ดีเอ็นเอบาร์โค้ดของหนอนผีเสื้อให้อาศัยและแมลงเบียนในพื้นที่จุฬาลงกรณ์มหาวิทยาลัย อำเภอแก่งคอย จังหวัดสระบุรี

นายพรเทพ เกื้อกิจ

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DNA BARCODING OF LEPIDOPTERAN HOSTS AND THEIR PARASITOIDS AT CHULALONGKORN UNIVERSITY AREA, KAENG KHOI DISTRICT, SARABURI PROVINCE

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A Thesis Submitted in Partial Fulfillment of the Requirements
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ปัจจุบันข้อมูลด้านความสัมพันธ์ระหว่างหนอนผีเสื้อและแมลงเบียนมีอยู่อย่างจำกัด เนื่องจากปัญหาด้านการเลี้ยงแมลงและการจัดจำแนกที่ถูกต้อง อย่างไรก็ตามความรู้นี้มีความสำคัญอย่างยิ่งต่อการควบคุมประชากรของแมลงศัตรูพืชด้วยชีววิธี โดยอาศัยแมลงเบียนเป็นแมลงศัตรูธรรมชาติ รวมถึงการทำความเข้าใจปฏิสัมพันธ์ระหว่างหนอนผีเสื้อให้อาศัยและแมลงเบียน ในช่วงไม่กี่ปีที่ผ่านมาวิธีการตรวจสอบดีเอ็นเอ ได้ถูกพัฒนาขึ้น และนำมาใช้ในการจัดจำแนกสิ่งมีชีวิตโดยใช้เทคนิคดีเอ็นเอบาร์โค้ด ช่วยให้จัดจำแนกหนอนผีเสื้อและแมลงเบียนได้อย่างแม่นยำและรวดเร็ว รวมถึงแก้ปัญหาต่าง ๆ จากการเลี้ยงแมลงให้อาศัย งานวิจัยนี้มีจุดมุ่งหมายเพื่อศึกษาเบื้องต้นเกี่ยวกับความสัมพันธ์ระหว่างหนอนผีเสื้อและแมลงเบียนในพื้นที่จุฬาลงกรณ์มหาวิทยาลัย อำเภอแก่งคอย จังหวัดสระบุรี ประเทศไทย โดยเก็บตัวอย่างทั้งหมด 28 ครั้ง ทุก 2 สัปดาห์ตั้งแต่เดือนพฤศจิกายน 2559 - พฤศจิกายน 2560 เก็บหนอนผีเสื้อได้ทั้งหมด 5,673 ตัว จัดจำแนกได้เป็น 25 วงศ์ โดยวงศ์ Noctuidae พบมากที่สุด ในขณะที่วงศ์ Drepanidae, Gracilariidae และ Nolidae พบได้น้อยที่สุด พบหนอนผีเสื้อที่ถูกเบียนโดยแมลงเบียนจำนวน 340 (~6%) ตัว ผลจากการทำดีเอ็นเอบาร์โค้ดแสดงให้เห็นว่ามีหนอนผีเสื้อที่ถูกเบียน 120 ชนิด และแมลงเบียน 113 ชนิด หนอนผีเสื้อให้อาศัยที่พบมากที่สุดคือ *Haritalodes derogate* (วงศ์ Crambidae) ส่วนแมลงเบียนที่พบมากที่สุดคือแมลงวันเบียน *Peribaea* sp.1 (วงศ์ Tachinidae) ความสัมพันธ์ของ *Orvasca subnotata* และ *Cotesia* sp.1 พบบ่อยที่สุดในพื้นที่การศึกษา ในแง่ความจำเพาะของความสัมพันธ์ พบว่า 80% ของแมลงเบียนมีความจำเพาะกับแมลงให้อาศัย และ 20% ของแมลงเบียนไม่มีความจำเพาะกับแมลงให้อาศัย จากงานวิจัยนี้สรุปได้ว่าเทคนิคการทำดีเอ็นเอบาร์โค้ดเป็นวิธีที่รวดเร็วและมีศักยภาพในการจัดจำแนกผีเสื้อให้อาศัยและแมลงเบียน และสามารถนำมาใช้สร้างสายใยอาหารระดับโมเลกุลระหว่างหนอนผีเสื้อให้อาศัยและแมลงเบียน ซึ่งการศึกษาด้านนี้ยังมีอยู่น้อยมากในพื้นที่เขตร้อน นอกจากนี้ความสัมพันธ์ของแมลงให้อาศัยและแมลงเบียนจากฐานข้อมูลสามารถนำไปประยุกต์ใช้ในการคัดเลือกแมลงศัตรูธรรมชาติเมื่อมีการระบาดของหนอนผีเสื้อศัตรูพืชในพื้นที่การเกษตร

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PORNTHAP KERKIG: DNA BARCODING OF LEPIDOPTERAN HOSTS AND THEIR PARASITOIDS AT CHULALONGKORN UNIVERSITY AREA, KAENG KHOI DISTRICT, SARABURI PROVINCE. ADVISOR: ASSOC. PROF. BUNTIKA AREEKUL BUTCHER, Ph.D., CO-ADVISOR: PROF. DONALD L.J. QUICKE, Ph.D., pp.

Relationships between caterpillars and their parasitoids are poorly known due to the limitation of insect rearing and accurate identification. However, this knowledge is very important for controlling agricultural insect pests using parasitoids as natural enemies in biological control programmes and also for understanding interactions between caterpillar hosts and their parasitoids. During the recent decades, DNA barcoding technique has been developed and used for molecular identification, it could help identify both caterpillars and their parasitoids accurately and fast, also solve the problems about insect rearing. This research aims to preliminary study the relationships between caterpillars and their parasitoids at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province, Thailand. A total of 28 collecting trips, every 2 weeks started from November 2015 - November 2016, caterpillars were collected by hand. In total 5,673 caterpillars which are classified into 25 lepidopteran families were recorded. Noctuidae was the most abundance caterpillars discovered from this study while Drepanidae, Gracilariidae and Nolidae were the least abundance of caterpillars. Off these, 340 (~6%) caterpillars were parasitised by parasitoids. DNA barcoding revealed 124 provisional species of parasitised caterpillars and 113 provisional species of parasitoids. The most abundant caterpillar hosts belonged to *Haritalodes derogate* (family Crambidae) and for the parasitoid, tachinid fly, *Peribaea* sp.1 was the most frequently parasitoid recorded from the parasitised caterpillars. *Orvasca subnotata* and *Cotesia* sp.1 was the most frequently recorded of host-parasitoid interaction in study area. In term of host-parasitoid specificity, 80% were specialist parasitoids and only 20% were generalist parasitoids. DNA barcoding method is a rapid and powerful tool for identifying lepidopteran hosts and parasitoids and highly effective on resolving complex host–parasitoid relationships by constructing molecular food web of trophic interactions in poorly for study areas of tropic region. Host–parasitoid relationships from the databases can be applied for selecting potential natural enemies when there are outbreaks of lepidopteran pests in agricultural areas.

Department:	Biology	Student's Signature	....
Field of Study:	Zoology	Advisor's Signature	....
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CHAPTER 1

INTRODUCTION

1.1 Rationale

At present, information on host–parasitoid relationships is limited, not only in the tropics, including Thailand, but also around the world. Accurate techniques for detecting and identifying parasitoids are essential for understanding and managing host–parasitoid interactions (Agusti et al., 2005). This poses daunting technical challenges because detecting and differentiating endoparasitic species within their hosts is rather difficult. Traditional method for studying host–parasitoid interactions is rearing wild–caught hosts until either parasitoid or adult host emerged. This method has limitations, notably hosts often die before they develop into adults, particular problem in the tropics dues to heat and humidity, and also problem of obtaining sufficient food plant for the caterpillars to feed on, which might be scarce or difficult to find.

Parasitoids have previously been detected within dipteran, lepidopteran, heteropteran, and homopteran hosts by DNA–based methods at high specificity and sensitivity (Greenstone, 2006). DNA barcoding is a highly standardized method for molecular identification, using a short genetic marker in an organism's DNA to identify species. A PCR (Polymerase Chain Reaction) is used to amplify DNA with primers of broadest possible target taxonomic group. This technique is a powerful tool to quantify the study of host–parasitoid interactions and species identification (Traugott et al., 2013). Hebert et al. (2004) suggested that a sequence of approximately 650 base pairs of the mitochondrial gene cytochrome C oxidase subunit I (COI, cox1) could be used as a taxonomic tool for animals. Many studies have shown that these COI genetic markers are generally effective in diagnosing species. DNA barcoding provides a fast and accurate way to recognising species and may additionally reveal the presence of cryptic species. Alternatively, barcoding may indicate that observed morphological cryptic species. Alternatively, barcoding may indicate that observed morphological variation might be intraspecific rather than the presence of multiple species (Smith et al., 2006; 2007; 2008)

Caterpillars (lepidopteran larvae) are an immature stage in the life cycle of butterflies and moths. Many species are major agricultural insect pests which may cause severe economic loss, especially in agricultural–based countries such as Thailand. More than 4,087 species of Lepidoptera have been identified in Thailand. Of these, 1,291 species in 6 families are butterflies and 2,796 species in approximately 64 families are moths (Dokchan, Pinkaew, and Klorvuttimontara, 2013; Ek-Amnuay, 2006; Hutacharen, Tubtim, and Dokmai, 2007). At present, more than 30% of agricultural products from Thailand are damaged by lepidopteran pests. In Thailand, caterpillars can be found throughout the year. In many tropic countries, including Thailand, very little is known about caterpillar taxonomy, biology and their interactions with their parasitoids and food plants.

Parasitoids are insects that feed on or within a still living host, other insects and occasionally other arthropods, which they eventually killed. Parasitoids play an important role in terrestrial ecosystem (Godfray, 1994) because they control the populations of other insects (Hassell, 2000; LaSalle and Gauld, 1993). Regulation of the population density of many of their hosts has important economic implications for pest species. Insect parasitoids comprised of 2 large groups, parasitoid wasps (many families) and parasitoid flies (predominantly the family Tachinidae) (Quicke, 1997; 2015) . All these parasitoids are difficult to identify morphologically and many species still undescribed.

The purpose of this research is to study the relationships between the lepidopteran hosts and their parasitoids using DNA barcoding to identify hosts and parasitoids. Two sampling methods were used to obtain hosts: hand collecting and a beating sheet. This would establish a preliminary database of the caterpillars and their natural enemies at the study site, Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province.

To study the relationships between lepidopteran hosts and their parasitoids, normally, adult parasitoids are easily collected, but then their hosts are unknown. A standard method to find out about host–parasitoid relationships is to rear the caterpillars until either adult of butterfly / moth or parasitoid emerges, however there are many problems with insect rearing, diseases (molds, bacteria, fungi), which may kill hosts in captivity, moreover providing food for the caterpillars to complete their development requires much effort, botanical expertise, and may not be practicable. Therefore, tosolve this problem, DNA barcoding was applied to both caterpillars and parasitoids which were collected from CU, Saraburi campus every 2 weeks from November 2015 to November 2016. Wild–caught caterpillars were tentatively identified to family level based on a published pictorial key. Each was then photographed to provide a record, given voucher number and dissected to determine whether or not they have been parasitised by parasitoid wasps or flies. For each parasitised caterpillar detected, tissue samples of both the caterpillar and its parasitoid were sent to the Canadian Centre for DNA Barcoding (Guelph, Ontario) for DNA barcoding and subsequent molecular identification. Their parasitism rates and relationships were also recorded by observation. This research can be summarised according to Figure 1-1.

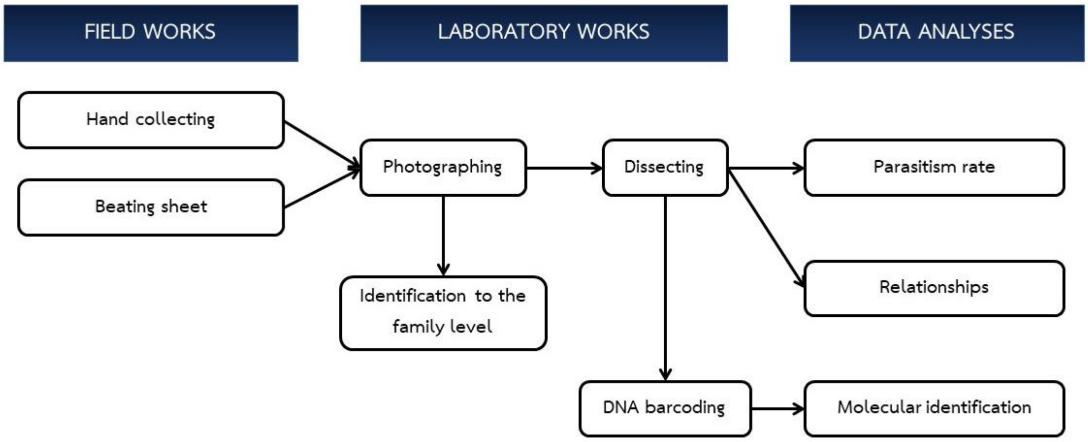


Figure 1 – 1 Flowchart summarised this thesis. There are 3 steps of the research, field work, laboratory work and data analyse

1.2 Objectives

1) Molecular identification of lepidopteran hosts and their parasitoids collected from Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province, using DNA barcoding technique
2) Study the interactions between (food–web) lepidopteran hosts and their parasitoids at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

CHAPTER 2

LITERATURE REVIEW

2.1 Relationships between the lepidoptera hosts and their parasitoids

Host–parasitoid relationships are trophic interactions within the ecosystem; they represent two trophic levels. These organisms have generally co–evolved in an arm–race. Insect hosts will be under selection to improve or gain new defense mechanisms to protect themselves from parasitoids, while the insect parasitoids will be selected to have effective host detection and parasitise mechanisms (Godfray, 1994; Poulin, 2011; Poulin and Randhawa, 2015).

2.1.1 Lepidopteran hosts

Caterpillars are the larval stage of insects, belonging to the order Lepidoptera, which comprises butterflies and moths. Insects in this group are highly diverse and have extraordinary range of survival techniques in all terrestrial ecosystems (James, Morgan, and Sourakov, 2018). At present, more than 180,000 species have been identified and described around the world (Capinera, 2008). In Thailand, more than 4,087 species of Lepidoptera have been recorded, though the total number is expected to be at least 20,000 species (Ek-Amnuay, 2012). Lepidopterans undergoes complete metamorphosis or holometabolism, with their life cycle consists of egg, larva, pupa, and adult (Gullan and Cranston, 2010). Developmental time depends on species, temperature and humidity. Normally, larvae grow under low temperature and humidity spend longer developmental time than under conditions with high temperature and humidity. Furthermore, species with larger size also take more time to develop than smaller–sized ones. Most caterpillars consume plants for food (herbivorous) though food consumption may be restricted to a particular time of day, especially night time. In some situations, more than 80% of plant damages may cause by caterpillars, so depending on the crop, caterpillars are frequently major agricultural pests. Thus, they can have a high economic impact, especially in agricultural based countries, including Thailand (Dokchan et al., 2013; Hutacharen et al., 2007). One of the most important lepidopteran pests, the diamondback moth (*Plutella xylostella* L., Lepidoptera: Plutellidae) which attacks *Brassica* vegetables, has a worldwide distribution. This moth creates a problem with annual primarily pesticide costs estimated to be 2.7 billion dollars and the yield losses to $4–5 billion (Furlong, Wright, and Dosdall, 2013). In Thailand, the diamondback moth was reported as the major pests in *Brassica* crops in Central and Northern regions of the country (Chansri, 2014; Rowell et al., 2005).

2.1.1.1 Caterpillar defenses

Depending on species, a female butterfly or moth can lay thousands of eggs during her adult lifetime. However, only a small percentage generally survive until adulthood (James et al., 2018). Since they have many factors causing mortality during an immature stage of lepidopteran, such as biotic enemies and abiotic factors, therefore to increase survival rate, high number of egg production and defense mechanisms during larval and pupal stages are used. These defensive systems are different among species and environment that they inhabit (Gentry and Dyer, 2002; Russell et al., 2009).

Herbivorous caterpillars have a variety of feeding behaviour that are different among caterpillar species. Leaf miner caterpillars feed only inside of leaves, creating tunnels and brown or white spots on the leaves. Free feeding caterpillars may consume entire leaves. Skeletonizers caterpillars consume leaves and left all veins of the leaf intact and creating a lacy appearance on the leaves. Other species are leaf roller caterpillars use silk to roll leaves and leaf–tiers use silk to stick different leaves together. In both cases the caterpillars eat the leaves from within them. These rolls and ties provide defense against parasitoids and birds as well as creating a more stable internal microclimate.

2.1.1.2 Control of lepidopteran pests

According to a survey by Food and Agriculture Organization of the United Nations (FAO), Thailand ranked at the 48th world ranking of agricultural area and came 5th world ranking on insecticide usage. The Thai government spent over 30,000 million baht per year for imported these synthetic chemicals for using in agriculture. Using high amount of chemicals resulted in health problems, 39% of farmers have risk from the use of these pesticides; chemicals contaminated in environment; more than 14,000 million baht was spent on external effects of pesticides (Alavanja, Hoppin, and Kamel, 2004; Payackso, 2017). As a result, Thailand has tried alternative methods to control insect pest population from pesticides to Integrated Pest Management (IPM) by applying multiple techniques of pest control methods based on ecological and economic principles (Ehi-Eromosele, Nwinyi, and Ajani, 2013).

Wangboonkong (1981) studied chemical control on bollworm or *Heliothis armige*ra (Hbn.) major cotton pests in Thailand. Normally, there are eight insecticides used for controlling bollworm. After applying synthetic pyrethroids the bollworm can evolve resistance to synthetic pyrethroids and furthermore, damage caused by the whitefly *Bemisia tabaci* (Genn.) (Hemiptera) has increased.

Idris and Grafius (1996) compared oviposition, egg hatch, larval survival and infestation level in *Plutella xylostella* or diamondback moth and parasitism rate, developmental time and sex ratio of *Diadegma insulare* (Cresson) in wild and cultivated Brassicaceae. Oviposition, egg hatch and larval survival were highest on the cultivated Brassicaceae, but developmental time of caterpillars was longer on the wild Brassicaceae compared with cultivated host plants. The parasitism rate was higher in moth larvae fed on *B. kaber* than on the wild Brassicaceae. Parasitised diamondback moth larvae use long time to develop when fed on *E. cheiranthoides*, *Thlaspi arvense* L., and *B. incana* and the female/male sex ratio was higher on *Brassica* species. The infestation was higher on broccoli than on the other *Brassica* crops. In the field, diamondback moth can reduce populations from increase impact of *D. insulare*. This research show increases the success of diamondback moth management programmes.

Fay and Halfpapp (1999) studied the activities of six species of fruit-piercing moths, *Eudocima fullonia* (Clerck), *E. jordani* (Holland), *E. materna* (L.), *E. salaminia* (Cramer), *E. aurantia* (Moore) and *E. cocalus* (Cramer) (Lepidoptera: Noctuidae), in lychee or carambola crops at northeastern Queensland between 1985 and 1993. The moths were least active in the driest season (July–October) and most abundant in the wet season (November–December). *E. fullonia* was the dominant species between November and mid–March and 95.5% of the moths on coastal lychees. *E. jordani* was major species in carambola crops during autumn. 77.9% of all moths caught in the study site were males. The activity of all moths arrived before midnight. The results show opportunities for pests control in tableland areas during the dry season.

Timprasert, Datta, and Ranamukhaarachchi (2014) interviewed 220 vegetable farmers in Nakhon Ratchasima Province to survey factors choosing of IPM. The farmers had 3 major reasons for using IPM such as insecticides are more expensive, negative effects on human health and the environment and almost insect pests were able to resist insecticides. After IPM training, the farmers had better knowledge and uncompromising acceptance on IPM. But, minority farmers rejected adoption of IPM, the non–IPM farmers belief that natural enemies cannot control insect pests and IPM cannot increase vegetable yields.

At present, biological pest control is a preferred method for eliminating natural insect pests using natural enemies (parasitoids or predators). Parasitoids are important insect natural enemies of pests, more than 80 percent successful of biological control programmes using parasitoids as natural enemies. Based on many researches, parasitoids are provided more powerful benefit than pesticides and reduces effects of pesticides. The most important and difficult process of biological pest control is to search for suitable natural enemies that can be recommended correctly with ecological knowledge but this method is difficult to produce natural enemies and distribute to farmers more than chemicals (Bale, Van Lenteren, and Bigler, 2008). For mass production, there are two types of rearing systems, first, short–term rearing system is to produce a relatively small number of parasitoids per day for releasing and hopefully long–term establishment. Secondly, long–term rearing system is mass production of parasitoids for a year–round, with approximately 4–1000 millions female parasitoids per week which are continuously being released to inundate the pest population (Smith, 1996; Wajnberg, Hassan, and Polaszek, 1994). Bompard et al. (2013) reported that the parasitoids with high searching behaviour are most effective as biocontrol agents due to their abilities to reduce pest population and higher performance of mating for population increase reproduction.

Xu et al. (2018) studied fitness and biocontrol effectiveness of the *Encarsia sophia* and the primary parasitoid *Eretmocerus hayati* for whitefly (*Bemisia tabaci*) control programme. For results, population of *En. sophia* increased faster and more killing effectiveness than *Er. hayati*. Therefore, *En. sophia* is the best choice as natural enemies for biological control of whitefly.

2.1.2 Parasitoids

A parasitoid is highly evolved organism and displays one of six main evolutionary strategies within the broader topic of parasitism (Table2-1) (Poulin and Randhawa, 2015). Parasitoids play an important role in terrestrial ecosystem because they control other insect populations, therefore, these insects influence or regulate the population density of their hosts (Quicke, 2015). Insect parasitoids comprise two large groups, parasitoid wasps and parasitoid flies (Quicke, 2012). Parasitoid larvae develop by feeding on the host arthropods, either internally or externally. However, when the parasitoid larva is fully grown, it always kills the host. At present, parasitoid can be divided into 2 major groups according to their development such as koinobiont and Idiobiont (Quicke, 1997). Most ectoparasitoids are idiobiont developmental strategies that hosts are restrained further development and immobilized after initial parasitisation. Because the hosts are allowed to move and molt, they could damage or remove from host. Normally, idiobiont can parasitise multiple host species called generalists. In contrast, hosts are parasitised by koinobiont parasitoids that the host can continue its development while parasitoid feeding upon it. Most endoparasitoids are koinobiont developmental strategies that hosts are only killed when the parasitoid develops into an adult. Koinobionts developmental strategies give them the advantage of a host that continues to grow larger and avoid predators (Gullan and Cranston, 2010).

Table 2 - 1 Six main evolutionary strategies of parasitism

Evolutionary strategies	**Definition**
Parasitic castrators	These parasites destroy reproductive ability of their host
Directly transmitted	These parasites can transmit directly to hosts without requirement of vector
Trophically transmitted	These parasites are transmitted by being eaten by a host
Vector-transmitted	These parasites rely on a third party, an intermediate host, where the parasite does not reproduce sexually to carry them from one definitive host to another
Parasitoids	These parasites live and eat on/inside other arthropods, when the larva became adult, it would eventually kill the host
Micropredators	Micropredators attacks more than one host, reducing each host's fitness at least a small amount, and is only in contact with any one host intermittently

Moreover, parasitoids have various behaviour of parasitism levels. First parasitoid that parasitises a host is called a primary parasitoid. Secondary parasitoid or hyperparasitoid is a parasitoid of the primary parasitoid. Hyperparasitoids also fall into two categories: facultative hyperparasitoids can be either primary parasitoids or secondary parasitoids depending on the situation, whereas obligate hyperparasitoids must always develop as hyperparasitoid. Levels of parasitoids can be up to five levels of parasitism.

In addition, multiple parasitism is two or more species of parasitoids parasitising the same host but without parasitising each other. If multiple parasitoids of the same parasitoids species cohabit in the same host, it is called superparasitism (Askew, 1961, 1971). Furthermore, parasitoids have two oviposition styles called solitary parasitoid and gregarious parasitoid. Solitary parasitoids normally produce one progeny per host, while gregarious parasitoids produce several progenies per host (Fisher, 1961).

Accurate techniques for detecting and identify parasitoids are essential to understand and manage host–parasitoid interaction (Agusti et al., 2005). This poses technical challenges because detecting and differentiating endoparasitic species within their hosts is rather difficult because of parasitoids' complex behaviour.

2.1.3 Current study of lepidopteran hosts and their parasitoids

Relationships among parasitoids and their hosts are very complex and studies about the relationships are difficult to establish because of many limitations. Traditional method to detect and discriminate parasitoids within their hosts is rearing field–collected hosts in the laboratory until either parasitoid or adult host emerge. This method has limitations such as hosts often die before developing into adults, pathogenic fungi and the difficulty of providing food plants for field–collected caterpillars to complete their development (Greenstone, 2006; Greenstone et al., 2005; Lukhtanov et al., 2009). However, the relationships among parasitoids and their hosts need to be studied because these relationships have important roles in terrestrial and agriculture ecosystems by controlling population of insect pests and other insects. Henry et al. (2010) reported that the ability to parasitise a host of biological control agents was defined as being genetically identity and the strength of heritable. This study is very limited because the organisms have complexity of biological interaction and most hosts are parasitised by parasitoids more than one species. The method for understand interaction between hosts and parasitoids in a large community such as tropical rainforest. One approach is to create a simple relationships diagram (one–host and one–parasitoid) or trophic link of hosts and parasitoids. Alternatively, one build real community features and attempts to relationship the patterns that may indicate of real structure (Godfray, 1994).

2.2 DNA barcode

Hebert, Cywinska, and Ball (2003) published a paper titled “Biological identifications through DNA barcodes” that proposed a new way to molecularly identify species called “DNA barcoding”, using amplified, sequenced, and analyzed in uniform region of the mitochondrial gene then compare with the sequences from the database (GenBank, BOLD). This technique would create a barcode that could identify biological organisms and a reference library for identifying the target DNA. DNA barcoding could reduce misidentification problem and confusion of species identification and give accurate species identification (Seifert et al., 2007; Stoeckle, Waggoner, and Ausubel, 2004). For almost all animals, cytochrome C oxidase I (*COI, cox1*), a 650 base–pair region in the mitochondrial gene is used as a standard barcode for almost all animal groups. Therefore, DNA barcoding is often perceived as a reliable, cost effective and easy molecular identification tool that is extremely useful for identifying mimicry, sibling and cryptic species and species with inter– or, intra–specific variation, especially for highly diverse taxa of many insect groups and can be used to identify ovary stage of development (eggs, larvae, pupae and adults) which are hardly achieved by other techniques (Hebert and Gregory, 2005; Hebert et al., 2004a).

2.2.1 DNA barcoding database

The use of DNA barcoding as a tool for studying diversity and identification of species requires a reference database that has been verified by professional taxonomists. Currently, BOLD and GenBank provide the largest publically accessible DNA sequence (including barcodes) databases searching for most similar sequences (Sonet et al., 2013).

The Barcode of Life Data System (BOLD) is a project to create public informatics workbench for management about DNA barcode records. From this system, researchers can create DNA barcode by assembling molecular, morphological and distributional data for acquisition, storage, analysis and publication of DNA barcode. The objective of BOLD is to collect referenced sequences of all species in the world (Ratnasingham and Hebert, 2007).

GenBank (R) is a public database, which is constructed and shared by National Center for Biotechnology Information (NCBI) by including nucleotide sequences and biological citations. This database compiles DNA sequences and amino acid sequences of proteins, and also including genomic taxonomy, protein mapping, and domain information. GenBank has many institutes for exchanging data in order to ascertain that data sets. Furthermore, it also has searching and analyzing systems of relating data. Basic Local Alignment Search Tool (BLAST) is a tool for searching sequence similarity of GenBank databases (Benson et al., 2008). BLAST is an algorithm for comparing biological sequence information that find sequences in the database which are similar to query sequences and searches high scoring sequence alignments between the query sequence and the target sequences in the database (Gollery, 2005).

2.2.2 DNA barcoding in Entomology

DNA barcoding for insect identification still has many limitations which can decrease its efficiency. There are over millions of insect species and most of them are still unknow to species, this could cause a limitation of DNA barcoding database. However, many studies show that it is still a reliable tool for species identification of Lepidoptera, Hymenoptera, Coleoptera and Diptera (Hajibabaei et al., 2006; Janzen et al., 2005; Jurado-Rivera et al., 2009; Pfenninger et al., 2007; Vaglia et al., 2008). Moreover, DNA barcoding could be used to study host–parasitoid relationships by showing trophic interaction of host–parasitoid and then used to analyse trophic level of organism in food webs. Gómez-Polo et al. (2016) shows that over the last 15 years, molecular tools create a molecular food web comprising seven species more than two trophic levels in a mediterranean lettuce crop that such technique is suited for studying predator–prey interaction in agricultural and improve biological control. In addition, it will fail to detect hybrids because the barcode is only from maternal DNA, there can be mitochondrial introgression, there can be cases where mitochondrial lineage sorting is still incomplete or distorted because of endosymbiotic bacteria such as *Wolbachia* (Jinbo, Kato, and Ito, 2011; Smith et al., 2012).

2.2.2.1 Cryptic species

Smith et al. (2006) used DNA barcoding to reveal a great deal of cryptic but host–specific species within the genus of parasitoid fly genus *Belvosia* (Diptera: Tachinidae). All the specimens had been reared from the caterpillars (Lepidoptera) at the Area de Conservación Guanacaste (ACG), northwestern Costa Rica. Barcoding not only discriminates 17 highly host–specific morphospecies, but it is also raises the species count to 32 by revealing that each of the three–generalist species are actually arrays of highly host–specific cryptic species.

2.2.2.2 limition of database

Zaldivar-Riverón et al. (2007) used DNA barcoding to investigate the doryctine braconid wasp fauna in the Chamela–Cuixmala Biosphere Reserve in Mexico. Three field trips had been carried out in the reserve and 468 specimens were collected. DNA barcoding detected 115 species of parasitic wasps belonging to the genus *Heterospilus* alone. Their sequence data also provided evidence to justify synonymizing *Ptesimogastroides* as a junior synonym of the *Ptesimogaster*.

Smith et al. (2008) used DNA barcodes to analyse 2,597 parasitoid wasps, belonging to 6 microgastrine braconid genera reared from the ACG. Barcoding and morphology discovered the same provisional species and that the biological entities revealed by these analyses are congruent with wasp host specificity. Therefore, DNA barcoding helps understanding the diversity and host–parasitoid specificity.

2.2.2.3 Trophic interaction

Hrček et al. (2011) used molecular methods by species-specific primers for detection complex of caterpillar–parasitoid food web from tropical rainforest in Papua New Guinea. From data, 93 trophic links between 37 host lepidopteran species and 46 parasitoid species include parasitic warps and parasitic flies this technique is useful for identification when host species is in the larval stage which is difficult to identify morphologically and host die during rearing and parasitoid specialization. Molecular helps to understand about parasitoid host specificity and new possibilities for food web structure and forecasts inference of species.

Wirta et al. (2014) studied networks of ecological antagonistic interactions in the High Arctic using parasitoid DNA sequenced collecting from the tissues of their hosts and host DNA sequenced collecting from the guts of adult parasitoids. For data analysis, molecular information from parasitoids and hosts and rearing data were revealed many interactions such as parasitoid’s host specialist role of predators with a cryptic lifestyle. These data can create network of host–parasitoid interactions that can be used to compare in food web structure.

Kitson et al. (2018) used nested tagging DNA metabarcoding for determining host–parasitoid interactions and parasitism rates in the larval stage of biological control parasitoids in the new environment. The use of next generation sequencing revealed complex community in the environment of all oak processionary moth (developmental stages *Thaumetopoea processionea*) that are parasitised by the primary parasitoid (*Carcelia iliaca*: Diptera: Tachinidae) and a secondary parasitoid (*Compsilura concinnata*: Diptera: Tachinidae). This methodology effectively resolved ecological networks of host–parasitoid relationships.

CHAPTER 3

MATERIALS AND METHODS

3.1 Study area

Field study was conducted in the secondary forest at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province (Figure 3-1 A, B). The study site is approximately 40 – 150 m above mean sea level, with the size of 538.24 Ha (Figure 3-1 C). The study site consists of secondary forests, which are mixed among deciduous and dry dipterocarp forests (80%) and grassland (20%). It was moist and green during the rainy season (May – November). Whereas it is very dry during the dry season (December – April) (Figure 3-2) (Vasinopas, 2009) and there was a large amount of leaf litter depositing on the ground lead to forest fire frequently (January – February) (Figure 3-3 A, B). The study area was divided into 35 randomly selected plot(s) (600 x 700 m^2) (Figure 3-4). So that, insect samples could be collected cover most of Chulalongkorn University area at Kaeng Khoi.

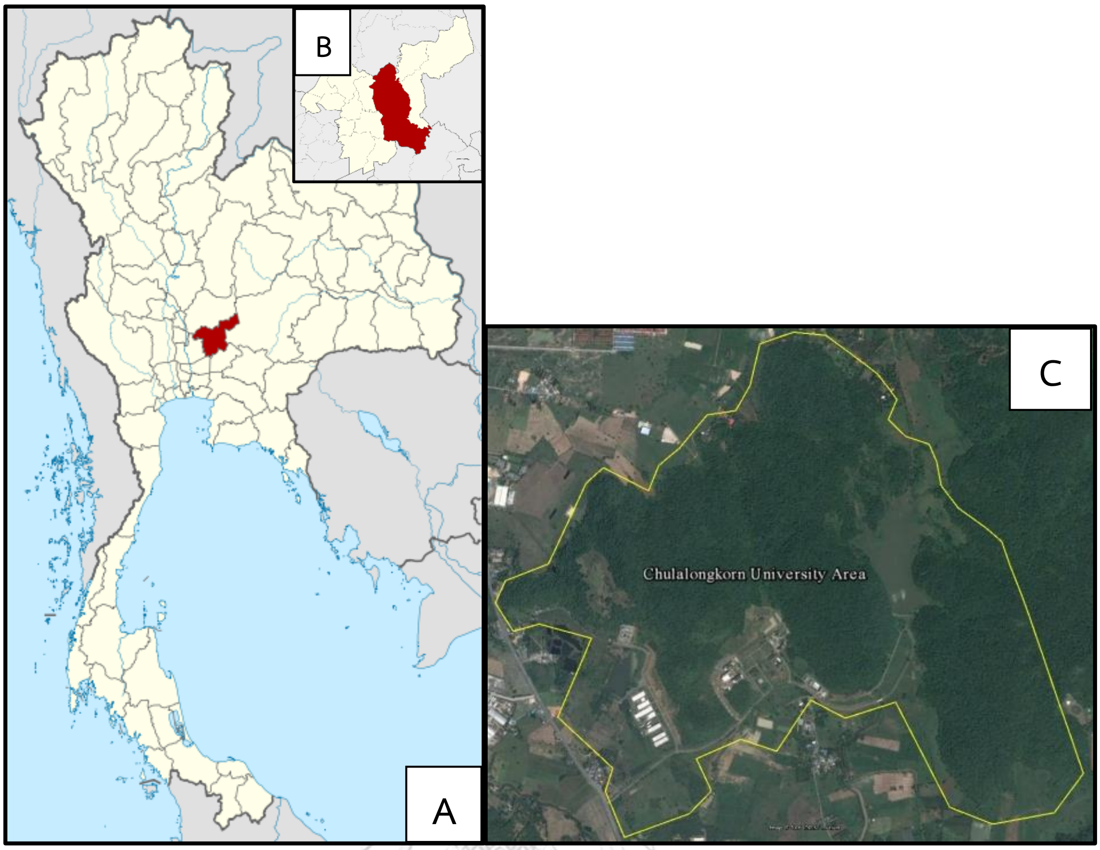


Figure 3 – 1 Map of the study area; A, map of Thailand shows where Saraburi Province located (red); B, map of Saraburi Province, Kaeng Khoi District is located at the red area; C, map of Chulalongkorn University Area at Kaeng Khoi (https://upload.wikimedia.org/wikipedia/commons/a/af/Thailand_Saraburi_locator_map.svg)

(https://upload.wikimedia.org/wikipedia/commons/6/67/Amphoe_1902.svg)

Figure 3 – 2 Habitats at the study sites: rainy season (May – November 2016: left) and dry season (December 2015 – April 2016; right)

Figure 3 – 3 A, Forest fires at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province (22 January 2016); B, habitat was changed after the fire

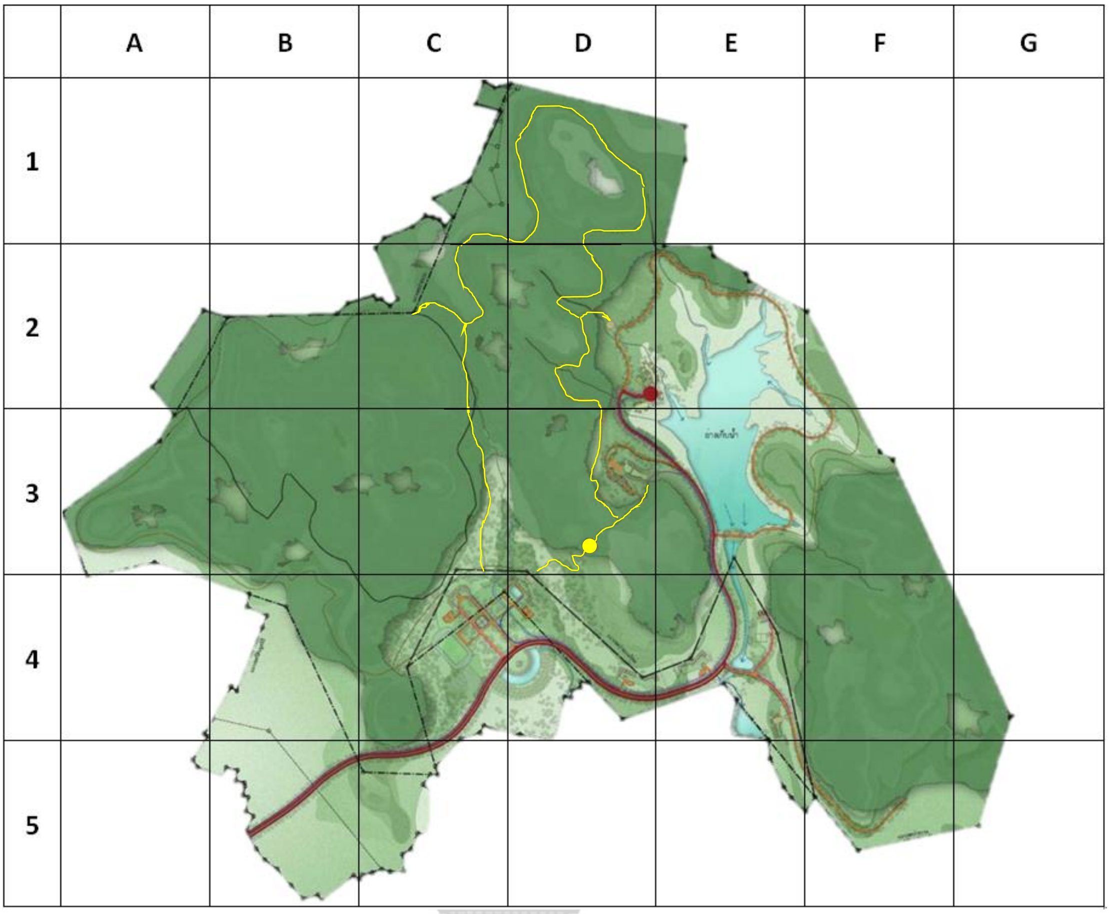


Figure 3 – 4 Forest division and numbering compartment on this study

Note: red line = main street; orange line = reservoir and grassland trail; yellow line = forest trail

3.2 Sample collection

3.2.1 Lepidopteran hosts

Larvae of lepidopteran hosts were collected from 2 randomly selected plots every 2 weeks at the study site from November 2015 – November 2016. The selected plots were changed randomly every collecting time. Samples collecting was conducted twice a day in two randomly selected plots, namely one plot from 6.00 AM to 9.00 AM and another plost from 4.00 PM to 6.00 PM using two methods.

3.2.1.1 Hand collecting

By using forceps and paintbrush (Figure 3-5 A, B). Searching for caterpillars by looking for traces of damaged leaves and holes on the stems that were probably been eaten by caterpillars. Also, flipping insect damaged from top to bottom to search for caterpillars. Wild-caught caterpillars were placed in 50 ml polypropylene centrifuge tubes containing 95% ethanol and a label was placed in each tube with the locality, date of collection and code number of the sampling plot of the study site.

3.2.1.2 Beating sheet

Beating sheet is a process of collecting insects that live or feed on higher leaves and branches of trees where a man can’t see or reach. This equipment can easily collect caterpillars by beating the branches of the tree with a stick, placed a beating sheet under the tree that being beaten (Figure 3-6 A). This tool was built from a white heavy cotton fabric (125×80 centimeters) stretches over, on an X-shaped frame (Figure 3-6 B). The caterpillars were fallen on the beating sheet, then placed them in 50 ml polypropylene centrifuge tubes containing 95% ethanol same as the hand collecting method. The label was placed in each tube with the locality, date of collection and code number of area on the study site.

Figure 3 – 5 A, caterpillars were collected using forceps and paintbrush, then preserved them in polypropylene centrifuge tubes filled with 95% ethanol.; B, wild–caught caterpillars were placed in polypropylene centrifuge tubes containing 95% ethanol in the study area

Figure 3 – 6 A, beating sheet was built from a cotton fabric and stretched over an X-shaped frame; B, beating sheet used to collect caterpillars, beating the branches with a stick, caterpillars would then fail on the beating sheet placed under the tree

3.2.2 Parasitoids

Parasitoids were discovered by dissecting the wild-caught caterpillars under the stereozoom microscope (Figure 3-7). Before disecting, wild-caught caterpillars were soaked in distilled water for eliminating ethanol in order to soften the caterpillars. Fine tip forceps were used for disecting. Before and after conducting, the forceps were flamed with an alchol burner to eliminate contaminating DNA from other organisims. If caterpillars had been parasitised by parasitoids (Figure 3-8), the tissue samples of both parasitoids (eggs or larvae) and parasitised caterpillars were placed in 96-well PCR plate containing absolute ethanol, then sending the PCR plates to CCDB (Canadian Centre for DNA Barcoding), Biodiversity Institute of Ontario, University of Guelph, Canada, for DNA barcoding.

3.3 Physical factors

Information about temperature, humidity, wind speed and rainfall were compared with the records by the Thai Meteorological Department (Lop Buri Provincial Meteorological Station). In additional, digital hygro-thermometer (HTC-2) was used to record the air temperature (°C) and air humidity (%) during the collecting times (6.00 – 9.00 AM and 4.00 – 6.00 PM.) at the study area.

Figure 3 – 7 Wild-caught caterpillar was dissected under the stereozoom microscope to see whether or not it had been parasitised by parasitoid

Figure 3 – 8 Parasitoid larva discovered inside the dissected caterpillar

3.3 Taxonomic processing

3.4.1 Photograph, given voucher numbers and study morphological characters of the specimens

Lepidopteran larvae were photographed using Olympus Stylus (TG─2 Tough) at the Integrative Ecology Laboratory, Department of Biology, Faculty of Science, Chulalongkorn University for roughly identification using pictorial identification key from "Lepidopterous Adults and Larvae" (Lewvanich, 2001) and "Plant Diseases and Insect Pests of Economic Importance" (Ek-Amnuay, 2010), to the family level of the Lepidoptera. Each specimen was given a voucher numbers then measured its length and width using digital vernier caliper (EagleOne) (Figure 3-9).

Figure 3 – 9 Measuring length and width of the wild-caught caterpillars using Vernier Caliper at the Integrative Ecology Laboratory

3.4.2 Molecular identification

Parasitised caterpillars and their parasitoids were identified using DNA barcoding method performed by CCDB. Standard barcoding protocols had been used to barcode all the specimens. First, DNA was extracted from the sample tissues by Chelex extraction method using enzyme proteinase K digestion. DNA was stored at 4 °C. The target 658-bp fragment of *COI* was varied using the standard insect primers LepF1/LepR1 (LepF1:5′–ATTCAACCAATCATAAAGATATTGG–3′;LepR1:5′–TAAACTTCTG GATGTCCAAAAAATCA–3′) (Hebert et al., 2004a). PCRs were carried out using a thermocycling profile of a cycle of 1 min at 94 °C, 5 cycles of 40 s at 94 °C, 40 s at 45 °C and 1 min at 72 °C, followed by 35 cycles of 40 s at 94 °C, 40 s at 51 °C and 1 min at 72 °C, with a final step of 5 min at 72 °C. PCR products were visualized on a 2% agarose E–gel® 96–well system (Invitrogen) and were bidirectionally sequenced using BigDye v3.1 and analysed on an ABI 3730xl DNA Analyzer (Applied Biosystems). Contigs were assembled using Sequencher v 4.0.5 (Gene Codes) and were subsequently aligned by eye in Bioedit (Hall, 1999) to ensure that there were no gaps or stop codons in the alignment. All DNA sequences will be deposited in both GenBank and BOLD databases by BLAST (Basic Local Alignment Search Tool) (Figure 3-10). The molecular identification was determination for identified at least to the family level. The sequences were query and reference using BLAST, BOLD, ABGD and NJ trees. Species identification base on the databases could be identified when the percentage of similarity score was higher than 97%. COI sequences of at least 559 base pairs (bp) were used to determine provisional species. The phylogenetic trees were built by neighbor joining (NJ) method in MEGA 7 (Figure 3-11).

