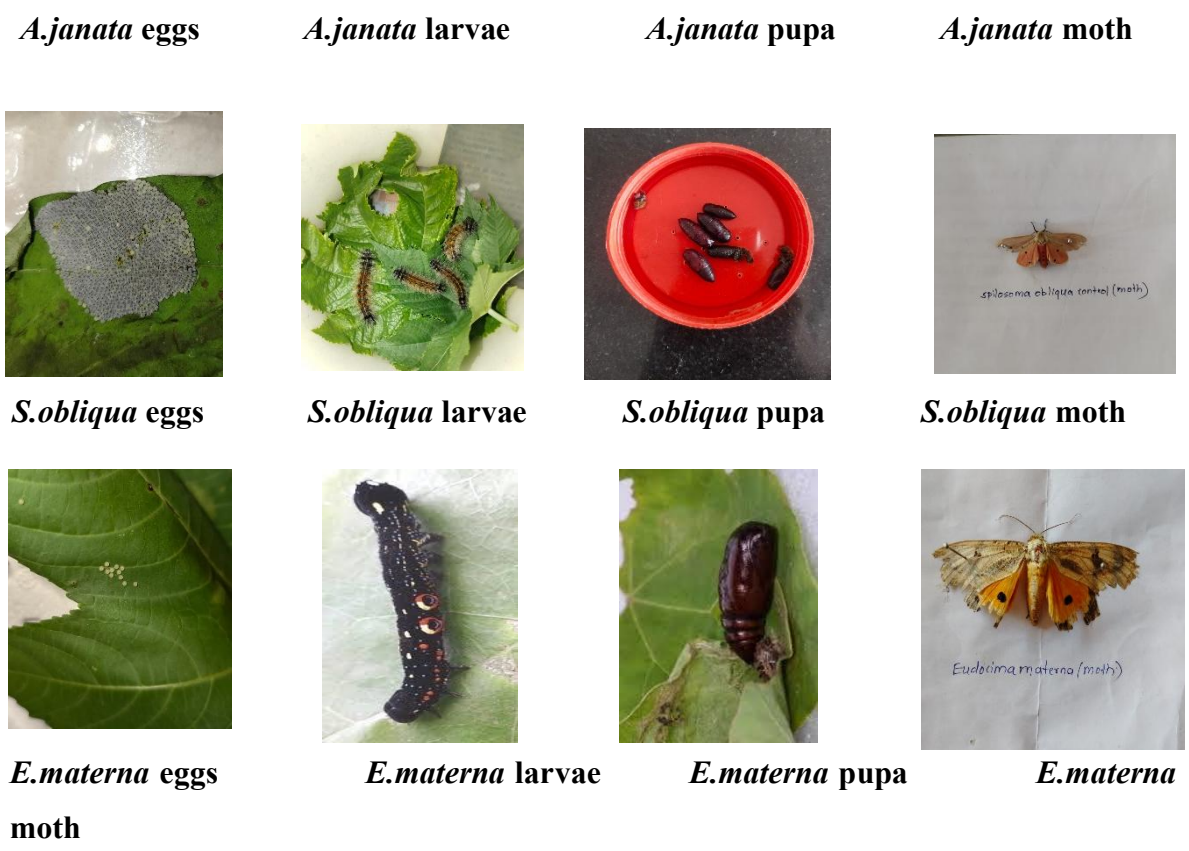

Figure 1. Life Cycle Stages of Selected Erebidae Moths (*Achaea janata*, *Spilosoma obliqua*, and *Eudocima materna*): Eggs, Larvae, Pupae, and Adult Forms.

Antibiotics and their impact on life cycle

Excreta from humans and animals, including urine and feces, often contain considerable concentrations of unmetabolized antibiotics, contributing to environmental contamination. In veterinary applications, the pathways of antibiotic release differ, as these compounds are more directly introduced into soil systems through animal waste, except in aquaculture where aquatic environments are primarily affected. Although many antibiotics are degraded relatively rapidly due to intense microbial activity in soils, certain compounds exhibit prolonged persistence, remaining detectable for extended periods [23].

Gut microbiota plays a fundamental role in the survival and physiological functioning of animals, including insects, by supplying essential digestive enzymes and nutritional support [24]. Microbial enzymes such as cellulases, hemicellulases, and pectinases facilitate the breakdown of plant cell wall components, thereby enabling the release of utilizable sugars like glucose for insect metabolism [25]. In lepidopteran insects, extensive genomic studies have identified

numerous genes encoding cellulolytic and carbohydrate-active enzymes within the gut microbiome, indicating the critical contribution of microbial symbionts in cellulose digestion [26]. Additionally, certain microbial taxa, such as *Rhodococcus* species in the gut of the gypsy moth, are capable of degrading complex compounds like monoterpenes, highlighting their role in detoxification processes [27].