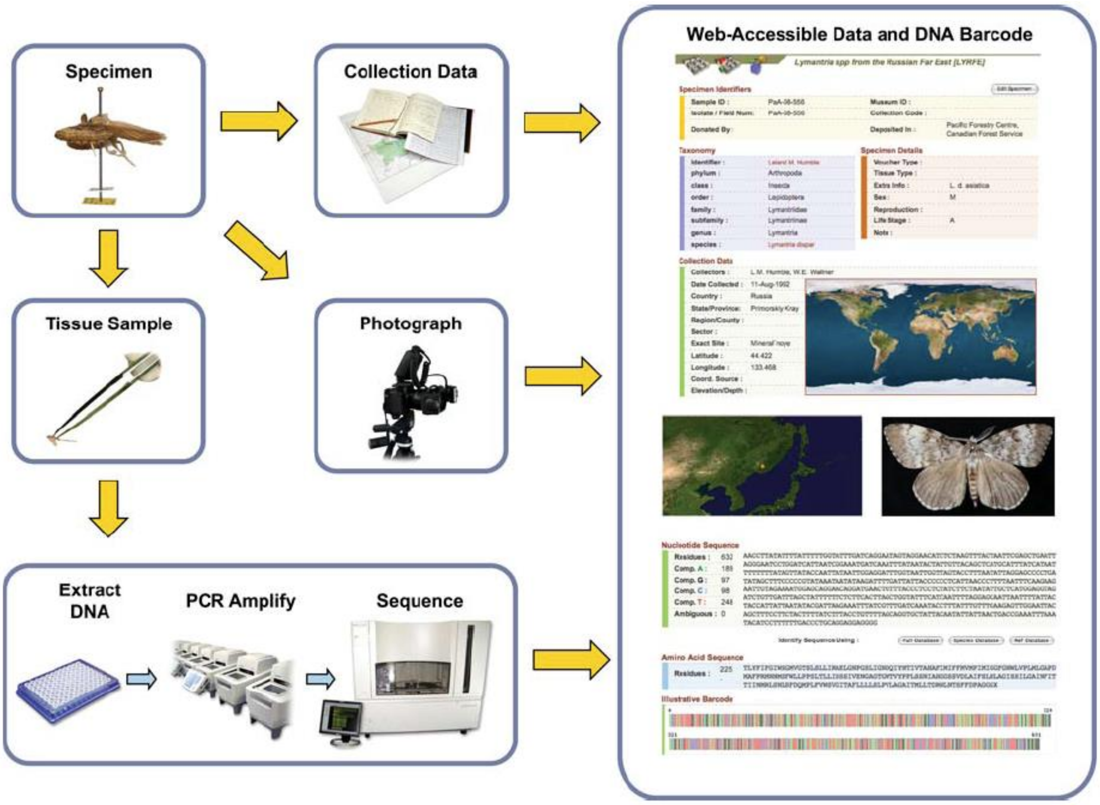
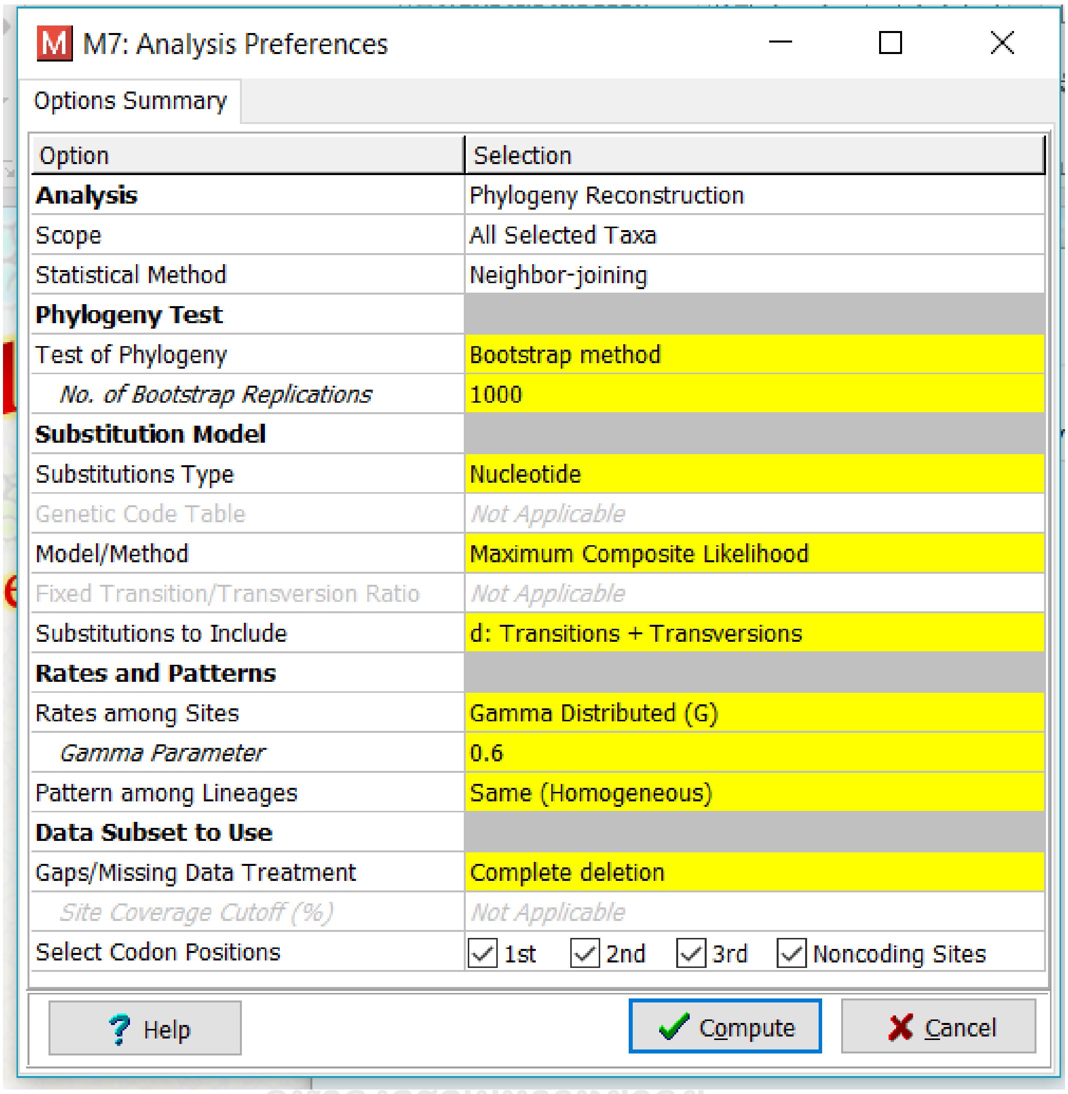


Figure 3 – 10 Standard barcoding protocols by Canadian Centre for DNA Barcoding, Centre for Biodiversity Genomics, University of Guelph, Canada (http://jeremydewaard.com/wp-content/uploads/2010/01/Floyd_et_al_fig_1.png)



Option	Selection
Analysis	Phylogeny Reconstruction
Scope	All Selected Taxa
Statistical Method	Neighbor-joining
Phylogeny Test	
Test of Phylogeny	Bootstrap method
No. of Bootstrap Replications	1000
Substitution Model	
Substitutions Type	Nucleotide
Genetic Code Table	*Not Applicable*
Model/Method	Maximum Composite Likelihood
Fixed Transition/Transversion Ratio	*Not Applicable*
Substitutions to Include	d: Transitions + Transversions
Rates and Patterns	
Rates among Sites	Gamma Distributed (G)
Gamma Parameter	0.6
Pattern among Lineages	Same (Homogeneous)
Data Subset to Use	
Gaps/Missing Data Treatment	Complete deletion
Site Coverage Cutoff (%)	*Not Applicable*
Select Codon Positions	☑ 1st ☑ 2nd ☑ 3rd ☑ Noncoding Sites

Figure 3 – 11 Options summary of neighbor joining method set to build phylogenetic trees in MEGA 7

3.4 Host–parasitoid interactions

Trophic relationships between lepidopteran hosts and their parasitoids were constructed from 34 collecting trips from 13 months (November 2015 – November 2016). Data of host-parasitoid interactions from the study area were evaluated statistically for their relationships, diversity and abundance. The data from host-parasitoid relationships also indicated to host specificity. For this study, spacilist refered to the parasitoid species that could parasitise only single host species while genaralist could parasitise more than one species. Diagram of the trophic links between lepidopteran host and their parasitoids were built using R command written by Donald L.J. Quicke in R version 3.4.0 (R Development Core Team, 2017).

3.5 Parasitism rate

Parasitism rate was calculated from the equation by Gómez-Marco et al. (2015). Parasitism rate equals to number of parasitised caterpillars divided by the total number of wild-caught caterpillars. Ggregarious parasitoids (more than one parasitoid larva per one host) were counted as one parasitism event on parasitised caterpillars (Figure 3-12).

$$\text{Parasitism rate} = \frac{\text{number of parasitised caterpillars}}{\text{total number of caterpillars}}$$

Figure 3 – 12 Gregarious parasitoids were observed within the dissected parasitised caterpillar under the stereozoom microscope

CHAPTER 4

RESULTS

4.1 Abundance of lepidopteran pests and morphological identification

Total of 28 collecting trips started from November 2015 to November 2016, 5,673 caterpillars were collected from the study side at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province (Figure 4-1). The highest number of caterpillars (837 individuals) were collected at 25 - 26 May 2016, while the lowest number of caterpillars (48 individuals) were collected at 18 - 19 March 2016 (Appendix A: Table A-1).

Caterpillars were classified into 23 families using the pictorial identification key by Lewvanich (2001) and Ek-Amnuay (2010): Bombycidae (n = 47); Crambidae (n = 1,430); Drepanidae (n = 1); Danaidae (n = 42); Erebidae (n = 447); Gelechiidae (n = 155); Geometridae (n = 696); Gracilariidae (n = 1); Hesperiidae (n = 81); Immidae (n = 76); Lasiocampidae (n = 5); Limacodidae (n = 125); Lycaenidae (n = 38); Noctuidae (n = 1,649); Nolidae (n = 1); Notodontidae (n = 8); Nymphalidae (n = 24); Papilionidae (n = 17); Pieridae (n = 779); Pterophoridae (n = 10); Pyralidae (n = 10); Sphingidae (n = 21) and Tortricidae (n = 10) (Figure 4-2; Appendix A: Table A-2). The abundance of caterpillars in each family varied depending on time of collection during the year. Noctuidae were the most abundance caterpillars found from this study while Nolidae, Gracilariidae and Drepanidae (Cyclidiidae) were the less collected caterpillars in this study.

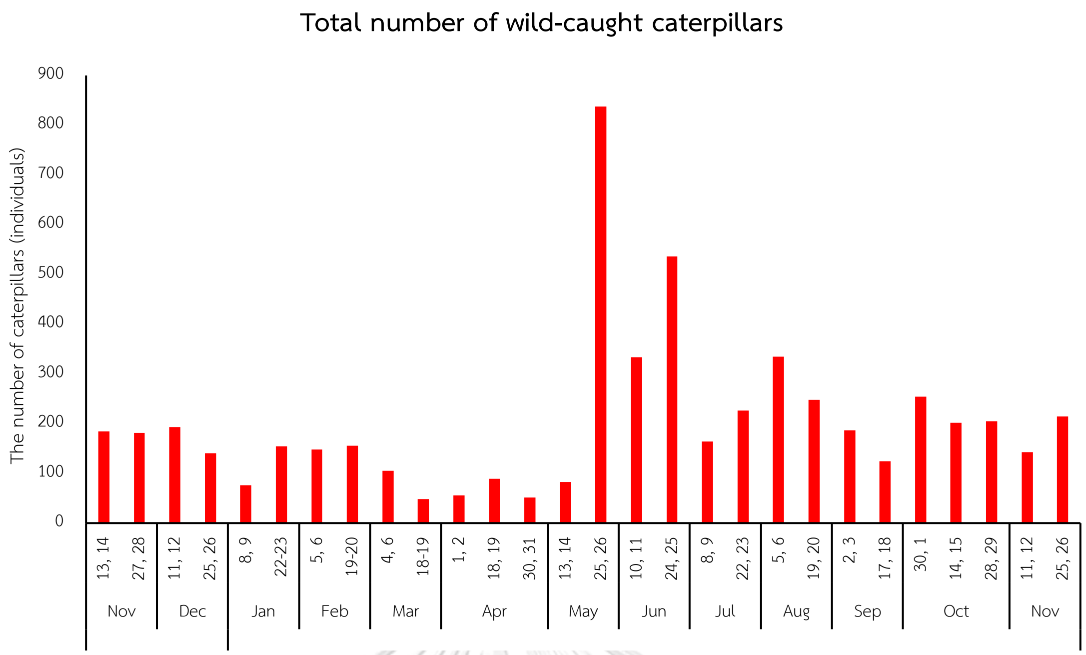


Figure 4 – 1 Number of wild-caught caterpillars collected each month started from November 2015 - November 2016 (28 collecting trips) at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

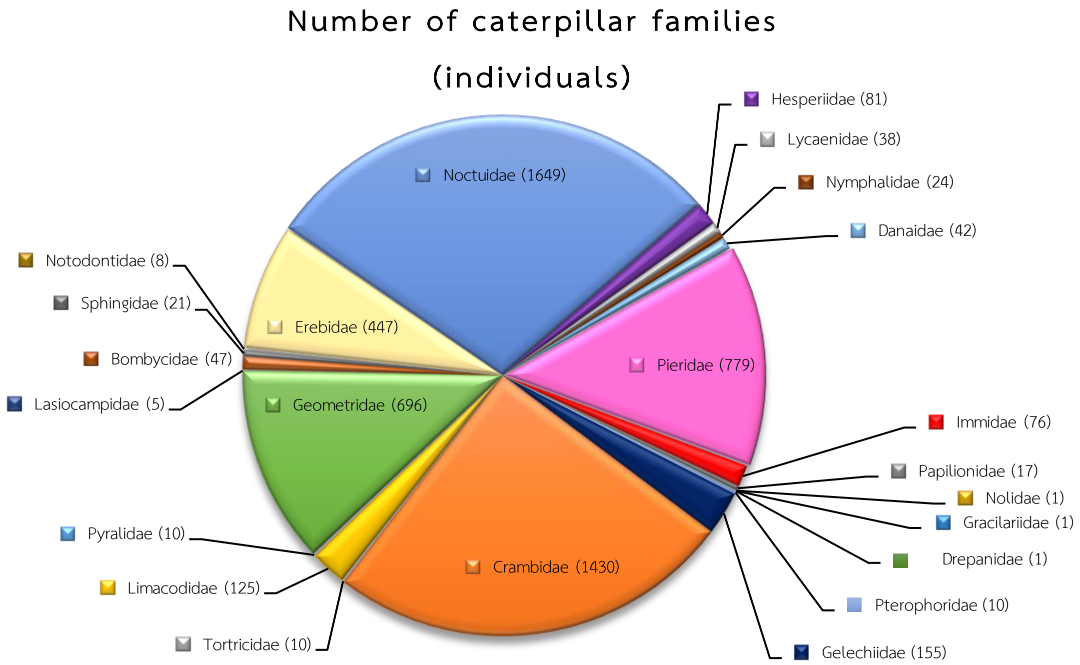


Figure 4 – 2 Diagram shows number of wild-caught caterpillars in each family (individuals) collected from November 2015 - November 2016 at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

4.2 Physical factors

Average field temperature, humidity, precipitation and wind speed were recorded from Thai Meteorological Department (TMD), Lopburi Provincial Agrometeorological Station. The range of TMD temperature during (November 2015 – November 2016) was 27.3 °C to 33.45 °C. The highest average of TMD temperature was 33.45 °C in April 2016 but the lowest average of TMD temperature was 27.3 °C in January 2016. October 2016 had the highest average of TMD humidity (82%) while February 2016 had the lowest average of TMD humidity (56%) (Figure 4-3; Appendix C).

From one year of observation, the wind speed was about 1.4 to 4.2 Knots, the highest range of wind speed (4.2 Knots) was in February 2016. The precipitation (total rainfall) from TMD records from 0 to 309 mm. and the highest TMD precipitation was 309 mm.

Season was determined from average field temperature and precipitation by using climograph. For this study, season was divided in to dry season (December 2015 to May 2016) and rainy season (June to October 2016).

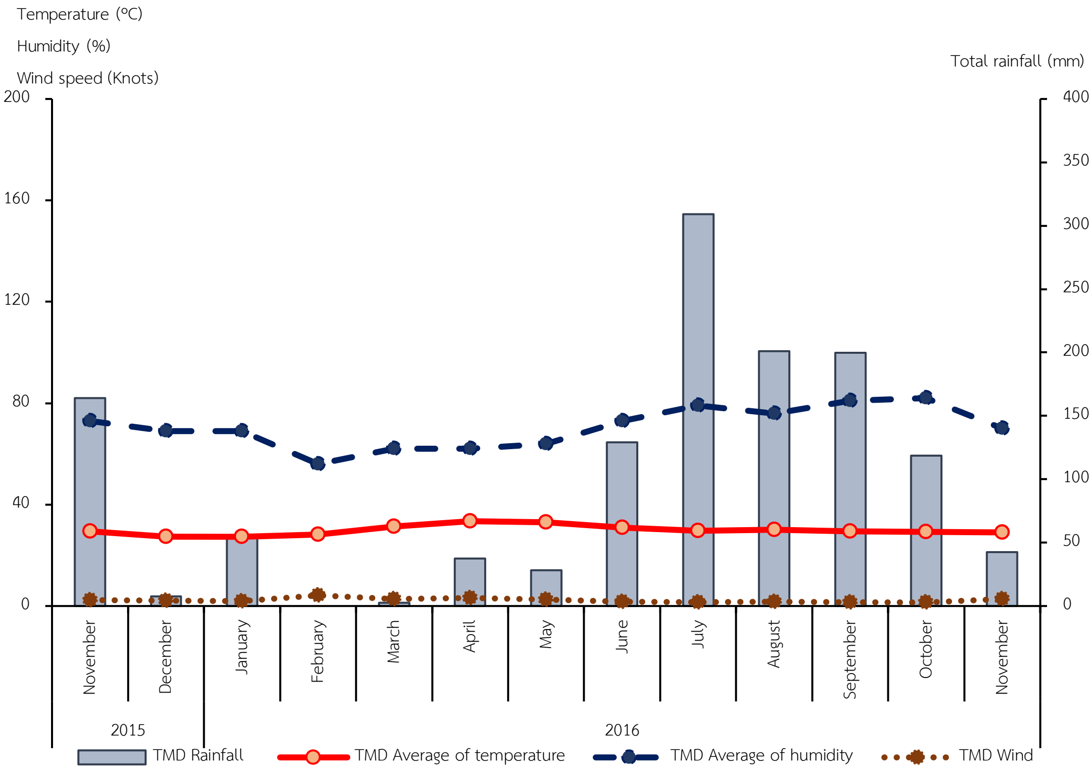


Figure 4 – 3 Climograph at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province based on air temperature, humidity, wind speed and precipitation recorded from November 2015 to November 2016

4.3 Parasitism rate

Off 5,673 caterpillars collected from this study 340 caterpillars were parasitised by parasitoids. Number of parasitised caterpillars each month is shown in Figure 4-4, late June 2016 had the highest number of parasitised caterpillars while late March and May 2016 had the lowest number of parasitised caterpillars. Early April 2016 had the highest rate of parasitism rate (~14%) while late May had the lowest parasitism rate (~0.2%) (Figure 4-4; Appendix A: Table A-1).

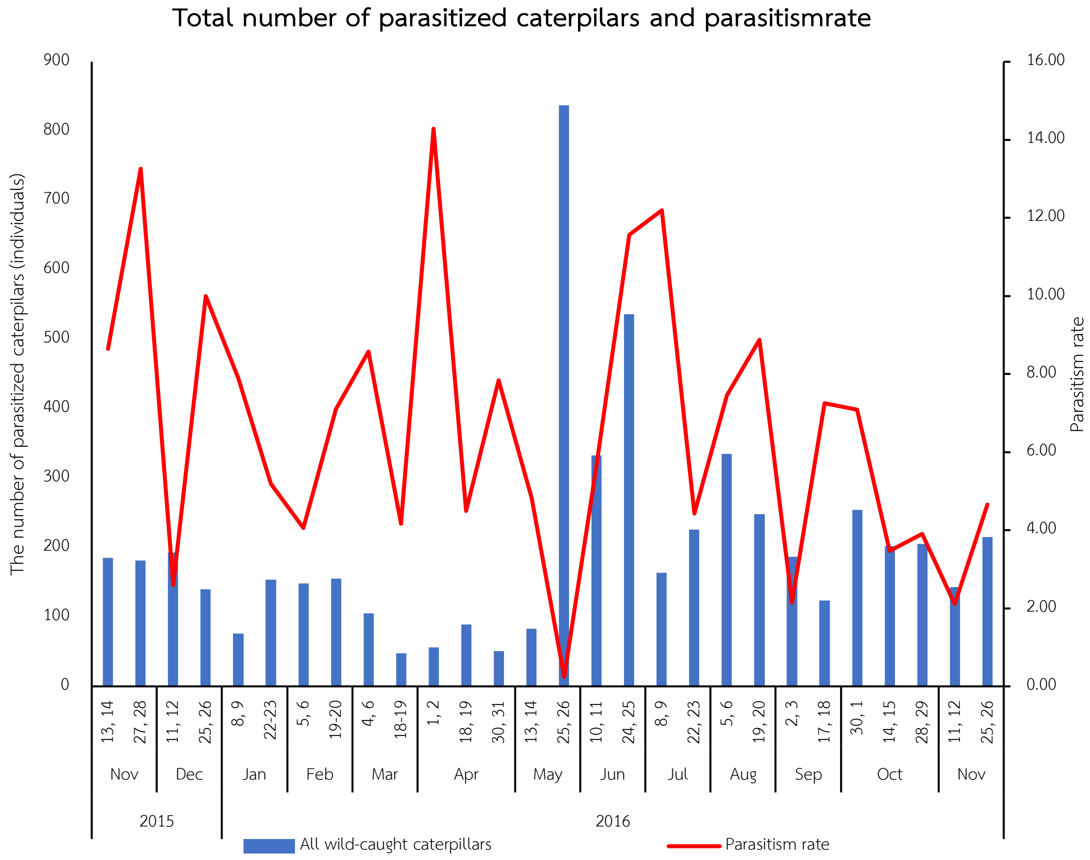

Total number of parasitized caterpilars and parasitismrate

Figure 4 – 4 Total number of parasitized caterpilars and parasitismrate recorded during the 28 collecting trips started from November 2015 - November 2016 at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

4.4 Barcoding analyses and molecular identification of the specimens

So far, a total of 883 specimens (both caterpillars (483) and parasitoids (400) were sent for DNA barcoding analyses, 749 (~85%) specimens were able to amplify for *COI*; of these 458 (~95%) are parasitised caterpillars and 291 (~73%) are parasitoids. Membership in a provisional species was determined using sequences contained at least 559 bp. DNA barcoding revealed 124 provisional species of parasitised caterpillars classified into 99 genera in 24 families (Table 4-1) and 113 provisional species of parasitoids classified into 40 genera in 7 families (Table 4-2) from GenBank and BOLD databases. The most abundant caterpillar hosts belonged to *Haritalodes derogate* (family Crambidae) (Figure 4-5 A). Tachinid flies *Peribaea* sp.1 (Figure 4-5 B) was the most abundant parasitoid. Using BLAST, BOLD system, tree and ABGD of all query and reference sequences, identification at least to the family level could be achieved (Appendix B).

Figure 4 – 5 A, Caterpillar of *Haritalodes derogate*; B, tachinid fly *Peribaea* sp.1 larva

Table 4 - 1 Tentative identification of parasitised caterpillars using DNA barcoding from GenBank and BOLD databases (numbers of individuals are shown in parentheses)

Family	**Species**	**Family**	**Species**
Crambidae		Erebidae	
Pyraustinae	*Haritalodes derogata* (36)	Lymantriinae	*Olene mendosa* (3)
	Hyalobathra brevialis (6)		*Orgyia postica* (4)
	Notarcha sp.1 (2)		*Orvasca subnotata* (14)
	Notarcha aurolinealis (4)		*Pantana* sp.1 (1)
	Notarcha obrinusalis (1)	Scoliopteryginae	*Dinumma* sp.1 (16)
	Orthospila sp.1 (3)	Euteliidae	Euteliidae sp.1 (1)
	Paliga damastesalis (1)		Euteliidae sp.2 (2)
	Parotis marinata (2)	Gelechiidae	
	Parotis sp.1 (3)		Gelechiidae sp.1 (1)
	Pyrausta panopealis (1)		Gelechiidae sp.2 (1)
	Desmia sp.1 (1)	Chelariinae	*Anarsia* sp.1 (1)
Spilomelinae	*Herpetogramma* sp.1 (3)	Gelechiinae	*Ardozyga* sp.1 (10)
	Herpetogramma platycapna (5)	Geometridae	
	Herpetogramma stultalis (4)	Ennominae	*Ascotis selenaria* (1)
	Orthospila orissusalis (2)		*Biston suppressaria* (2)
	Orthospila sp.1 (1)		*Casbia* sp.1 (1)
	Protonoceras leucocosma (1)		*Chiasmia nora* (5)
	Pycnarmon sp.1 (1)		*Chiasmia* sp.1 (24)
	Synclera sp.1 (2)		*Chiasmia* sp.2 (3)
	Spilomelinae sp.1 (1)		*Chiasmia* sp.3 (5)
Elachistidae			*Cleora repulsaria* (1)
Stenomatinae	*Antaeotricha* sp.1 (2)		*Hyperythra lutea* (1)
Erebidae			*Hyposidra talaca* (5)
Aganainae	*Asota caricae* (4)		*Macaria abydata* (2)
	Asota sp.1 (2)		*Petelia medardaria* (1)
Arctiinae	*Eilema* sp.1 (1)		*Petelia paroobathra* (1)
	Ormetica sp.1 (1)		*Synegia* sp.1 (1)
Boletobiinae	*Condate* sp.1 (1)	Geometrinae	*Chlorocoma* sp.1 (1)
Calpinae	*Plecoptera reflexa* (2)		*Hemithea* sp.1 (1)
Catocalinae	*Rhesala* sp.1 (10)		*Spaniocentra* sp.1 (2)
Erebinae	*Arctia virginalis* (1)	Larentiinae	*Chloroclystis ablechra* (1)
	Episparina tortuosalis (2)		*Eois* sp.1 (2)
	Rhesalides curvata (27)	Sterrhinae	*Scopula floslactata* (2)
	Avitta ophiusalis (2)	Gracilariidae	Gracillariidae sp.1 (1)
	Spirama helicina (22)	Hesperiidae	
Herminiinae	*Palthis* sp.1 (1)	Coeliadinae	*Hasora chromus* (1)
	Progonia sp.1 (1)	Hyblaeidae	*Hyblaea puera* (2)

Table 4 - 2 (cont.) Tentative identification of parasitised caterpillars using DNA barcoding from GenBank and BOLD databases (numbers of individuals are shown in parentheses)

Family	Species	Family	Species
Immidae	*Imma* sp.1 (26)	Noctuidae	
Limacodidae		Plusiinae	*Plusiopalpa adrasta* (1)
Limacodinae	*Darna sybilla* (1)		*Chrysodeixis eriosoma* (3)
	Thosea sp.1 (1)	Nolidae	
	Parasa media (1)	Chloephorinae	*Selepa* sp.1 (6)
Lycaenidae		Nymphalidae	
Polyommatinae	*Castalius rosimon* (3)	Danainae	*Danaus chrysippus* (4)
Theclinae	*Arhopala pseudocentaurus* (1)	Oecophoridae	
Noctuidae		Oecophorinae	*Compsotropha* sp.1 (1)
Acontiinae	*Acontia* sp.1 (3)	Stathmopodinae	*Vanicela* sp.1 (1)
	Hyperstrotia sp.1 (13)	Papilionidae	
	Hyperstrotia sp.2 (1)	Papilioninae	*Papilio clytia* (1)
Amphipyrinae	*Callyna* sp.1 (1)		*Papilio polytes* (1)
	Chasmina sp.1 (2)	Pieridae	
	Chasmina tenuilinea (5)	Coliadinae	*Eurema hecabe* (5)
	Condica sp.1 (1)	Pterophoridae	
Bagisarinae	*Amyna axis* (2)	Pterophorinae	*Sphenarches anisodactylus* (1)
	Xanthodes sp.1 (1)	Pyralidae	
Catocalinae	*Achaea* sp.1 (2)	Phycitinae	*Assara* sp.1 (1)
	Arsacia rectalis (6)		*Phycita* sp.1 (3)
	Bastilla amygdalis (1)		*Ptyobathra atrisquamella* (1)
	Hulodes caranea (1)		*Sciota virgatella* (1)
	Hypospila bolinoides (1)		*Thylacoptila* sp.1 (6)
	Marcipa sp.1 (1)		*Tylochares* sp.1 (1)
	Mocis trifasciata (1)		Phycitinae sp.1 (24)
	Plecoptera quaesita (2)		Pyralidae sp.1 (3)
	Plecoptera reflexa (1)	Saturniidae	
	Spirama helicina (1)	Saturniinae	*Attacus atlas* (1)
	Tamba sp.1 (2)	Sphingidae	
	Zale exhausta (6)	Macroglossinae	*Macroglossum belis* (1)
Condicinae	*Condica illecta* (3)	Thyrididae	
Erebinae	*Pericyma mendax* (12)	Siculodinae	Picrostomastis subrosealis (1)
Euteliinae	*Penicillaria jocosatrix* (1)	Striglininae	*Striglina* sp.1 (1)
Noctuinae	*Sasunaga longiplaga* (1)	Tortricidae	
	Spodoptera litura (5)	Tortricinae	*Archips machlopis* (2)

Table 4 - 3 Tentative identification of parasitoids specimens using DNA barcoding from GenBank and BOLD databases (numbers of individuals are shown in parentheses)

Family	Species
Hymenoptera	
Bethylidae	
Bethylinae	Bethylinae sp.1 (1)
Braconidae	
	Braconidae sp.1 (2)
	Braconidae sp.2 (6)
Agathidinae	*Zosteragathis contrasta* (8)
Cheloninae	*Chelonus* sp.1 (1)
	Chelonus sp.2 (1)
	Chelonus sp.3 (1)
	Chelonus sp.4 (1)
	Chelonus sp.5 (5)
	Phanerotoma sp.1 (5)
	Phanerotoma sp.2 (1)
	Phanerotoma sp.3 (12)
	Cheloninae sp.1 (3)
Meteorinae	*Meteorus* sp.1 (1)
Microgastrinae	Microgastrinae sp.1 (1)
	Microgastrinae sp.2 (2)
	Microgastrinae sp.3 (1)
	Microgastrinae sp.4 (2)
	Apanteles sp.1 (1)
	Apanteles sp.2 (1)
	Apanteles sp.3 (1)
	Apanteles sp.4 (8)
	Apanteles sp.5 (2)
	Apanteles sp.6 (11)
	Apanteles sp.7 (1)
	Apanteles sp.8 (1)
	Cotesia ruficrus (5)
	Cotesia sp.1 (13)
	Cotesia sp.2 (6)
	Cotesia sp.3 (1)
	Diolcogaster sp.1 (4)
	Diolcogaster sp.2 (2)
	Diolcogaster sp.3 (1)
	Diolcogaster sp.4 (3)
	Dolichogenidea cerialis (5)
	Dolichogenidea sp.1 (2)
	Dolichogenidea sp.2 (1)
Braconidae	
	Dolichogenidea sp.3 (1)
	Dolichogenidea sp.4 (1)
	Dolichogenidea sp.5 (3)
	Dolichogenidea sp.6 (5)
	Dolichogenidea sp.7 (1)
	Dolichogenidea sp.8 (1)
	Dolichogenidea sp.9 (2)
	Dolichogenidea sp.10 (4)
	Dolichogenidea sp.11 (4)
	Dolichogenidea sp.12 (2)
	Dolichogenidea sp.13 (1)
	Dolichogenidea sp.14 (1)
	Dolichogenidea sp.15 (1)
	Dolichogenidea sp.16 (3)
	Dolichogenidea sp.17 (3)
	Dolichogenidea sp.18 (1)
	Dolichogenidea sp.19 (1)
	Glyptapanteles sp.1 (2)
	Glyptapanteles sp.2 (1)
	Glyptapanteles sp.3 (3)
	Glyptapanteles sp.4 (2)
	Glyptapanteles sp.5 (5)
	Glyptapanteles sp.6 (1)
	Glyptapanteles sp.7 (1)
	Glyptapanteles sp.8 (4)
	Glyptapanteles sp.9 (2)
	Glyptapanteles sp.10 (1)
	Iconella sp.1 (1)
	Microplitis sp.1 (1)
	Parapanteles athamasae (1)
	Snellenius sp.1 (1)
	Wilkinsonellus sp.1 (3)
Orgilinae	*Orgilus* sp.1 (1)
Rogadinae	*Aleiodes contemptus* (1)
	Aleiodes sp.1 (1)
Chalcididae	
Chalcidinae	Brachymeria sp.1 (1)
Eulophidae	
	Eulophidae sp.1 (1)

Table 4 - 4 (cont.) Tentative identification of parasitoids specimens using DNA barcoding from GenBank and BOLD databases (numbers of individuals are shown in parentheses)

Family	Species	Family	Species
Hymenoptera		**Diptera**	
Eulophidae	Eulophidae sp.2 (1)	Muscidea	*Potamia* sp.1 (3)
	Eulophidae sp.3 (1)	Tachinidae	
	Eulophidae sp.4 (11)		Tachinidae sp.1 (1)
	Eulophidae sp.5 (2)		Tachinidae sp.2 (1)
Eulophinae	*Elachertus* sp.1 (1)		Tachinidae sp.3 (1)
	Elachertus sp.2 (3)		Tachinidae sp.4 (4)
	Elachertus sp.3 (11)		Tachinidae sp.5 (1)
	Euplectrus sp.1 (2)	Exoristinae	*Belvosia* sp.1 (1)
	Euplectrus sp.2 (2)		*Belvosia* sp.2 (1)
	Euplectrus sp.3 (2)		*Blepharella* sp.1 (1)
	Hemiptarsenus sp.1 (1)		*Chaetoglossa* sp.1 (1)
	Hyssopus sp.1 (1)		*Chrysoexorista* sp.1 (1)
Ichneumonidae			*Cyzenis* sp.1 (1)
Campopleginae	*Casinaria* sp.1 (1)		*Drino inconspicua* (4)
	Diadegma sp.1 (1)		*Eumea* sp.1 (1)
	Venturia sp.1 (4)		*Exorista xanthaspis* (1)
Ichneumoninae	*Holcojoppa* sp1 (1)		*Houghia* sp.1 (1)
Ophioninae	*Enicospilus* sp.1 (2)		*Lespesia* sp.1 (1)
			Pseudoperichaeta nigrolineata (4)
			Senometopia sp.1 (1)
			Sturmia sp.1 (1)
		Tachininae	*Peribaea* sp.1 (20)
			Siphona sp.1 (1)

4.5 Relationships between host and parasitoids

Three hundred and fourty parasitised caterpillars revealed the interaction between caterpillars and their parasitoids in Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province. Some species of caterpillars could be parasitised by more than 6 species of parasitoids. *Chiasmia* sp.1 (Figure 4-6) was parasitised with the highest number (7) of parasitoid species. *Phanerotoma* sp.1 (Figure 4-7) was a parasitoid of 6 species of lepidopteran host. Host–parasitoid interaction between *Orvasca subnotata* and *Cotesia* sp.1 was the most frequently recorded (Figure 4-8). From the molecular food web, 88 specialist and 22 generalist parasitoid species were discovered from dissecting wild–caught caterpillars (Table 4-3) (Figure 4-9). Generalist and specialist species could be determined from number of trophic line in molecular food web.

Twelve species of Crambidae were parasitised by parasitic wasps 13 species in the subfamilies Cheloninae, Microgastrinae and Campopleginae and a parasitic flies species in the subfamily Exoristinae. *Haritalodes derogate* was the most abundant lepidopteran hosts while *Apanteles* sp.4 was the most abundant parasitoids of Crambidae. Off these, 12 and 2 species were classified as specialists and generalists, respectively (Figure 4-10; Appendix D: Figure D-1).

Figure 4 – 6 Caterpillar of *Chiasmia* sp.1

Figure 4 – 7 Braconid wasp *Phanerotoma* sp.1 larva

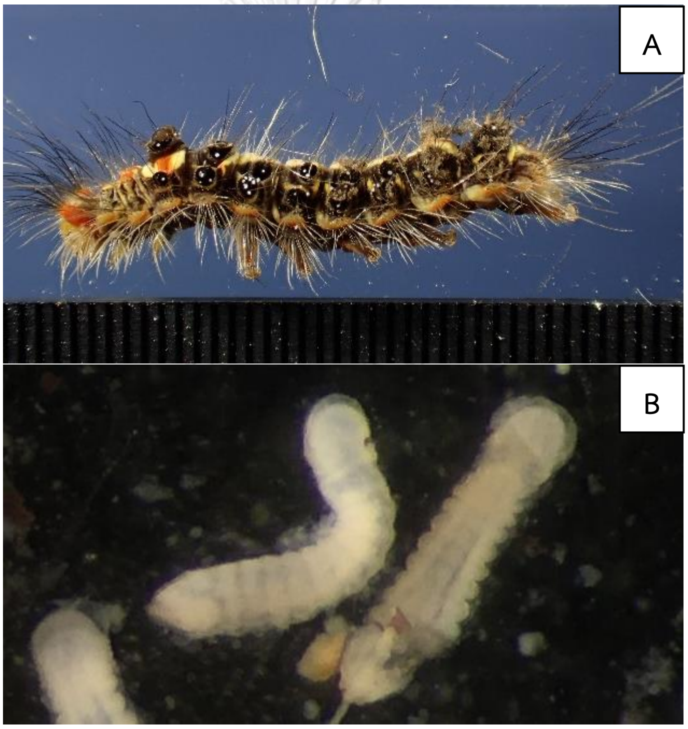


Figure 4 – 8 The most frequently recorded host–parasitoid interaction between; A, *Orvasca subnotata* and B, *Cotesia* sp.1

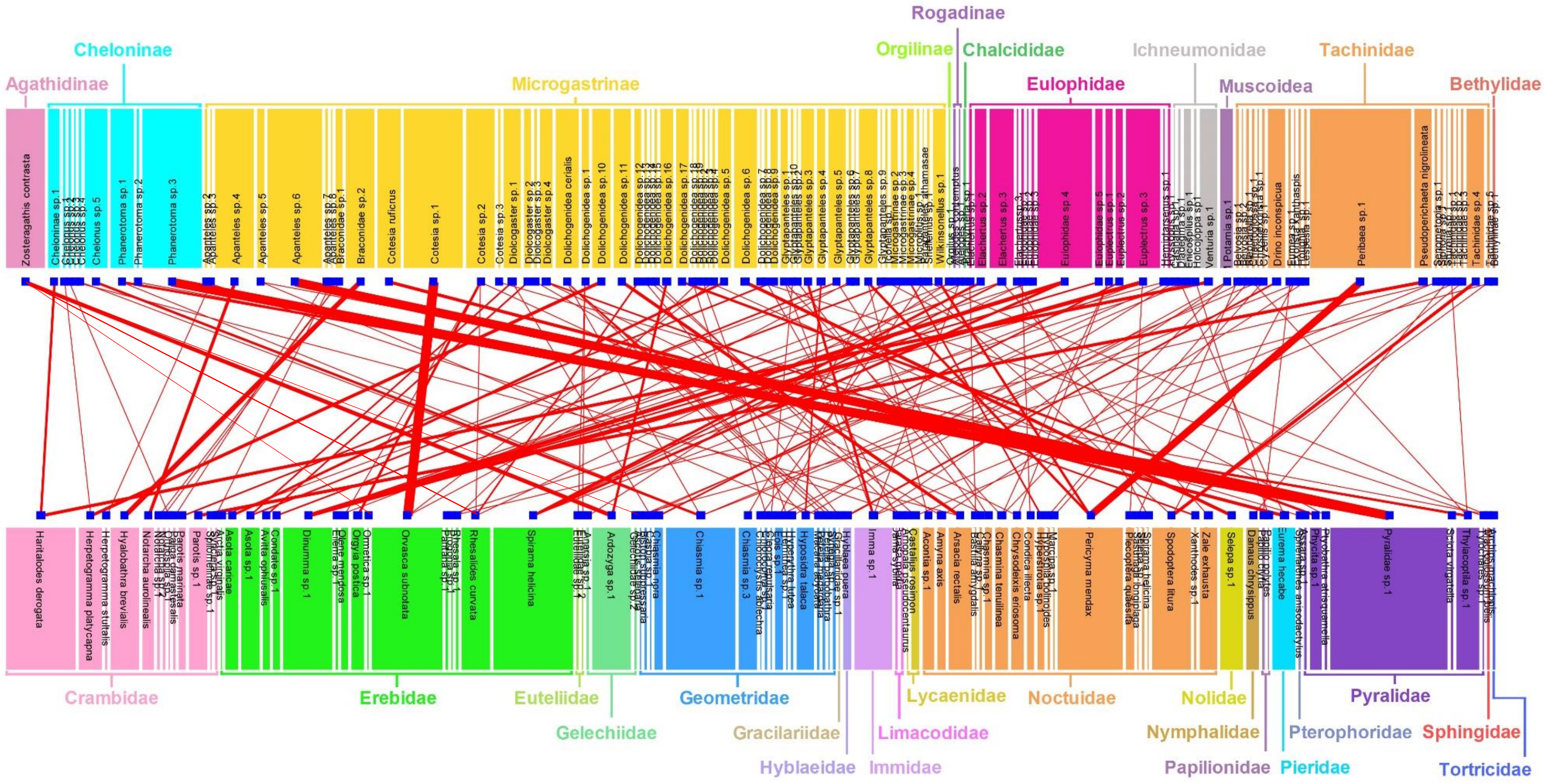


Figure 4 – 9 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host (bottom) and their parasitoids (above) detected by dissect from caterpillars. Different colours represent different insect groups (family or subfamily)

Table 4 - 5 Specialist and generalist parasitoid species were recorded from molecular food web of host–parasitoid relationship in Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

Specialist species			
Aleiodes contemptus	*Chrysoexorista* sp.1	*Dolichogenidea* sp.7	*Hyssopus* sp.1
Aleiodes sp.1	*Cotesia* sp.1	*Dolichogenidea* sp.8	*Iconella* sp.1
Apanteles sp.2	*Cotesia* sp.3	*Dolichogenidea* sp.9	*Lespesia* sp.1
Apanteles sp.3	*Cyzenis* sp.1	*Elachertus* sp.1	Microgastrinae sp.2
Apanteles sp.5	*Diadegma* sp.1	*Elachertus* sp.2	Microgastrinae sp.3
Apanteles sp.6	*Diolcogaster* sp.2	Eulophidae sp.1	Microgastrinae sp.4
Apanteles sp.7	*Diolcogaster* sp.3	Eulophidae sp.2	*Microplitis* sp.1
Apanteles sp.8	*Dolichogenidea* sp.10	Eulophidae sp.3	*Orgilus* sp.1
Belvosia sp.1	*Dolichogenidea* sp.11	Eulophidae sp.5	*Parapanteles athamasae*
Belvosia sp.2	*Dolichogenidea* sp.12	*Eumea* sp.1	*Phanerotoma* sp.2
Bethylinae sp.1	*Dolichogenidea* sp.13	*Euplectrus* sp.2	*Pseudoperichaeta nigrolineata*
Blepharella sp.1	*Dolichogenidea* sp.14	*Exorista xanthaspis*	*Senometopia* sp.1
Brachymeria sp.1	*Dolichogenidea* sp.15	*Glyptapanteles* sp.10	*Siphona* sp.1
Braconidae sp.1	*Dolichogenidea* sp.16	*Glyptapanteles* sp.2	*Snellenius* sp.1
Braconidae sp.2	*Dolichogenidea* sp.17	*Glyptapanteles* sp.3	*Sturmia* sp.1
Casinaria sp.1	*Dolichogenidea* sp.18	*Glyptapanteles* sp.4	Tachinidae sp.1
Chaetoglossa sp.1	*Dolichogenidea* sp.19	*Glyptapanteles* sp.6	Tachinidae sp.2
Cheloninae sp.1	*Dolichogenidea* sp.2	*Glyptapanteles* sp.7	Tachinidae sp.3
Chelonus sp.1	*Dolichogenidea* sp.3	*Glyptapanteles* sp.9	Tachinidae sp.4
Chelonus sp.2	*Dolichogenidea* sp.4	*Hemiptarsenus* sp.1	Tachinidae sp.5
Chelonus sp.3	*Dolichogenidea* sp.5	*Holcojoppa* sp1	*Venturia* sp.1
Chelonus sp.4	*Dolichogenidea* sp.6	*Houghia* sp.1	*Wilkinsonellus* sp.1
Generalist species			
Apanteles sp.4	*Dolichogenidea cerialis*	*Euplectrus* sp.1	*Phanerotoma* sp.1
Chelonus sp.5	*Dolichogenidea* sp.1	*Euplectrus* sp.3	*Phanerotoma* sp.3
Cotesia ruficrus	*Drino inconspicua*	*Glyptapanteles* sp.1	*Potamia* sp.1
Cotesia sp.2	*Elachertus* sp.3	*Glyptapanteles* sp.5	*Zosteragathis contrasta*
Diolcogaster sp.1	*Enicospilus* sp.1	*Glyptapanteles* sp.8	
Diolcogaster sp.4	Eulophidae sp.4	*Peribaea* sp.1	

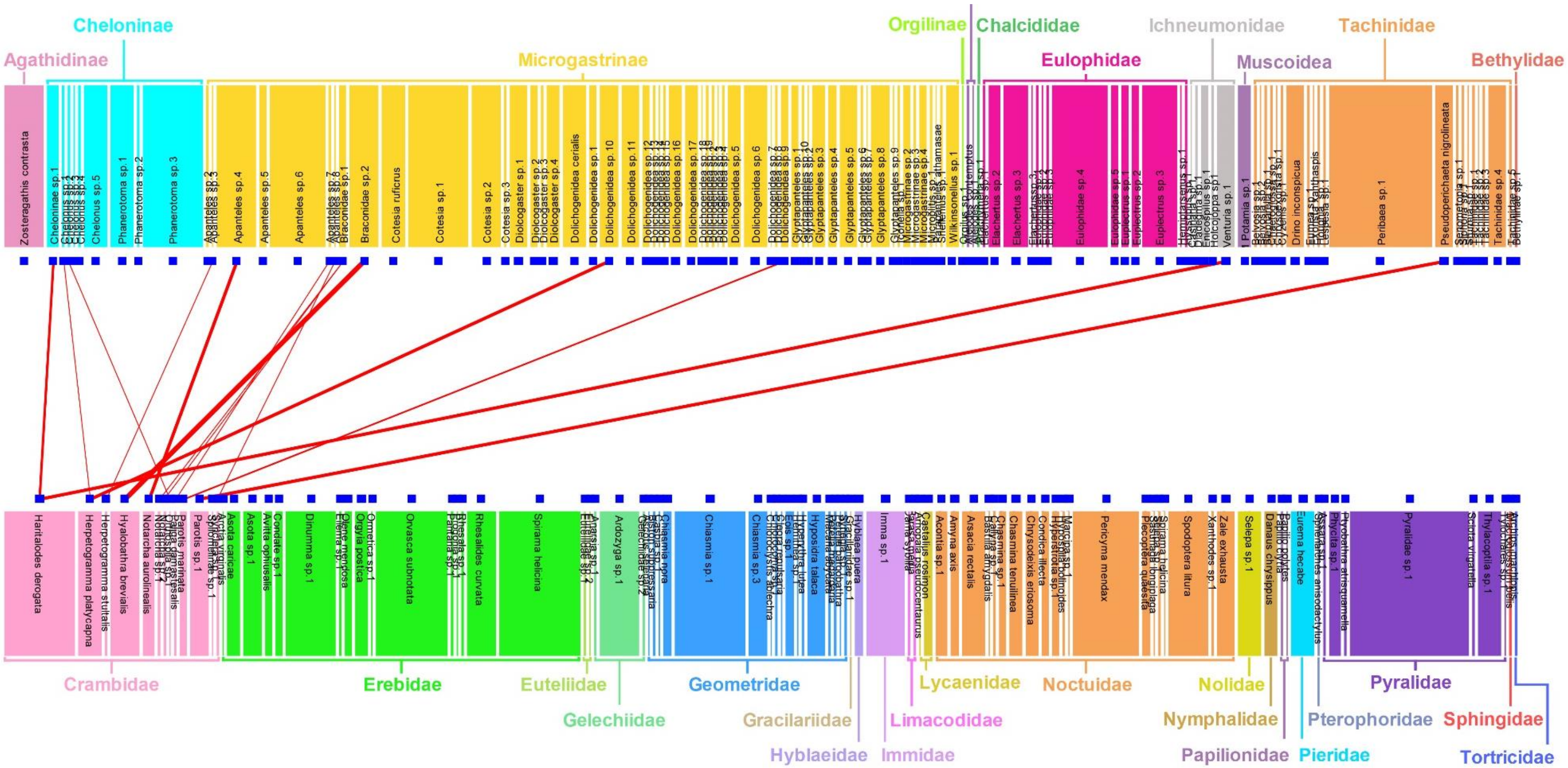


Figure 4 – 10 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Crambidae (bottom) and their parasitoids (above)

Sixteen species of Erebidae were parasitised by 23 species of parasitic wasps in the subfamilies Agathidinae, Microgastrinae, Rogadinae, Chalcidinae, Eulophinae and Ophioninae and 2 species of parasitic flies in the subfamily Tachininae. *Spirama helicina* was the most abundant of lepidopteran host species while *Cotesia* sp.1 was the most abundant of parasitoids in the family Crambidae. Specialists and generalists were identified to 20 and 5 species, respectively (Figure 4-11; Appendix D: Figure D-3).

Sixteen species of caterpillars in the family Geometridae were parasitised by 16 species of parasitic wasps in the subfamilies Cheloninae, Microgastrinae, Rogadinae, Eulophinae, Campopleginae and Ophioninae and 5 species of parasitic flies in the subfamilies Tachininae and Azeliinae. *Chiasmia* sp.1 and *Peribaea* sp.1 were the most abundant of lepidopteran host and parasitoid, respectively. Off these, 17 and 4 species were classified as specialists and generalists, respectively (Figure 4-12; Appendix D: Figure D-6).

For Noctuidae, 19 species of lepidopteran hosts were parasitised by 13 species of parasitic wasps in the subfamilies Cheloninae, Microgastrinae and Eulophinae, and 16 species of parasitic flies in the subfamilies Tachininae, Exoristinae and Azeliinae. The most abundant caterpillars and parasitoids species were *Pericyma mendax* and *Peribaea* sp.1. Specialists and generalists were identified to 19 and 10. species, respectively (Figure 4-13; Appendix D: Figure D-13).

Seven species of the Pyralidae were parasitised by 7 species of parasitic wasps in the subfamilies Cheloninae and Microgastrinae and 2 species of the parasitic flies in the subfamily Exoristinae. *Pyralidae* sp.1 was the most abundant lepidopteran hosts while *Apanteles* sp.6 and *Phanerotoma* sp.3 were the most abundant parasitoids. Off these, 7 and 2 species were classified as specialists and generalists, respectively (Figure 4-14; Appendix D: Figure D-20).

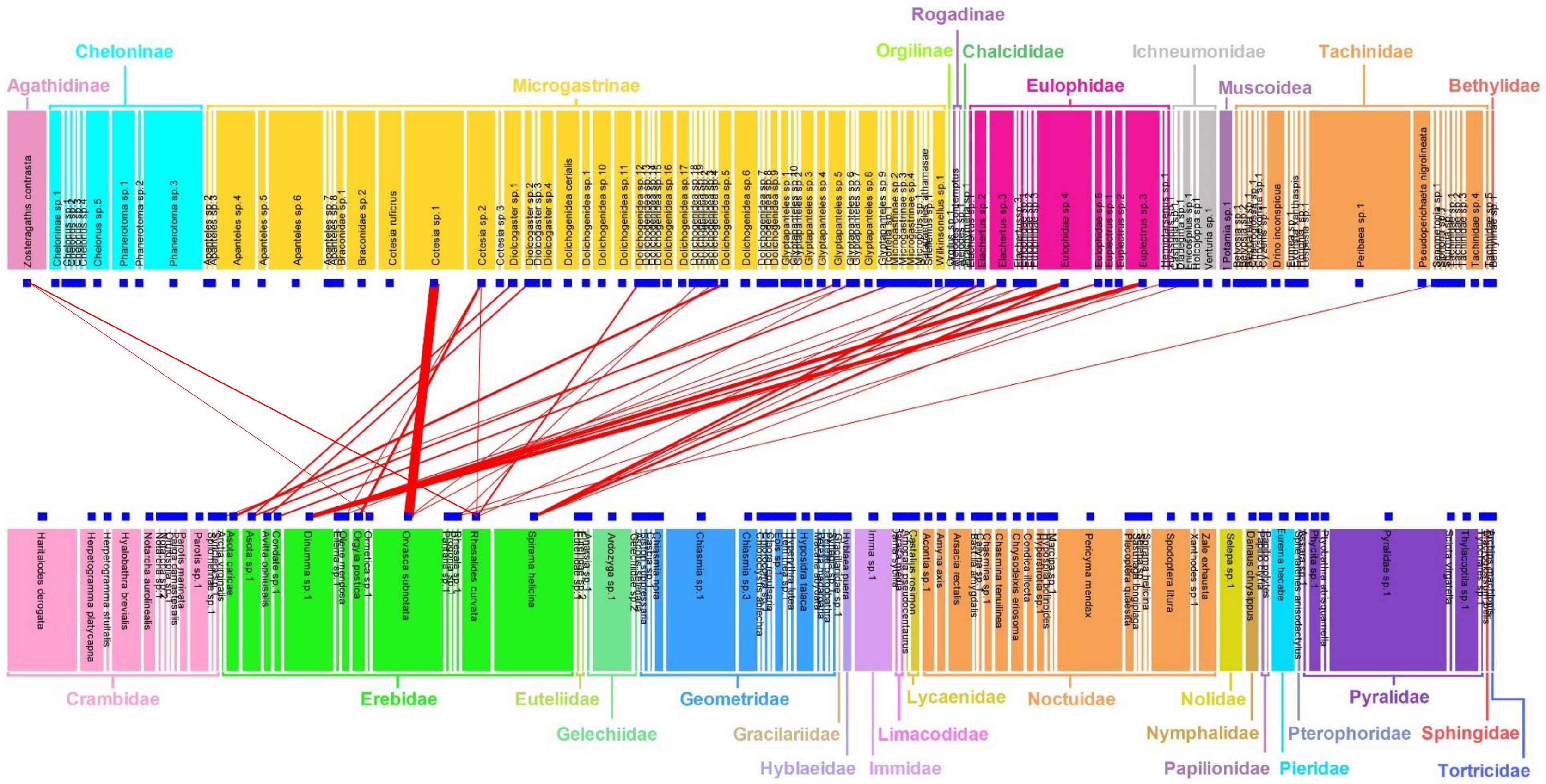


Figure 4 – 11 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Erebidae (bottom) and their parasitoids (above)

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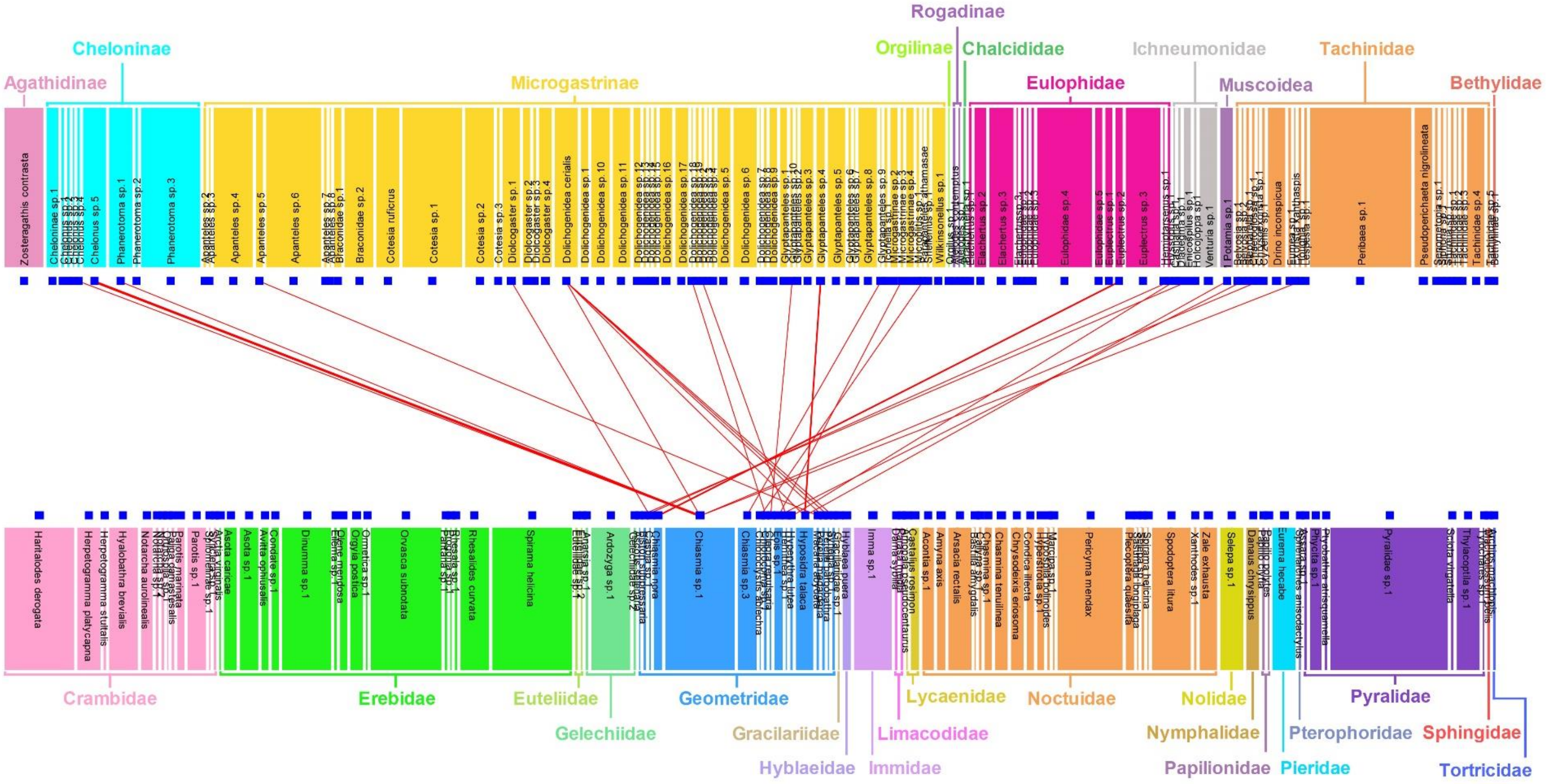

Figure 4 – 12 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Geometridae (bottom) and their parasitoids (above)

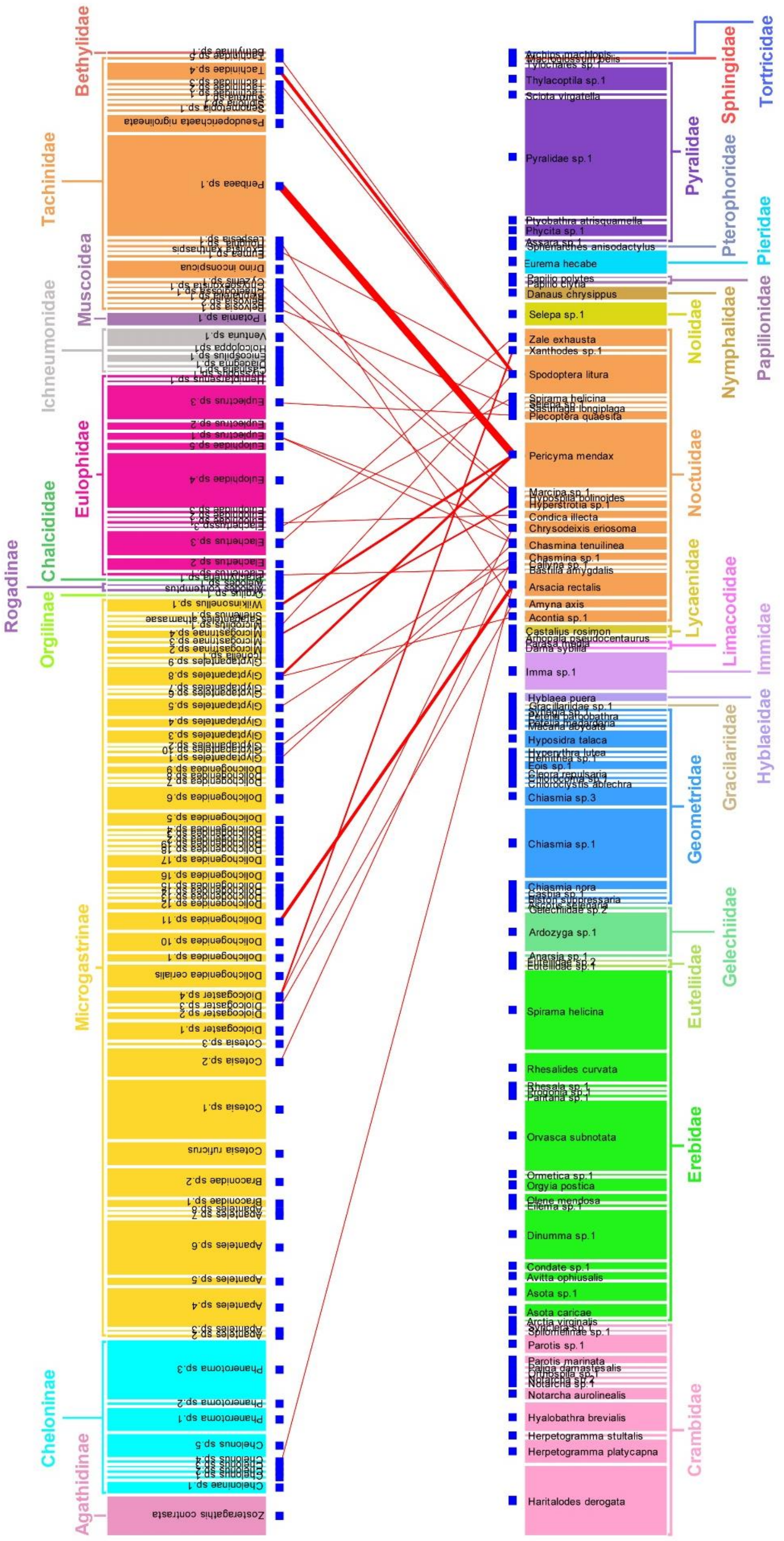

Figure 4 – 13 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Noctuidae (bottom) and their parasitoids (above)

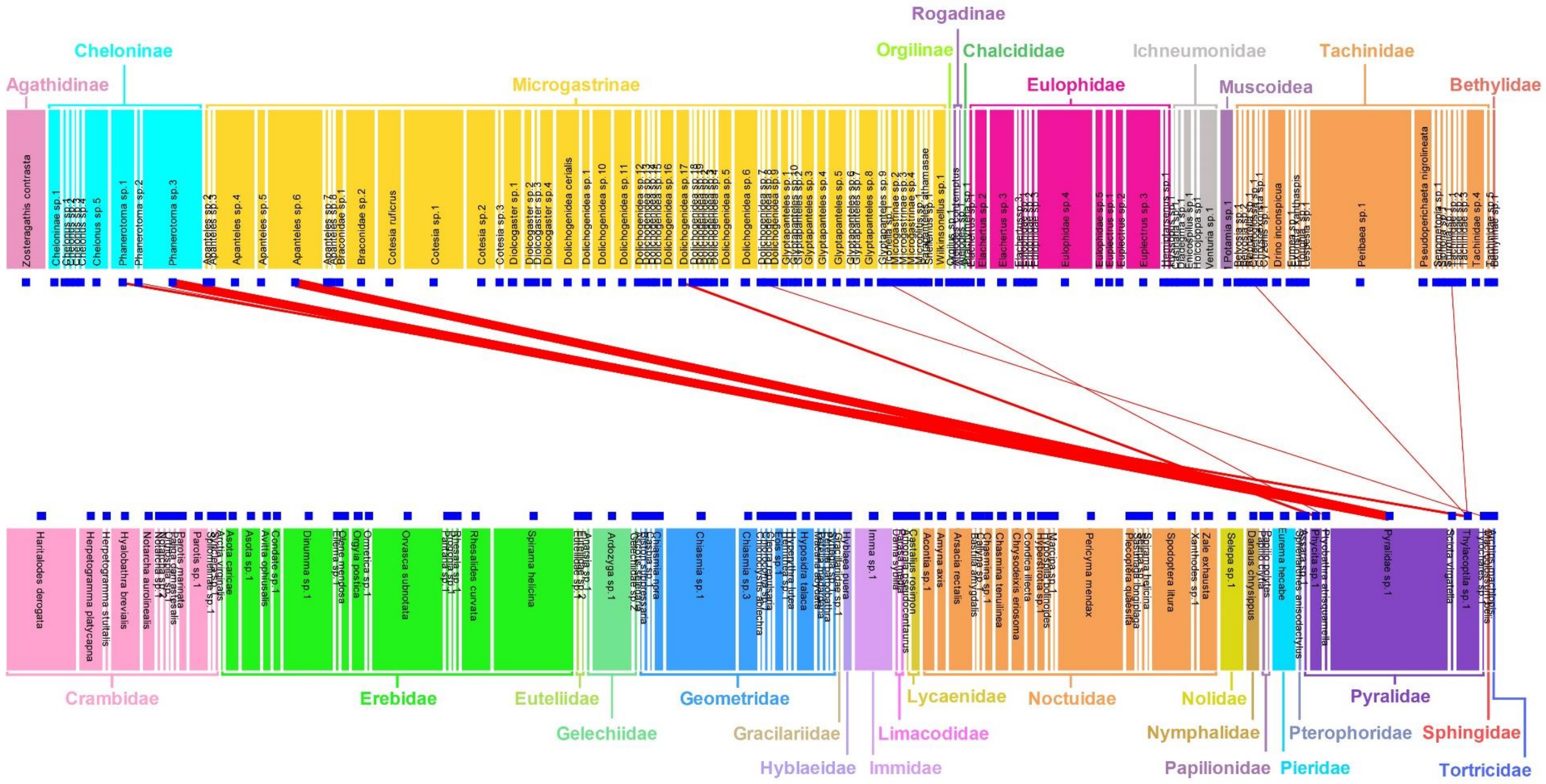

Figure 4 – 14 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Pyralidae (bottom) and their parasitoids (above)

For other families of caterpillars, Gelechiidae was parasitised by only 3 specialist species of parasitic wasps in the subfamilies Microgastrinae, Orgilinae and Bethylinae and a generalist species in the subfamily Agathidinae (Figure 4-15; Appendix D: Figure D-5). Immidae was parasitised by 3 specialist species of parasitic wasps and 3 generalist species in the subfamilies Microgastrinae, Rogadinae, Eulophinae, Azeliinae and Exoristinae (Figure 4-16; Appendix D: Figure D-10). Family Lycaenidae was parasitised by 3 specialist species of parasitic wasps in the subfamilies Microgastrinae and Exoristinae (Figure 4-17; Appendix D: Figure D-12). Family Pieridae was parasitised by a specialist species and a generalist species of parasitic wasps in the subfamilies Campopleginae and Microgastrinae, respectively (Figure 4-18; Appendix D: Figure D-18). Family Papilionidae was parasitised by a specialist species of parasitic wasps (Ichneumoninae) and a species of parasitic fly in the Exoristinae (Figure 4-19; Appendix D: Figure D-17). Finally, parasitic wasps in the subfamily Microgastrinae can parasitised 6 families of caterpillars as follows Euteliidae (Figure 4-20; Appendix D: Figure D-4), Limacodidae (Figure 4-21; Appendix D: Figure D-11), Nolidae (Figure 4-22; Appendix D: Figure D-14), Pterophoridae (Figure 4-23; Appendix D: Figure D-19), Sphingidae (Figure 4-24; Appendix D: Figure D-22). and Tortricidae (Figure 4-25; Appendix D: Figure D-24). while families Hyblaeidae (Figure 4-26; Appendix D: Figure D-9). and Nymphalidae (Figure 4-27 ; Appendix D: Figure D-15) were only parasitised by parasitic flies in the subfamily Exoristinae only.

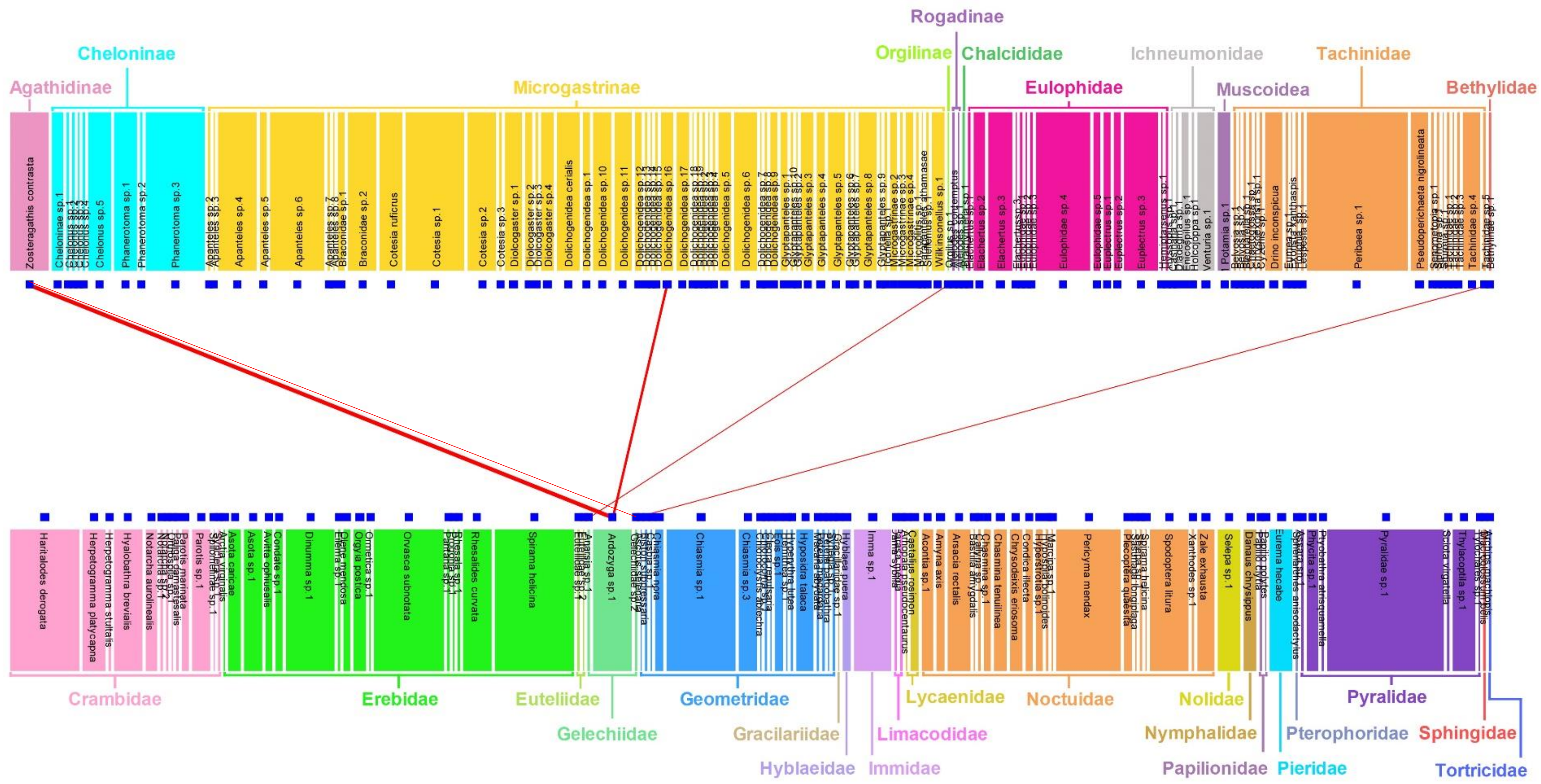

Figure 4 – 15 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Gelechiidae (bottom) and their parasitoids (above)

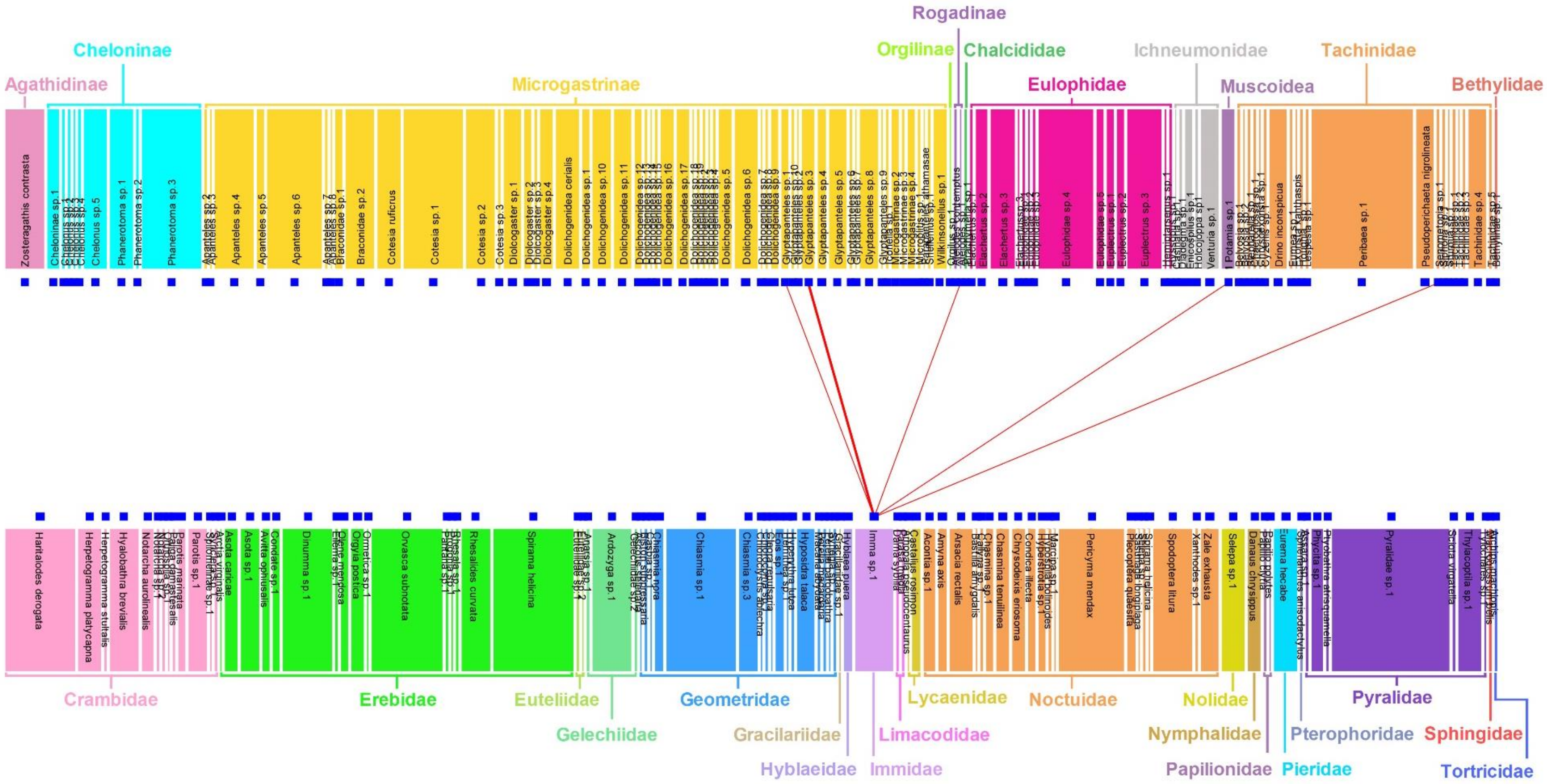

Figure 4 – 16 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Immidae (bottom) and their parasitoids (above)

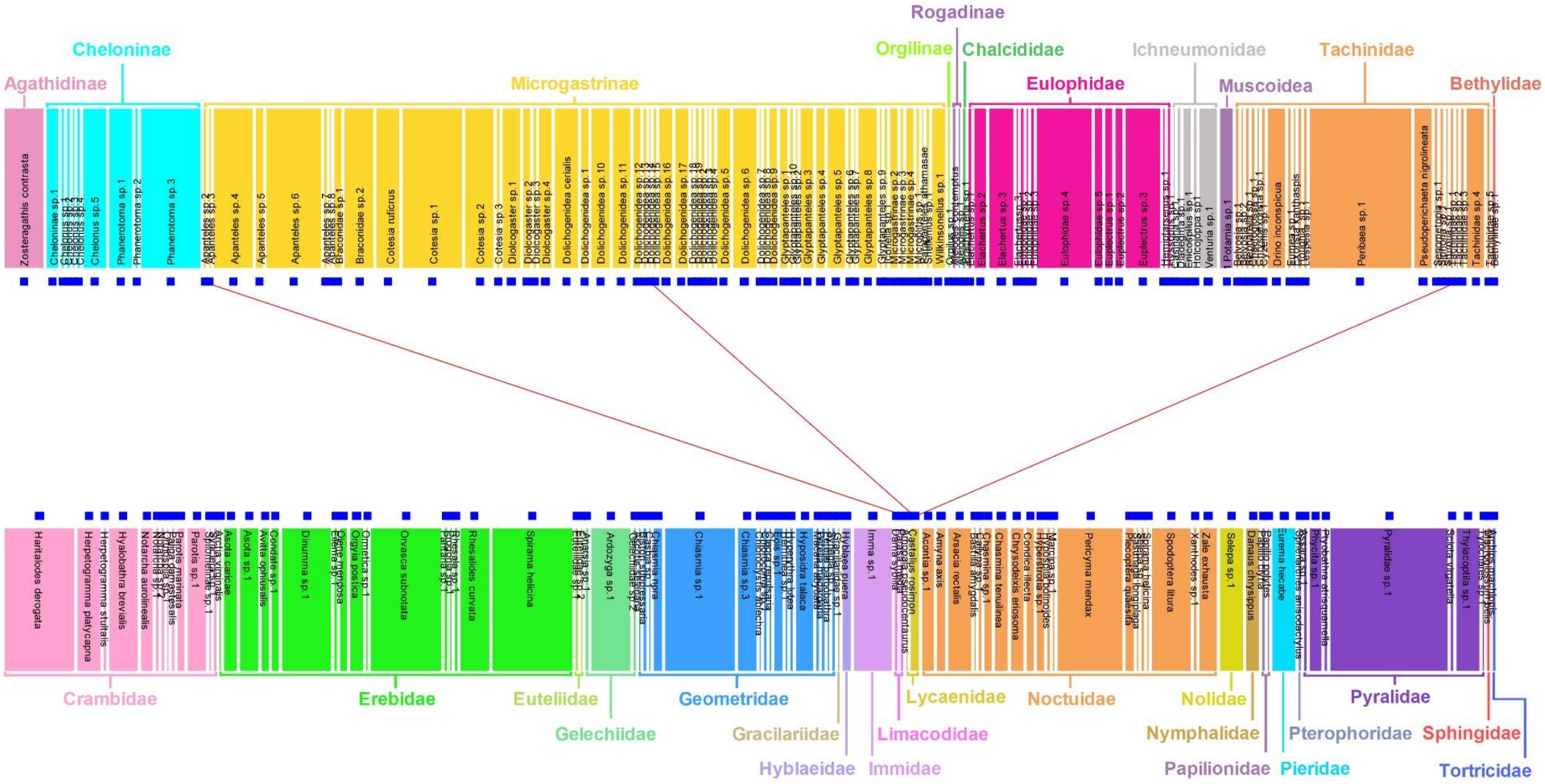

Figure 4 – 17 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Lycaenidae (bottom) and their parasitoids (above)

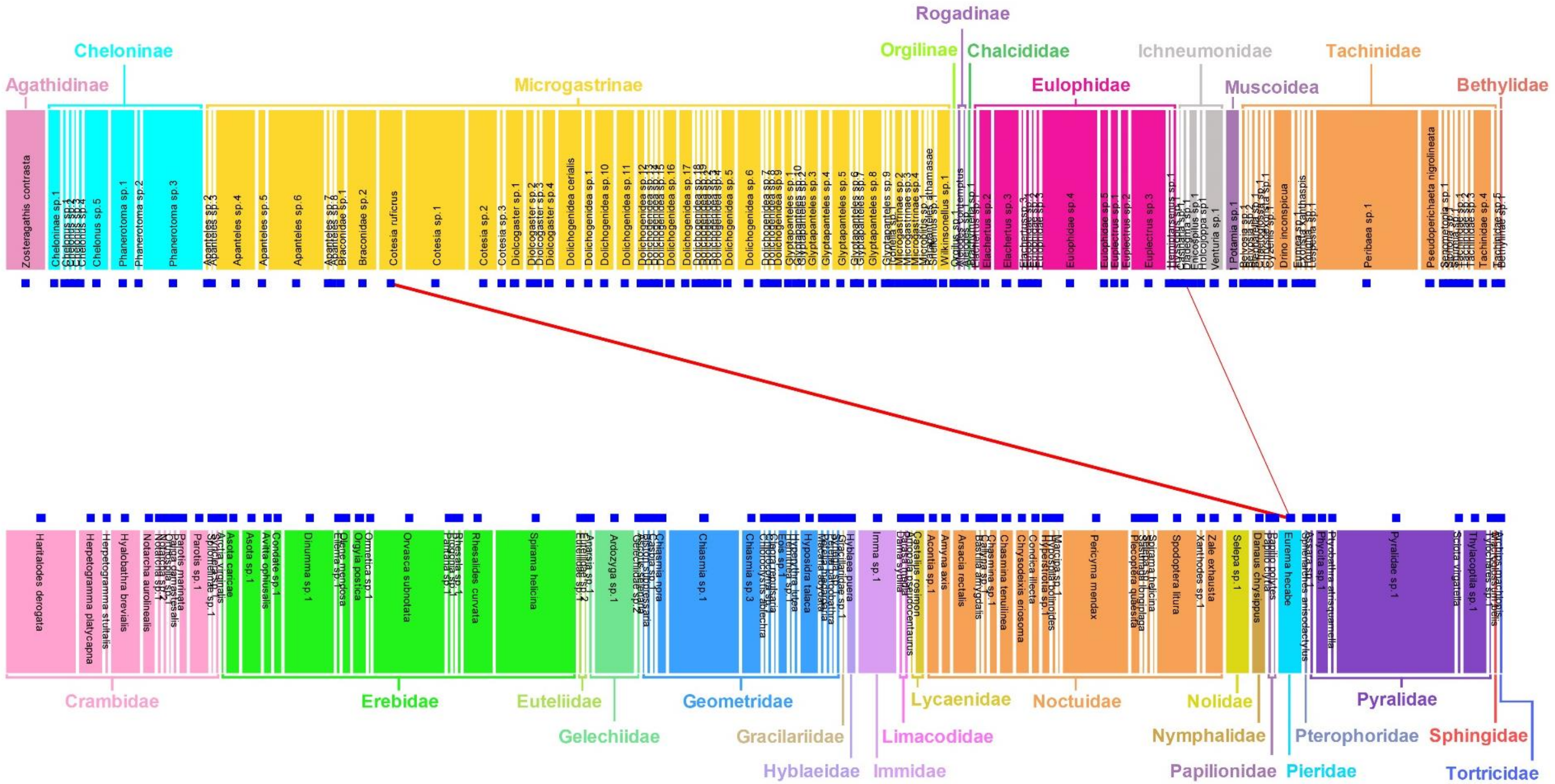

Figure 4 – 18 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Pieridae (bottom) and their parasitoids (above)

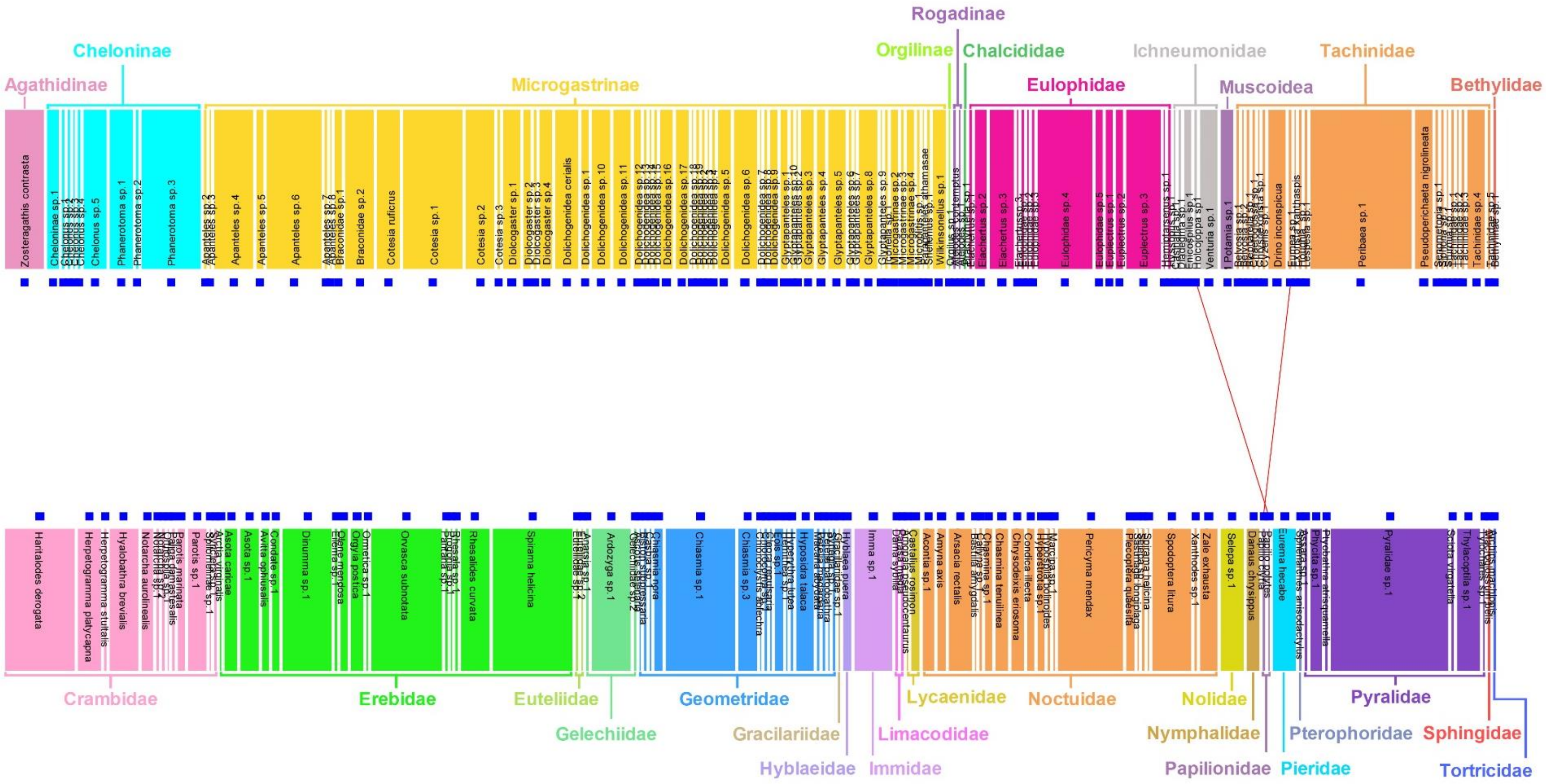

Figure 4 – 19 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Papilionidae (bottom) and their parasitoids (above)

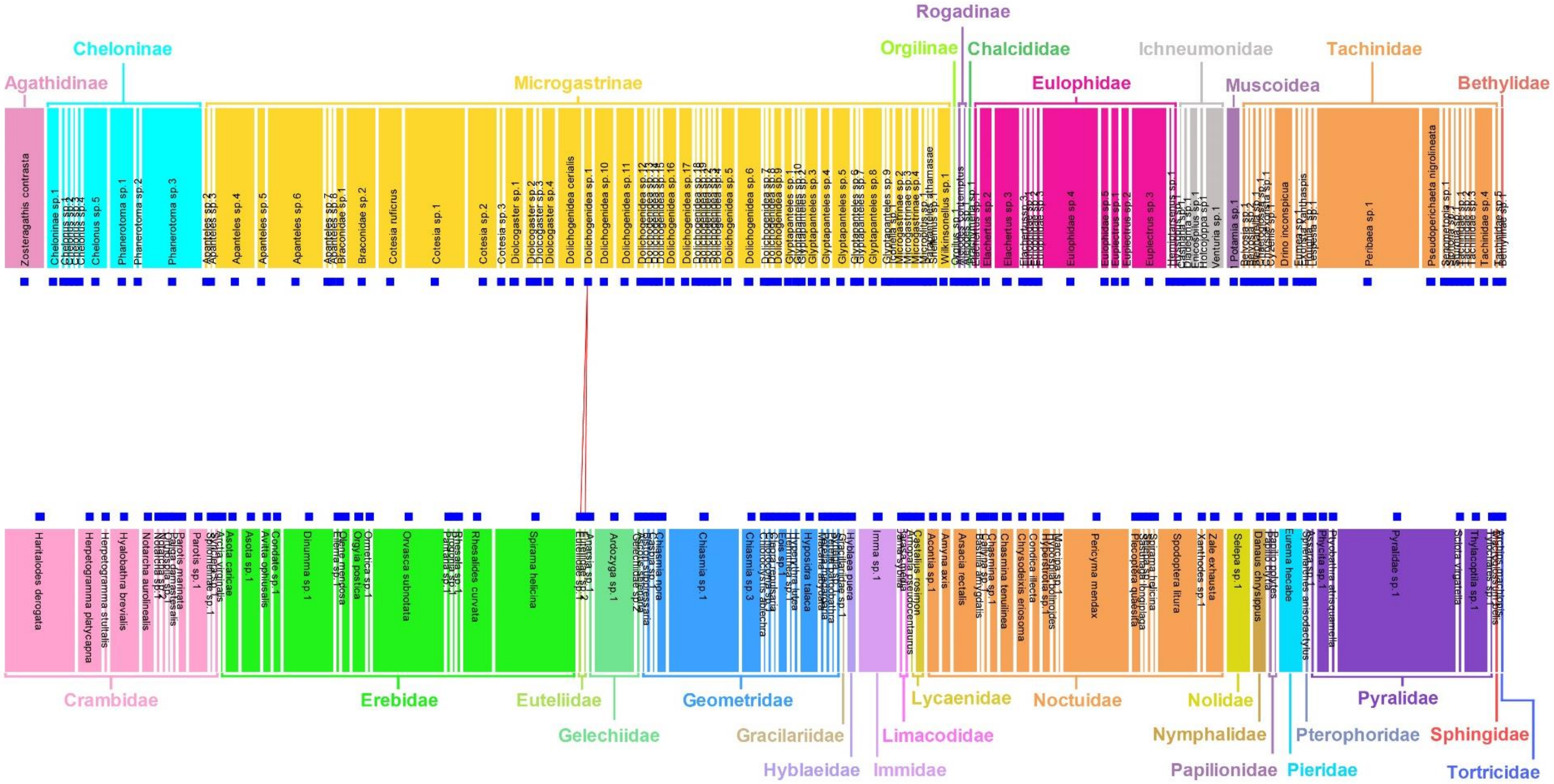

Figure 4 – 20 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Euteliidae (bottom) and their parasitoids (above)