Experimental evidence further suggests that antibiotic exposure can disrupt gut microbial communities, leading to adverse effects on insect physiology, including reduced flight performance, impaired development, and decreased reproductive capacity.

Antibiotic exposure has been shown to negatively influence flight performance in both male and female insects. In particular, male offspring exhibit a significant reduction in flight capacity compared to untreated control groups, while female offspring also display a declining trend in flight ability under similar conditions [28].

Tetracycline, a broad-spectrum antibiotic naturally synthesized by *Streptomyces* species, functions by inhibiting protein synthesis in bacterial cells [29]. It is effective against a wide range of microorganisms, including Gram-positive and Gram-negative bacteria, as well as atypical pathogens such as *rickettsiae, mycoplasmas, and chlamydiae* [30]. In insect studies, tetracycline is commonly employed to eliminate intracellular symbionts like *Wolbachia* and other associated bacterial communities [31].

Due to its broad-spectrum activity, tetracycline treatment can substantially disrupt the native gut microbiota, often leading to the removal of a large proportion of bacterial populations. However, such disturbances may result in ecological shifts within the microbial community, where previously suppressed or resistant bacterial species proliferate to occupy the vacated niches. Recolonization of the gut microbiota over successive generations may therefore be attributed to the survival and expansion of tetracycline-resistant bacterial strains that persist despite antibiotic treatment [32,33].

Species	Group	Initial larvae (N)	Larvae pupated (n)	Pupation success (%)	Mean larval duration (days)	Abnormal pupae (n)	Adults emerged (n)	Adult emergence (%)	Mean pupal duration (days)	Deformed adults (n)	Sex ratio (M:F)	Remarks
Achaea janata	Control	30	26	86.7	14.2	2	24	92.3	9.1	1	13:11	Normal growth
Achaea janata	Tetracycline	30	20	66.7	17.6	6	14	70.0	11.8	4	8:6	Delayed development
Eudocima materna	Control	30	25	83.3	15.0	3	23	92.0	9.5	1	12:11	Normal pupation
Eudocima materna	Tetracycline	30	19	63.3	18.3	7	13	68.4	12.2	3	7:6	Reduced emergence
Spilosoma obliqua	Control	30	27	90.0	13.6	1	26	96.3	8.8	0	14:12	High survival
Spilosoma obliqua	Tetracycline	30	21	70.0	16.9	5	16	76.2	11.3	2	9:7	Moderate delay

Table 2: Effect of antibiotic Treatment on Development, Pupation, and Adult Emergence of Selected Erebidae Moths.

Antibiotic treatment has been found to significantly influence the developmental biology of selected Erebidae moths by disrupting their gut microbiota (as shown in Table 2). The removal or suppression of beneficial symbiotic bacteria adversely affects larval growth, resulting in prolonged developmental duration, reduced feeding efficiency, and lower weight gain. Consequently, pupation is often delayed and may exhibit reduced success rates, with some individuals forming weak or malformed pupae. Furthermore, the emergence of adults is frequently compromised, with decreased emergence rates, reduced vitality, and shorter lifespan observed in treated groups compared to controls. These effects highlight the critical role of gut-associated microorganisms in supporting normal physiological processes, including nutrient assimilation, metabolism, and hormonal regulation during metamorphosis. Overall, antibiotic-induced alterations in microbial communities can impair successful completion of the life cycle in Erebidae moths, emphasizing the importance of microbiota in insect development and survival.

Future perspective and conclusion

The present study revealed that tetracycline treatment reduced bacterial diversity in insects, although it did not completely eliminate the microbial community or render them entirely aposymbiotic. Antibiotic exposure caused noticeable alterations in the structure of gut microbiota, affecting both the relative abundance and distribution of bacterial taxa. Importantly, these changes persisted across generations, as similar microbial shifts were observed in offspring even in the absence of direct antibiotic treatment. This finding highlights the potential for long-term and transgenerational impacts of antibiotic use, which is particularly significant given its widespread application in research, veterinary, and clinical settings. Furthermore, identifying specific gut symbionts involved in the detoxification of plant secondary metabolites opens new opportunities for developing targeted biopesticide strategies. Such approaches could disrupt pest adaptation mechanisms while minimizing reliance on conventional broad-spectrum chemical pesticides.

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