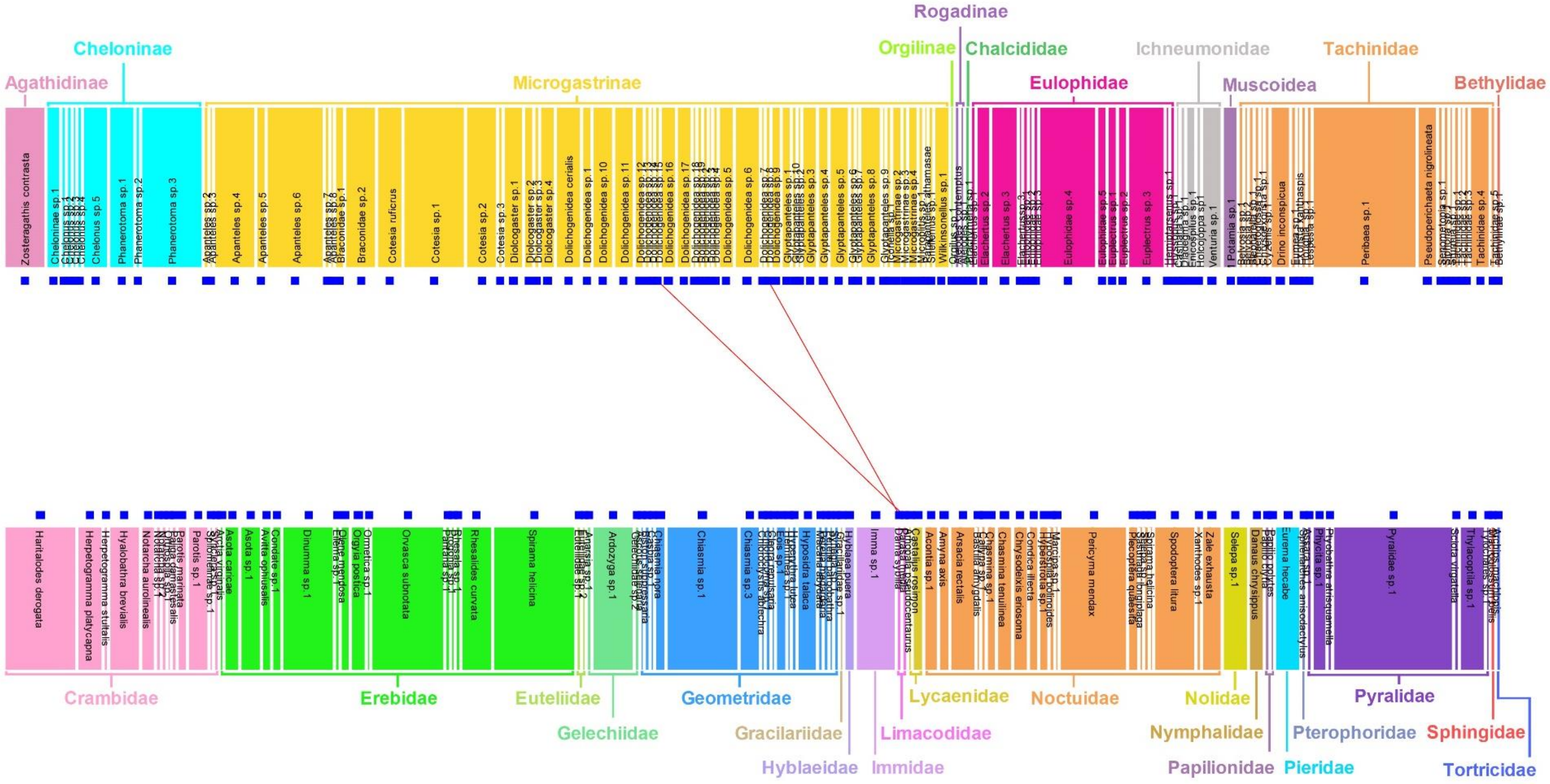

Figure 4 – 21 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Limacodidae (bottom) and their parasitoids (above)

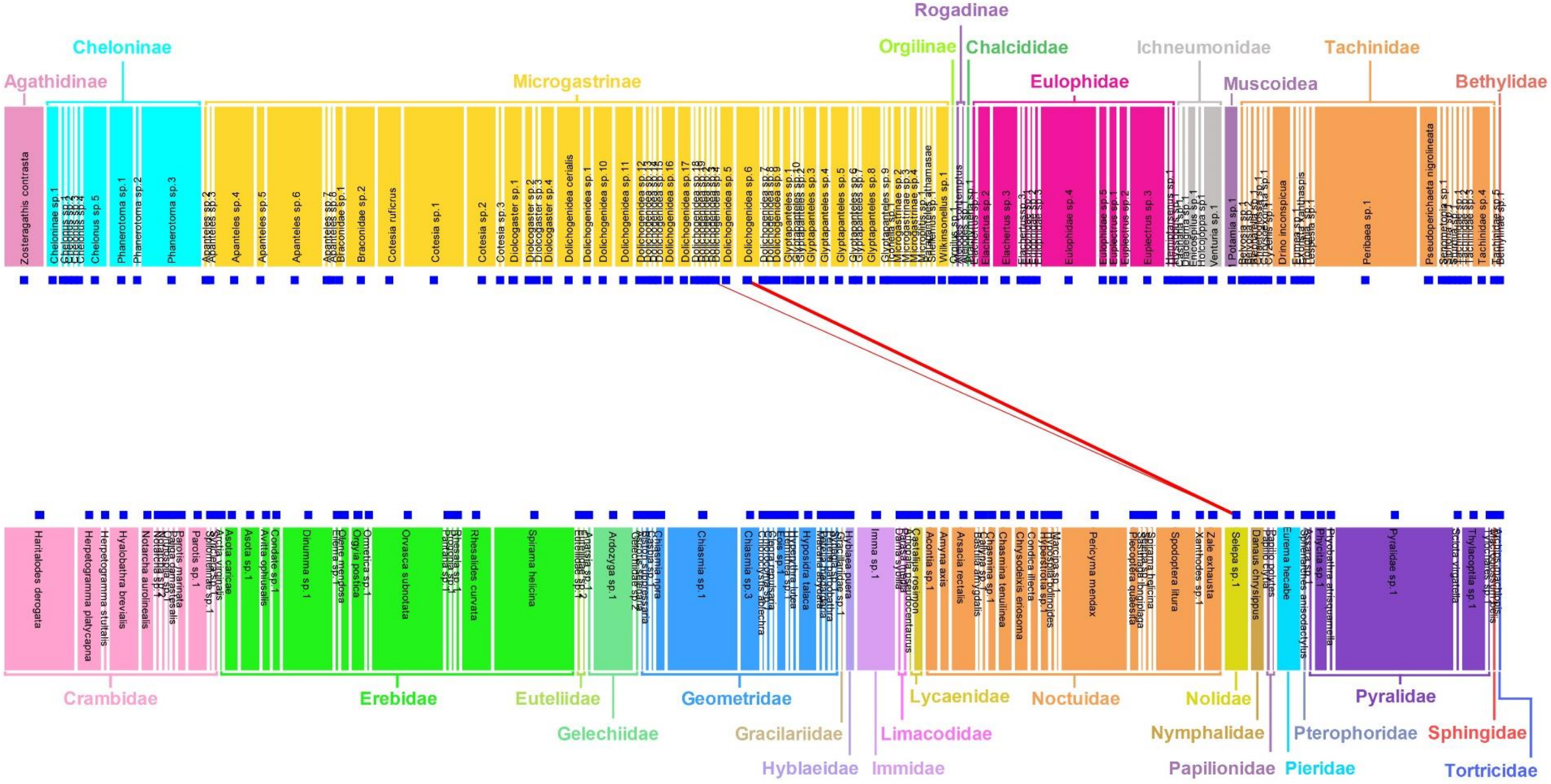

Figure 4 – 22 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Nolidae (bottom) and their parasitoids (above)

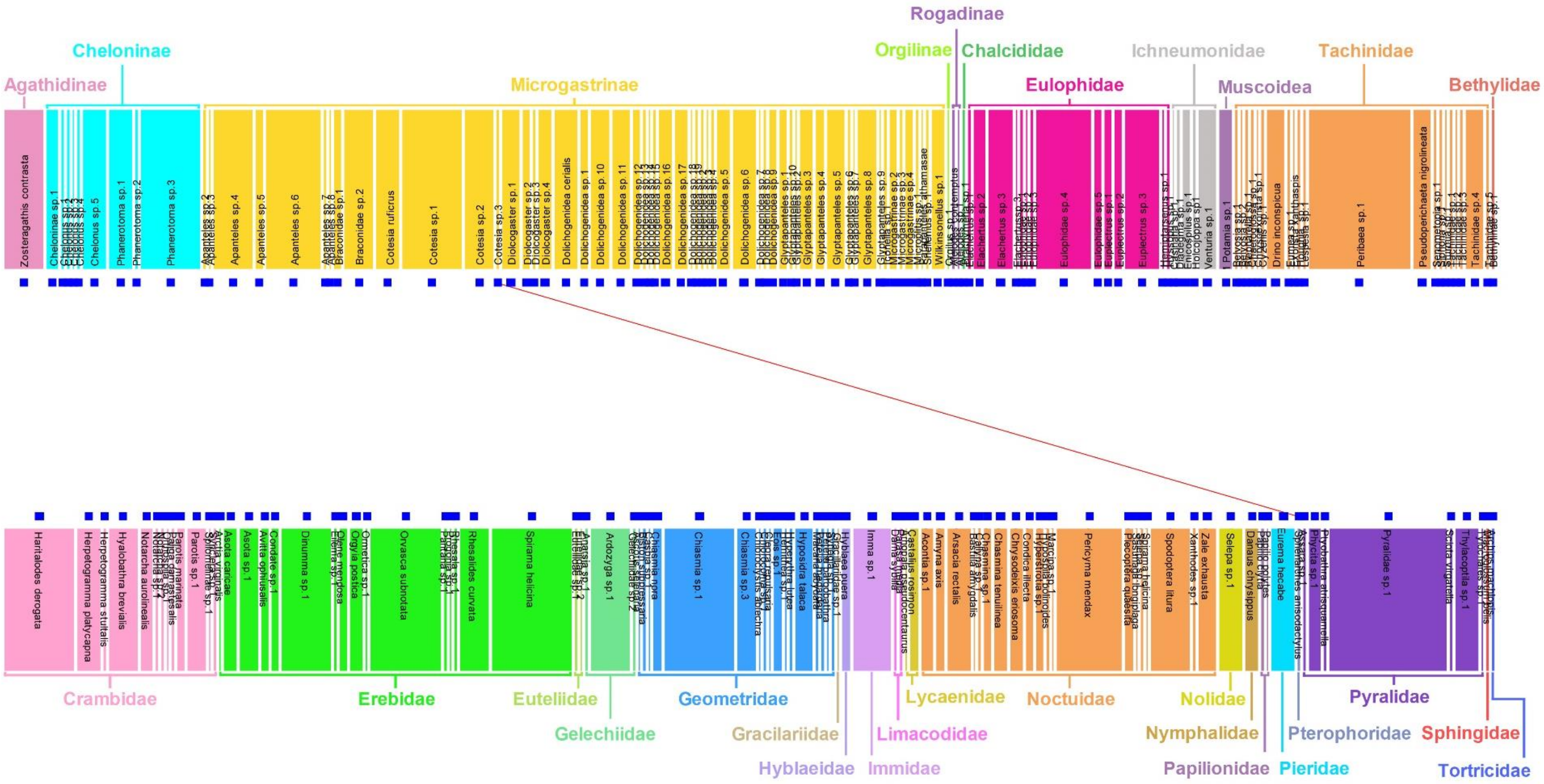

Figure 4 – 23 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Pterophoridae (bottom) and their parasitoids (above)

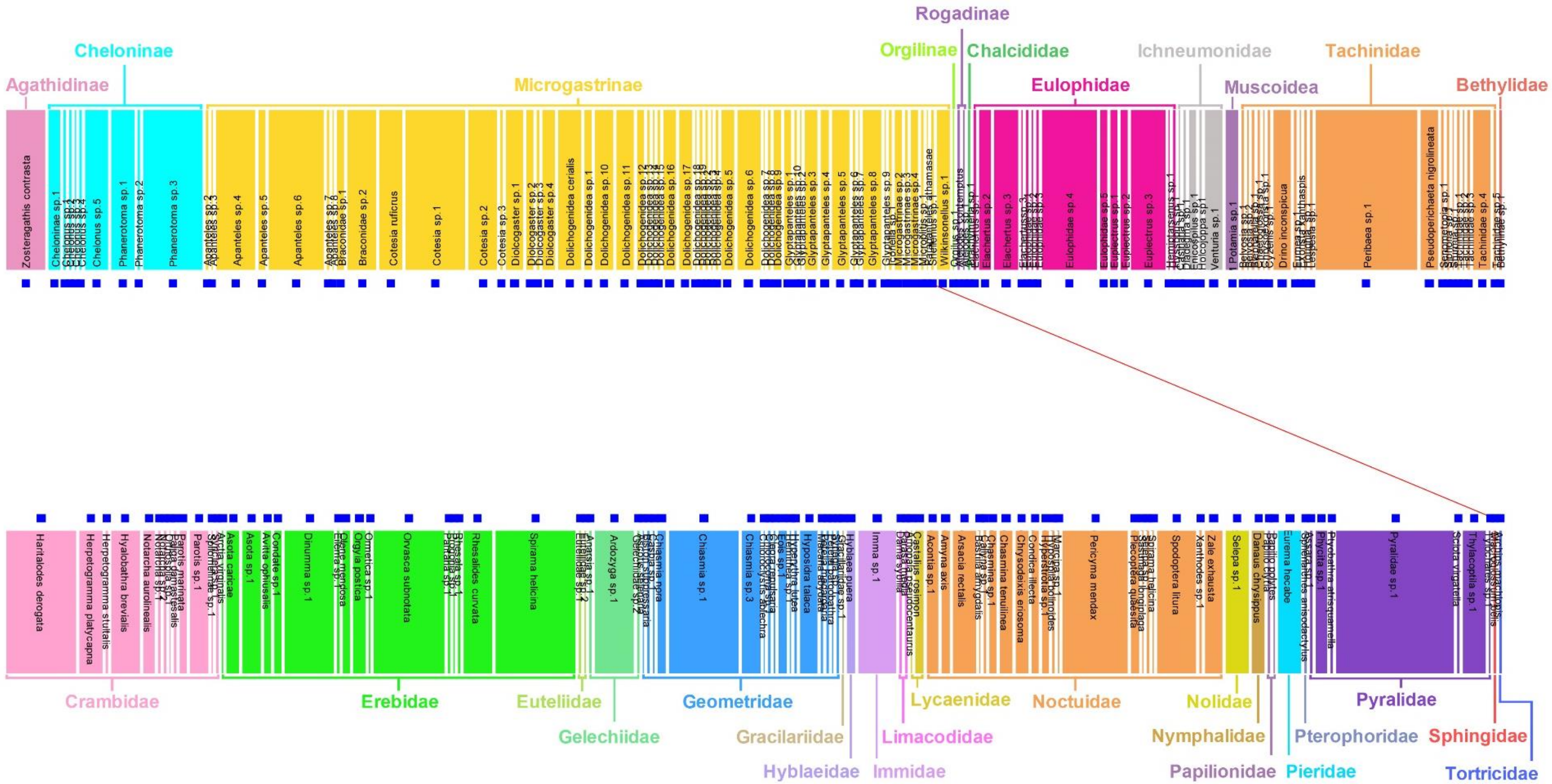

Figure 4 – 24 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Sphingidae (bottom) and their parasitoids (above)

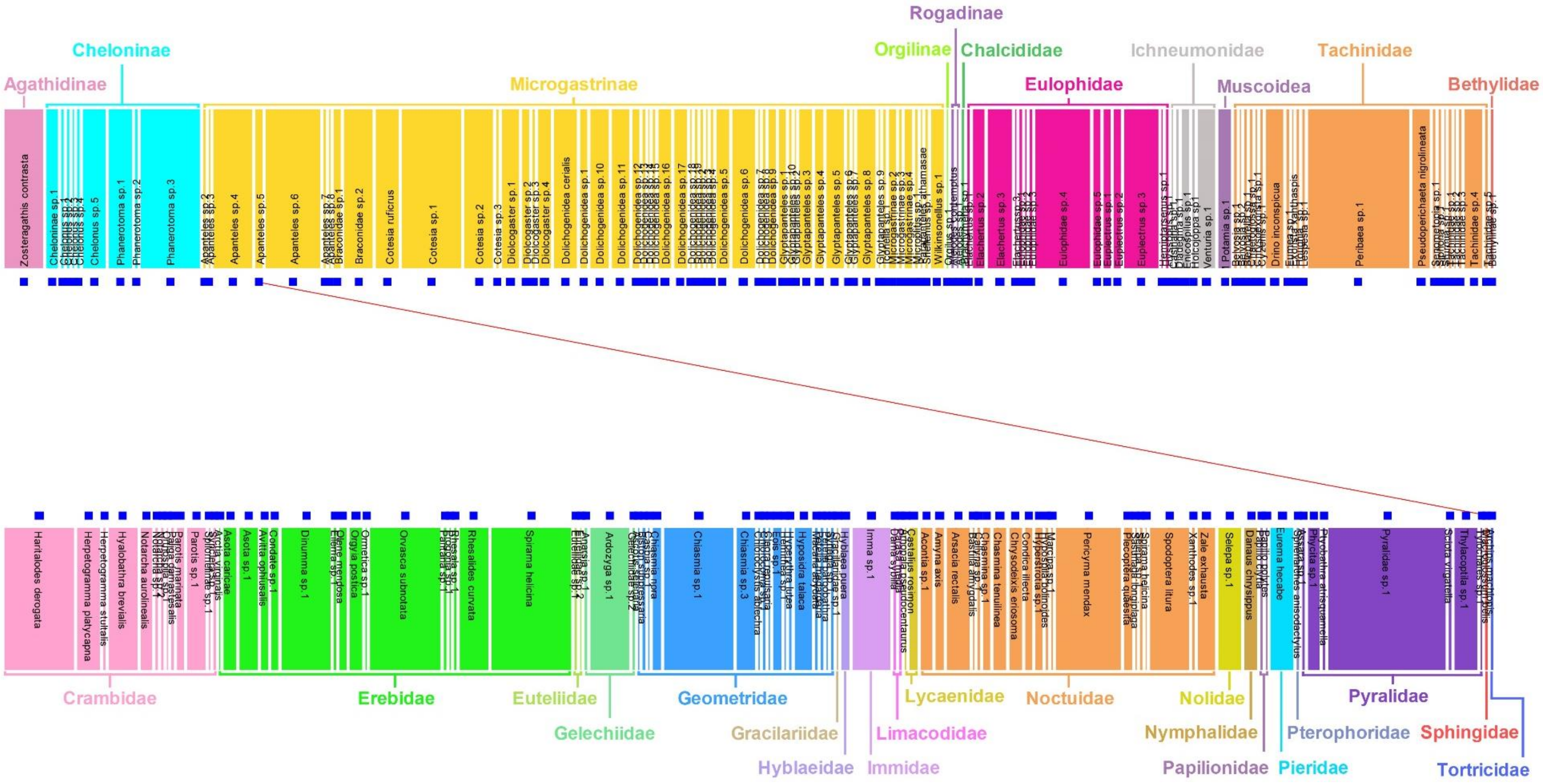

Figure 4 – 25 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Tortricidae (bottom) and their parasitoids (above)

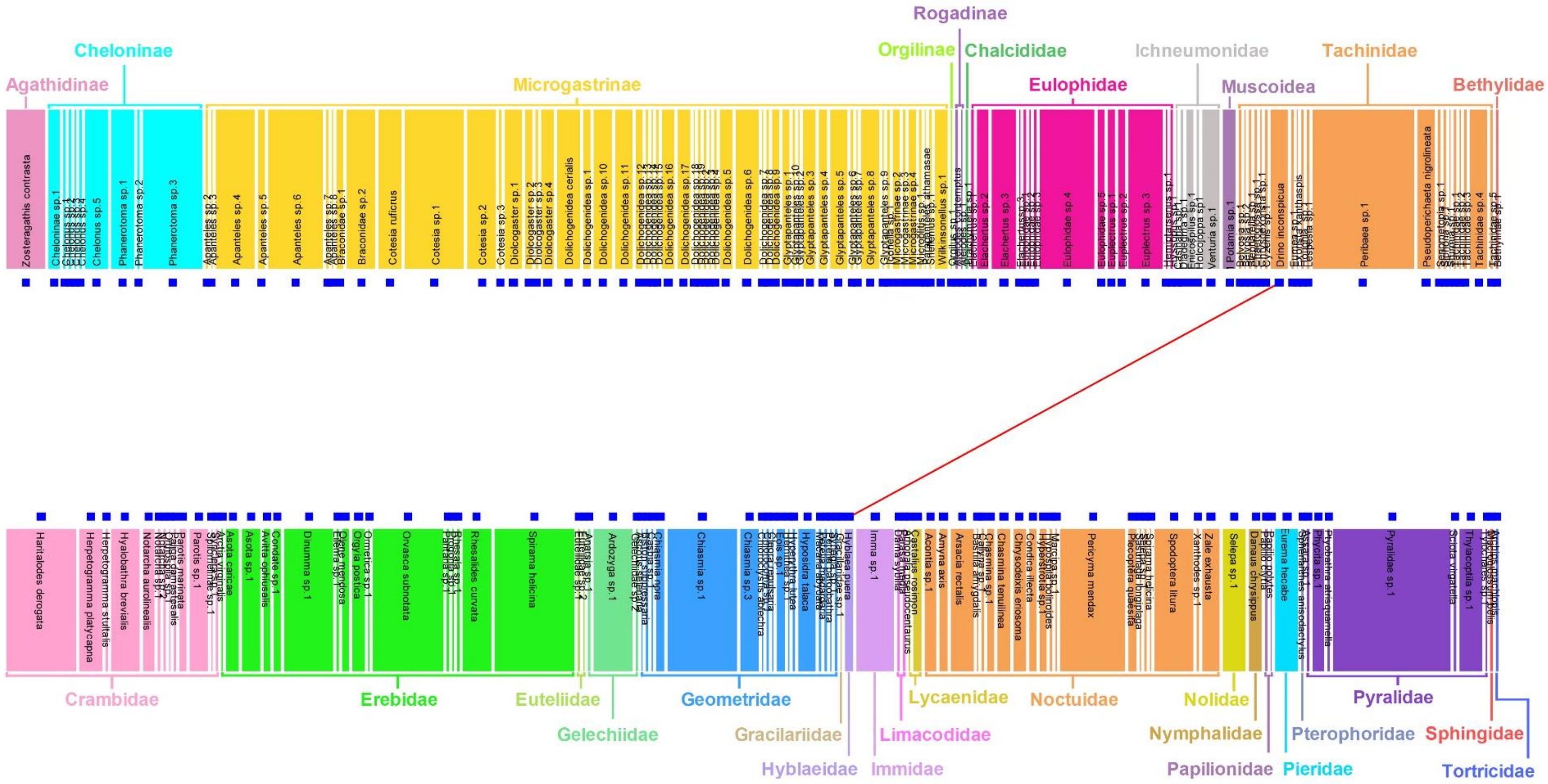

Figure 4 – 26 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Hyblaeidae (bottom) and their parasitoids (above)

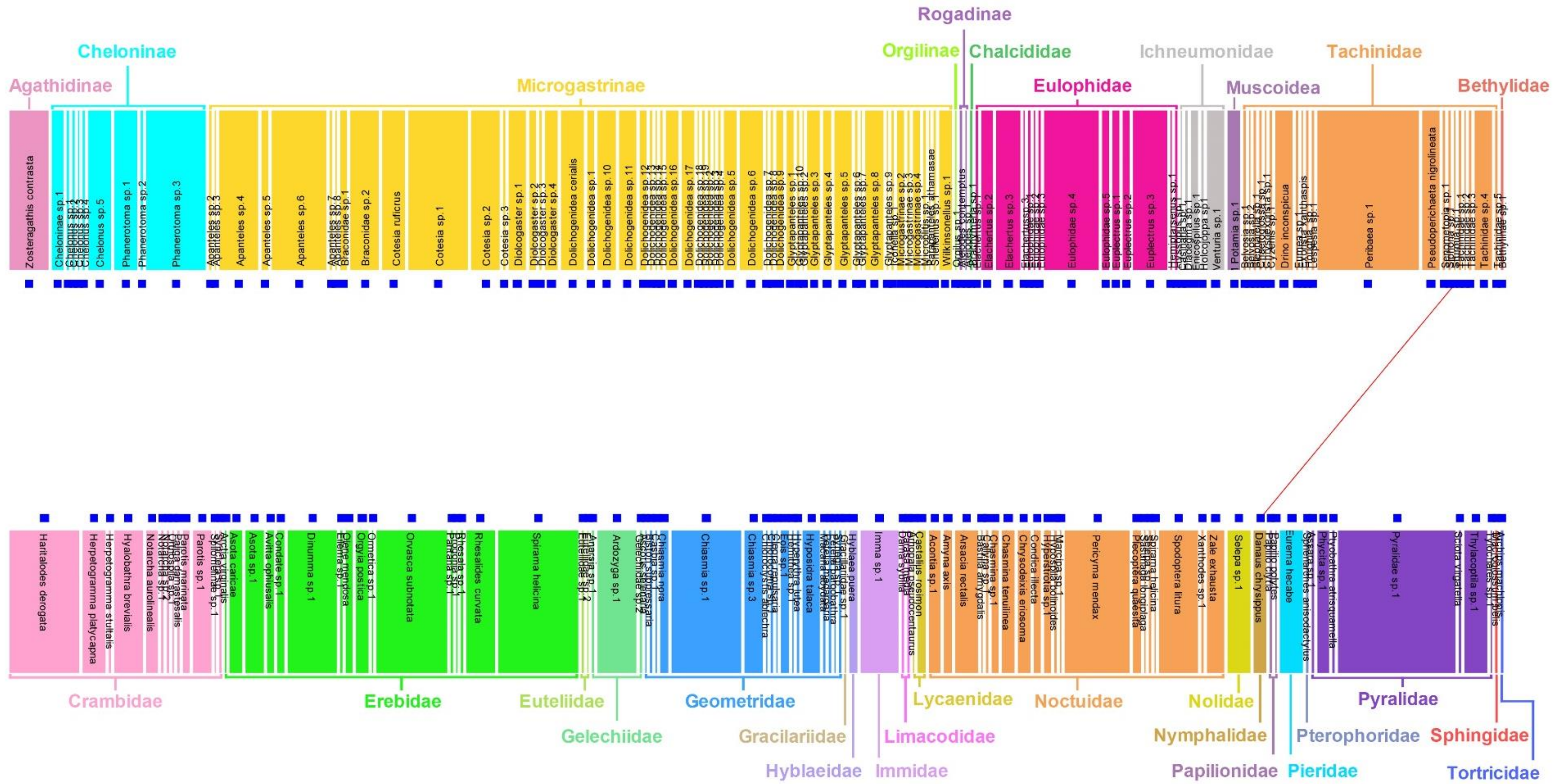

Figure 4 – 27 Molecular food web shows relationships of trophic links (red lines) between lepidopteran host in family Nymphalidae (bottom) and their parasitoids (above)

CHAPTER 5

DISCUSSION

This research is the first preliminary molecular food web construction caterpillar of host–parasitoids in Thailand. Caterpillar hosts were collected from a large secondary forest to study the parasitoids inside them. Wild–caught caterpillars were dissected so that parasitoid as well as host tissue samples could be obtained. The DNA barcoding technique was used to identify the lepidopteran host and parasitoid larvae because the target specimens in this study cannot be identified from morphological characteristics; both being in the larval stage make them exceedingly difficult to identify. By this technique, identification of lepidopteran hosts and their parasitoids was successful to various levels, and the data allowed a molecular food web of host–parasitoid relationships to be constructed.

Abundance of lepidopteran hosts and physical factors

The abundance of lepidopteran larvae that were detected and collected was associated with seasonal factors. Caterpillars were least abundant and least diverse during the late dry season (late March to early May 2016) but higher in abundance and species diversity when precipitation and humidity were increasing (late May to late June 2016). During one year of sampling, Thailand was affected by the El Niño phenomenon which lead to drought conditions (Thaiturapaisan, 2015). Therefore, the number of caterpillars reduced dramatically most likely due to lacking of suitable food plants. A previous study in Brazil similarly revealed that temperature fluctuation and drought caused by the El Niño effect resulted in reduction of survivability of caterpillars (Santos et al., 2017). However, the impact of the El Niño phenomenon varies depending on the part of the world, and in contrast to the drought in Thailand, some other places experienced other climatic effects such as heavier than normal rainfall, stronger winds and increased of temperature (Bravo-Cabrera et al., 2010).

Identification of caterpillar host species by morphological characteristics is very difficult in Thailand because there are only a few studies on taxonomy and biology of lepidopteran larvae. However, using external characters of larger caterpillar hosts can allow them to be classified roughly as far as family level. In this research, Noctuidae is the most abundance caterpillars, and it is the most diverse family of Lepidoptera in the world, with approximately 35,000 described species or 20% of the whole order (Kononenko and Pinratana, 2005) and most noctuid larvae are easily colleced by both beating sheet and hand collecting. According to previous studies, Noctuidae were recorded as the most abundance and diverse species in Thailand (Dokchan et al., 2013). Drepanidae, Gracilariidae, Nolidae had low abundance in this study. Drepanidae is a rare subfamily, which consists only 14 described species of Lepidoptera around the world (Chu and Wang, 1987; Inoue, 1962; Spitsyn, Bolotov, and Kogut, 2018). Many Gracillariidae are pest that live in and eat leaf tissue of plants (leaf miners), with small body size (4-20 mm) (Davis, 1994), while Nolidae mostly has small body with dull coloration (Heppner, 1991) and some nolid moths live in and eat inside leaf galls (Ito and Hattori, 1983), in Thailand a lot of species are associated with bamboos and palms, and may be out of reach. Thus, the life histories of these group (Gracilariidae, and Nolidae) made them less likely to be encountered during this investigation. Therefore, there are limitations of collecting which would have led to the low abundance of tree-feeding caterpillars collected in this study.

Parasitism rate of wild–caught caterpillars

Dissecting wild–caught caterpillars for parasitoids is successful. Previous studies suggested that using dissection method was superior than rearing method because rearing of caterpillar hosts is very difficult due to the need for maintaining food plant supply, time and effort needed, and premature host death procedure (Agusti et al., 2005; Laurenne et al., 2000; Tilmon et al., 2000). These can be overcome in large scale studies such as those of Professor Dan Janzen (http://janzen.sas.upenn.edu/Wadults /searchpara.lasso) in Costa Rica, but those projects involve dedicated buildings and large teams of botanically trained parataxonomists. The dissection employed here is therefore more accurate and appropriate given the resources available (Day, 1994).

Based on the results of dissecting wild–caught caterpillars, the proportion of parasitised individuals was highes abundant in early rainy season after increasing population (late June 2016) while in late dry season (both late March and late May 2016) had low abundance of the parasitised caterpillars. Previous study revealed that population trends between host and its parasitoids is obviously changed when the population of host increased, then the population of parasitoid also increased, but the increase in parasitisation rate may take more time (Blanco-Metzler, Watt, and Cosens, 2009). Therefore, these results based on the principle of predator–prey theory (Berryman, 1992; Gilpin, 1974; Horning and Mellish, 2012).

From November 2015 to November 2016, the highest parasitism rate (14%) occurred in early April while early December had the lowest parasitism rate (~0.2%). The highest parasitism rate of this study was a bit higher than normally stated of rate of 10% (Feener Jr and Brown, 1997; Godfray, 1994) but there is likely high variation. Finding parasitism rate by dissection method is very controversial because this method is difficult to find eggs and early instar parasitoids larvae (Symondson and Hemingway, 1997), but a previous study by Smith et al. (2008) reported that the parasitism rate calculated from dissection method was not different from rearing method.

Barcoding analyses and molecular identification of the specimens

Caterpillar host tissues were collected from tissues–rich parts and away from the parasitised area while the parasitoid’s tissues were collected from internal tissues to prevent contamination of DNA between host and parasitoid. Off all the insect tissues sent to CCDB for DNA barcoding, 95% of parasitised caterpillar specimens and 73% of parasitoid specimens were successfully barcoded. Previous study revealed that the success of barcoding in parasitoids was lower than caterpillar hosts because of wrong identification of tissue fragments and cross–amplification of DNA between caterpillar hosts and their parasitoids using universal primer, ectoparasitoids and small size of caterpillars and parasitoids. Cross–amplification is an important limitation of creating DNA barcoding for micro–lepidopteran hosts and small developmental stages. However, this problem was rarely found in larger caterpillars and parasitoids (Hrček et al., 2013). DNA barcoding of parasitised caterpillars and parasitoid revealed 58 genera in 20 families and 28 genera in 6 families, respectively. Specimen identification was compared using four methods BLAST, BOLD, ABGD and NJ trees, these techniques are important to obtain accurate identification. Quality and size of the reference library is the most important part for reliable identification and accurate. *Peribaea* sp.1, a tachinid fly was the most frequent parasitoid found in this study. Furthermore, this is the first report of any *Peribaea* in Thailand. Hussain and Annamalai (2008) reported that *Peribaea* is an alien invasive genus from biological control management of beet armyworm (small mottled willow moth) (Noctuidae: *Spodoptera exigua*) that an important pest of various economic crops such as onions, brinjal, legumes and crucifers in throughout most of the tropics including Thailand and Malaysia.

Relationships between host and parasitoids

A trophic food web of host–parasitoid relationships were created by the dissection method combined with DNA barcoding. The results of this study were supported by suggestion of previous studies that the number of lepidopteran larvae should be relatively high and PCR technique should be specific for detecting all developmental stages of parasitoids. However, this method is powerful tool for concealed hosts (woodboring, fruit feeding and gall–making insects, leaf miner) and applicable to use for multiparasitism and hyperparasitism (Hrček et al., 2013). Moreover, dissection is a quick method for creating food web of host–parasitoid relationships (Hrček et al., 2011; Santos et al., 2017). From the molecular food web, 88 apparently specialist and 22 generalist parasitoid species were found. Number of specialist was higher than generalist parasitoid species. Therefore, these results agree with Smith et al. (2006, 2007) studied parasitic flies in the family Tachinidae using DNA barcoding in tropical area and found that over 87% of parasitic flies were specialists. Theoretically, specialist parasitoid species are highly adaptive in respond to environmental changes and highly co–evolved to cope with their host defenses (Kassen, 2002). The molecular food web created in this study indicates high diversity and complexity of host–parasitoid relationships, even though the data were obtained from rather ecologically disturbed areas affected human activities and forest fires. These results are preliminary study of host–parasitoid interaction and should be further studies in other natural habitats.

From this study, 35 species of lepidopteran hosts were important insect pests that have outbreaks in many agricultural areas around the world, including Thailand. The results of trophic food web of host–parasitoid relationships in the secondary forest areas shown that the most species of lepidopteran pests in this study were different from pest species in the previous studies. In addition, the lepidopteran pest have never been reported about their parasitoids before (Table 5-1). Finally, the database of this study is very important that can be applied to discover native natural enemies for biological control programmes in agricultural areas around this study area.

Table 5 - 1 Lepidopteran pests and their parasitoids recorded from molecular food web of host–parasitoid relationship in Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

Lepidopteran host species	**Host plants**	**Parasitoids recorded from previous study**	**Parasitoids recorded from this study**
Amyna axis	Genus *Amaranthus,* genus *Croton,* genus *Celosia,* genus *Digera,* genus *Helianthus,* genus *Chenopodium,* genus *Spinacia,* genus *Ipomoea,* genus *Ricinus,* genus *Arachis,* genus *Crotalaria,* genus *Medicago,* genus *Phaseolus,* genus *Hibiscus,* genus *Cardiospermum,* genus *Solanum,* genus *Corchorus* and genus *Parasponia* (Wagner and Binns, 2010)	—	*Diolcogaster* sp. *Lespesia* sp.
Archips machlopis	Genus *Rumex,* genus *Citrus,* genus *Litchi,* genus *Salix,* genus *Medicago, Gloriosa superba* (climbing Lily), *Cedrela toonica* (Indian mahogany) and *Camellia sinensis* (tea) (Pratt et al., 2016)	—	*Apanteles* sp.
Arctia virginalis	Generalist feeding on many vegetation (Powell and Opler, 2009)	Tachinid flies (Karban et al., 2013)	*Glyptapanteles* sp.
Arsacia rectalis	Genus *Dalbergia* (Robinson et al., 2001)	—	*Chelonus* sp. *Dolichogenidea* sp.
Ascotis selenaria	*Artemisia campestris* (Wormwood), *Sambucus* sp., *Rosa* sp. (rose), *Rubus fruticosus* (blackberry), *Cytisus scoparius* (broom), *Taraxacum* sp., *Betula* sp. (birch), *Arbutus* sp., *Pimpinella* sp., *Melilotus* sp. (clover), *Euphorbia* sp. (cypress spurge), *Mimosa longifolia* (acacia), *Mimosa dealbata, Salvia* sp., *Salix glabra, Prosopis juliflora* (prosopis), *Delonix regia* and *Shorea robusta* (sal) (Pratap and Thapa, 1988; Rabindra et al., 2003)	—	*Enicospilus* sp.
Asota caricae	Genus *Broussonetia,* genus *Ficus,* genus *Mesuam,* genus *Shorea* and genus *Tectona* (Browne, 1968)	—	*Dolichogenidea* sp.

Table 5 - 2 (cont.) Lepidopteran pests and their parasitoids were recorded from molecular food web of host–parasitoid relationship in Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

Lepidopteran host species	Host plants	Parasitoids recorded from previous study	Parasitoids recorded from this study
Bastilla amygdalis	Genus *Phyllanthus* (Poole, 1989)	—	*Elachertus* sp.
Biston suppressaria	Genus *Acacia,* genus *Albizia,* genus *Eucalyptus, Cassia auriculata* (matura tea tree)*, Camellia sinensis* (tea)*, Chrysanthemum indicum* (Guldaudi)*, Dalbergia latifolia* (blackwood)*, Litchi chinensis* (lychee)*, Mangifera indica* (mango)*, Paulownia tomentosa* (Paulownia)*, Phyllanthus emblica* (emblic)*, Prunus domestica* (European plum)*, Prunus salicina* (Japanese plum)*, Psidium guajava* (guava) and *Vernicia fordii* (tung tree)	*Apanteles* sp. (Danthanarayana and Kathiravetpillai, 1969)	*Hyssopus* sp.
Castalius rosimon	*Zizyphus jujuba* (Chinese date) (Bingham, 1907)	—	*Dolichogenidea* sp. and Tachinid flies
Chiasmia nora	Genus *Acacia* but adult males feed mammalian body fluids (Kumar, Kumar, and Seth, 2016)	—	*Euplectrus* sp.
Chrysodeixis eriosoma	More than sixty species of plants (Roberts, 1979)	—	*Diolcogaster* sp. and *Euplectrus* sp.
Condica illecta	Gnus *Asteraceae , Ageratum houstonianum* (blue billygoat weed), *Bidens pilosa* (Spanish needle) and *Calendula officinalis* (Calendula) (Mathur and Singh, 1961; Pholboon, 1965)	—	*Cotesia ruficrus* and Eulophidae sp.
Danaus chrysippus	Host plants are from several families, most importantly in family Asclepiadoideae	*Charops* sp. Tachinid flies (Edmunds, 1976)	*Sturmia* sp. and *Drino inconspicua*

Table 5 - 3 (cont.) Lepidopteran pests and their parasitoids were recorded from molecular food web of host–parasitoid relationship in Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

Lepidopteran host species	Host plants	Parasitoids recorded from previous study	Parasitoids recorded from this study
Eurema hecabe	*Abrus precatorius* (crab's eye), *Falcataria moluccana* (Moluccan albizia), genus *Acacia*, genus *Aeschynomene*, family Leguminosae, family Euphorbiaceae and family *Cucurbitaceae* (Robinson et al., 2010)	*Nasonia vitripennis* (Narita et al., 2007)	*Cotesia* sp. and *Diadegma* sp.
Haritalodes derogata	*Abelmoschus esculentus* (okra), *Ceiba pentandra* (kapok), *Corchorus* (jutes), *Corchorus capsularis* (white jute), *Corchorus olitorius* (jute), *Durio zibethinus* (durian), *Gossypium* (cotton), *Hibiscus* (rosemallows), *Manihot esculenta* (cassava), *Solanum lycopersicum* (tomato) and *Solanum melongena* (aubergine)	*Apanteles* sp. and *Chelonus* sp. (Ek-Amnuay, 2010)	*Apanteles* sp., *Chelonus* sp. and *Venturia* sp.
Herpetogramma platycapna	*Angiopteris evecta* (giant fern) (Ghazali et al., 2014)	*Aprostocetus* sp. and *Alabagrus texanus*	*Chelonus* sp. and *Dolichogenidea* sp.
Herpetogramma stultalis	Family Amaranthaceae, family Lamiaceae, genus *Coleus* and *Hyptis brevipes* (Chibolita) (Fernandez-Triana et al., 2017)	*Apanteles* sp. (Fernandez-Triana et al., 2017)	*Apanteles* sp.
Hyblaea puera	*Tectona grandis* (teak) (Tripathy, Rout, and Das, 2018)	*Palexorisa solennis*, *Sympiesis hyblaeae*, *Brachymeria lasus*, *Eriborus gardneri*, *Stictopisthus* sp. and *Echthromorpha agrestoria notulatoria* (Nair, Mohanadas, and Sudheendrakumar, 1997; Surekha et al., 1996)	*Drino inconspicua*

Table 5 - 4 (cont.) Lepidopteran pests and their parasitoids were recorded from molecular food web of host–parasitoid relationship in Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

Lepidopteran host species	Host plants	Parasitoids recorded from previous study	Parasitoids recorded from this study
Hyperythra lutea	Genus *Gouania* (Singh, 1958)	—	*Glyptapanteles* sp.
Hyposidra talaca	Tea plantations (Majumdar and Ghosh, 2004)	—	*Dolichogenidea cerialis, Glyptapanteles* sp. and *Potamia* sp.
Hypospila bolinoides	Genus *Derris* (Hampson, 1892)	—	*Blepharella* sp.
Macroglossum belis	*Strychnos angustiflora* (narrow-flowered poison-nut), *Strychnos nux-vomica* (strychnos), *Saprosoma indicum* and *Spermadictyon suaveolans* (Hindi) (Pittaway and Kitching, 2018)	—	*Snellenius* sp.
Notarcha aurolinealis	*Sida rhombifolia* (Paddy's lucerne) (Orr and Kitching, 1999)	—	*Apanteles* sp.
Olene mendosa	Genus *Citrus*, *Solanum tuberosum* (potato), *Tamarindus indica* (tamarind), *Cedrus deodara* (deodar cedar), *Acacia nilotica* (gum arabic tree), *Mangifera indica* (mango), *Camelia sinensis* (green tea), *Ricinus communis* (castor oil plant) and *Salmalia malabarica* (silk cotton tree) (Das, 1990; Shamila, Charan, and Pandey, 2002)	*Theronia* sp. (Erniwati and Ubaidillah, 2011)	*Cotesia* sp. and *Diolcogaster* sp.

Table 5 - 5 (cont.) Lepidopteran pests and their parasitoids were recorded from molecular food web of host–parasitoid relationship in Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

Lepidopteran host species	Host plants	Parasitoids recorded from previous study	Parasitoids recorded from this study
Orgyia postica	Genus *Buchanania, Mangifera, Durio, Ochroma, Casuarina, Terminalia, Shorea, Hevea, Ricinus, Pelargonium, Cinnamomum, Acacia, Albizia, Caesalpina, Cajanus, Cassia, Dalbergia, Erythrina, Pithecellobium, Pterocarpus, Sesbania, Xylia, Lagerstroemia, Eucalyptus, Tristania, Zizyphus, Malus, Coffea, Citrus, Santalum, Dimocarpus, Litchi, Nephelium, Theobroma, Camellia, Grewia* and *Tectona* (Fasih et al., 1989)	*Telenomus* sp.	*Cotesia* sp.
Orvasca subnotata	*Dalbergia odorifera* (fragrant rosewood) (Zhou et al., 2015) and *Brassica* sp. (Chansri, 2014)	—	*Cotesia* sp., *Dolichogenidea* sp. and *Glyptapanteles* sp.
Paliga damastesalis	*Tectona grandis* (teak) (Chey, 2000)	—	*Apanteles* sp.
Papilio clytia	*Alseodaphne semecarpifolia, Cinnamomum camphora* (camphor tree), *Cinnamonum macrocarpum, Cinnamomum verum* (Ceylon cinnamon tree), *Litsea chinensis, Litsea deccansis and Tetranthera apetala* (Barraud, 1934)	—	*Eumea* sp.
Papilio polytes	*Aegle marmelos* (bael), *Atalantia racemosa, Citrus aurantifolia, Citrus grandis, Citrus limon, Citrus medica, Citrus sinensis, Glycosmis arborea, Murraya koenigii* (curry leaf) and *Murraya paniculata* (orange jessamine) (Kunte, 2006)	Chalcid wasps (Barraud, 1934)	*Holcojoppa* sp.

Table 5 - 6 (cont.) Lepidopteran pests and their parasitoids were recorded from molecular food web of host–parasitoid relationship in Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

Lepidopteran host species	Host plants	Parasitoids recorded from previous study	Parasitoids recorded from this study
Parasa media	*Coffea arabica* (coffee), *Hevea brasiliensis* (rubber), *Elaeis guineensis* (oil palm), *Theobroma cacao* (cocoa), *Manihot esculenta* (cassava), *Camellia sinensis* (tea), *Cocos nucifera* (coconut), genus *Musa* (banana), *Psophocarpus tetragonolobus* (winged bean) and *Mangifera indica* (mango)	Cuckoo wasp (*Chrysis shanghaiensis*) (Sevastopulo, 1937)	*Dolichogenidea* sp.
Parotis marinata	*Rauwolfia vomitoria* (Lin, 1997)	—	*Dolichogenidea* sp.
Pericyma mendax	*Acacia mearnsii* (black wattle), *Acacia* sp. and family Fabaceae (Martiré et al., 2008; Pinhey, 1975)	—	*Glyptapanteles* sp., *Wilkinsonellus* sp. and *Peribaea* sp.
Petelia medardaria	*Gouania leptostachya, Ziziphus incurva, Ziziphus jujube, Ziziphus mauritiana, Ziziphus oenoplia, Ziziphus rugosa* and *Hovenia dulcis.*	*Dolichogenidea cerialis* (Halperin, 1986)	*Dolichogenidea cerialis*
Sphenarches anisodactylus	*Brillantaisia lamium* (brillantaisia), *Caperonia castaneifolia* (birdseye), *Phaseolus vulgaris* (beans), *Hibiscus mutabilis* (Dixie Marshmallow), *Thalia geniculata* (fireflag), *Mimosa pudica* (sensitive plant), *Averrhoa bilimbi* (cucumber Tree), *Passiflora foetida* (stinking passionflower), *Antirrhinum majus* (snapdragons), *Theobroma cacao* (cocoa) and *Lantana camara* (lantana camara) (Cassani, Habeck, and Matthews, 1990)	—	*Cotesia* sp.

Table 5 - 7 (cont.) Lepidopteran pests and their parasitoids were recorded from molecular food web of host–parasitoid relationship in Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

Lepidopteran host species	**Host plants**	**Parasitoids recorded from previous study**	**Parasitoids recorded from this study**
Spodoptera litura	Highly polyphagous over 112 host plant species into 40 families (Abbas, Shad, and Razaq, 2012; Ahmad, Saleem, and Sayyed, 2009)	*Microplitis* sp. and *Exorista xanthaspis* (Ahangama and Gilstrap, 2007; Yan et al., 2018)	*Microplitis* sp. and *Exorista xanthaspis*

CHAPTER 6

CONCLUSION AND RECOMMENDATION

Conclusion

A total of 5,673 caterpillars were collected by two collecting methods, beating sheet and hand collecting in 28 collecting trips during November 2015 to November 2016 in Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province. The highest number of caterpillars were founded in early rainy season (late May 2016) and the lowest number of caterpillar were founded in late dry season (late March 2016).

Wild–caught caterpillars were initially classified roughly by pictorial key into 25 Lepidoptera families, of which Noctuidae were the most abundant Drepanidae, Gracilariidae, Nolidae and Satyridae were the least abundance of caterpillars.Off these, 340 wilds–caught caterpillars were found to be parasitised by parasitoids. The highest number of parasitised caterpillars were founded in late June 2016 while the lowest number of parasitised caterpillars were founded in late March and May 2016. Parasitism rate was highest rate in early April 2016 and the lowest in the late May 2015.

From DNA barcoding, 749 (~85%) of the samples were successfully barcoded for *COI*. Of these, 458 (~95%) were parasitised caterpillar specimens and 291 (~73%) parasitoid specimens. Of these 124 could be provisionally identified provisional species, 99 to genera and 24 to families for the hosts and 113 provisional species, 40 genera in 7 families for the parasitoids. The most abundant caterpillar hosts belonged to *Haritalodes derogate* (family Crambidae) while the most abundant parasitoids belonged to *Peribaea* sp.1 (family Tachinidae).

From molecular food web model, a species of caterpillar host could be parasitised by more than 6 species of parasitoids. *Chiasmia* sp.1 was parasitised with the highest number of parasitoid species. *Phanerotoma* sp.1 was a parasitoid of 6 species of lepidopteran host. *Orvasca subnotata* and *Cotesia* sp. 1 was the most frequently recorded of host–parasitoid interaction. For specificity of host–parasitoid species, the specialist (80%) parasitoid species were significantly higher than generalist (20%) parasitoid species.

DNA barcoding methods is a rapid and powerful tool for identifying larvae of lepidopteran hosts and parasitoids and highly effective to resolve complex host–parasitoid relationships by construct molecular food web of trophic interaction in poorly study area of tropic region better than traditional methods.

Finally, host–parasitoid relationships from the databases can be applied to choose potential natural enemies when there are outbreaks of lepidopteran pests in agricultural areas.

Recommendations

Study of host–parasitoid relationships should be conducted in natural habitats to construct databases of molecular food web which will be benefit for research on co–evolution, conservation natural resources management and biological control programmes.

The caterpillar should be collected during night time which will help to compare diurnal and nocturnal species of lepidopteran hosts and their parasitoids.

Adult of lepidopteran hosts and their parasitoids should be collected to make completely the databases which will have both adult and larvae information.

Parasitoids found in this study should be reared and study of their potential ability for pest control.

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APPENDICES

APPENDIX A

ABUNDANCE OF LEPIDOPTERAN PESTS AND MORPHOLOGICAL IDENTIFICATION

Table A - 1 Total number of wild–caught caterpillars, normal caterpillars, parasitised caterpillars and parasitism rates recorded during the 28 collecting trips started from November 2015 to November 2016 at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

Year/Month/Date			Wild–caught caterpillars	Normal caterpillars	Parasitised Caterpillars	Parasitism rate
2015	Nov	13, 14	185	169	16	8.65
		27, 28	181	157	24	13.26
	Dec	11, 12	193	188	5	2.59
		25, 26	140	126	14	10.00
2016	Jan	8, 9	76	70	6	7.89
		22-23	154	146	8	5.19
	Feb	5, 6	148	142	6	4.05
		19-20	155	144	11	7.10
	Mar	4, 6	105	96	9	8.57
		18-19	48	46	2	4.17
	Apr	1, 2	56	48	8	14.29
		18, 19	89	85	4	4.49
		30, 31	51	47	4	7.84
	May	13, 14	83	79	4	4.82
		25, 26	837	835	2	0.24
	Jun	10, 11	333	314	19	5.71
		24, 25	536	474	62	11.57
	Jul	8, 9	164	144	20	12.20
		22, 23	226	216	10	4.42
	Aug	5, 6	335	310	25	7.46
		19, 20	248	226	22	8.87
	Sep	2, 3	187	183	4	2.14
		17, 18	124	115	9	7.26
	Oct	30, 1	254	236	18	7.09
		14, 15	202	195	7	3.47
		28, 29	205	197	8	3.90
	Nov	11, 12	143	140	3	2.10
		25, 26	215	205	10	4.65
Total			5673	5333	340	5.99

Table A - 2 Abundance of caterpillar families recorded during the 28 collecting trips started from November 2015 to November 2016 at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

Family of lepidoptera	Year/Month/Date																												Individuals
	2015				2016																								
	Nov		Dec		Jan		Feb		Mar		Apr			May		Jun		Jul		Aug		Sep		Oct			Nov		
	13,14	27,28	11,12	25,26	8,9	22,23	5,6	19,20	5,6	18,19	1,2	18,19	30,1	13,14	25,26	10,11	24,25	8,9	22,23	5,6	19,20	2,3	16,17	30,1	14,15	28,29	11,12	25,26	
Bombycidae	-	-	-	4	-	-	-	-	-	-	-	-	8	-	-	-	-	-	24	-	-	2	-	5	-	-	3	1	47
Crambidae	81	42	99	35	16	9	72	111	38	9	18	67	4	77	25	252	46	66	22	12	144	10	57	37	44	20	8	9	1430
Drepanidae	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1
Danaidae	-	-	-	-	-	4	-	27	-	2	6	1	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	42
Erebidae	17	49	6	11	8	60	3	1	1	1	-	-	1	-	14	6	79	7	3	37	9	20	2	13	33	44	8	14	447
Gelechiidae	14	5	-	4	1	3	6	1	2	3	-	-	-	-	98	1	-	-	-	4	3	6	3	-	1	-	-	-	155
Geometridae	27	26	15	49	16	7	10	-	25	1	-	-	1	3	-	26	237	35	25	38	18	27	9	22	13	21	15	30	696
Gracilariidae	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Hesperiidae	-	3	4	-	-	-	3	-	-	-	3	-	-	-	-	-	37	2	3	1	-	8	5	-	-	1	4	6	81
Immidae	1	-	7	9	-	1	6	-	2	1	-	-	-	-	-	-	1	-	2	16	4	1	2	4	7	8	1	3	76
Lasiocampidae	-	-	2	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	5
Limacodidae	1	-	3	1	1	-	-	5	-	-	-	-	-	-	-	-	16	-	18	1	23	12	6	2	29	4	1	2	125
Lycaenidae	1	1	11	-	1	7	2	-	2	3	1	-	1	-	2	-	-	-	2	1	-	1	-	-	-	1	1	-	38
Noctuidae	40	50	30	27	17	50	39	7	29	21	28	15	27	2	123	46	118	50	120	223	44	79	33	167	66	102	39	57	1649
Nolidae	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
Notodontidae	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	7	8
Nymphalidae	-	-	2	-	2	-	-	-	-	-	-	-	-	1	-	1	-	1	1	-	-	10	-	-	3	-	-	3	24
Papilionidae	-	-	1	-	10	-	-	-	-	-	-	-	-	-	3	-	-	1	1	-	-	1	-	-	-	-	-	-	17
Pieridae	-	4	-	-	2	12	5	2	1	7	-	-	7	-	572	-	1	1	-	1	1	6	7	2	1	3	63	81	779

Table A - 2 (cont.) Abundance of caterpillar families recorded during the 28 collecting trips started from November 2015 to November 2016 at Chulalongkorn University Area, Kaeng Khoi District, Saraburi Province

Family of lepidoptera	Year/Month/Date																												Individuals
	2015				2016																								
	Nov		Dec		Jan		Feb		Mar		Apr			May		Jun		Jul		Aug		Sep		Oct			Nov		
	13,14	**27,28**	**11,12**	**25,26**	**8,9**	**22,23**	**5,6**	**19,20**	**5,6**	**18,19**	**1,2**	**18,19**	**30,1**	**13,14**	**25,26**	**10,11**	**24,25**	**8,9**	**22,23**	**5,6**	**19,20**	**2,3**	**16,17**	**30,1**	**14,15**	**28,29**	**11,12**	**25,26**	
Pterophoridae	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	4	-	-	4	1	-	-	10
Pyralidae	-	-	6	-	-	1	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	10
Sphingidae	-	1	-	-	-	-	-	-	5	-	-	5	-	-	-	-	1	-	5	-	1	-	-	2	1	-	-	-	21
Tortricidae	3	-	7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	10
Total	185	181	193	140	76	154	148	155	105	48	56	89	51	83	837	333	536	164	226	335	248	187	124	254	202	205	143	215	5673

APPENDIX B

MOLECULAR IDENTIFICATION OF THE SPECIMENS

Table B - 1 Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH096-16	SRKk011038	685	*Macroglossum belis*	99	*Macroglossum belis*	99.83	Sphingidae	*Macroglossum belis*
BBTH097-16	PL011001	685	*Papilio polytes*	99	*Papilio polytes*	99.85	Papilionidae	*Papilio polytes*
BBTH098-16	SRKk012104	686	*Condica illecta*	100	*Condica illecta*	100	Noctuidae	*Condica illecta*
BBTH099-16	SRKk011060	686	*Papilio clytia*	99	*Papilio clytia*	99.85	Papilionidae	*Papilio clytia*
BBTH100-16	SRKk011047	626	*Hypodoxa emiliaria*	92	*Spaniocentra* sp.	98.69	Geometridae	*Spaniocentra* sp.1
BBTH101-16	SS011001	669	*Sasunaga tenebrosa*	94	*Sasunaga longiplaga*	100	Noctuidae	*Sasunaga longiplaga*
BBTH102-16	SRKk012027	686	*Hyblaea puera*	100	*Hyblaea puera*	100	Hyblaeidae	*Hyblaea puera*
BBTH103-16	SRKk012022	682	*Hyblaea puera*	100	*Hyblaea puera*	100	Hyblaeidae	*Hyblaea puera*
BBTH104-16	SY011001	685	*Attacus atlas*	100	*Attacus atlas*	100	Saturniidae	*Attacus atlas*
BBTH105-16	SRKk012028	682	*Hypospila bolinoides*	100	*Hypospila bolinoides*	100	Noctuidae	*Hypospila bolinoides*
BBTH106-16	SRKk012073	694	*Salebriaria engeli*	93	Ambesa sp.	93	Pyralidae	Phycitinae sp.1
BBTH107-16	SRKk021007	690	*Scoparia biplagialis*	91	Gelechiidae sp.	92.47	Gelechiidae	Gelechiidae sp.1
BBTH108-16	SRKk021012	638	*Ardozyga* sp.	92	Gelechiidae sp.	92.46	Gelechiidae	*Ardozyga* sp.1
BBTH109-16	SRKk021010	685	*Ardozyga* sp.	92	Gelechiidae sp.	92.96	Gelechiidae	*Ardozyga* sp.1
BBTH110-16	SRKk021040	686	*Ardozyga* sp.	93	Gelechiidae sp.	92.96	Gelechiidae	*Ardozyga* sp.1
BBTH111-16	SRKk021033	686	*Crypsiphona ocultaria*	92	*Spaniocentra* sp.	98.92	Geometridae	*Spaniocentra* sp.1
BBTH112-16	SRKk021050	686	*Arsacia rectalis*	94	*Arsacia rectalis*	99.66	Noctuidae	*Arsacia rectalis*
BBTH113-16	SRKk021054	640	*Parotis atlitalis*	90	Syllepte placophaea	90.66	Pyralidae	*Tylochares* sp.1
BBTH115-16	SRKk021044	686	*Arsacia rectalis*	94	*Arsacia rectalis*	99.66	Noctuidae	*Arsacia rectalis*
BBTH116-16	SRKk021062	687	*Ardozyga* sp.	93	Gelechiidae sp.	92.8	Gelechiidae	*Ardozyga* sp.1
BBTH117-16	SRKk021063	689	*Ardozyga sp.*	93	Gelechiidae sp.	92.8	Gelechiidae	*Ardozyga sp.1*
BBTH118-16	SRKk022033	672	*Selepa discigera*	95	Selepa sp.	96.67	Nolidae	*Selepa sp.1*

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH119-16	SRKk022052	683	*Condate* sp.1	93	Condate sp.	92.34	Erebidae	*Condate* sp.1
BBTH120-16	SRKk022043	694	*Selepa discigera*	95	*Selepa* sp.	96.65	Nolidae	*Selepa* sp.1
BBTH121-16	SRKk022044	686	*Biston suppressaria*	99	*Biston suppressaria*	100	Geometridae	*Biston suppressaria*
BBTH122-16	SRKk022064	693	*Herpetogramma licarsisalis*	92	*Eclipsiodes* sp.	92.32	Crambidae	*Herpetogramma* sp.1
BBTH123-16	SRKk022074	655	*Ardozyga* sp.	92	Gelechiidae sp.	92.61	Gelechiidae	*Ardozyga* sp.1
BBTH124-16	SRKk022072	686	*Ardozyga* sp.	93	Gelechiidae sp.	92.8	Gelechiidae	*Ardozyga* sp.1
BBTH125-16	SRKk022077	696	*Godonela* sp.	99	*Chiasmia nora*	99.54	Geometridae	*Chiasmia nora*
BBTH126-16	SRKk022075	686	*Ardozyga* sp.	92	Gelechiidae sp.	92.8	Gelechiidae	*Ardozyga* sp.1
BBTH127-16	SRKk032019	686	*Ascotis selenaria*	97	*Ascotis dianaria*	97.7	Geometridae	*Ascotis selenaria*
BBTH128-16	SRKk031015	680	*Thaduka multicaudata*	99	*Arhopala pseudocentaurus*	99.83	Lycaenidae	*Arhopala pseudocentaurus*
BBTH129-16	SRKk031035	698	*Ormetica pauperis*	88	*Ormetica pauperis*	88.23	Erebidae	*Ormetica* sp.1
BBTH130-16	SRKk031011	691	*Imma loxoscia*	91	Immidae sp.	100	Immidae	*Imma* sp.1
BBTH131-16	SRKk031028	686	*Imma loxoscia*	91	Immidae sp.	100	Immidae	*Imma* sp.1
BBTH132-16	SRKk031033	683	*Spirama helicina*	99	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH133-16	SRKk031060	648	*Asota kinabaluensis*	92	*Ponometia acutus*	92.26	Erebidae	*Asota* sp.1
BBTH134-16	SRKk031059	633	*Asota kinabaluensis*	92	*Asota kinabaluensis*	92.43	Erebidae	*Asota* sp.1
BBTH135-16	SRKk031052	689	*Ardozyga* sp.	92	Gelechiidae sp.	92.63	Gelechiidae	*Ardozyga* sp.1
BBTH136-16	SRKk031061	639	*Sphenarches anisodactylus*	99	*Sphenarches anisodactylus*	100	Pterophoridae	*Sphenarches anisodactylus*
BBTH137-16	SRKk031055	685	*Chrysodeixis includens*	95	*Plusiopalpa adrasta*	100	Noctuidae	*Plusiopalpa adrasta*
BBTH138-16	SRKk031066	682	*Ardozyga* sp.	93	Gelechiidae sp.	92.8	Gelechiidae	*Ardozyga* sp.1
BBTH139-16	SRKk031095	685	*Avitta ophiusalis*	100	*Avitta ophiusalis*	100	Erebidae	*Avitta ophiusalis*
BBTH140-16	SRKk031097	661	*Avitta ophiusalis*	98	*Avitta ophiusalis*	97.46	Erebidae	*Avitta ophiusalis*

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH141-16	SRKk032115	687	*Zale exhausta*	93	*Zale exhausta*	99.39	Noctuidae	*Zale exhausta*
BBTH142-16	SRKk032112	679	*Dinumma mediobrunnea*	93	*Dinumma* sp.	100	Erebidae	*Dinumma* sp.1
BBTH143-16	SRKk032113	687	*Neolithocolletis hikomonticola*	89	Gracillariidae sp.	90.31	Gracilariidae	Gracillariidae sp.1
BBTH144-16	SRKk032111	683	*Spirama helicina*	99	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH145-16	SRKk032107	685	*Spirama helicina*	100	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH146-16	SRKk032042	682	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH147-16	SRKk032040	686	*Amyna axis*	100	*Amyna axis*	100	Noctuidae	*Amyna axis*
BBTH148-16	SRKk032027	693	*Amyna axis*	99	*Amyna axis*	96.69	Noctuidae	*Amyna axis*
BBTH149-16	SRKk032035	685	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH150-16	SRKk032025	679	*Dinumma mediobrunnea*	93	*Dinumma* sp.	100	Erebidae	*Dinumma* sp.1
BBTH151-16	SRKk032033	672	*Imma loxoscia*	91	Immidae sp.	100	Immidae	*Imma* sp.1
BBTH153-16	SRKk032061	648	*Salepa disciterga*	95	*Selepa* sp.	96.86	Nolidae	*Selepa* sp.1
BBTH154-16	SRKk032050	627	*Cyana arenbergeri*	93	Euteliidae sp.	93.96	Euteliidae	Euteliidae sp.1
BBTH155-16	SRKk032068	688	*Plecoptera quaesita*	93	*Arctia virginalis*	100	Erebidae	*Arctia virginalis*
BBTH156-16	SRKk032074	687	*Thalassodes antithetica*	95	*Chlorocoma* sp.	98.31	Geometridae	*Chlorocoma* sp.1
BBTH157-16	SRKk032082	683	*Dichomeris limosellus*	92	Gelechiidae sp.	92.45	Gelechiidae	Gelechiidae sp.2
BBTH158-16	SRKk032077	685	*Spirama helicina*	99	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH159-16	SRKk032071	682	*Salepa disciterga*	95	*Selepa* sp.	96.65	Nolidae	*Selepa* sp.1
BBTH160-16	SRKk032075	687	*Spirama helicina*	99	*Spirama helicina*	99.69	Erebidae	*Spirama helicina*
BBTH161-16	SRKk032066	686	*Dinumma mediobrunnea*	93	*Dinumma* sp.	100	Erebidae	*Dinumma* sp.1
BBTH162-16	SRKk032093	685	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH163-16	SRKk032090	683	*Parasemia plantaginis*	93	Euteliidae sp.	96.62	Euteliidae	Euteliidae sp.2

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH164-16	SRKk032097	688	*Parasemia plantaginis*	93	Euteliidae sp.	96.77	Euteliidae	Euteliidae sp.2
BBTH165-16	SRKk041012	686	*Haritalodes derogata*	99	*Haritalodes derogata*	99.85	Crambidae	*Haritalodes derogata*
BBTH166-16	SRKk041028	686	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH167-16	SRKk041052	685	*Picrostomastis subrosealis*	94	*Picrostomastis subrosealis*	94.13	Thyrididae	Picrostomastis subrosealis
BBTH168-16	SRKk041058	685	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH169-16	SRKk041075	673	*Herpetogramma platycapna*	100	*Herpetogramma platycapna*	100	Crambidae	*Herpetogramma platycapna*
BBTH170-16	SRKk041079	685	*Asota caricae*	100	*Asota caricae*	100	Erebidae	*Asota caricae*
BBTH171-16	SRKk042017	636	*Rhectocraspeda periusalis*	94	*Parotis* sp.	99.68	Crambidae	*Parotis* sp.1
BBTH172-16	SRKk042006	687	*Plecoptera reflexa*	100	*Plecoptera reflexa*	100	Noctuidae	*Plecoptera reflexa*
BBTH173-16	SRKk042003	685	*Glyphodes* sp.1	92	*Compsotropha selenias*	91.91	Oecophoridae	*Compsotropha* sp.1
BBTH174-16	SRKk042042	685	*Rhectocraspeda periusalis*	94	*Parotis* sp.	99.54	Crambidae	*Parotis* sp.1
BBTH175-16	SRKk042053	686	*Chasmina tenuilinea*	97	*Chasmina tenuilinea*	99.85	Noctuidae	*Chasmina tenuilinea*
BBTH176-16	SRKk042025	688	*Chasmina tenuilinea*	97	*Chasmina tenuilinea*	99.85	Noctuidae	*Chasmina tenuilinea*
BBTH177-16	SRKk042076	685	*Pardoxia graellsi*	98	*Xanthodes* sp.	100	Noctuidae	*Xanthodes* sp.1
BBTH178-16	SRKk042074	688	*Chasmina tenuilinea*	96	*Chasmina tenuilinea*	99.54	Noctuidae	*Chasmina tenuilinea*
BBTH179-16	SRKk042073	683	*Herpetogramma stultalis*	99	*Herpetogramma stultalis*	99.69	Crambidae	*Herpetogramma stultalis*
BBTH180-16	SRKk042099	686	*Rhectocraspeda periusalis*	94	*Parotis* sp.	99.85	Crambidae	*Parotis* sp.1
BBTH181-17	SRKk042089	687	*Notarcha aurolinealis*	98	*Notarcha aurolinealis*	98.77	Crambidae	*Notarcha aurolinealis*
BBTH182-18	SRKk042090	652	*Notarcha aurolinealis*	98	*Notarcha aurolinealis*	98.74	Crambidae	*Notarcha aurolinealis*
BBTH183-19	SRKk042106	653	*Notarcha aurolinealis*	98	*Notarcha aurolinealis*	98.74	Crambidae	*Notarcha aurolinealis*
BBTH184-20	SRKk051007	559	*Orvasca subnotata*	99	*Euproctis trispila*	100	Erebidae	*Orvasca subnotata*
BBTH185-21	SRKk051010	595	*Orvasca subnotata*	99	*Orvasca subnotata*	100	Erebidae	*Orvasca subnotata*

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH186-22	SRKk051013	686	Noctuidae sp.	100	Pericyma mendax	100	Noctuidae	Pericyma mendax
BBTH187-23	SRKk051011	648	*Orvasca subnotata*	99	*Orvasca subnotata*	100	Erebidae	*Orvasca subnotata*
BBTH188-24	SRKk051009	705	*Orvasca subnotata*	99	*Orvasca subnotata*	100	Erebidae	*Orvasca subnotata*
BBTH189-25	SRKk051036	686	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH190-26	SRKk051038	670	*Orvasca subnotata*	99	*Orvasca subnotata*	100	Erebidae	*Orvasca subnotata*
BBTH192-16	SRKk051033	673	*Selepa discigera*	95	*Selepa* sp.	96.67	Nolidae	*Selepa* sp.1
BBTH193-16	SRKk051037	680	*Godonela* sp.	99	*Chiasmia nora*	99.54	Geometridae	*Chiasmia nora*
BBTH194-16	SRKk051028	679	*Spirama helicina*	99	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH195-16	SRKk051024	679	*Dinumma mediobrunnea*	93	*Dinumma* sp.	100	Erebidae	*Dinumma* sp.1
BBTH196-16	SRKk051050	679	*Anarsia* sp.	96	*Anarsia* sp.	96.53	Gelechiidae	*Anarsia* sp.1
BBTH197-16	SRKk051055	679	*Imma loxoscia*	91	Immidae sp.	100	Immidae	*Imma* sp.1
BBTH198-16	SRKk051046	680	*Melanolophia canadaria*	93	*Casbia celidosema*	93.52	Geometridae	*Casbia* sp.1
BBTH199-16	SRKk052038	690	*Orvasca subnotata*	99	*Orvasca subnotata*	100	Erebidae	*Orvasca subnotata*
BBTH200-16	SRKk052041	676	*Orvasca subnotata*	99	*Orvasca subnotata*	99.85	Erebidae	*Orvasca subnotata*
BBTH201-16	SRKk052066	682	*Petelia medardaria*	95	*Petelia paroobathra*	97.7	Geometridae	*Petelia paroobathra*
BBTH202-16	SRKk052064	683	*Pyrausta panopealis*	97	*Pyrausta panopealis*	99.46	Crambidae	*Pyrausta panopealis*
BBTH203-16	SRKk052065	683	*Petelia medardaria*	99	*Petelia medardaria*	99.85	Geometridae	*Petelia medardaria*
BBTH204-16	SRKk052097	681	*Castalius rosimon*	100	*Castalius rosimon*	100	Lycaenidae	*Castalius rosimon*
BBTH205-16	SRKk052098	686	*Orvasca subnotata*	99	*Orvasca subnotata*	100	Erebidae	*Orvasca subnotata*
BBTH207-16	SRKk052127	673	*Hemithea aestivaria*	93	*Hemithea* sp.	99.85	Geometridae	*Hemithea* sp.1
BBTH208-16	SRKk052165	680	*Parasa media*	97	*Parasa media*	99.85	Limacodidae	*Parasa media*
BBTH209-16	SRKk061024	680	*Chrysodeixis eriosoma*	100	*Chrysodeixis eriosoma*	100	Noctuidae	*Chrysodeixis eriosoma*

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH210-16	SRKk061042	679	*Eurema hecabe*	100	*Eurema hecabe*	100	Pieridae	*Eurema hecabe*
BBTH211-16	SRKk061060	679	*Chrysodeixis eriosoma*	100	*Chrysodeixis eriosoma*	100	Noctuidae	*Chrysodeixis eriosoma*
BBTH213-16	SRKk061068	665	*Hyposidra talaca*	97	*Hyposidra talaca*	99.85	Geometridae	*Hyposidra talaca*
BBTH214-16	SRKk061085	683	*Chrysodeixis eriosoma*	100	*Chrysodeixis eriosoma*	100	Noctuidae	*Chrysodeixis eriosoma*
BBTH215-16	SRKk062013	679	*Herpetogramma licarsisalis*	92	*Haritalodes polycymalis*	93.24	Crambidae	*Herpetogramma* sp.1
BBTH216-16	SRKk062039	633	Noctuidae sp.	94	*Marcipa* sp.	93.91	Noctuidae	*Marcipa* sp.1
BBTH217-16	SRKk062040	680	*Ophyx sp.1*	93	*Episparina tortuosalis*	100	Erebidae	*Episparina tortuosalis*
BBTH218-16	SRKk062062	644	*Chasmina pulchra*	93	*Chasmina pulchra*	93.72	Noctuidae	*Chasmina* sp.1
BBTH219-16	SRKk062051	683	*Tamba* sp.	93	*Haemanota* sp.	93.27	Noctuidae	*Tamba sp.1*
BBTH220-16	SRKk062063	676	*Ectropis* sp.1	96	*Synegia* sp.	99.85	Geometridae	*Synegia* sp.1
BBTH221-16	SRKk062082	679	*Anarsia* sp.	90	*Orthospila orissusalis*	100	Crambidae	*Orthospila orissusalis*
BBTH223-16	SRKk062122	685	*Plecoptera quaesita*	99	*Plecoptera quaesita*	99.69	Noctuidae	*Plecoptera quaesita*
BBTH224-16	SRKk062115	683	*Anarsia* sp.	90	*Orthospila orissusalis*	100	Crambidae	*Orthospila orissusalis*
BBTH225-16	SRKk071031	682	*Orthospila orissusalis*	95	*Orthospila* sp.	100	Crambidae	*Orthospila* sp.1
BBTH226-16	SRKk071026	649	*Haritalodes derogata*	99	*Haritalodes derogata*	99.69	Crambidae	*Haritalodes derogata*
BBTH227-16	SRKk071028	679	*Orthospila orissusalis*	95	*Orthospila* sp.	100	Crambidae	*Orthospila* sp.1
BBTH228-16	SRKk071054	637	*Orthospila orissusalis*	95	*Orthospila* sp.	100	Crambidae	*Orthospila* sp.1
BBTH229-16	SRKk071070	560	*Orgyia australis*	100	*Orgyia postica*	100	Erebidae	*Orgyia postica*
BBTH230-16	SRKk072031	686	*Notarcha chrysoplasta*	98	*Notarcha obrinusalis*	99	Crambidae	*Notarcha obrinusalis*
BBTH231-16	SRKk072032	637	*Scopula* sp.1	92	*Eois nympha*	93.18	Geometridae	*Eois* sp.1
BBTH232-16	SRKk072053	683	*Orvasca subnotata*	99	*Orvasca subnotata*	100	Erebidae	*Orvasca subnotata*
BBTH233-16	SRKk072061	684	*Orvasca subnotata*	100	*Orvasca subnotata*	99.85	Erebidae	*Orvasca subnotata*

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH234-16	SRKk072064	680	*Chasmina tenuilinea*	96	*Chasmina tenuilinea*	99.54	Noctuidae	*Chasmina tenuilinea*
BBTH235-16	SRKk072069	684	*Imma loxoscia*	91	Immidae sp.	100	Immidae	*Imma* sp.1
BBTH236-16	SRKk072070	683	*Chasmina tenuilinea*	97	*Chasmina tenuilinea*	100	Noctuidae	*Chasmina tenuilinea*
BBTH237-16	SRKk072084	678	*Callyna leucosticha*	93	*Callyna leucosticha*	92.97	Noctuidae	*Callyna* sp.1
BBTH238-16	SRKk072092	646	*Hyposidra talaca*	97	*Hyposidra talaca*	99.52	Geometridae	*Hyposidra talaca*
BBTH239-16	SRKk072101	680	*Dasychira alboschistacea*	92	*Olene mendosa*	99.69	Erebidae	*Olene mendosa*
BBTH240-16	SRKk072102	644	*Hyposidra talaca*	97	*Hyposidra talaca*	99.84	Geometridae	*Hyposidra talaca*
BBTH241-16	SRKk081009	685	*Orvasca subnotata*	99	*Orvasca subnotata*	100	Erebidae	*Orvasca subnotata*
BBTH242-16	SRKk081011	680	Noctuidae sp.	100	*Pericyma mendax*	100	Noctuidae	*Pericyma mendax*
BBTH243-16	SRKk081014	681	Noctuidae sp.	100	*Pericyma mendax*	100	Noctuidae	*Pericyma mendax*
BBTH244-16	SRKk081016	644	Noctuidae sp.	100	*Pericyma mendax*	100	Noctuidae	*Pericyma mendax*
BBTH245-16	SRKk081026	680	Noctuidae sp.	100	*Pericyma mendax*	100	Noctuidae	*Pericyma mendax*
BBTH246-16	SRKk081046	679	Noctuidae sp.	100	*Pericyma mendax*	100	Noctuidae	*Pericyma mendax*
BBTH247-16	SRKk081047	679	Noctuidae sp.	100	*Pericyma mendax*	100	Noctuidae	*Pericyma mendax*
BBTH248-16	SRKk081048	643	*Eurema hecabe*	99	*Eurema hecabe*	100	Pieridae	*Eurema hecabe*
BBTH249-16	SRKk081052	686	*Hyposidra talaca*	98	*Hyposidra talaca*	99.54	Geometridae	*Hyposidra talaca*
BBTH250-16	SRKk081054	672	*Eurema hecabe*	99	*Eurema hecabe*	100	Pieridae	*Eurema hecabe*
BBTH251-16	SRKk081056	679	Noctuidae sp.	100	*Pericyma mendax*	100	Noctuidae	*Pericyma mendax*
BBTH252-16	SRKk081057	656	Noctuidae sp.	99	*Pericyma mendax*	100	Noctuidae	*Pericyma mendax*
BBTH253-16	SRKk081059	666	Noctuidae sp.	100	*Pericyma mendax*	100	Noctuidae	*Pericyma mendax*
BBTH254-16	SRKk081095	673	Noctuidae sp.	100	*Pericyma mendax*	100	Noctuidae	*Pericyma mendax*
BBTH255-16	SRKk081096	680	Noctuidae sp.	100	*Pericyma mendax*	100	Noctuidae	*Pericyma mendax*

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH256-16	SRKk082014	680	*Herpetogramma stultalis*	99	*Herpetogramma stultalis*	99.69	Crambidae	*Herpetogramma stultalis*
BBTH257-16	SRKk082019	683	*Notarcha aurolinealis*	98	*Notarcha aurolinealis*	98.77	Crambidae	*Notarcha aurolinealis*
BBTH258-16	SRKk082027	683	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH259-16	SRKk082031	683	*Herpetogramma platycapna*	100	*Herpetogramma platycapna*	100	Crambidae	*Herpetogramma platycapna*
BBTH260-16	SRKk082037	655	*Herpetogramma platycapna*	100	*Herpetogramma platycapna*	100	Crambidae	*Herpetogramma platycapna*
BBTH261-16	SRKk082056	679	*Herpetogramma platycapna*	100	*Herpetogramma platycapna*	100	Crambidae	*Herpetogramma platycapna*
BBTH262-16	SRKk082059	700	*Dasychira alboschistacea*	92	*Olene mendosa*	99.85	Erebidae	*Olene mendosa*
BBTH263-16	SRKk082061	679	*Orvasca subnotata*	99	*Orvasca subnotata*	99.85	Erebidae	*Orvasca subnotata*
BBTH264-16	SRKk082068	680	*Herpetogramma platycapna*	100	*Herpetogramma platycapna*	100	Crambidae	*Herpetogramma platycapna*
BBTH265-16	SRKk091011	679	*Hyphorma minax*	89	*Darna sybilla*	98.62	Limacodidae	*Darna sybilla*
BBTH266-16	SRKk091037	680	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH267-16	SRKk091046	679	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH268-16	SRKk092003	659	*Parotis marinata*	99	*Parotis marinata*	98.99	Crambidae	*Parotis marinata*
BBTH269-16	SRKk092110	679	*Parotis marinata*	99	*Parotis marinata*	99.17	Crambidae	*Parotis marinata*
BBTH907-17	SRKk 101010	658	*Orvasca subnotata*	99	*Orvasca subnotata*	99.85	Erebidae	*Orvasca subnotata*
BBTH908-17	SRKk 101033	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH909-17	SRKk 101036	658	*Chiasmia* sp.	99	*Chiasmia* sp.	99.85	Geometridae	*Chiasmia* sp.1
BBTH910-17	SRKk 102008	658	*Archips machlopis*	99	-	-	Tortricidae	*Archips machlopis*
BBTH911-17	SRKk 102045	623	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH912-17	SRKk 102047	658	*Rhesala sp.*	94	-	-	Erebidae	*Rhesala* sp.1
BBTH913-17	SRKk 102049	658	*Chiasmia* sp.	99	*Chiasmia* sp.	99.85	Geometridae	*Chiasmia* sp.2
BBTH914-17	SRKk 102052	658	*Imma loxoscia*	92	Immidae sp.	100	Immidae	*Imma* sp.1

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH915-17	SRKk 102055	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH916-17	SRKk 102056	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH917-17	SRKk 102068	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH918-17	SRKk 102070	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH919-17	SRKk 102071	658	*Rhesala sp.*	94	-	-	Erebidae	*Rhesala* sp.1
BBTH920-17	SRKk 102072	658	*Imma loxoscia*	91	Immidae sp.	100	Immidae	*Imma* sp.1
BBTH921-17	SRKk 111006	658	*Macaria abydata*	100	*Macaria abydata*	100	Geometridae	*Macaria abydata*
BBTH922-17	SRKk 111010	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH923-17	SRKk 112017	658	*Archips machlopis*	95	-	-	Tortricidae	*Archips machlopis*
BBTH924-17	SRKk 112030	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH925-17	SRKk 112031	658	*Orgyia australis*	100	Orgyia postica	100	Erebidae	*Orgyia postica*
BBTH926-17	SRKk 112035	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH927-17	SRKk 121007	658	*Eurema hecabe*	99	-	-	Pieridae	*Eurema hecabe*
BBTH928-17	SRKk 121010	658	*Orgyia australis*	100	Orgyia postica	100	Erebidae	*Orgyia postica*
BBTH929-17	SRKk 121019	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH930-17	SRKk 122001	658	*Danaus chrysippus*	100	-	-	Nymphalidae	*Danaus chrysippus*
BBTH931-17	SRKk 122014	658	*Castalius rosimon*	100	-	-	Lycaenidae	*Castalius rosimon*
BBTH932-17	SRKk 122038	658	*Synclera* sp.1	97	*Synclera* sp.	97.94	Crambidae	*Synclera* sp.1
BBTH933-17	SRKk 122041	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH934-17	SRKk 122075	658	Spilomelinae sp.1	99	-	-	Crambidae	Spilomelinae sp.1
BBTH935-17	SRKk 131028	658	*Chloroclystis ablechra*	93	-	-	Geometridae	*Chloroclystis ablechra*
BBTH936-17	SRKk 131036	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH937-17	SRKk 131037	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH938-17	SRKk 131043	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH939-17	SRKk 132064	658	*Herpetogramma* sp.	92	-	-	Crambidae	*Herpetogramma* sp.1
BBTH940-17	SRKk 132046	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH941-17	SRKk 142034	658	*Desmia* sp.1	90	-	-	Crambidae	*Desmia* sp.1
BBTH942-17	SRKk 142044	658	*Antaeotricha* sp.	90	-	-	Elachistidae	*Antaeotricha* sp.1
BBTH943-17	SRKk 142059	658	*Antaeotricha* sp.	90	-	-	Elachistidae	*Antaeotricha* sp.1
BBTH944-17	SRKk 142071	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH945-17	SRKk 142072	658	*Thylacoptila* sp.1	98	-	-	Pyralidae	*Thylacoptila* sp.1
BBTH946-17	SRKk 142073	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH947-17	SRKk 142075	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH948-17	SRKk 142084	658	*Ptyobathra atrisquamella*	97	-	-	Pyralidae	*Ptyobathra atrisquamella*
BBTH949-17	SRKk 142089	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH950-17	SRKk 142096	658	*Thylacoptila* sp.1	98	-	-	Pyralidae	*Thylacoptila* sp.1
BBTH951-17	SRKk 142108	658	*Thylacoptila* sp.1	98	-	-	Pyralidae	*Thylacoptila* sp.1
BBTH952-17	SRKk 151009	658	*Selepa* sp.1	95	-	-	Nolidae	*Selepa* sp.1
BBTH953-17	SRKk 151028	658	Phycitinae sp.	93	-	-	Pyralidae	Phycitinae sp.1
BBTH954-17	SRKk 151029	658	Phycitinae sp.	93	-	-	Pyralidae	Phycitinae sp.1
BBTH955-17	SRKk 152026	658	*Spirama helicina*	99	-	-	Noctuidae	*Spirama helicina*
BBTH956-17	SRKk 152027	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH957-17	SRKk 152036	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH958-17	SRKk 152037	637	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH959-17	SRKk 152038	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH960-17	SRKk 152041	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH961-17	SRKk 161018	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.67	Erebidae	*Rhesalides curvata*
BBTH962-17	SRKk 161019	658	*Asota caricae*	100	*Asota caricae*	100	Erebidae	*Asota caricae*
BBTH963-17	SRKk 171021	658	*Rhesala sp.*	94	-	-	Erebidae	*Rhesala* sp.1
BBTH964-17	SRKk 171027	658	*Rhesala sp.*	94	-	-	Erebidae	*Rhesala* sp.1
BBTH965-17	SRKk 171031	658	*Rhesala sp.*	94	-	-	Erebidae	*Rhesala* sp.1
BBTH966-17	SRKk 172002	658	*Danaus chrysippus*	100	-	-	Nymphalidae	*Danaus chrysippus*
BBTH967-17	SRKk 172008	658	*Danaus chrysippus*	100	-	-	Nymphalidae	*Danaus chrysippus*
BBTH968-17	SRKk 172010	658	*Notarcha* sp.2	98	-	-	Crambidae	*Notarcha* sp.1
BBTH969-17	SRKk 172015	658	*Rhesala sp.*	94	-	-	Erebidae	*Rhesala* sp.1
BBTH970-17	SRKk 172016	658	*Notarcha* sp.2	98	-	-	Crambidae	*Notarcha* sp.1
BBTH971-17	SRKk 181020	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH972-17	SRKk 182045	658	*Phycita roborella*	95	-	-	Pyralidae	*Phycita sp.1*
BBTH973-17	SRKk 182047	658	*Phycita roborella*	95	-	-	Pyralidae	*Phycita sp.1*
BBTH974-17	SRKk 182049	658	*Phycita roborella*	95	-	-	Pyralidae	*Phycita sp.1*
BBTH975-17	SRKk 191023	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH976-17	SRKk 191029	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH977-17	SRKk 191030	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH978-17	SRKk 191033	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH979-17	SRKk 211010	622	*Danaus chrysippus*	100	-	-	Nymphalidae	*Danaus chrysippus*
BBTH980-17	SRKk 211021	658	*Assara* sp.1	95	-	-	Pyralidae	*Assara* sp.1

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH981-17	SRKk 212016	658	*Plecoptera reflexa*	100	-	-	Erebidae	*Plecoptera reflexa*
BBTH982-17	SRKk 212028	658	*Plecoptera reflexa*	100	-	-	Erebidae	*Plecoptera reflexa*
BBTH983-17	SRKk 201491	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH984-17	SRKk 202285	658	*Paliga damastesalis*	99	-	-	Crambidae	*Paliga damastesalis*
BBTH985-17	SRKk 221023	658	*Orthospila* sp.1	95	-	-	Crambidae	*Orthospila* sp.1
BBTH986-17	SRKk 221042	639	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.3
BBTH987-17	SRKk 222086	658	*Sciota virgatella*	94	-	-	Pyralidae	*Sciota virgatella*
BBTH988-17	SRKk 222153	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH989-17	SRKk 222157	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH990-17	SRKk 222161	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH991-17	SRKk 222173	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH992-17	SRKk 222186	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH993-17	SRKk 222192	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH994-17	SRKk 222197	639	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH995-17	SRKk 222199	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH996-17	SRKk 222203	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH997-17	SRKk 222207	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH998-17	SRKk 222209	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH999-17	SRKk 222211	658	Pyralidae sp.	99	-	-	Pyralidae	Pyralidae sp.1
BBTH1190-17	SRKk 222212	658	Pyralidae sp.	99	Pyralidae sp.	99.89	Pyralidae	Pyralidae sp.1
BBTH1191-17	SRKk 222214	658	Pyralidae sp.	99	Pyralidae sp.	99.69	Pyralidae	Pyralidae sp.1
BBTH1192-17	SRKk 222221	658	Pyralidae sp.	99	Pyralidae sp.	99.54	Pyralidae	Pyralidae sp.1

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH1193-17	SRKk 222231	658	*Plecoptera quaesita*	99	*Plecoptera quaesita*	99.69	Noctuidae	*Plecoptera quaesita*
BBTH1194-17	SRKk 231041	658	*Spirama helicina*	99	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH1195-17	SRKk 231045	658	*Chiasmia* sp.	99	*Chiasmia* sp.	99.83	Geometridae	*Chiasmia* sp.3
BBTH1196-17	SRKk 231046	658	*Chiasmia* sp.	99	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.3
BBTH1197-17	SRKk 231051	658	*Dinumma deponens*	94	*Dinumma sp.*	100	Erebidae	*Dinumma* sp.1
BBTH1198-17	SRKk 231067	658	*Dinumma deponens*	95	*Dinumma sp.*	100	Erebidae	*Dinumma* sp.1
BBTH1199-17	SRKk 231069	658	*Chiasmia* sp.	99	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.3
BBTH1200-17	SRKk 231075	658	*Spirama helicina*	100	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH1201-17	SRKk 231079	658	*Spirama helicina*	100	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH1202-17	SRKk 231098	658	*Dinumma deponens*	94	*Dinumma sp.*	100	Erebidae	*Dinumma* sp.1
BBTH1203-17	SRKk 231108	658	*Dinumma deponens*	94	*Dinumma sp.*	100	Erebidae	*Dinumma* sp.1
BBTH1204-17	SRKk 231116	658	*Spirama helicina*	99	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH1205-17	SRKk 231119	658	*Spirama helicina*	99	*Spirama helicina*	100	Erebidae	*Spirama helicina*
BBTH1206-17	SRKk 231120	658	*Spirama helicina*	99	*Spirama helicina*	100	Erebidae	*Spirama helicina*
BBTH1207-17	SRKk 231121	658	*Zale exhausta*	93	*Zale exhausta*	99.39	Noctuidae	*Zale exhausta*
BBTH1208-17	SRKk 231128	658	*Dinumma deponens*	94	*Dinumma sp.*	100	Erebidae	*Dinumma* sp.1
BBTH1209-17	SRKk 231129	658	*Dinumma deponens*	94	*Dinumma sp.*	99.85	Erebidae	*Dinumma* sp.1
BBTH1210-17	SRKk 231134	658	*Spirama helicina*	99	*Spirama helicina*	100	Erebidae	*Spirama helicina*
BBTH1211-17	SRKk 231136	658	*Dinumma deponens*	94	*Dinumma sp.*	100	Erebidae	*Dinumma* sp.1
BBTH1212-17	SRKk 231137	658	*Spirama helicina*	99	*Spirama helicina*	100	Erebidae	*Spirama helicina*
BBTH1213-17	SRKk 231142	658	*Zale exhausta*	93	*Zale exhausta*	99.39	Noctuidae	*Zale exhausta*
BBTH1214-17	SRKk 231143	658	*Dinumma deponens*	94	*Dinumma sp.*	99.85	Erebidae	*Dinumma* sp.1

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH1215-17	SRKk 231144	658	*Spirama helicina*	99	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH1216-17	SRKk 231147	658	*Spirama helicina*	99	*Spirama helicina*	100	Erebidae	*Spirama helicina*
BBTH1217-17	SRKk 231167	658	*Spirama helicina*	99	*Spirama helicina*	100	Erebidae	*Spirama helicina*
BBTH1218-17	SRKk 231184	658	*Spirama helicina*	99	*Spirama helicina*	100	Erebidae	*Spirama helicina*
BBTH1219-17	SRKk 231185	658	*Dinumma deponens*	95	*Dinumma deponens*	94.44	Erebidae	*Dinumma* sp.1
BBTH1220-17	SRKk 232005	658	*Spodoptera litura*	100	*Spodoptera litura*	100	Noctuidae	*Spodoptera litura*
BBTH1221-17	SRKk 232006	658	*Hyalobathra brevialis*	99	*Hyalobathra brevialis*	99.66	Crambidae	*Hyalobathra brevialis*
BBTH1222-17	SRKk 232007	658	*Hyalobathra brevialis*	99	*Hyalobathra brevialis*	99.49	Crambidae	*Hyalobathra brevialis*
BBTH1223-17	SRKk 232010	658	*Hyalobathra brevialis*	99	*Hyalobathra brevialis*	99.49	Crambidae	*Hyalobathra brevialis*
BBTH1224-17	SRKk 232013	658	*Condica illecta*	100	*Condica illecta*	100	Noctuidae	*Condica illecta*
BBTH1225-17	SRKk 232015	658	*Spodoptera litura*	100	*Spodoptera litura*	100	Noctuidae	*Spodoptera litura*
BBTH1226-17	SRKk 232019	658	*Condica illecta*	100	*Condica illecta*	100	Noctuidae	*Condica illecta*
BBTH1227-17	SRKk 232020	658	*Hyalobathra brevialis*	99	*Hyalobathra brevialis*	99.49	Crambidae	*Hyalobathra brevialis*
BBTH1228-17	SRKk 232023	658	*Thylacoptila* sp.	98	*Thylacoptila paurosema*	99.39	Pyralidae	*Thylacoptila* sp.1
BBTH1229-17	SRKk 232027	658	*Thylacoptila* sp.	98	*Thylacoptila paurosema*	99.23	Pyralidae	*Thylacoptila* sp.1
BBTH1230-17	SRKk 232029	658	*Thylacoptila* sp.	98	*Thylacoptila paurosema*	99.39	Pyralidae	*Thylacoptila* sp.1
BBTH1231-17	SRKk 232030	658	*Spodoptera litura*	100	*Spodoptera litura*	100	Noctuidae	*Spodoptera litura*
BBTH1232-17	SRKk 232074	658	*Spodoptera litura*	100	*Spodoptera litura*	100	Noctuidae	*Spodoptera litura*
BBTH1233-17	SRKk 232087	658	*Hyalobathra brevialis*	99	*Hyalobathra brevialis*	99.49	Crambidae	*Hyalobathra brevialis*
BBTH1234-17	SRKk 232097	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1235-17	SRKk 232105	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1236-17	SRKk 232111	658	*Chiasmia* sp.	99	*Chiasmia* sp.	99.85	Geometridae	*Chiasmia* sp.1

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH1237-17	SRKk 232115	658	*Eurema hecabe*	99	*Eurema hecabe*	100	Pieridae	*Eurema hecabe*
BBTH1238-17	SRKk 232119	658	*Chiasmia* sp.	99	*Chiasmia* sp.	99.54	Geometridae	*Chiasmia* sp.1
BBTH1239-17	SRKk 232129	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1240-17	SRKk 232132	658	*Chiasmia* sp.	99	*Chiasmia* sp.	99.85	Geometridae	*Chiasmia* sp.1
BBTH1241-17	SRKk 232136	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1242-17	SRKk 232137	526	*Hyalobathra brevialis*	99	*Hyalobathra brevialis*	99.78	Crambidae	*Hyalobathra brevialis*
BBTH1243-17	SRKk 232155	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1244-17	SRKk 232170	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1245-17	SRKk 232182	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1246-17	SRKk 232189	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1247-17	SRKk 232190	658	*Spodoptera litura*	100	*Spodoptera litura*	100	Noctuidae	*Spodoptera litura*
BBTH1248-17	SRKk 232196	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.84	Erebidae	*Rhesalides curvata*
BBTH1249-17	SRKk 232210	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1250-17	SRKk 232211	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.69	Crambidae	*Haritalodes derogata*
BBTH1251-17	SRKk 232222	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1252-17	SRKk 232223	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1253-17	SRKk 232226	658	*Chiasmia* sp.	100	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.1
BBTH1254-17	SRKk 232242	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.69	Crambidae	*Haritalodes derogata*
BBTH1255-17	SRKk 232284	658	*Bastilla amygdalis*	99	-	-	Noctuidae	*Bastilla amygdalis*
BBTH1256-17	SRKk 241030	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.69	Crambidae	*Haritalodes derogata*
BBTH1257-17	SRKk 241031	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.85	Crambidae	*Haritalodes derogata*
BBTH1258-17	SRKk 241038	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.69	Crambidae	*Haritalodes derogata*

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH1259-17	SRKk 241039	658	*Spirama helicina*	99	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH1260-17	SRKk 241043	658	*Zale exhausta*	93	*Zale exhausta*	99.39	Noctuidae	*Zale exhausta*
BBTH1261-17	SRKk 241044	658	*Zale exhausta*	93	*Zale exhausta*	99.39	Noctuidae	*Zale exhausta*
BBTH1262-17	SRKk 242038	658	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH1263-17	SRKk 242041	658	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH1264-17	SRKk 242052	658	*Acontia thapsina*	96	-	-	Noctuidae	*Acontia* sp.1
BBTH1265-17	SRKk 242055	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.85	Crambidae	*Haritalodes derogata*
BBTH1266-17	SRKk 242057	658	*Acontia thapsina*	96	-	-	Noctuidae	*Acontia* sp.1
BBTH1267-17	SRKk 242061	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.85	Crambidae	*Haritalodes derogata*
BBTH1268-17	SRKk 242063	658	*Biston suppressaria*	99	*Biston suppressaria*	100	Geometridae	*Biston suppressaria*
BBTH1269-17	SRKk 242068	658	*Acontia thapsina*	96	-	-	Noctuidae	*Acontia* sp.1
BBTH1270-17	SRKk 242072	658	*Arsacia rectalis*	94	Arsacia rectalis	99.66	Noctuidae	*Arsacia rectalis*
BBTH1271-17	SRKk 242073	658	*Arsacia rectalis*	94	Arsacia rectalis	99.54	Noctuidae	*Arsacia rectalis*
BBTH1272-17	SRKk 242077	658	*Arsacia rectalis*	94	Arsacia rectalis	99.54	Noctuidae	*Arsacia rectalis*
BBTH1273-17	SRKk 242091	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.69	Crambidae	*Haritalodes derogata*
BBTH1274-17	SRKk 242103	658	*Godonela* sp.	99	*Chiasmia nora*	99.54	Geometridae	*Chiasmia nora*
BBTH1275-17	SRKk 242105	658	*Godonela* sp.	99	*Chiasmia nora*	99.54	Geometridae	*Chiasmia nora*
BBTH1276-17	SRKk 251028	658	*Asota caricae*	100	*Asota caricae*	100	Erebidae	*Asota caricae*
BBTH1277-17	SRKk 251067	658	*Asota caricae*	100	*Asota caricae*	100	Erebidae	*Asota caricae*
BBTH1278-17	SRKk 251083	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.84	Erebidae	*Rhesalides curvata*
BBTH1279-17	SRKk 251091	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.68	Erebidae	*Rhesalides curvata*
BBTH1280-17	SRKk 252025	658	*Chiasmia* sp.	98	*Chiasmia* sp.	99	Geometridae	*Chiasmia* sp.3

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH1281-17	SRKk 252034	658	*Herpetogramma stultalis*	100	*Herpetogramma stultalis*	100	Crambidae	*Herpetogramma stultalis*
BBTH1282-17	SRKk 252056	658	*Mocis trifasciata*	99	*Mocis trifasciata*	100	Noctuidae	*Mocis trifasciata*
BBTH1283-17	SRKk 252060	658	*Scopula floslactata*	99.05	*Scopula* sp.	99.05	Geometridae	*Scopula floslactata*
BBTH1284-17	SRKk 252076	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.68	Erebidae	*Rhesalides curvata*
BBTH1589-18	SRKk 342047	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1
BBTH1618-18	SRKk 331082	658	*Eois ambarilla*	94	-	-	Geometridae	*Eois* sp.1
BBTH1619-18	SRKk 331085	658	*Hulodes caranea*	97	*Hulodes caranea*	100	Noctuidae	*Hulodes caranea*
BBTH1620-18	SRKk 341004	658	*Hyperythra rubricata*	95	*Hyperythra lutea*	97.11	Geometridae	*Hyperythra lutea*
BBTH1621-18	SRKk 341005	526	*Melese* sp.	92	*Pantana* sp.	99.39	Erebidae	*Pantana* sp.
BBTH1622-18	SRKk 341014	658	*Progonia* sp.	97	-	-	Erebidae	*Progonia sp.1*
BBTH1623-18	SRKk 341026	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.68	Erebidae	*Rhesalides curvata*
BBTH1624-18	SRKk 341043	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.68	Erebidae	*Rhesalides curvata*
BBTH1626-18	SRKk 341054	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1
BBTH1627-18	SRKk 341065	658	*Dasychira alboschistacea*	92	*Olene mendosa*	99.84	Erebidae	*Olene mendosa*
BBTH1628-18	SRKk 342033	658	*Eilema plana*	96	-	-	Erebidae	*Eilema* sp.1
BBTH1629-18	SRKk 342047	658	*Imma* sp.	91	*Imma* sp.	91.71	Immidae	*Imma* sp.1
BBTH1665-18	SRKk 252083	658	*Herpetogramma stultalis*	100	*Herpetogramma stultalis*	100	Crambidae	*Herpetogramma stultalis*
BBTH1666-18	SRKk 261002	658	*Spirama helicina*	99	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH1667-18	SRKk 261004	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1
BBTH1668-18	SRKk 261019	658	*Chiasmia* sp.	99	*Chiasmia* sp.	100	Geometridae	*Chiasmia* sp.2
BBTH1669-18	SRKk 261037	658	*Godonela* sp.	99	*Chiasmia nora*	99.54	Geometridae	*Chiasmia nora*
BBTH1670-18	SRKk 261049	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH1671-18	SRKk 261057	658	*Castalius rosimon*	100	*Castalius rosimon*	100	Lycaenidae	*Castalius rosimon*
BBTH1672-18	SRKk 261059	658	*Imma* sp.	91	*Imma* sp.	91.71	Immidae	*Imma* sp.1
BBTH1673-18	SRKk 261067	658	*Spirama helicina*	99	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH1674-18	SRKk 261082	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1675-18	SRKk 261086	658	*Arsacia rectalis*	94	Arsacia rectalis	99.66	Noctuidae	*Arsacia rectalis*
BBTH1676-18	SRKk 261087	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1
BBTH1677-18	SRKk 261089	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1
BBTH1678-18	SRKk 261091	658	*Imma* sp.	91	*Imma* sp.	91.71	Immidae	*Imma* sp.1
BBTH1679-18	SRKk 261100	658	*Rhesala sp.*	94	-	-	Erebidae	*Rhesala* sp.1
BBTH1680-18	SRKk 261107	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1681-18	SRKk 261123	658	*Rhesalides curvata*	97	*Rhesalides curvata*	96.68	Erebidae	*Rhesalides curvata*
BBTH1682-18	SRKk 261139	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1
BBTH1683-18	SRKk 262010	658	*Hasora chromus*	100	*Hasora chromus*	100	Hesperiidae	*Hasora chromus*
BBTH1684-18	SRKk 262065	658	*Achaea echo*	93	-	-	Noctuidae	*Achaea* sp.1
BBTH1685-18	SRKk 262077	658	*Tamba* sp.	93	*Haemanota* sp.	93.27	Noctuidae	*Tamba sp.1*
BBTH1686-18	SRKk 262084	658	*Macaria abydata*	100	*Macaria abydata*	100	Geometridae	*Macaria abydata*
BBTH1687-18	SRKk 262121	658	*Achaea echo*	93	-	-	Noctuidae	*Achaea* sp.1
BBTH1688-18	SRKk 262127	658	*Rhesala* sp.	94	-	-	Erebidae	*Rhesala* sp.1
BBTH1689-18	SRKk 262146	658	*Rhesala* sp.	94	-	-	Erebidae	*Rhesala* sp.1
BBTH1690-18	SRKk 262151	658	*Zale exhausta*	93	*Zale exhausta*	93.27	Noctuidae	*Zale exhausta*
BBTH1691-18	SRKk 271005	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1
BBTH1692-18	SRKk 271006	658	*Hyposidra talaca*	98	*Hyposidra talaca*	99.54	Geometridae	*Hyposidra talaca*

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH1693-18	SRKk 271033	658	*Synclera* sp.	97	*Synclera* sp.	97.94	Crambidae	*Synclera* sp.1
BBTH1694-18	SRKk 271050	658	*Dinumma deponens*	94	*Dinumma deponens*	94.34	Erebidae	*Dinumma* sp.1
BBTH1695-18	SRKk 271052	658	*Spirama helicina*	99	*Spirama helicina*	99.85	Erebidae	*Spirama helicina*
BBTH1697-18	SRKk 272024	658	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH1698-18	SRKk 272032	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.69	Crambidae	*Haritalodes derogata*
BBTH1699-18	SRKk 272034	658	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH1700-18	SRKk 272041	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.39	Crambidae	*Haritalodes derogata*
BBTH1701-18	SRKk 272047	658	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH1702-18	SRKk 272051	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.39	Crambidae	*Haritalodes derogata*
BBTH1703-18	SRKk 272055	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.39	Crambidae	*Haritalodes derogata*
BBTH1704-18	SRKk 272057	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.85	Crambidae	*Haritalodes derogata*
BBTH1705-18	SRKk 272062	658	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH1706-18	SRKk 272063	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.69	Crambidae	*Haritalodes derogata*
BBTH1707-18	SRKk 272070	658	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH1708-18	SRKk 272075	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.39	Crambidae	*Haritalodes derogata*
BBTH1709-18	SRKk 272076	658	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH1710-18	SRKk 272081	658	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*
BBTH1711-18	SRKk 272094	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.85	Crambidae	*Haritalodes derogata*
BBTH1712-18	SRKk 272113	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.69	Crambidae	*Haritalodes derogata*
BBTH1713-18	SRKk 281064	658	*Scopula floslactata*	97	*Scopula* sp.	100	Geometridae	*Scopula floslactata*
BBTH1714-18	SRKk 282013	658	*Protonoceras leucocosma*	97	*Protonoceras leucocosma*	97.45	Crambidae	*Protonoceras leucocosma*
BBTH1715-18	SRKk 282044	658	*Condica circuita*	93	-	-	Noctuidae	*Condica* sp.1

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH1716-18	SRKk 282067	658	*Chasmina pulchra*	93	*Chasmina pulchra*	93.72	Noctuidae	*Chasmina* sp.1
BBTH1717-18	SRKk 291019	526	*Haritalodes derogata*	99	*Haritalodes derogata*	99.69	Crambidae	*Haritalodes derogata*
BBTH1718-18	SRKk 291045	658	*Vanicela xenadelpha*	92	-	-	Oecophoridae	*Vanicela* sp.1
BBTH1720-18	SRKk 292010	658	*Thosea sinensis*	93	-	-	Limacodidae	*Thosea* sp.1
BBTH1721-18	SRKk 292017	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1
BBTH1722-18	SRKk 292029	658	*Palthis* sp.	93	-	-	Erebidae	*Palthis sp.1*
BBTH1723-18	SRKk 292033	658	*Rhesala* sp.	94	-	-	Erebidae	*Rhesala* sp.1
BBTH1724-18	SRKk 292036	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1
BBTH1725-18	SRKk 292037	658	*Pycnarmon* sp.	100	*Pycnarmon* sp.	100	Crambidae	*Pycnarmon* sp.
BBTH1726-18	SRKk 301003	658	*Ophyx* sp.	93	*Episparina tortuosalis*	100	Erebidae	*Episparina tortuosalis*
BBTH1727-18	SRKk 301091	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1728-18	SRKk 301092	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1729-18	SRKk 301095	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1730-18	SRKk 301105	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1731-18	SRKk 301108	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1732-18	SRKk 301116	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1
BBTH1733-18	SRKk 301121	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1734-18	SRKk 301132	658	*Imma* sp.	91	*Imma* sp.	91.71	Immidae	*Imma* sp.1
BBTH1735-18	SRKk 301141	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1736-18	SRKk 301144	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1737-18	SRKk 301154	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1738-18	SRKk 302031	658	*Haritalodes derogata*	100	*Haritalodes derogata*	100	Crambidae	*Haritalodes derogata*

Table B - 1 (cont.) Tentative identification (ID) of parasitised caterpillar specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH1739-18	SRKk 302047	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.85	Crambidae	*Haritalodes derogata*
BBTH1740-18	SRKk 302055	658	*Imma* sp.	91	*Imma* sp.	91.71	Immidae	*Imma* sp.1
BBTH1741-18	SRKk 302063	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.85	Crambidae	*Haritalodes derogata*
BBTH1742-18	SRKk 302064	658	*Haritalodes derogata*	99	*Haritalodes derogata*	99.69	Crambidae	*Haritalodes derogata*
BBTH1743-18	SRKk 302066	658	*Hyperstrotia nana*	94	-	-	Noctuidae	*Hyperstrotia* sp.2
BBTH1745-18	SRKk 311042	658	*Imma* sp.	91	*Imma* sp.	91.71	Immidae	*Imma* sp.1
BBTH1747-18	SRKk 311052	658	*Dinumma deponens*	94	*Dinumma deponens*	94.34	Erebidae	*Dinumma* sp.1
BBTH1748-18	SRKk 311066	658	*Dinumma deponens*	94	*Dinumma deponens*	94.34	Erebidae	*Dinumma* sp.1
BBTH1749-18	SRKk 312083	635	*Penicillaria jocosatrix*	99	*Penicillaria jocosatrix*	100	Noctuidae	*Penicillaria jocosatrix*
BBTH1750-18	SRKk 312084	658	*Striglina buergersi*	91	-	-	Thyrididae	*Striglina* sp.1
BBTH1751-18	SRKk 321008	658	*Chiasmia* sp.	99	*Chiasmia* sp.	99.68	Geometridae	*Chiasmia* sp.2
BBTH1752-18	SRKk 321014	658	*Orvasca subnotata*	99	*Orvasca subnotata*	99.85	Erebidae	*Orvasca subnotata*
BBTH1754-18	SRKk 322051	658	*Imma* sp.	91	*Imma* sp.	91.71	Immidae	*Imma* sp.1
BBTH1755-18	SRKk 322076	658	*Orgyia postica*	100	*Orgyia australis*	100	Erebidae	*Orgyia postica*
BBTH1756-18	SRKk 322099	658	*Imma* sp.	91	*Imma* sp.	91.55	Immidae	*Imma* sp.1
BBTH1757-18	SRKk 322102	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1758-18	SRKk 322118	658	*Hyperstrotia flaviguttata*	94	-	-	Noctuidae	*Hyperstrotia* sp.1
BBTH1759-18	SRKk 331075	658	*Cleora repulsaria*	96	*Cleora repulsaria*	99.83	Geometridae	*Cleora repulsaria*

Table B - 2 Tentative identification (ID) of parasitoids specimens using DNA barcoding from Genbank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH001-16	SRKk011038	570	*Snellenius* sp.1	95	Braconidae sp.	99.64	Braconidae	*Snellenius* sp.1
BBTH002-16	PL011001	582	*Holcojoppa mactator*	94	*Holcojoppa mactator*	94.43	Ichneumonidae	*Holcojoppa* sp1
BBTH003-16	SRKk012104	595	Eulophidae sp.1	88	Eulophidae sp.1	100	Eulophidae	Eulophidae sp.1
BBTH004-16	SRKk011060	639	*Eumea caesar*	91	*Eumea caesar*	90.98	Tachinidae	*Eumea* sp.1
BBTH006-16	SS011001	680	*Belvosia* sp.1	91	Tachinidae sp.	92.32	Tachinidae	*Belvosia* sp.1
BBTH007-16	SRKk012027	640	*Drino inconspicua*	93	*Drino solennis*	98.27	Tachinidae	*Drino inconspicua*
BBTH008-16	SRKk012022	679	*Drino inconspicua*	92	*Drino solennis*	98.27	Tachinidae	*Drino inconspicua*
BBTH010-16	SRKk012028	684	*Blepharella lateralis*	97	*Blepharella* sp.	98.62	Tachinidae	*Blepharella* sp.1
BBTH013-16	SRKk021012	635	*Therophilus festivus*	95	*Zosteragathis contrasta*	100	Braconidae	*Zosteragathis contrasta*
BBTH014-16	SRKk021010	669	*Therophilus festivus*	95	*Zosteragathis contrasta*	100	Braconidae	*Zosteragathis contrasta*
BBTH017-16	SRKk021050	651	*Apanteles* sp.1	95	Braconidae sp.	95.83	Braconidae	*Dolichogenidea* sp.11
BBTH018-16	SRKk021054	633	Microgastrinae sp.4	98	*Dolichogenidea* sp.	97.71	Braconidae	*Dolichogenidea* sp.7
BBTH019-16	SRKk021059	681	*Apanteles* sp.4	99	*Apanteles* sp.4	100	Braconidae	*Apanteles* sp.1
BBTH020-16	SRKk021044	679	*Apanteles* sp.1	95	Braconidae sp.	95.79	Braconidae	*Dolichogenidea* sp.11
BBTH022-16	SRKk021063	633	*Apanteles* sp.2	96	*Dolichogenidea* sp.	98.69	Braconidae	*Dolichogenidea* sp.16
BBTH024-16	SRKk022052	681	*Dolichogenidea* sp.2	94	*Dolichogenidea* sp.2	93.65	Braconidae	Microgastrinae sp.2
BBTH025-16	SRKk022052	679	*Dolichogenidea* sp.2	94	*Dolichogenidea* sp.2	93.73	Braconidae	Microgastrinae sp.2
BBTH027-16	SRKk022044	677	*Elachertus* sp.2	90	*Hyssopus nigritulus*	90.97	Eulophidae	*Hyssopus* sp.1
BBTH029-16	SRKk022074	680	*Apanteles* sp.2	97	*Dolichogenidea* sp.	98.69	Braconidae	*Dolichogenidea* sp.16
BBTH030-16	SRKk022072	682	*Therophilus festivus*	95	*Zosteragathis contrasta*	100	Braconidae	*Zosteragathis contrasta*
BBTH032-16	SRKk022075	669	*Therophilus festivus*	95	*Zosteragathis contrasta*	100	Braconidae	*Zosteragathis contrasta*
BBTH033-16	SRKk032019	635	*Enicospilus* sp.1	85	Ichneumonidae sp.1	87.97	Ichneumonidae	*Enicospilus* sp.1

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH034-16	SRKk031015	684	*Apanteles* sp.4	92	Microgastrinae sp.	92.75	Braconidae	*Apanteles* sp.2
BBTH035-16	SRKk031011	671	*Senometopia intermedia*	93	Tachinidae	97.27	Tachinidae	*Senometopia* sp.1
BBTH036-16	SRKk031035	621	*Therophilus festivus*	95	*Zosteragathis contrasta*	100	Braconidae	*Zosteragathis contrasta*
BBTH037-16	SRKk031028	681	Microgastrinae sp.16	93	Glyptapanteles	92.88	Braconidae	*Glyptapanteles* sp.3
BBTH038-16	SRKk031033	675	*Elachertus* sp.6	90	Eulophidae sp.	90.08	Eulophidae	*Elachertus* sp.3
BBTH039-16	SRKk031060	665	Microgastrinae sp.18	97	Braconidae	96.76	Braconidae	*Glyptapanteles* sp.5
BBTH040-16	SRKk031060	680	*Diolcogaster* sp.2	91	*Diolcogaster* sp.2	91.36	Braconidae	*Diolcogaster* sp.1
BBTH041-16	SRKk031059	679	Microgastrinae sp.18	97	Braconidae	96.76	Braconidae	*Glyptapanteles* sp.5
BBTH042-16	SRKk031059	683	*Diolcogaster* sp.2	91	*Diolcogaster* sp.2	91.44	Braconidae	*Diolcogaster* sp.1
BBTH043-16	SRKk031052	682	*Therophilus festivus*	95	*Zosteragathis contrasta*	100	Braconidae	*Zosteragathis contrasta*
BBTH044-16	SRKk031061	641	*Cotesia* sp.2	99	*Cotesia* sp.2	100	Braconidae	*Cotesia* sp.3
BBTH046-16	SRKk031066	606	*Apanteles* sp.2	96	*Dolichogenidea sp.*	98.85	Braconidae	*Dolichogenidea* sp.16
BBTH047-16	SRKk031095	680	*Diolcogaster* sp.1	99	*Diolcogaster* sp.1	99.67	Braconidae	*Diolcogaster* sp.2
BBTH048-16	SRKk031097	633	*Diolcogaster* sp.1	100	*Diolcogaster* sp.1	99.84	Braconidae	*Diolcogaster* sp.2
BBTH049-16	SRKk032115	636	*Elachertus* sp.8	90	Eulophidae	89.71	Eulophidae	*Elachertus* sp.3
BBTH050-16	SRKk032112	619	*Elachertus* sp.8	88	Eulophidae	89.8	Eulophidae	*Elachertus* sp.3
BBTH051-16	SRKk032113	680	*Apanteles* sp.3	93	Dolichogenidea	93.39	Braconidae	*Dolichogenidea* sp.13
BBTH052-16	SRKk032111	606	*Elachertus* sp.7	89	Elachertus	89.57	Eulophidae	*Elachertus* sp.2
BBTH054-16	SRKk032042	678	*Therophilus festivus*	96	*Zosteragathis contrasta*	100	Braconidae	*Zosteragathis contrasta*
BBTH055-16	SRKk032040	684	Lespesia sp.1	92	Tachinidae	100	Tachinidae	*Lespesia* sp.1
BBTH056-16	SRKk032027	602	*Diolcogaster* sp.3	87	Braconidae	95.78	Braconidae	*Diolcogaster* sp.3
BBTH057-16	SRKk032035	573	*Brachymeria femorata*	90	Brachymeria rugosa	92.24	Chalcididae	Brachymeria sp.1

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH058-16	SRKk032025	656	*Euplectrus* sp.4	90	Eulophidae	91	Eulophidae	*Elachertus* sp.3
BBTH060-16	SRKk032049	621	*Dolichogenidea* sp.1	91	Parapanteles	92.11	Braconidae	Microgastrinae sp.1
BBTH061-16	SRKk032061	632	Microgastrinae sp.10	97	Dolichogenidea	96.73	Braconidae	*Dolichogenidea* sp.6
BBTH062-16	SRKk032050	644	Microgastrinae sp.3	96	Dolichogenidea cerialis	97.28	Braconidae	*Dolichogenidea* sp.1
BBTH063-16	SRKk032068	680	Microgastrinae sp.20	97	Glyptapanteles	96.75	Braconidae	*Glyptapanteles* sp.7
BBTH064-16	SRKk032074	680	Microgastrinae sp.5	95	Dolichogenidea	95.22	Braconidae	*Dolichogenidea* sp.18
BBTH065-16	SRKk032082	647	Bethylinae sp.1	90	Bethylinae sp.1	89.33	Bethylidae	Bethylinae sp.1
BBTH066-16	SRKk032077	627	*Elachertus* sp.8	89	Eulophidae	89.6	Eulophidae	*Elachertus* sp.2
BBTH067-16	SRKk032071	652	Microgastrinae sp.9	97	Dolichogenidea	96.73	Braconidae	*Dolichogenidea* sp.6
BBTH068-16	SRKk032071	679	Microgastrinae sp.10	97	Dolichogenidea	96.76	Braconidae	*Dolichogenidea* sp.6
BBTH069-16	SRKk032075	636	*Elachertus* sp.7	89	Eulophidae	88.95	Eulophidae	*Elachertus* sp.2
BBTH070-16	SRKk032066	633	*Euplectrus* sp.5	89	*Hemiptarsenus*	89.19	Eulophidae	*Hemiptarsenus* sp.1
BBTH071-16	SRKk032093	653	*Therophilus festivus*	96	*Zosteragathis contrasta*	100	Braconidae	*Zosteragathis contrasta*
BBTH072-16	SRKk032090	680	Microgastrinae sp.3	96	Dolichogenidea cerialis	97.22	Braconidae	*Dolichogenidea* sp.1
BBTH074-16	SRKk041012	683	*Venturia canescens*	89	Ichneumonidae	92.82	Ichneumonidae	*Venturia* sp.1
BBTH075-16	SRKk041028	684	*Venturia canescens*	90	Ichneumonidae	93.01	Ichneumonidae	*Venturia* sp.1
BBTH078-16	SRKk041075	680	Microgastrinae sp.13	98	Dolichogenidea	97.38	Braconidae	*Dolichogenidea* sp.10
BBTH079-16	SRKk041079	632	Microgastrinae sp.8	99	Dolichogenidea	98.2	Braconidae	*Dolichogenidea* sp.5
BBTH080-16	SRKk042017	679	*Pseudoperichaeta nigrolineata*	99	*Pseudoperichaeta nigrolineata*	98.97	Tachinidae	*Pseudoperichaeta nigrolineata*
BBTH084-16	SRKk042042	679	*Pseudoperichaeta nigrolineata*	99	*Pseudoperichaeta nigrolineata*	98.97	Tachinidae	*Pseudoperichaeta nigrolineata*
BBTH085-16	SRKk042042	623	*Pseudoperichaeta nigrolineata*	99	*Pseudoperichaeta nigrolineata*	98.93	Tachinidae	*Pseudoperichaeta nigrolineata*
BBTH087-16	SRKk042053	626	*Euplectrus* sp.1	90	*Euplectrus* sp.1	90.1	Eulophidae	*Euplectrus* sp.1

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH088-16	SRKk042076	633	*Diolcogaster* sp.5	87	Diolcogaster	88.53	Braconidae	*Diolcogaster* sp.4
BBTH090-16	SRKk042073	678	*Apanteles* sp.5	99	*Apanteles* sp.5	100	Braconidae	*Apanteles* sp.3
BBTH091-16	SRKk042099	683	*Pseudoperichaeta nigrolineata*	99	*Pseudoperichaeta nigrolineata*	98.97	Tachinidae	*Pseudoperichaeta nigrolineata*
BBTH092-16	SRKk042089	647	*Apanteles* sp.6	99	*Apanteles* sp.6	100	Braconidae	*Apanteles* sp.4
BBTH093-16	SRKk042090	679	*Apanteles* sp.6	98	*Apanteles* sp.6	100	Braconidae	*Apanteles* sp.4
BBTH094-16	SRKk042106	680	*Apanteles* sp.6	98	*Apanteles* sp.6	100	Braconidae	*Apanteles* sp.4
BBTH095-16	SRKk051007	627	Microgastrinae sp.22	98	Cotesia	96.89	Braconidae	*Cotesia* sp.1
BBTH287-16	SRKk051010	684	Microgastrinae sp.23	98	Cotesia	97.4	Braconidae	*Cotesia* sp.1
BBTH288-16	SRKk051013	691	*Peribaea tibialis*	89	Tachinidae	92.04	Tachinidae	*Peribaea* sp.1
BBTH289-16	SRKk051011	667	Microgastrinae sp.23	98	Cotesia	97.4	Braconidae	*Cotesia* sp.1
BBTH290-16	SRKk051009	684	Microgastrinae sp.21	98	Cotesia	97.07	Braconidae	*Cotesia* sp.1
BBTH292-16	SRKk051038	682	Microgastrinae sp.24	98	Cotesia	97.24	Braconidae	*Cotesia* sp.1
BBTH293-16	SRKk051030	683	Microgastrinae sp.24	98	Cotesia	97.24	Braconidae	*Cotesia* sp.1
BBTH294-16	SRKk051033	680	Microgastrinae sp.10	97	Dolichogenidea	96.76	Braconidae	*Dolichogenidea* sp.6
BBTH295-16	SRKk051033	683	Microgastrinae sp.6	95	Dolichogenidea	95.52	Braconidae	*Dolichogenidea* sp.3
BBTH296-16	SRKk051037	676	*Euplectrus* sp.3	90	Elachertus	89.25	Eulophidae	*Euplectrus* sp.2
BBTH298-16	SRKk051028	678	*Euplectrus* sp.6	90	Eulophidae	90.03	Eulophidae	*Elachertus* sp.3
BBTH299-16	SRKk051024	656	*Euplectrus* sp.4	90	Eulophidae	91.05	Eulophidae	*Elachertus* sp.3
BBTH300-16	SRKk051050	683	*Orgilus* sp.1	90	*Orgilus* sp.1	90.71	Braconidae	*Orgilus* sp.1
BBTH301-16	SRKk051055	684	Microgastrinae sp.16	93	Glyptapanteles	92.88	Braconidae	*Glyptapanteles* sp.3
BBTH302-16	SRKk051046	686	*Diolcogaster* sp.2	91	Diolcogaster	91.44	Braconidae	*Diolcogaster* sp.1
BBTH303-16	SRKk052038	683	Microgastrinae sp.23	98	Cotesia	97.4	Braconidae	*Cotesia* sp.1

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH304-16	SRKk052041	600	Microgastrinae sp.23	98	Cotesia	97.09	Braconidae	*Cotesia* sp.1
BBTH305-16	SRKk052066	681	Microgastrinae sp.1	97	Dolichogenidea cerialis	99.67	Braconidae	*Dolichogenidea cerialis*
BBTH307-16	SRKk052065	681	Microgastrinae sp.1	97	Dolichogenidea cerialis	99.67	Braconidae	*Dolichogenidea cerialis*
BBTH309-16	SRKk052097	682	*Parapanteles eros*	96	Dolichogenidea	94.39	Braconidae	*Dolichogenidea* sp.14
BBTH310-16	SRKk052098	684	Microgastrinae sp.23	98	Cotesia	97.4	Braconidae	*Cotesia* sp.1
BBTH312-16	SRKk052127	680	Microgastrinae sp.4	96	Dolichogenidea	96.3	Braconidae	*Dolichogenidea* sp.2
BBTH313-16	SRKk052165	683	Microgastrinae sp.6	95	Dolichogenidea cerialis	95.42	Braconidae	*Dolichogenidea* sp.15
BBTH314-16	SRKk061024	682	*Diolcogaster* sp.4	88	Diolcogaster	88.72	Braconidae	*Diolcogaster* sp.4
BBTH315-16	SRKk061042	680	*Cotesia* sp.1	98	Cotesia	98.32	Braconidae	Cotesia ruficrus
BBTH316-16	SRKk061060	673	*Euplectrus* sp.1	90	Eulophidae	90.45	Eulophidae	*Euplectrus* sp.1
BBTH318-16	SRKk061068	684	Microgastrinae sp.17	94	Parapanteles	94.38	Braconidae	*Glyptapanteles* sp.4
BBTH319-16	SRKk061085	684	*Diolcogaster* sp.5	88	Diolcogaster	88.55	Braconidae	*Diolcogaster* sp.4
BBTH321-16	SRKk062039	684	*Cyzenis albicans*	92	Tachinidae	94.01	Tachinidae	*Cyzenis* sp.1
BBTH322-16	SRKk062042	682	*Meteorus* sp.1	99	*Meteorus* sp.1	95.89	Braconidae	*Meteorus* sp.1
BBTH323-16	SRKk062062	683	Microgastrinae sp.18	97	Glyptapanteles	96.08	Braconidae	*Glyptapanteles* sp.5
BBTH324-16	SRKk062062	637	*Cotesia* sp.4	98	*Cotesia* sp.4	98.18	Braconidae	*Cotesia* sp.2
BBTH326-16	SRKk062063	680	Microgastrinae sp.2	97	Dolichogenidea cerialis	98.69	Braconidae	*Dolichogenidea cerialis*
BBTH328-16	SRKk062102	563	Microgastrinae sp.18	96	Glyptapanteles	96.04	Braconidae	*Glyptapanteles* sp.5
BBTH329-16	SRKk062122	684	Microgastrinae sp.19	96	Glyptapanteles	95.42	Braconidae	*Glyptapanteles* sp.5
BBTH332-16	SRKk071026	682	*Venturia canescens*	89	Ichneumonidae	92.91	Ichneumonidae	*Venturia* sp.1
BBTH335-16	SRKk071070	680	*Cotesia* sp.4	98	Cotesia	98.15	Braconidae	*Cotesia* sp.2
BBTH337-16	SRKk072032	684	*Belvosia* sp.2	92	Tachinidae	93.39	Tachinidae	*Belvosia* sp.2

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH338-16	SRKk072053	679	Microgastrinae sp.23	98	Cotesia	97.4	Braconidae	*Cotesia* sp.1
BBTH339-16	SRKk072061	662	Microgastrinae sp.7	94	Dolichogenidea	94.44	Braconidae	*Dolichogenidea* sp.4
BBTH340-16	SRKk072064	683	Microgastrinae sp.14	96	Glyptapanteles creatonoti	95.58	Braconidae	*Glyptapanteles* sp.1
BBTH341-16	SRKk072069	682	Microgastrinae sp.14	96	Glyptapanteles creatonoti	95.58	Braconidae	*Glyptapanteles* sp.1
BBTH342-16	SRKk072070	684	*Potamia* sp.	90	*Potamia* sp.	90.63	Muscidea	*Potamia* sp.1
BBTH343-16	SRKk072084	684	Microgastrinae sp.15	97	Glyptapanteles	96.91	Braconidae	*Glyptapanteles* sp.2
BBTH344-16	SRKk072092	684	Microgastrinae sp.2	97	Dolichogenidea cerialis	98.69	Braconidae	*Dolichogenidea cerialis*
BBTH345-16	SRKk072101	679	*Cotesia* sp.3	98	Cotesia	98.46	Braconidae	*Cotesia* sp.2
BBTH346-16	SRKk072102	683	Microgastrinae sp.17	94	Parapanteles	94.38	Braconidae	*Glyptapanteles* sp.4
BBTH347-16	SRKk081009	680	Microgastrinae sp.24	98	Cotesia	97.24	Braconidae	*Cotesia* sp.1
BBTH348-16	SRKk081011	684	*Wilkinsonellus* sp.2	98	*Wilkinsonellus* sp.2	97.54	Braconidae	*Wilkinsonellus* sp.1
BBTH349-16	SRKk081014	683	*Peribaea tibialis*	90	Agromyzidae	93.11	Tachinidae	*Peribaea* sp.1
BBTH350-16	SRKk081016	683	*Wilkinsonellus* sp.1	97	*Wilkinsonellus* sp.1	97.39	Braconidae	*Wilkinsonellus* sp.1
BBTH351-16	SRKk081026	680	*Wilkinsonellus* sp.2	98	*Wilkinsonellus* sp.2	97.54	Braconidae	*Wilkinsonellus* sp.1
BBTH352-16	SRKk081046	683	*Glyptapanteles* sp.1	98	Glyptapanteles	97.56	Braconidae	*Glyptapanteles* sp.8
BBTH353-16	SRKk081047	621	*Peribaea tibialis*	90	*Agromyzidae* sp.	93.11	Tachinidae	*Peribaea* sp.1
BBTH354-16	SRKk081048	684	*Diadegma semiclausum*	88	Ichneumonidae	92.59	Ichneumonidae	*Diadegma* sp.1
BBTH355-16	SRKk081052	684	*Potamia* sp.	90	*Potamia* sp.	90.63	Muscidea	*Potamia* sp.1
BBTH356-16	SRKk081054	680	*Cotesia* sp.1	98	Cotesia	98.32	Braconidae	*Cotesia ruficrus*
BBTH357-16	SRKk081056	684	*Peribaea tibialis*	90	*Agromyzidae* sp.	92.77	Tachinidae	*Peribaea* sp.1
BBTH358-16	SRKk081057	684	*Peribaea tibialis*	90	*Agromyzidae* sp.	92.77	Tachinidae	*Peribaea* sp.1
BBTH359-16	SRKk081059	650	*Peribaea tibialis*	90	*Agromyzidae* sp.	92.82	Tachinidae	*Peribaea* sp.1

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH360-16	SRKk081059	684	*Peribaea tibialis*	90	*Agromyzidae* sp.	92.77	Tachinidae	*Peribaea* sp.1
BBTH361-16	SRKk081095	683	*Peribaea tibialis*	90	*Agromyzidae* sp.	92.77	Tachinidae	*Peribaea* sp.1
BBTH362-16	SRKk081096	684	*Peribaea tibialis*	90	*Agromyzidae* sp.	92.77	Tachinidae	*Peribaea* sp.1
BBTH365-16	SRKk082027	684	*Venturia canescens*	89	Ichneumonidae	92.83	Ichneumonidae	*Venturia* sp.1
BBTH366-16	SRKk082031	684	Microgastrinae sp.13	98	*Dolichogenidea* sp.	97.38	Braconidae	*Dolichogenidea* sp.10
BBTH367-16	SRKk082037	683	Microgastrinae sp.13	98	*Dolichogenidea* sp.	97.22	Braconidae	*Dolichogenidea* sp.10
BBTH368-16	SRKk082056	684	Microgastrinae sp.13	98	*Dolichogenidea* sp.	97.38	Braconidae	*Dolichogenidea* sp.10
BBTH369-16	SRKk082059	683	*Diolcogaster* sp.2	91	*Diolcogaster* sp.	91.44	Braconidae	*Diolcogaster* sp.1
BBTH370-16	SRKk082061	682	Microgastrinae sp.23	98	*Cotesia* sp.	97.4	Braconidae	*Cotesia* sp.1
BBTH371-16	SRKk082068	680	*Chelonus* sp.1	93	*Chelonus* sp.	99.23	Braconidae	*Chelonus* sp.1
BBTH372-16	SRKk091011	680	Microgastrinae sp.11	95	*Dolichogenidea* sp.	95.37	Braconidae	*Dolichogenidea* sp.8
BBTH375-16	SRKk092003	680	Microgastrinae sp.12	98	*Dolichogenidea* sp.	98.04	Braconidae	*Dolichogenidea* sp.9
BBTH376-16	SRKk092110	683	Microgastrinae sp.12	98	*Dolichogenidea* sp.	98.04	Braconidae	*Dolichogenidea* sp.9
BBTH1000-17	SRKk 101010	658	*Cotesia* sp.3	98	Cotesia sp.3	97.4	Braconidae	*Cotesia* sp.1
BBTH1001-17	SRKk 101033	592	Tachinidae sp.	93	*Chrysoexorista* sp.1	93.3	Tachinidae	*Chrysoexorista* sp.1
BBTH1003-17	SRKk 102008	658	*Apanteles* sp.5	92	*Apanteles* sp.5	92.3	Braconidae	*Apanteles* sp.5
BBTH1015-17	SRKk 102072	642	*Euplectrus* sp.8	97.65	*Euplectrus* sp.8	90	Eulophidae	*Elachertus* sp.3
BBTH1018-17	SRKk 112017	658	*Apanteles* sp.5	92	*Apanteles* sp.5	92.3	Braconidae	*Apanteles* sp.5
BBTH1020-17	SRKk 112031	658	*Cotesia* sp.7	98	*Cotesia* sp.7	99.85	Braconidae	*Cotesia* sp.2
BBTH1022-17	SRKk 121007	658	*Cotesia* sp.5	99	*Cotesia* sp.5	98.32	Braconidae	*Cotesia ruficrus*
BBTH1023-17	SRKk 121010	658	*Cotesia* sp.7	99	*Cotesia* sp.7	98.32	Braconidae	*Cotesia* sp.2
BBTH1025-17	SRKk 122001	658	*Sturmia* sp.1	95	*Sturmia bella*	94.8	Tachinidae	*Sturmia* sp.1

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH1026-17	SRKk 122014	658	Tachinidae sp.2	94	Tachinidae sp.2	94	Tachinidae	Tachinidae sp.2
BBTH1027-17	SRKk 122038	658	*Apanteles* sp.1	89	Braconidae	88.89	Braconidae	*Apanteles* sp.8
BBTH1028-17	SRKk 122041	658	*Houghia* sp.1	93	*Houghia bivittata*	93	Tachinidae	*Houghia* sp.1
BBTH1029-17	SRKk 122075	658	*Apanteles* sp.4	99	*Apanteles* sp.4	99.83	Braconidae	*Apanteles* sp.4
BBTH1030-17	SRKk 131028	658	*Parapanteles athamasae*	96	*Parapanteles* sp.	95.24	Braconidae	*Parapanteles athamasae*
BBTH1031-17	SRKk 131036	658	*Apanteles* sp.6	92	*Apanteles kubensis*	91.69	Braconidae	*Apanteles* sp.6
BBTH1032-17	SRKk 131037	658	*Apanteles* sp.6	92	*Apanteles kubensis*	91.69	Braconidae	*Apanteles* sp.6
BBTH1033-17	SRKk 131043	658	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.3
BBTH1039-17	SRKk 142071	628	*Phanerotoma flava*	93	*Phanerotoma* sp.3	99.15	Braconidae	*Phanerotoma* sp.1
BBTH1040-17	SRKk 142072	658	*Phanerotoma flava*	93	*Phanerotoma* sp.1	98.72	Braconidae	*Phanerotoma* sp.1
BBTH1043-17	SRKk 142084	658	*Iconella* sp.1	93	*Iconella* sp.1	92.91	Braconidae	*Iconella* sp.1
BBTH1045-17	SRKk 142096	658	*Phanerotoma flava*	93	*Phanerotoma* sp.1	98.72	Braconidae	*Phanerotoma* sp.1
BBTH1046-17	SRKk 142108	658	*Phanerotoma* sp.1	93	*Phanerotoma* sp.1	98.72	Braconidae	*Phanerotoma* sp.1
BBTH1047-17	SRKk 151009	658	*Dolichogenidea* sp.7	94	*Dolichogenidea* sp.7	96.76	Braconidae	*Dolichogenidea* sp.6
BBTH1050-17	SRKk 152026	652	*Euplectrus* sp.7	90	*Euplectrus* sp.7	99.38	Eulophidae	*Elachertus* sp.3
BBTH1057-17	SRKk 161019	658	*Dolichogenidea* sp.5	99	*Dolichogenidea* sp.5	97.99	Braconidae	*Dolichogenidea* sp.5
BBTH1061-17	SRKk 172002	658	*Drino inconspicua*	94	Tachinidae sp.	99.39	Tachinidae	*Drino inconspicua*
BBTH1062-17	SRKk 172008	500	*Drino inconspicua*	94	Tachinidae sp.	99.39	Tachinidae	*Drino inconspicua*
BBTH1063-17	SRKk 172010	658	Braconidae sp.1	96	Braconidae sp.	99.15	Braconidae	Braconidae sp.1
BBTH1065-17	SRKk 172015	635	*Dolichogenidea* sp.17	95	*Dolichogenidea* sp.17	97.44	Braconidae	*Dolichogenidea* sp.19
BBTH1066-17	SRKk 172016	658	Braconidae sp.1	96	Braconidae sp.	99.15	Braconidae	Braconidae sp.1
BBTH1067-17	SRKk 181020	658	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.3

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH1068-17	SRKk 182045	658	*Dolichogenidea* sp.16	90	*Iconella andydeansi*	90.55	Braconidae	*Dolichogenidea* sp.17
BBTH1069-17	SRKk 182047	658	*Dolichogenidea* sp.17	90	*Iconella* sp.	90.55	Braconidae	*Dolichogenidea* sp.17
BBTH1070-17	SRKk 182049	658	*Dolichogenidea* sp.18	90	*Iconella* andydeansi	90.55	Braconidae	*Dolichogenidea* sp.17
BBTH1071-17	SRKk 191023	658	*Apanteles* sp.6	92	*Apanteles kubensis*	91.55	Braconidae	*Apanteles* sp.6
BBTH1072-17	SRKk 191029	658	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.3
BBTH1073-17	SRKk 191030	658	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.3
BBTH1074-17	SRKk 191033	658	*Apanteles* sp.6	92	*Apanteles kubensis*	91.69	Braconidae	*Apanteles* sp.6
BBTH1076-17	SRKk 211021	658	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.3
BBTH1079-17	SRKk 201491	658	*Apanteles* sp.6	93	*Phanerotoma* sp.	95.32	Braconidae	*Apanteles* sp.6
BBTH1080-17	SRKk 202285	658	*Apanteles* sp.7	91	*Apanteles brunnistigma*	90.74	Braconidae	*Apanteles* sp.7
BBTH1081-17	SRKk 221023	634	*Chelonus* sp.1	89	*Chelonus* sp.1	88.75	Braconidae	*Chelonus* sp.2
BBTH1082-17	SRKk 221042	658	*Glyptapanteles* sp.9	97	Glyptapanteles sp.9	97.05	Braconidae	*Glyptapanteles* sp.9
BBTH1083-17	SRKk 222086	658	*Phanerotoma flava*	93	*Phanerotoma* sp.2	98.56	Braconidae	*Phanerotoma* sp.1
BBTH1084-17	SRKk 222153	639	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.2
BBTH1085-17	SRKk 222157	658	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.3
BBTH1087-17	SRKk 222173	658	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.3
BBTH1088-17	SRKk 222186	658	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.3
BBTH1089-17	SRKk 222192	658	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.3
BBTH1090-17	SRKk 222197	658	*Apanteles* sp.6	92	*Apanteles kubensis*	91.69	Braconidae	*Apanteles* sp.6
BBTH1091-17	SRKk 222199	658	*Apanteles* sp.6	92	*Apanteles kubensis*	91.69	Braconidae	*Apanteles* sp.6
BBTH1092-17	SRKk 222203	658	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.3
BBTH1093-17	SRKk 222207	658	*Phanerotoma flava*	93	*Phanerotoma* sp.4	95.32	Braconidae	*Phanerotoma* sp.3

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH1094-17	SRKk 222209	658	*Apanteles* sp.6	92	*Apanteles kubensis*	91.69	Braconidae	*Apanteles* sp.6
BBTH1285-17	SRKk 222211	658	*Phanerotoma flava*	93	*Phanerotoma* sp.	95.32	Braconidae	*Phanerotoma* sp.3
BBTH1286-17	SRKk 222212	658	*Apanteles* sp.	92	*Apanteles kubensis*	91.55	Braconidae	*Apanteles* sp.6
BBTH1287-17	SRKk 222214	658	*Apanteles* sp.	91	*Apanteles kubensis*	91.4	Braconidae	*Apanteles* sp.6
BBTH1288-17	SRKk 222221	658	*Apanteles* sp.	92	*Apanteles kubensis*	91.55	Braconidae	*Apanteles* sp.6
BBTH1289-17	SRKk 222231	626	*Euplectrus paulheberti*	89	*Euplectrus paulheberti*	89.11	Eulophidae	*Euplectrus* sp.3
BBTH1290-17	SRKk 231041	658	*Peribaea tibialis*	90	*Phytomyptera* sp.	90.6	Tachinidae	*Peribaea* sp.1
BBTH1291-17	SRKk 231045	658	*Peribaea tibialis*	90	*Phytomyptera* sp.	90.6	Tachinidae	*Peribaea* sp.1
BBTH1292-17	SRKk 231046	658	*Peribaea tibialis*	90	*Phytomyptera* sp.	90.25	Tachinidae	*Peribaea* sp.1
BBTH1295-17	SRKk 231069	658	*Peribaea tibialis*	90	*Phytomyptera* sp.	90.43	Tachinidae	*Peribaea* sp.1
BBTH1296-17	SRKk 231075	652	*Euplectrus* sp.	90	*Euplectrus scottshawi*	89.41	Eulophidae	*Elachertus* sp.3
BBTH1297-17	SRKk 231079	652	Eulophidae sp.	89	-	-	Eulophidae	*Elachertus* sp.3
BBTH1298-17	SRKk 231098	652	Eulophidae sp.	89	-	-	Eulophidae	Eulophidae sp.4
BBTH1299-17	SRKk 231108	652	Eulophidae sp.	89	-	-	Eulophidae	Eulophidae sp.4
BBTH1300-17	SRKk 231116	652	Eulophidae sp.	89	-	-	Eulophidae	Eulophidae sp.4
BBTH1301-17	SRKk 231119	652	Eulophidae sp.	89	-	-	Eulophidae	Eulophidae sp.4
BBTH1302-17	SRKk 231120	652	Eulophidae sp.	89	-	-	Eulophidae	Eulophidae sp.4
BBTH1303-17	SRKk 231121	652	Eulophidae sp.	89	-	-	Eulophidae	Eulophidae sp.4
BBTH1304-17	SRKk 231128	636	Eulophidae sp.	89	Eulophidae sp.	89.1	Eulophidae	Eulophidae sp.3
BBTH1305-17	SRKk 231129	568	Eulophidae sp.	89	Eulophidae sp.	88.77	Eulophidae	Eulophidae sp.5
BBTH1306-17	SRKk 231134	652	Eulophidae sp.	90	Eulophidae sp.	89.81	Eulophidae	Eulophidae sp.4
BBTH1307-17	SRKk 231136	631	Eulophidae sp.	89	Eulophidae sp.	89.28	Eulophidae	Eulophidae sp.5

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH1309-17	SRKk 231142	652	Eulophidae sp.	89	Eulophidae sp.	89.42	Eulophidae	Eulophidae sp.4
BBTH1310-17	SRKk 231143	652	Eulophidae sp.	89	Eulophidae sp.	89.16	Eulophidae	Eulophidae sp.4
BBTH1311-17	SRKk 231144	615	Eulophidae sp.	89	Eulophidae sp.	89.44	Eulophidae	Eulophidae sp.4
BBTH1312-17	SRKk 231147	633	Eulophidae sp.	89	Eulophidae sp.	90.28	Eulophidae	Eulophidae sp.2
BBTH1313-17	SRKk 231167	652	Eulophidae sp.	89	Eulophidae sp.	89.41	Eulophidae	*Euplectrus* sp.3
BBTH1314-17	SRKk 231184	626	*Euplectrus* sp.	89	Eulophidae sp.	88.76	Eulophidae	*Euplectrus* sp.3
BBTH1316-17	SRKk 232005	626	*Exorista xanthaspis*	100	*Exorista xanthaspis*	100	Tachinidae	*Exorista xanthaspis*
BBTH1317-17	SRKk 232006	658	Braconidae sp.	92	Braconidae sp.	91.67	Braconidae	Braconidae sp.2
BBTH1318-17	SRKk 232007	658	Braconidae sp.	92	Braconidae sp.	91.67	Braconidae	Braconidae sp.2
BBTH1319-17	SRKk 232010	658	Braconidae sp.	92	Braconidae sp.	96.6	Braconidae	Braconidae sp.2
BBTH1321-17	SRKk 232015	658	Tachinidae sp.	99	-	-	Tachinidae	Tachinidae sp.4
BBTH1322-17	SRKk 232015	658	Tachinidae sp.	99	-	-	Tachinidae	Tachinidae sp.4
BBTH1323-17	SRKk 232019	658	*Cotesia* sp.	99	*Cotesia ruficrus*	98.66	Braconidae	*Cotesia ruficrus*
BBTH1324-17	SRKk 232020	658	Braconidae sp.	92	-	-	Braconidae	Braconidae sp.2
BBTH1326-17	SRKk 232027	619	Tachinidae sp.	93	-	-	Tachinidae	Tachinidae sp.1
BBTH1327-17	SRKk 232029	658	*Chaetoglossa picticornis*	93	-	-	Tachinidae	Chaetoglossa sp.1
BBTH1328-17	SRKk 232030	658	Tachinidae sp.	99	-	-	Tachinidae	Tachinidae sp.4
BBTH1329-17	SRKk 232074	658	Tachinidae sp.	99	-	-	Tachinidae	Tachinidae sp.4
BBTH1330-17	SRKk 232074	622	Tachinidae sp.	100	-	-	0	Tachinidae sp.5
BBTH1331-17	SRKk 232074	658	Tachinidae sp.	95	-	-	Tachinidae	Tachinidae sp.3
BBTH1332-17	SRKk 232087	658	Braconidae sp.	92	-	-	Braconidae	Braconidae sp.2
BBTH1334-17	SRKk 232105	658	*Peribaea tibialis*	90	*Phytomyptera* sp.	90.6	Tachinidae	*Peribaea* sp.1

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH1335-17	SRKk 232111	633	*Peribaea tibialis*	90	*Phytomyptera* sp.	90.19	Tachinidae	*Peribaea* sp.1
BBTH1336-17	SRKk 232115	658	*Cotesia* sp.	98	*Cotesia ruficrus*	98.15	Braconidae	*Cotesia ruficrus*
BBTH1337-17	SRKk 232119	639	*Peribaea tibialis*	90	*Phytomyptera* sp.	90.43	Tachinidae	*Peribaea* sp.1
BBTH1338-17	SRKk 232129	658	Microgastrinae sp.	97	*Dolichogenidea cerialis*	99.51	Braconidae	*Dolichogenidea cerialis*
BBTH1340-17	SRKk 232136	658	*Peribaea tibialis*	90	*Phytomyptera* sp.	90.43	Tachinidae	*Peribaea* sp.1
BBTH1341-17	SRKk 232137	658	Braconidae sp.	92	-	-	Braconidae	Braconidae sp.2
BBTH1342-17	SRKk 232155	637	*Peribaea tibialis*	90	*Phytomyptera* sp.	90.6	Tachinidae	*Peribaea* sp.1
BBTH1343-17	SRKk 232170	658	*Chelonus* sp.	89	-	-	Braconidae	*Chelonus* sp.5
BBTH1344-17	SRKk 232182	658	*Peribaea tibialis*	90	*Phytomyptera* sp.	90.6	Tachinidae	*Peribaea* sp.1
BBTH1346-17	SRKk 232190	658	*Microplitis* sp.	100	*Microplitis* sp.	99.83	Braconidae	*Microplitis* sp.1
BBTH1347-17	SRKk 232196	658	*Dolichogenidea* sp.	95	*Dolichogenidea* sp.	97.59	Braconidae	*Dolichogenidea* sp.12
BBTH1349-17	SRKk 232211	658	*Apanteles* sp.	98	*Apanteles* sp.	97.02	Braconidae	*Apanteles* sp.4
BBTH1350-17	SRKk 232222	658	*Chelonus* sp.	95	-	-	Braconidae	*Chelonus* sp.4
BBTH1351-17	SRKk 232223	658	*Chelonus* sp.	89	-	-	Braconidae	*Chelonus* sp.5
BBTH1352-17	SRKk 232226	658	*Peribaea tibialis*	90	*Phytomyptera* sp.	90.6	Tachinidae	*Peribaea* sp.1
BBTH1353-17	SRKk 232242	658	*Apanteles* sp.	98	*Apanteles* sp.	97.02	Braconidae	*Apanteles* sp.4
BBTH1354-17	SRKk 232284	626	*Elachertus* sp.	89	-	-	Eulophidae	*Elachertus* sp.1
BBTH1355-17	SRKk 241030	658	Cheloninae sp.	93	-	-	Braconidae	Cheloninae sp.1
BBTH1356-17	SRKk 241031	658	Cheloninae sp.	93	-	-	Braconidae	Cheloninae sp.1
BBTH1357-17	SRKk 241038	658	*Apanteles* sp.	98	*Apanteles* sp.	97.02	Braconidae	*Apanteles* sp.4
BBTH1360-17	SRKk 241044	652	Eulophidae sp.	89	-	-	Eulophidae	Eulophidae sp.4
BBTH1361-17	SRKk 242038	658	Cheloninae sp.	93	-	-	Braconidae	Cheloninae sp.1

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query Sequence	GenBank		BOLD		Final ID	
			ID	%	ID	%	Family	Species
BBTH1362-17	SRKk 242041	658	*Chelonus* sp.	95	-	-	Braconidae	*Chelonus* sp.5
BBTH1363-17	SRKk 242052	658	Microgastrinae sp.	99	*Glyptapanteles* sp.	99.69	Braconidae	*Glyptapanteles* sp.8
BBTH1364-17	SRKk 242055	658	*Chelonus* sp.	89	-	-	Braconidae	*Chelonus* sp.5
BBTH1365-17	SRKk 242057	658	Microgastrinae sp.	97	*Glyptapanteles* sp.	99.69	Braconidae	*Glyptapanteles* sp.8
BBTH1366-17	SRKk 242061	658	*Chelonus* sp.	89	-	-	Braconidae	*Chelonus* sp.5
BBTH1368-17	SRKk 242068	658	Microgastrinae sp.	96	*Glyptapanteles* sp.	99.54	Braconidae	*Glyptapanteles* sp.8
BBTH1369-17	SRKk 242072	658	*Apanteles* sp.	95	*Dolichogenidea* sp.	95.21	Braconidae	*Dolichogenidea* sp.11
BBTH1370-17	SRKk 242073	658	*Chelonus* sp.	91	-	-	Braconidae	*Chelonus* sp.3
BBTH1371-17	SRKk 242077	658	*Apanteles* sp.	95	*Dolichogenidea* sp.	95.21	Braconidae	*Dolichogenidea* sp.11
BBTH1372-17	SRKk 242091	658	*Apanteles* sp.	98	*Apanteles* sp.	97.02	Braconidae	*Apanteles* sp.4
BBTH1374-17	SRKk 242105	652	*Elachertus* sp.	89	-	-	Eulophidae	*Euplectrus* sp.2
BBTH1376-17	SRKk 251067	658	Microgastrinae sp.	98	*Dolichogenidea lacteicolor*	97.69	Braconidae	*Dolichogenidea* sp.5
BBTH1378-17	SRKk 251091	658	*Dolichogenidea* sp.	95	*Dolichogenidea* sp.	97.59	Braconidae	*Dolichogenidea* sp.12
BBTH1570-18	SRKk 321014	658	Microgastrinae sp.	98	*Glyptapanteles* sp.	97.4	Braconidae	*Glyptapanteles* sp.6
BBTH1572-18	SRKk 322051	658	*Potamia* sp.	90	*Pararhinoleucophenga setipes*	90.94	Muscidea	*Potamia* sp.1
BBTH1573-18	SRKk 322076	658	*Cotesia* sp.	98	*Cotesia* sp.	98.46	Braconidae	*Cotesia* sp.2
BBTH1574-18	SRKk 322099	658	*Aleiodes* sp.	90	-	-	Braconidae	*Aleiodes* sp.1
BBTH1575-18	SRKk 322102	658	Microgastrinae sp.	95	-	-	Braconidae	Microgastrinae sp.4
BBTH1576-18	SRKk 322118	658	Microgastrinae sp.	95	-	-	Braconidae	Microgastrinae sp.4
BBTH1577-18	SRKk 331075	658	*Glyptapanteles* sp.	96	-	-	Braconidae	*Glyptapanteles* sp.10
BBTH1578-18	SRKk 331082	658	Microgastrinae sp.	92	-	-	Braconidae	Microgastrinae sp.3
BBTH1580-18	SRKk 341004	658	*Casinaria* sp.	92	-	-	Ichneumonidae	*Casinaria* sp.1

Table B - 2 (cont.) Tentative identification (ID) of parasitoids specimens using DNA barcoding from GenBank and BOLD databases, ABGD and phylogenetic tree

Code	Sample ID	Query	GenBank		BOLD		Final ID	
		Sequence	ID	%	ID	%	Family	Species
BBTH1581-18	SRKk 341005	658	*Enicospilus* sp.	94	-	-	Ichneumonidae	*Enicospilus* sp.1
BBTH1582-18	SRKk 341014	658	*Siphona hokkaidensis*	89	-	-	Tachinidae	*Siphona* sp.1
BBTH1585-18	SRKk 341052	658	Microgastrinae sp.	97	-	-	Braconidae	*Glyptapanteles* sp.9
BBTH1586-18	SRKk 341054	648	Microgastrinae sp.	99	-	-	Braconidae	*Glyptapanteles* sp.3
BBTH1588-18	SRKk 342033	658	*Aleiodes divergerus*	98	*Aleiodes contemptus*	100	Braconidae	*Aleiodes contemptus*
BBTH1581-18	SRKk 341005	658	*Enicospilus* sp.	94	-	-	Ichneumonidae	*Enicospilus* sp.1
BBTH1582-18	SRKk 341014	658	*Siphona hokkaidensis*	89	-	-	Tachinidae	*Siphona* sp.1
BBTH1585-18	SRKk 341052	658	Microgastrinae sp.	97	-	-	Braconidae	*Glyptapanteles* sp.9

APPENDIX C

PHYSICAL FACTORS BY THAI METEOROLOGICAL DEPARTMENT

Table C-1 Average temperature, humidity, precipitation and wind speed recorded by Thai Meteorological Department (Lopburi Provincial Agrometeorological Station) during November 2015 – November 2016

Year	Month	Thai Meteorological Department Data			
		Average of temperature (°C)	Average of humidity (%)	Precipitation (mm)	Wind (Knots)
2015	November	29.55	73	163.9	2.4
	December	27.35	69	7.8	2.1
2016	January	27.3	69	54.8	2
	February	28.2	56	0	4.2
	March	31.45	62	2.6	2.8
	April	33.45	62	37.4	3.1
	May	33	64	28.1	2.5
	June	30.85	73	129.2	1.8
	July	29.6	79	309	1.5
	August	30.15	76	201.1	1.8
	September	29.4	81	199.9	1.5
	October	29.2	82	118.7	1.4
	November	29.05	70	42.4	2.7

APPENDIX D

PHOTOGRAPH OF LEPIDOPTERAN HOSTS AND THEIR PARASITOIDS

Figure D - 1 Photograph of the parasitised caterpillars in family Crambidae; A, *Haritalodes derogate*; B, *Hyalobathra brevialis*; C, *Notarcha aurolinealis*; D, *Notarcha obrinusalis*; E, *Orthospila* sp.1; F, *Paliga damastesalis*; G, *Parotis marinata*; H, *Parotis* sp.1

Figure D - 1 (cont.) Photograph of the parasitised caterpillars in family Crambidae; I, *Pyrausta panopealis*; J, *Herpetogramma platycapna*; K, *Herpetogramma* sp.1; L, *Herpetogramma stultalis*; M, *Notarcha* sp.1; N, *Orthospila orissusalis*; O, *Orthospila* sp.1; P, *Protonoceras leucocosma*

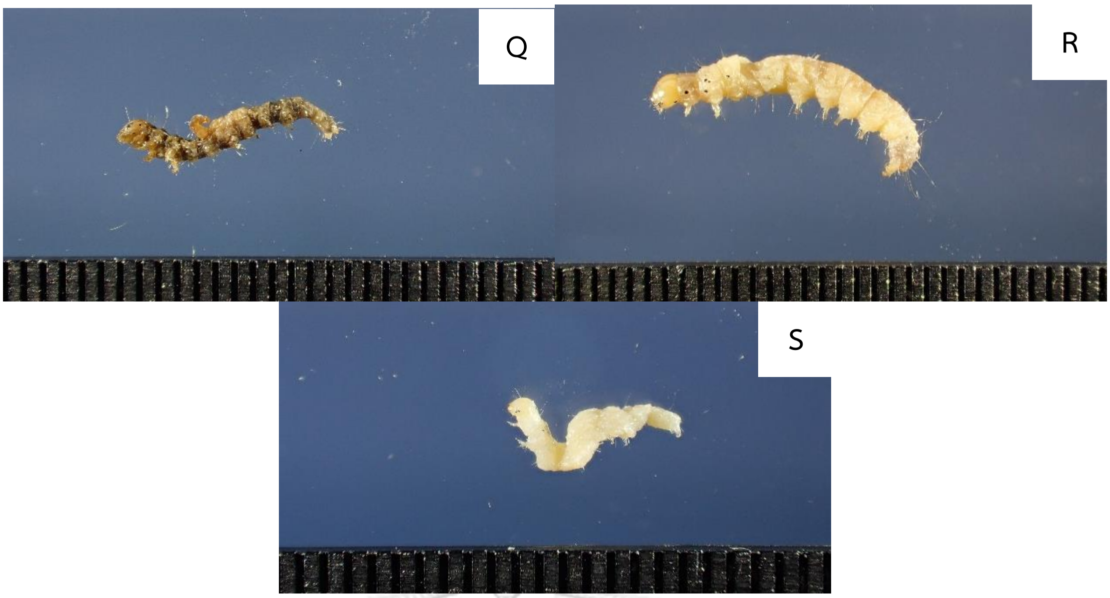

Figure D - 1 (cont.) Photograph of the parasitised caterpillars in family Crambidae; Q, *Pycnarmon* sp.; R, *Synclera* sp.1; S, *Spilomelinae* sp.1

Figure D - 2 Photograph of the parasitised caterpillars in family Elachistidae; A, *Antaeotricha* sp.1

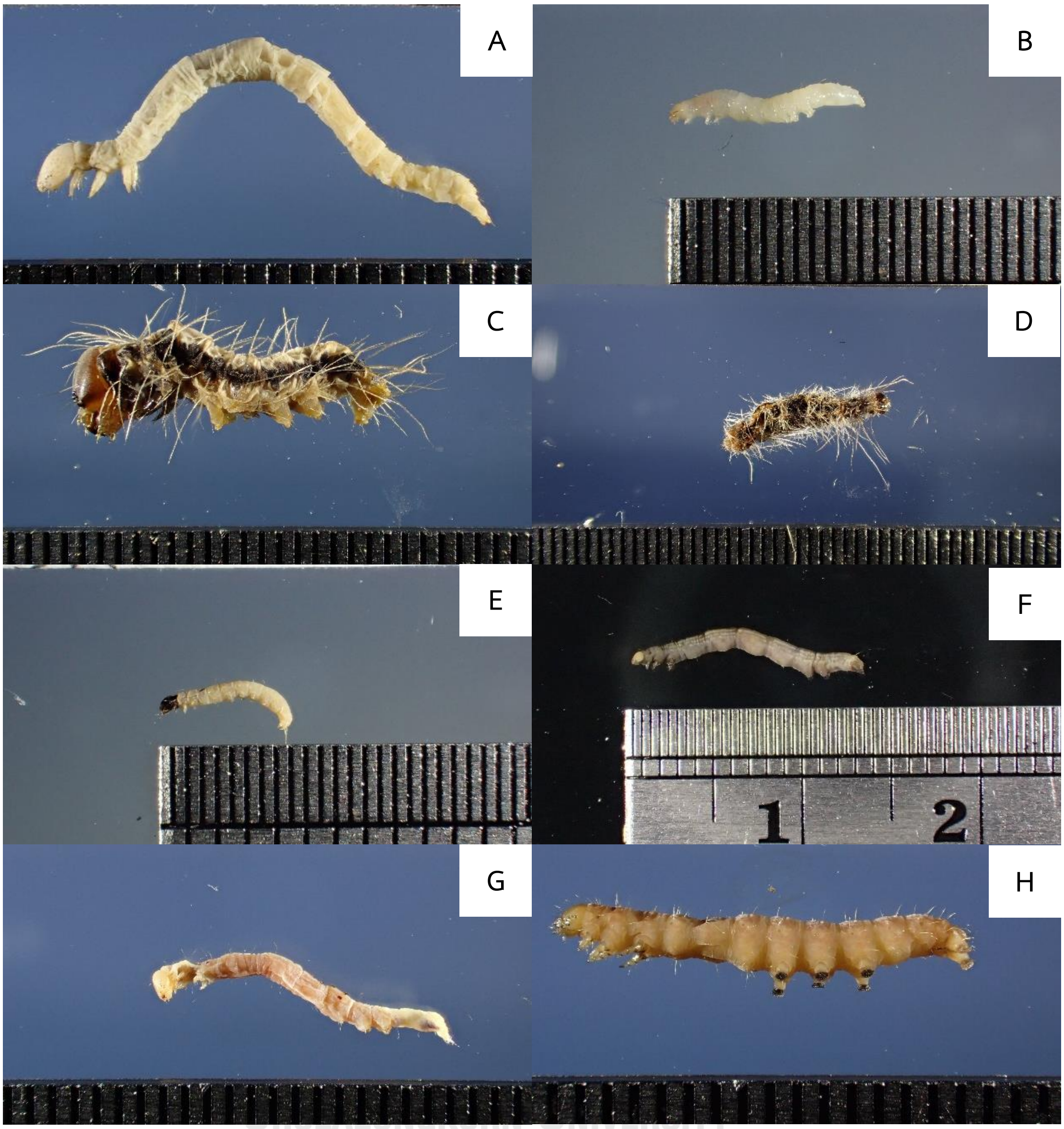

Figure D - 3 Photograph of the parasitised caterpillars in family Erebidae; A, *Dinumma* sp.1; B, *Asota* sp.1; C, *Asota caricae*; D, *Eilema* sp.1; E, *Ormetica* sp.1; F, *Condate* sp.1; G, *Plecoptera reflexa*; H, *Rhesala* sp.1

Figure D - 3 (cont.) Photograph of the parasitised caterpillars in family Erebidae; I, *Arctia virginalis*; J, *Episparina tortuosalis*; K, *Rhesalides curvata*; L, *Avitta ophiusalis*; M, *Spirama helicina*; N, *Palthis* sp.1; O, *Olene mendosa*

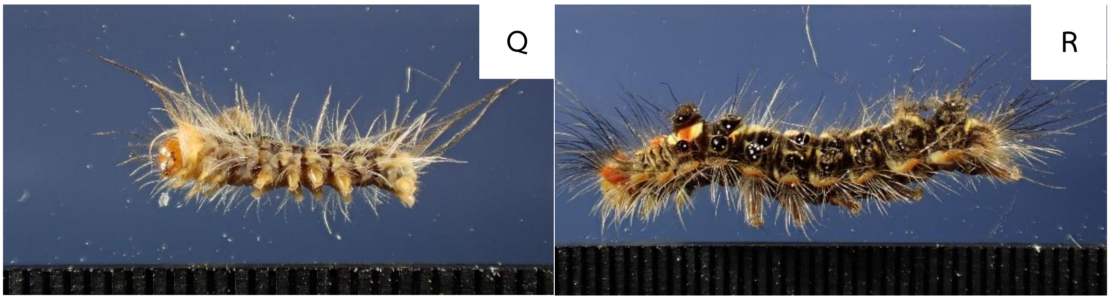

Figure D - 3 (cont.) Photograph of the parasitised caterpillars in family Erebidae; Q, *Orgyia postica*; R, *Orvasca subnotata*;

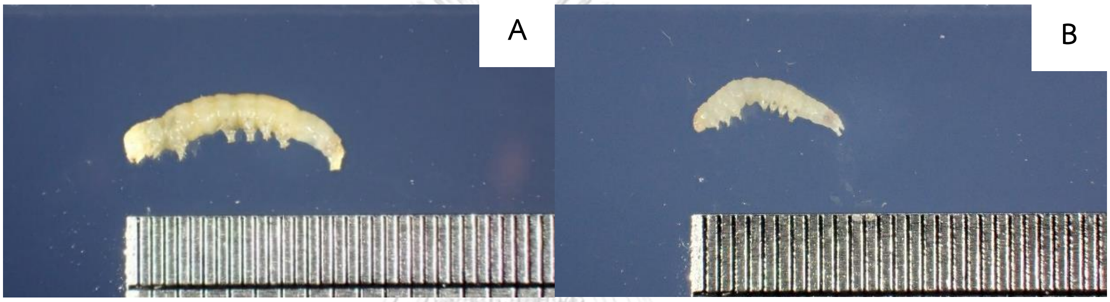

Figure D - 4 Photograph of the parasitised caterpillars in family Euteliidae; A, Euteliidae sp.1; B, Euteliidae sp.2

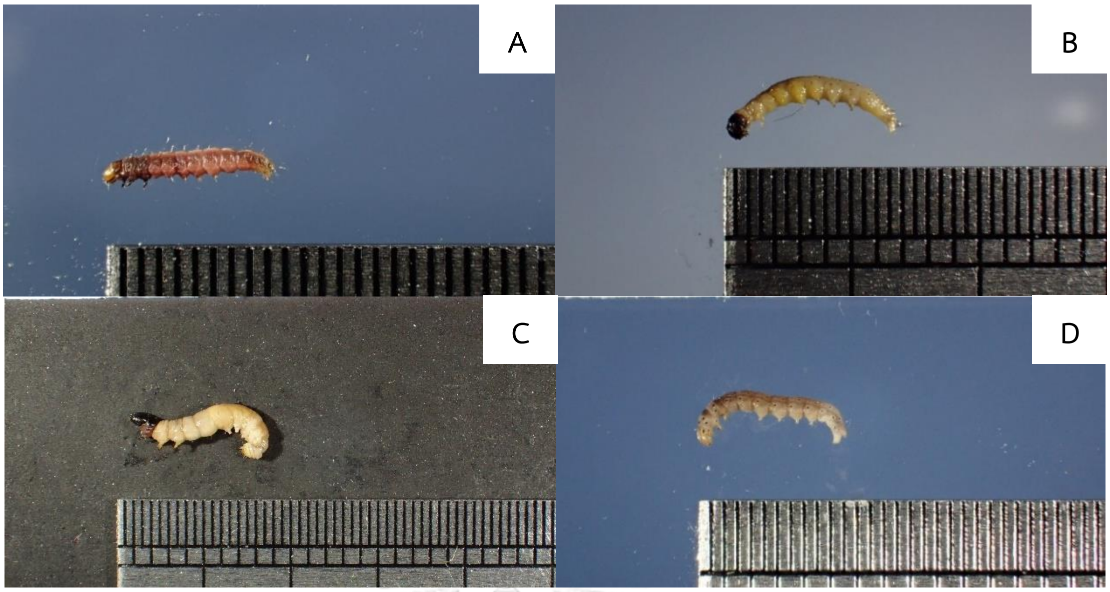

Figure D - 5 Photograph of the parasitised caterpillars in family Gelechiidae; A, *Anarsia* sp.1; B, *Ardozyga* sp.1; C, Gelechiidae sp.1; D, Gelechiidae sp.2

Figure D - 6 Photograph of the parasitised caterpillars in family Geometridae; A, *Chiasmia nora*; B, *Synegia* sp.1; C, *Casbia* sp.1; D, *Ascotis selenaria*

Figure D - 6 (cont.) Photograph of the parasitised caterpillars in family Geometridae; E, *Biston suppressaria*; F, *Chiasmia* sp.1; G, *Chiasmia* sp.2; H, *Chiasmia* sp.3; I, *Cleora repulsaria*; J, *Hyposidra talaca*; K, *Macaria abydata*; L, *Petelia medardaria*

Figure D - 6 (cont.) Photograph of the parasitised caterpillars in family Geometridae; L, *Petelia paroobathra*; M, *Chlorocoma* sp.1; N, *Hemithea* sp.1; O, *Spaniocentra* sp.1; P, *Chloroclystis ablechra*; Q, *Eois* sp.1; R, *Scopula floslactata*

Figure D - 7 Photograph of the parasitised caterpillars in family Gracilariidae; A, Gracillariidae sp.1

Figure D - 8 Photograph of the parasitised caterpillars in family Hesperiidae; A, *Hasora chromus*

Figure D - 9 Photograph of the parasitised caterpillars in family Hyblaeidae; A, *Hyblaea puera*

Figure D - 10 Photograph of the parasitised caterpillars in family Immidae; A, *Imma* sp.1

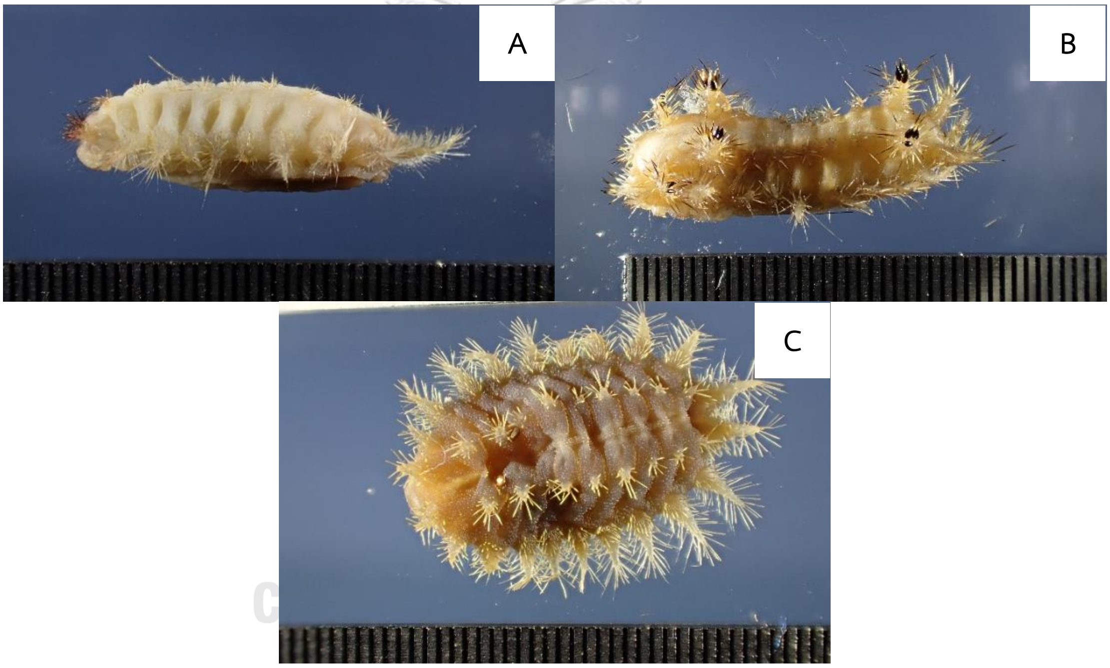

Figure D - 11 Photograph of the parasitised caterpillars in family Limacodidae; A, *Darna sybilla*; B, *Thosea* sp.1; C, *Parasa media*

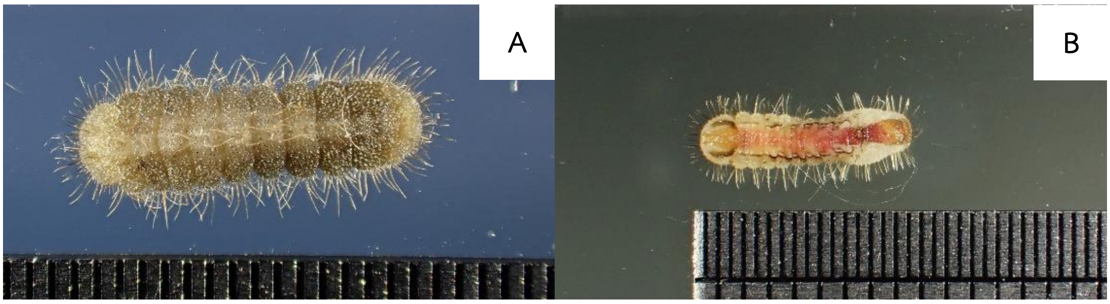

Figure D - 12 Photograph of the parasitised caterpillars in family Lycaenidae; A, *Castalius rosimon*; B, *Arhopala pseudocentaurus*

Figure D - 13 Photograph of the parasitised caterpillars in family Noctuidae; A, *Plusiopalpa adrasta*; B, *Condica illecta*; C, *Spodoptera litura*; D, Acontia sp.1; E, *Hyperstrotia* sp.1; F, *Hyperstrotia* sp.2

Figure D - 13 (cont.) Photograph of the parasitised caterpillars in family Noctuidae; G, *Callyna* sp.1; H, *Chasmina* sp.1; I, *Chasmina tenuilinea*; J, *Condica* sp.1; K, *Amyna axis*; L, *Xanthodes* sp.1; M, *Achaea* sp.1; N, *Arsacia rectalis*

Figure D - 13 (cont.) Photograph of the parasitised caterpillars in family Noctuidae; O, *Bastilla amygdalis*; P, *Hulodes caranea*; Q, *Hypospila bolinoides*; R, *Marcipa* sp.1; S, *Mocis trifasciata*; T, *Plecoptera quaesita*; U, *Plecoptera reflexa*; V, *Spirama helicina*

Figure D - 13 (cont.) Photograph of the parasitised caterpillars in family Noctuidae; W, *Tamba* sp.1; X, *Zale exhausta*; Y, *Condica illecta*; Z, *Pericyma mendax*; AA, *Penicillaria jocosatrix*; AB, *Chrysodeixis eriosoma*

Figure D - 14 Photograph of the parasitised caterpillars in family Nolidae; A, *Selepa* sp.1

Figure D - 15 Photograph of the parasitised caterpillars in family Nymphalidae; A, *Danaus chrysippus*

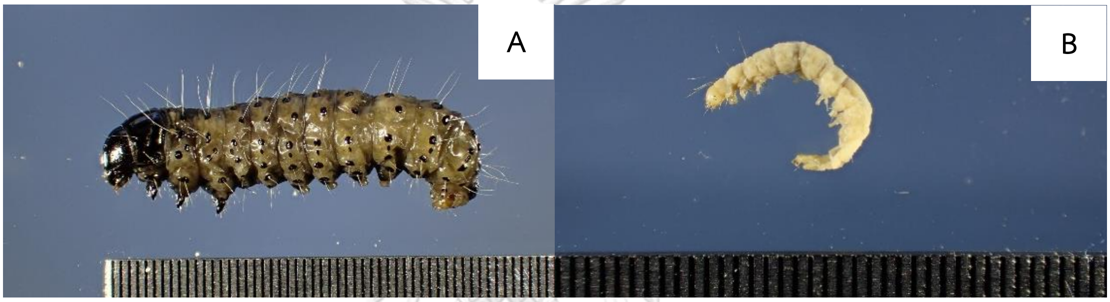

Figure D - 16 Photograph of the parasitised caterpillars in family Oecophoridae; A, *Compsotropha* sp.1; B, *Vanicela* sp.1

Figure D - 17 Photograph of the parasitised caterpillars in family Papilionidae; A, Papilio clytia

Figure D - 18 Photograph of the parasitised caterpillars in family Pieridae; A, *Eurema hecabe*

Figure D - 19 Photograph of the parasitised caterpillars in family Pterophoridae; A, *Tylochares* sp.1

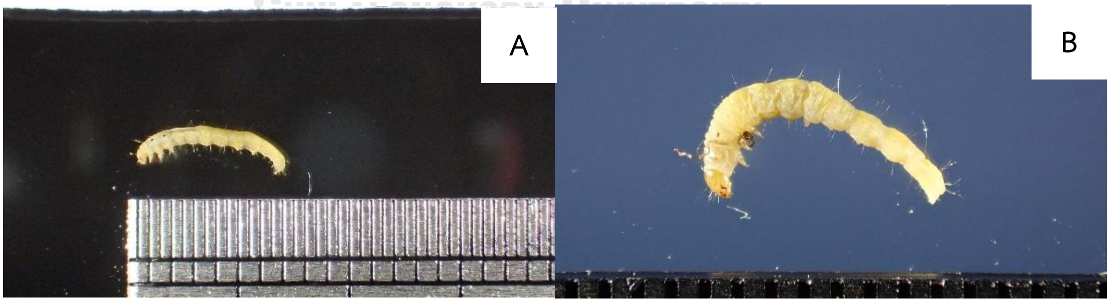

Figure D - 20 Photograph of the parasitised caterpillars in family Pyralidae; A, *Tylochares* sp.1; B, *Assara* sp.1

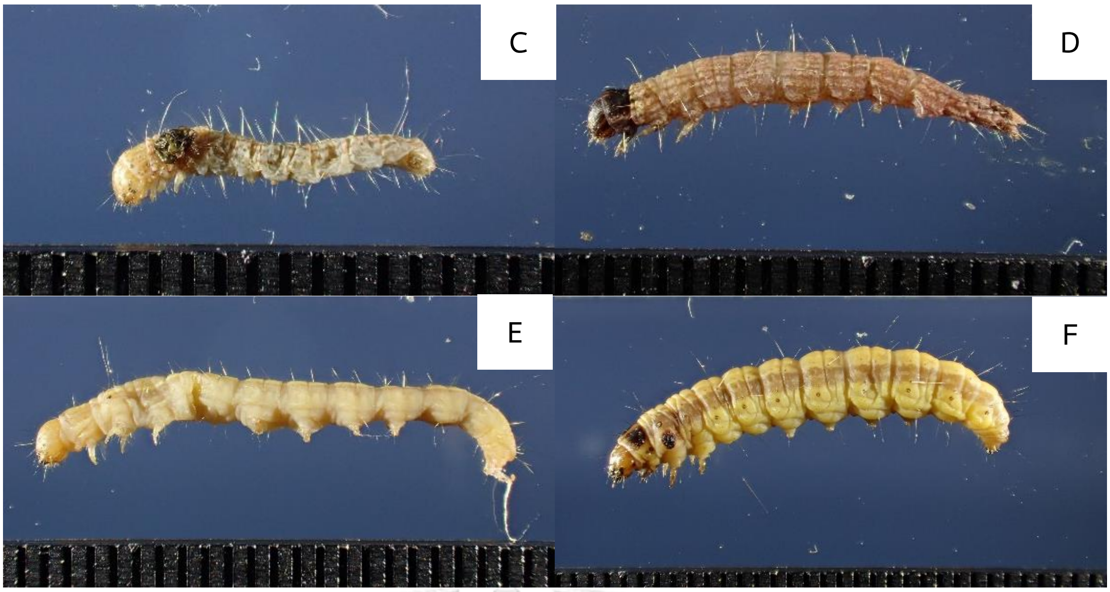

Figure D - 20 (cont.) Photograph of the parasitised caterpillars in family Pyralidae; C, *Phycita* sp.1; D, *Ptyobathra atrisquamella*; E, *Sciota virgatella*; F, *Thylacoptila* sp.1

Figure D - 21 Photograph of the parasitised caterpillars in family Saturniidae; A, *Attacus atlas*

Figure D - 22 Photograph of the parasitised caterpillars in family Sphingidae; A, *Macroglossum belis*

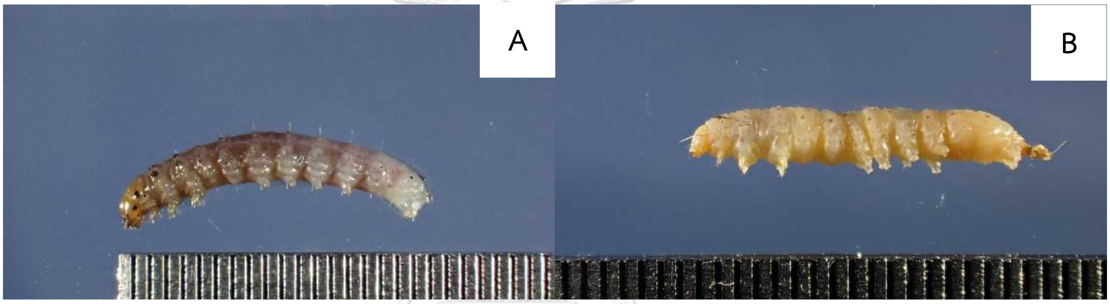

Figure D - 23 Photograph of the parasitised caterpillars in family Thyrididae; A, *Picrostomastis subrosealis*; B. *Striglina* sp.1

Figure D - 24 Photograph of the parasitised caterpillars in family Tortricidae; A, *Archips machlopis*

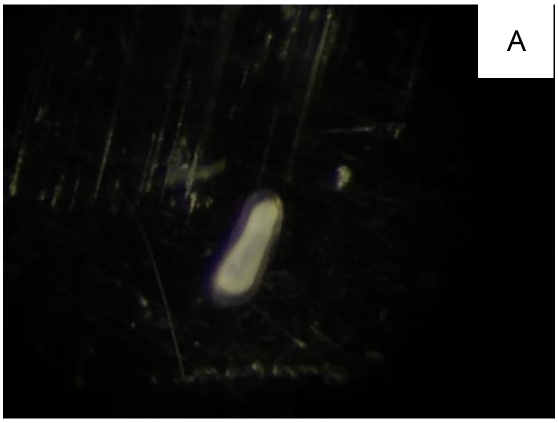

Figure D - 25 Photograph of the parasitoids in family Bethylidae, subfamily Bethylinae; A, Bethylinae sp.1

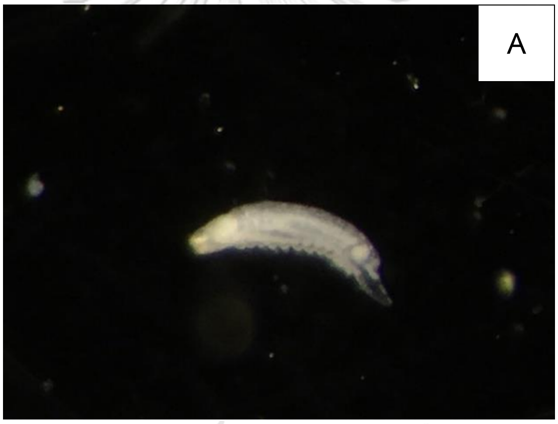

Figure D 26 Photograph of the parasitoids in family Braconidae, subfamily Agathidinae; A, *Zosteragathis contrasta*

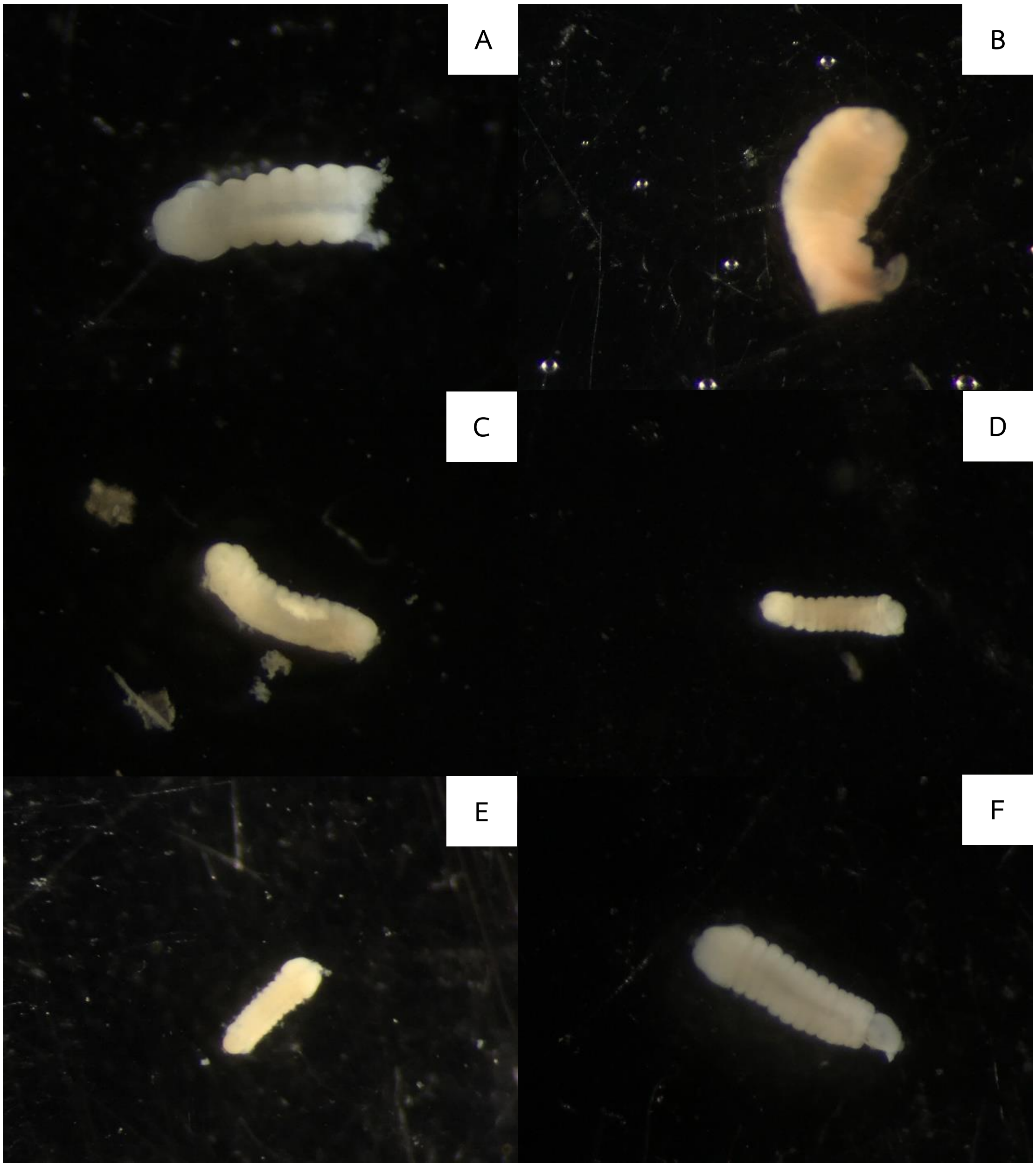

Figure D - 27 Photograph of the parasitoids in family Braconidae, subfamily Cheloninae; A, *Chelonus* sp.1; B, *Chelonus* sp.2; C, *Chelonus* sp.3; D, *Chelonus* sp.4; E, *Chelonus* sp.5; F, *Phanerotoma* sp.1

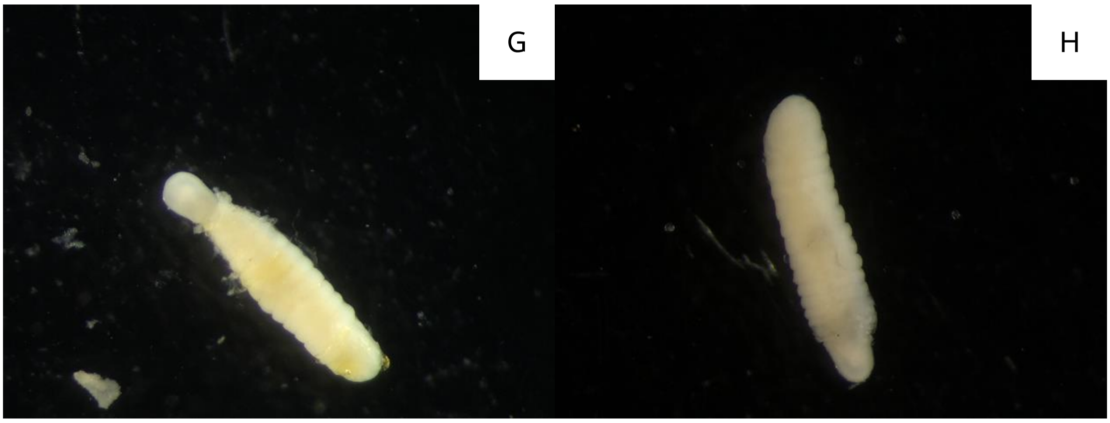

Figure D - 27 (cont.) Photograph of the parasitoids in family Braconidae, subfamily Cheloninae; G, *Phanerotoma* sp.2; H, *Phanerotoma* sp.3

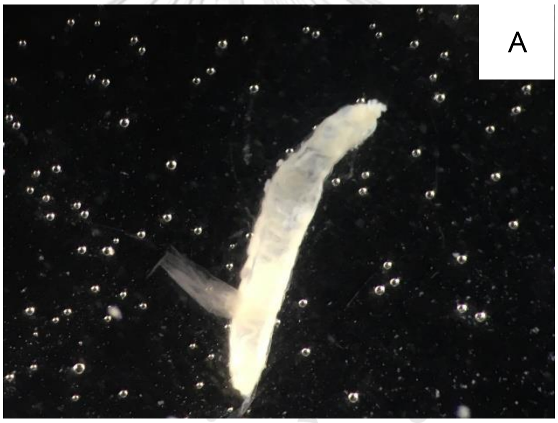

Figure D - 28 Photograph of the parasitoids in family Braconidae, subfamily Meteorinae; A. *Meteorus* sp.1

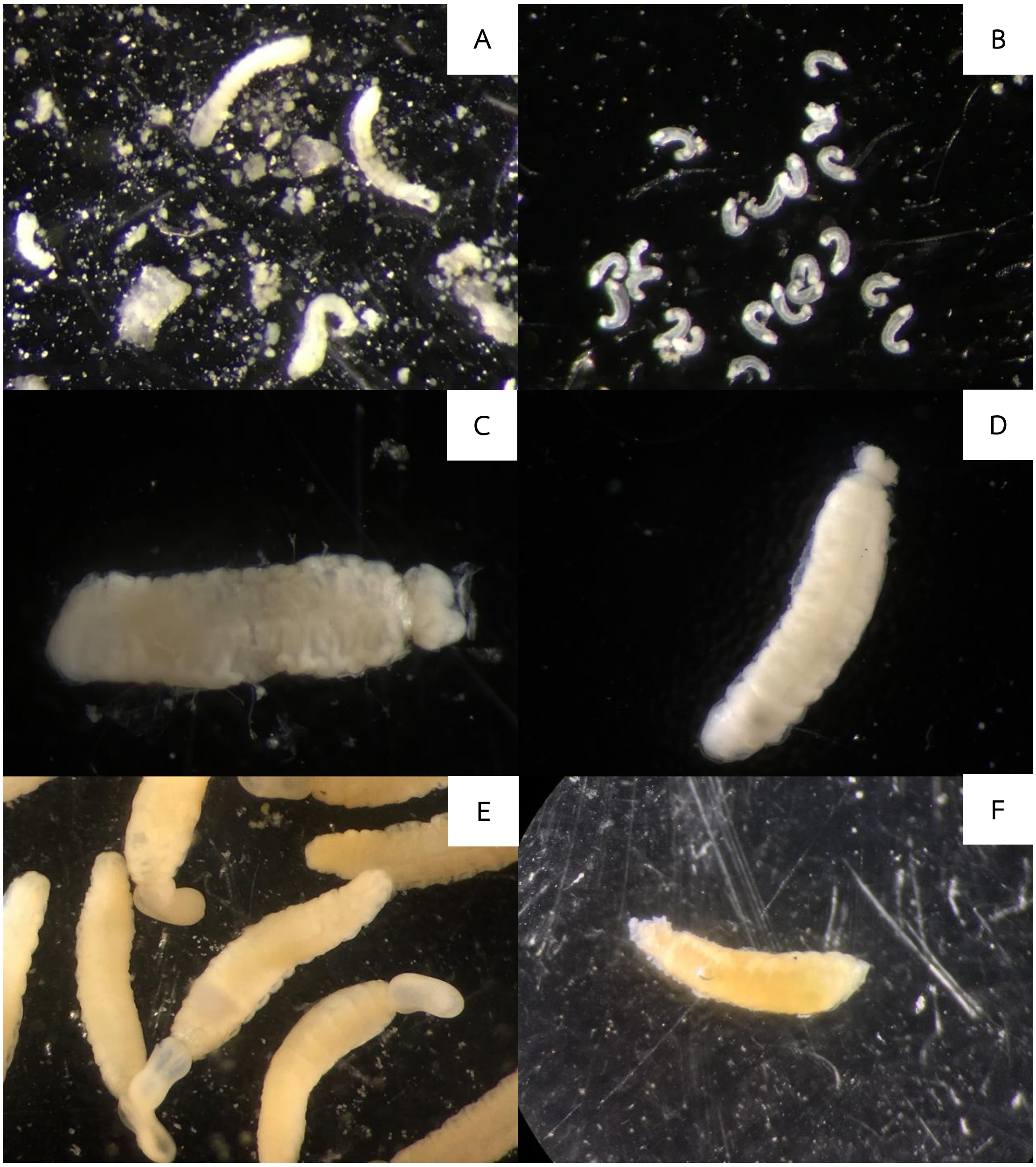

Figure D - 29 Photograph of the parasitoids in family Braconidae, subfamily Microgastrinae; A. *Apanteles* sp.1; B, *Apanteles* sp.2; C, *Apanteles* sp.3; D, *Apanteles* sp.4; E, *Apanteles* sp.5; F, *Apanteles* sp.6

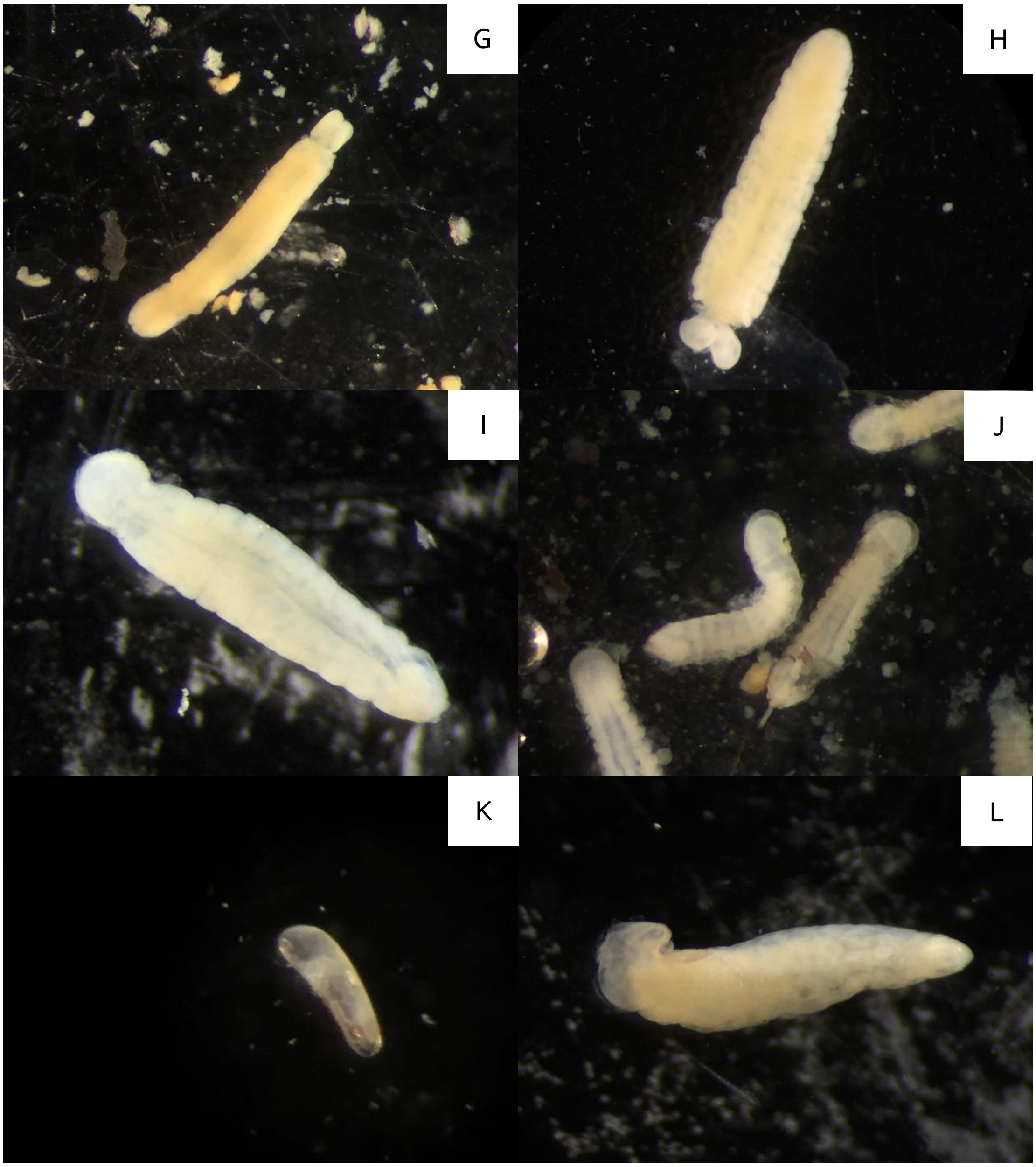

Figure D - 29 (cont.) Photograph of the parasitoids in family Braconidae, subfamily Microgastrinae; G. *Apanteles* sp.7; H, *Apanteles* sp.8; I, *Cotesia ruficrus*; J, *Cotesia* sp.1; K, *Cotesia* sp.2; L, *Cotesia* sp.3

Figure D - 29 (cont.) Photograph of the parasitoids in family Braconidae, subfamily Microgastrinae; M. *Diolcogaster* sp.1; N, *Diolcogaster* sp.2; O, *Diolcogaster* sp.3; P, *Diolcogaster* sp.4; Q, *Dolichogenidea cerialis*; R, *Dolichogenidea* sp.1

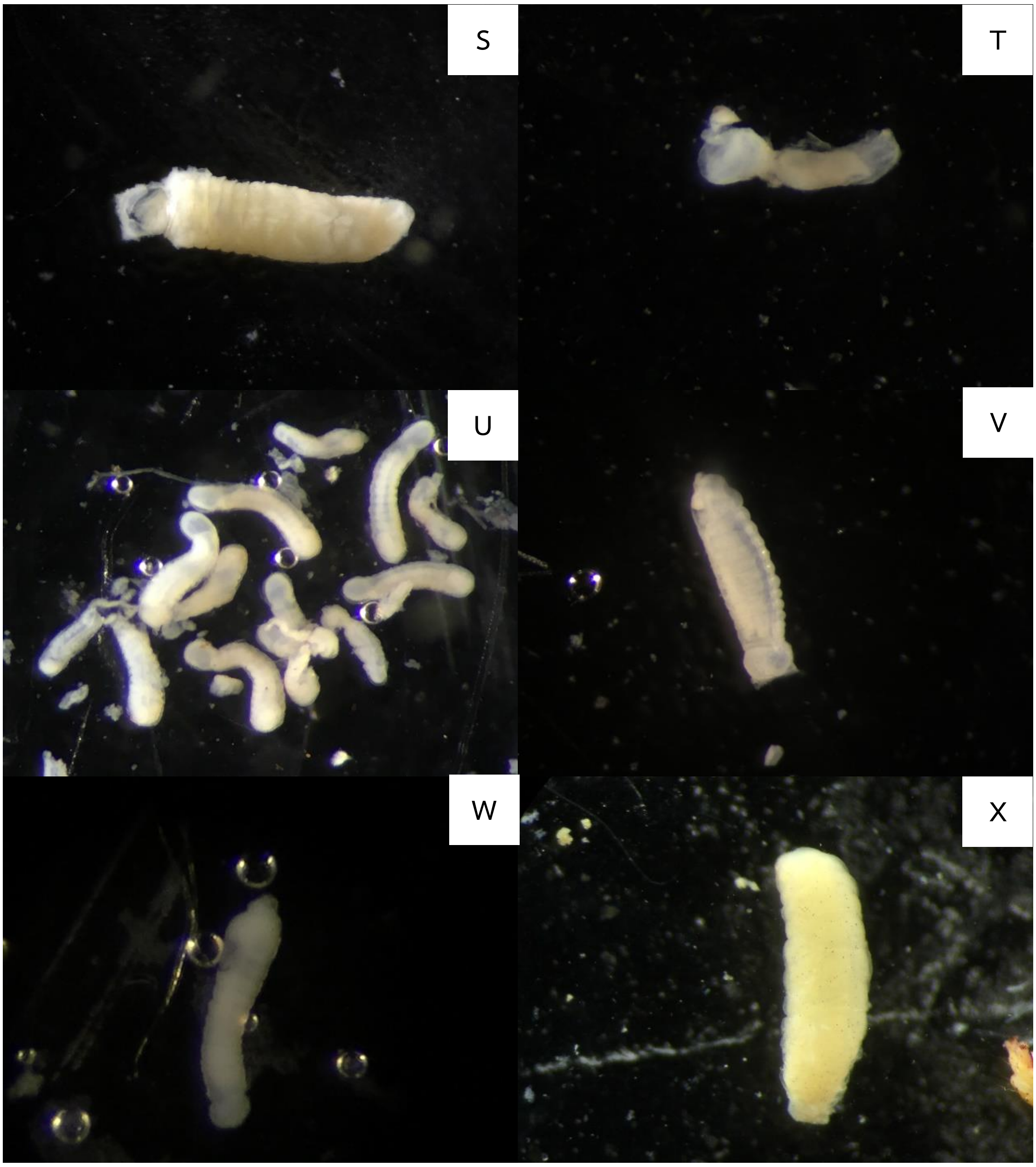

Figure D - 29 (cont.) Photograph of the parasitoids in family Braconidae, subfamily Microgastrinae; S. *Dolichogenidea* sp.2; T, *Dolichogenidea* sp.3; U, *Dolichogenidea* sp.4; V, *Dolichogenidea* sp.5; W, *Dolichogenidea* sp.6; X, *Dolichogenidea* sp.7

Figure D - 29 (cont.) Photograph of the parasitoids in family Braconidae, subfamily Microgastrinae; Y. *Dolichogenidea* sp.8; Z, *Dolichogenidea* sp.9; AA, *Dolichogenidea* sp.10; AB, *Dolichogenidea* sp.11; AC, *Dolichogenidea* sp.12; AD, *Dolichogenidea* sp.13

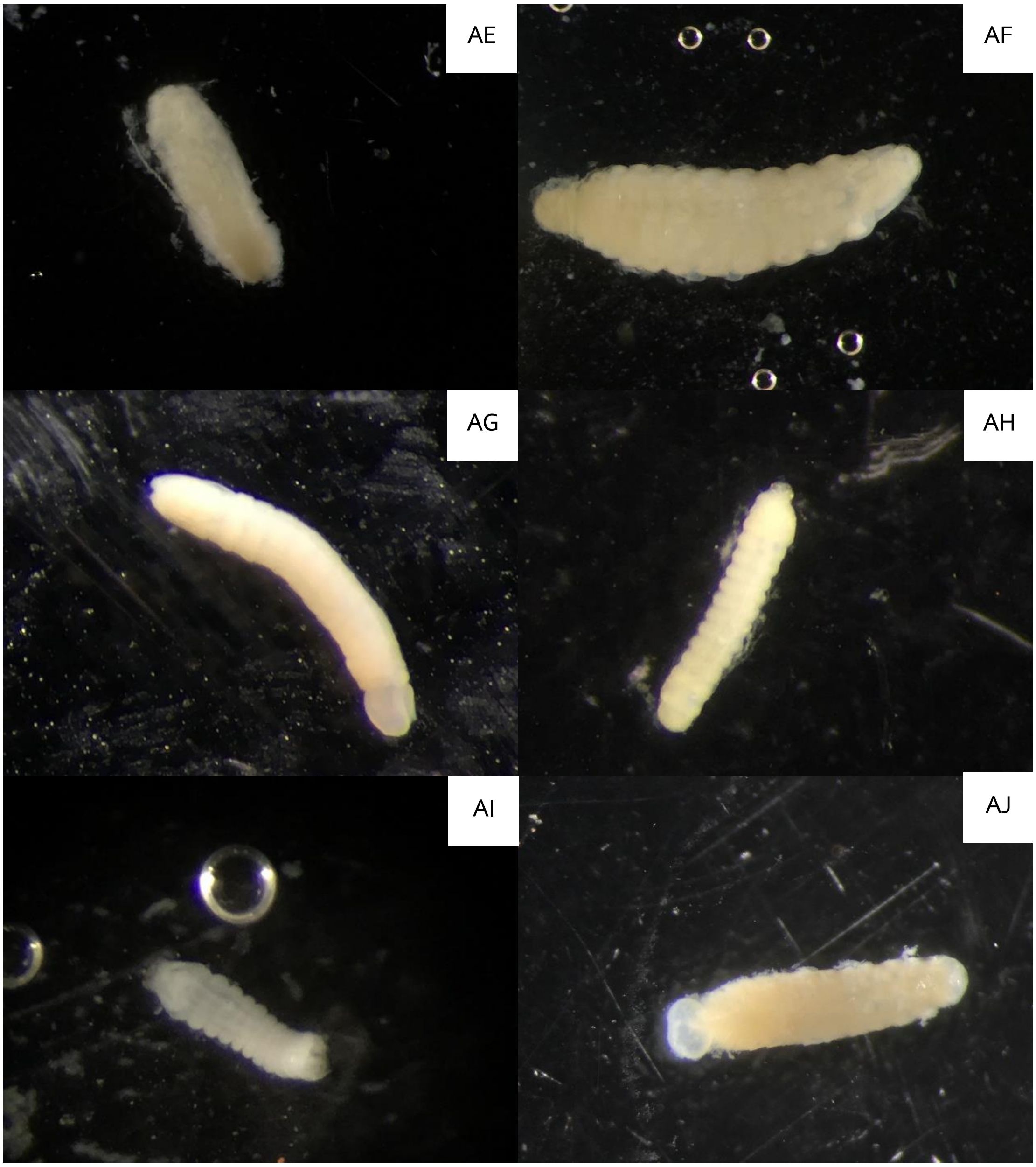

Figure D - 29 (cont.) Photograph of the parasitoids in family Braconidae, subfamily Microgastrinae; AE. *Dolichogenidea* sp.14; AF, *Dolichogenidea* sp.15; AG, *Dolichogenidea* sp.16; AH, *Dolichogenidea* sp.17; AI, *Dolichogenidea* sp.18; AJ, *Dolichogenidea* sp.19

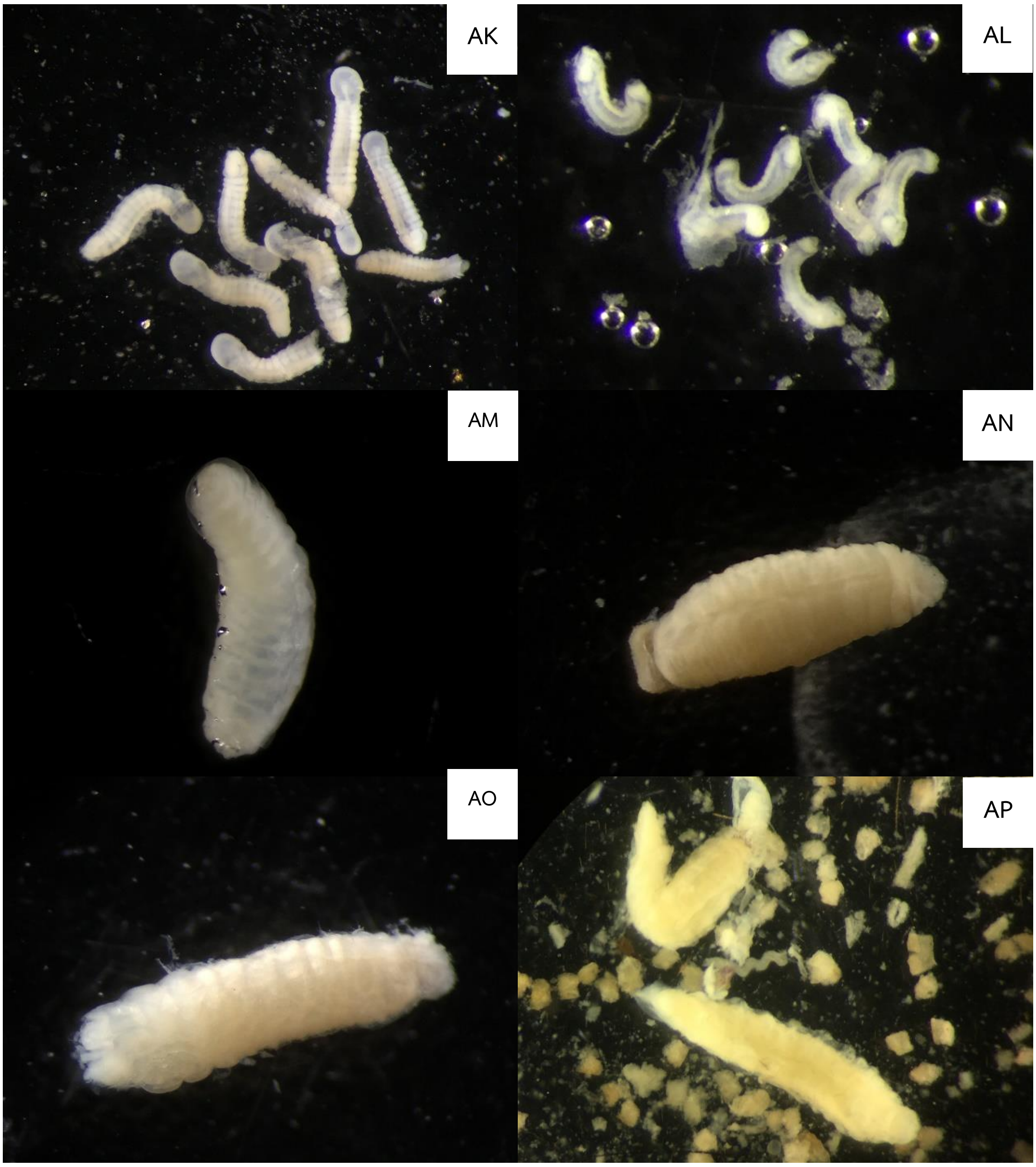

Figure D - 29 (cont.) Photograph of the parasitoids in family Braconidae, subfamily Microgastrinae; AK. *Glyptapanteles* sp.1; AL, *Glyptapanteles* sp.2; AM, *Glyptapanteles* sp.3; AN, *Glyptapanteles* sp.4; AO, *Glyptapanteles* sp.5; AP, *Glyptapanteles* sp.6

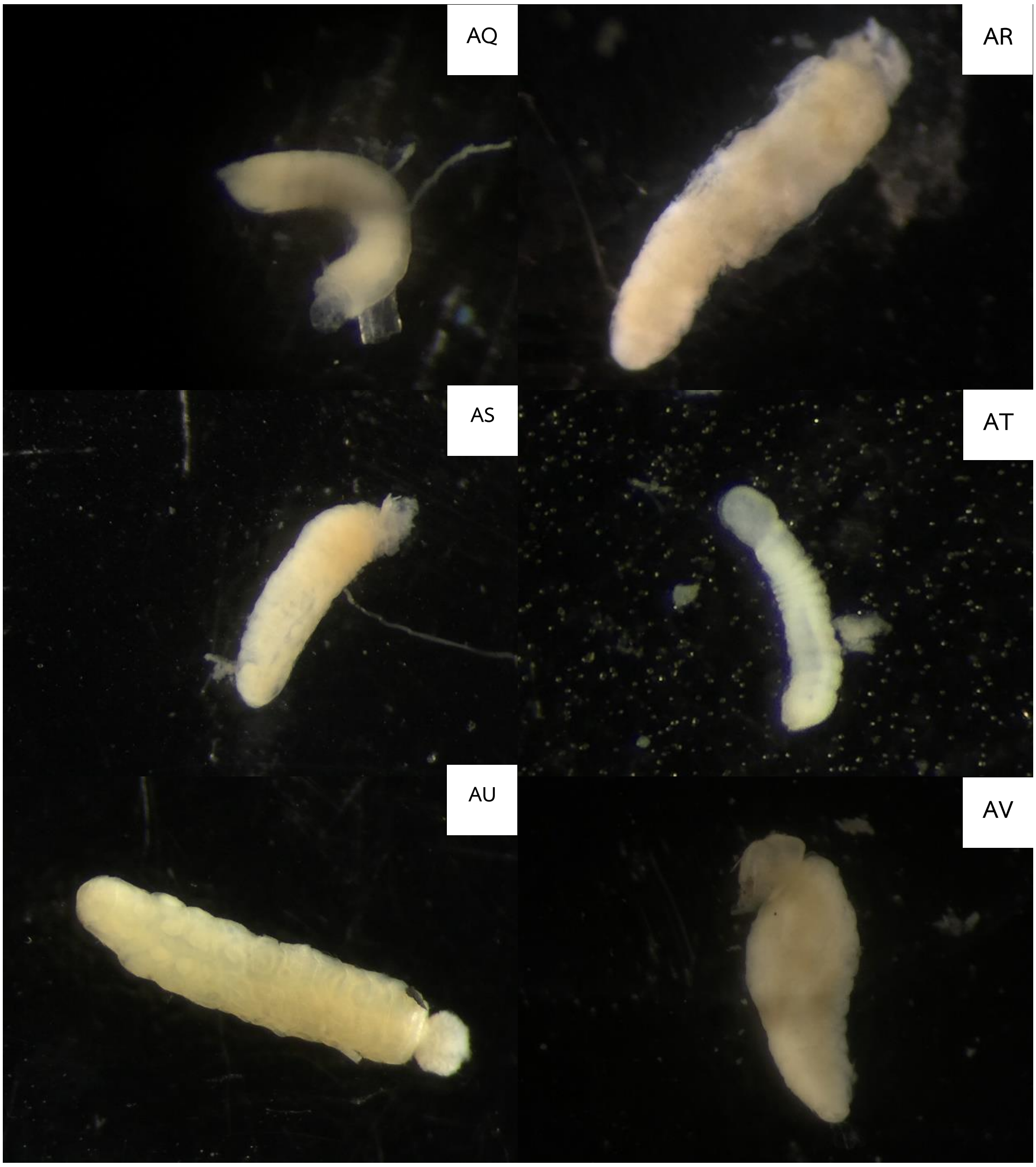

Figure D - 29 (cont.) Photograph of the parasitoids in family Braconidae, subfamily Microgastrinae; AQ. *Glyptapanteles* sp.7; AR, *Glyptapanteles* sp.8; AS, *Glyptapanteles* sp.9; AT, *Glyptapanteles* sp.10; AU, *Iconella* sp.1; AV, *Microplitis* sp.1

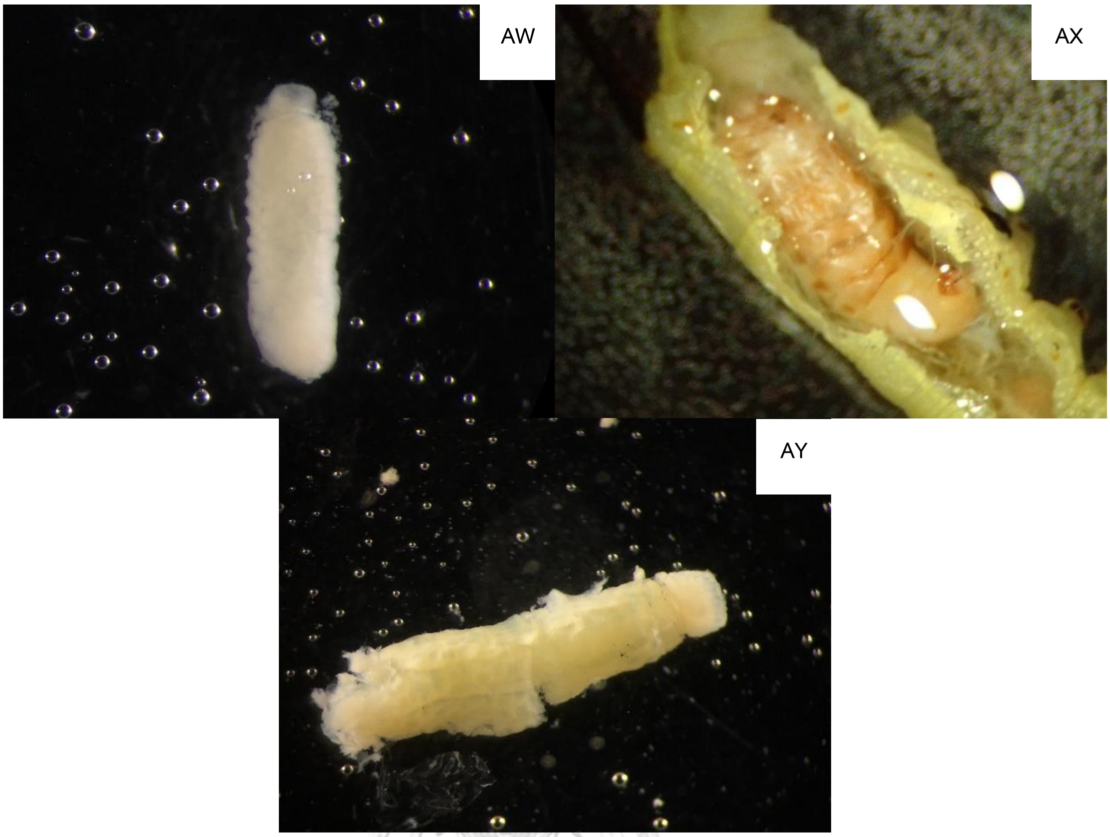

Figure D - 29 (cont.) Photograph of the parasitoids in family Braconidae, subfamily Microgastrinae; AW. *Parapanteles athamasae*; AX, *Snellenius* sp.1; AY, *Wilkinsonellus* sp.1

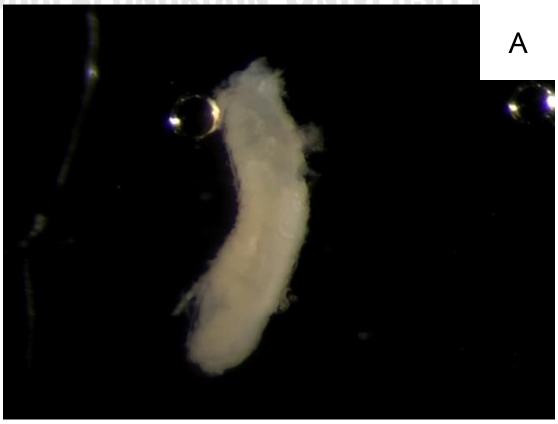

Figure D - 30 Photograph of the parasitoids in family Braconidae, subfamily Orgilinae; A, *Orgilus* sp.1

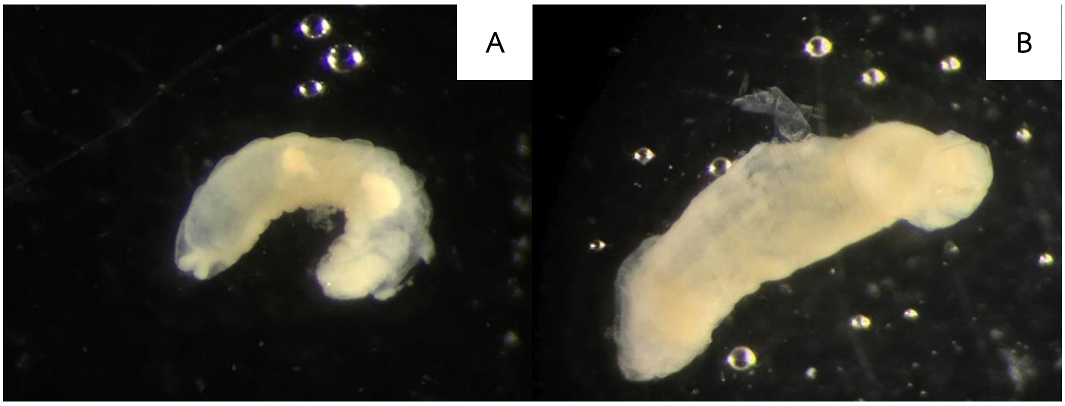

Figure D - 31 Photograph of the parasitoids in family Braconidae, subfamily Rogadinae; A, *Aleiodes contemptus*; B, *Aleiodes* sp.1

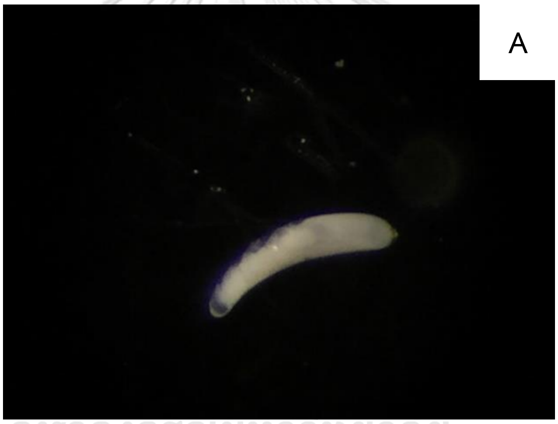

Figure D - 32 Photograph of the parasitoids in family Chalcididae; A, *Brachymeria* sp.1

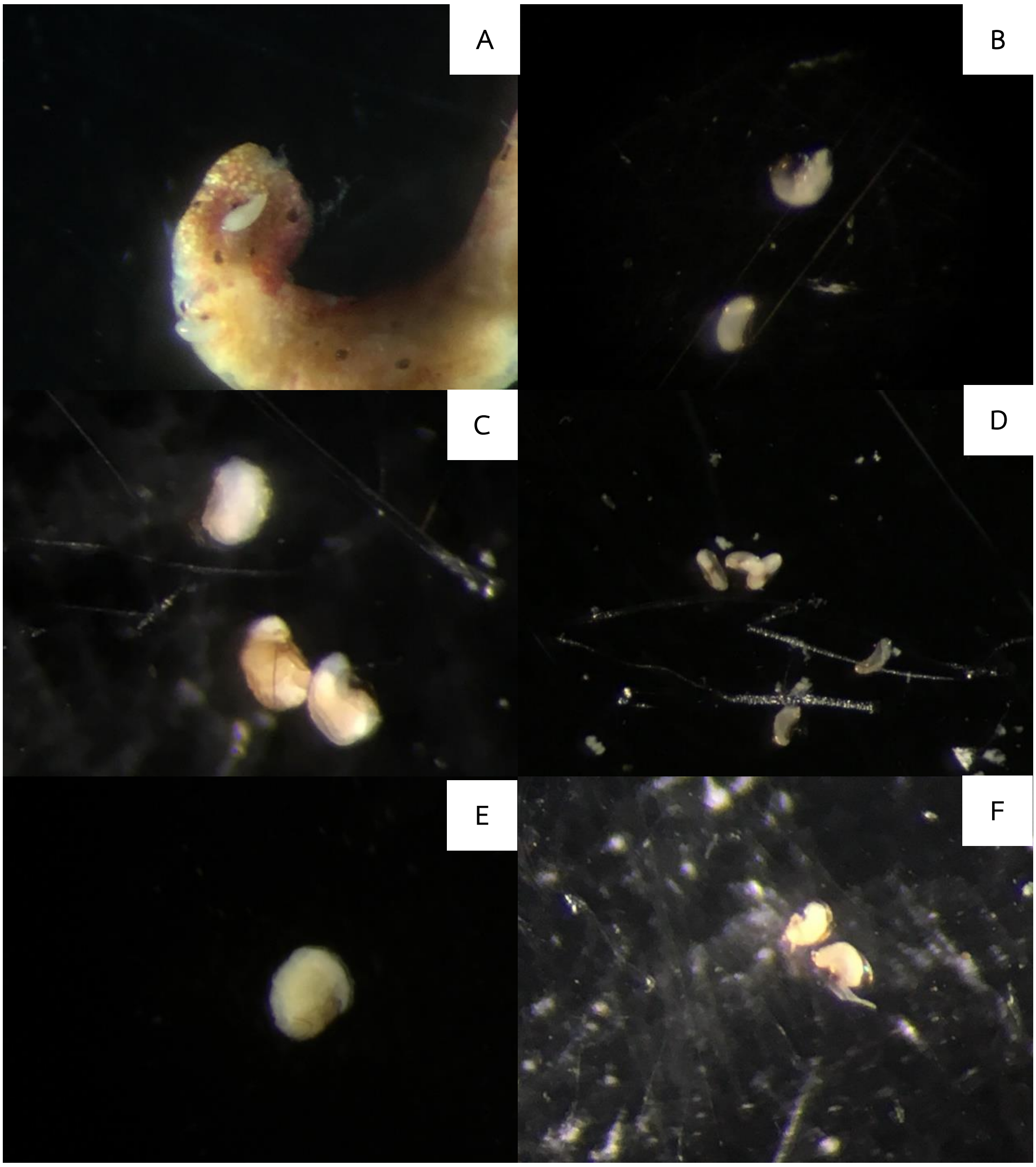

Figure D - 33 Photograph of the parasitoids in family Eulophidae; A, *Elachertus* sp.1; B, *Elachertus* sp.2; C, *Elachertus* sp.3; D, *Euplectrus* sp.1; E, *Euplectrus* sp.2; F, *Euplectrus* sp.3

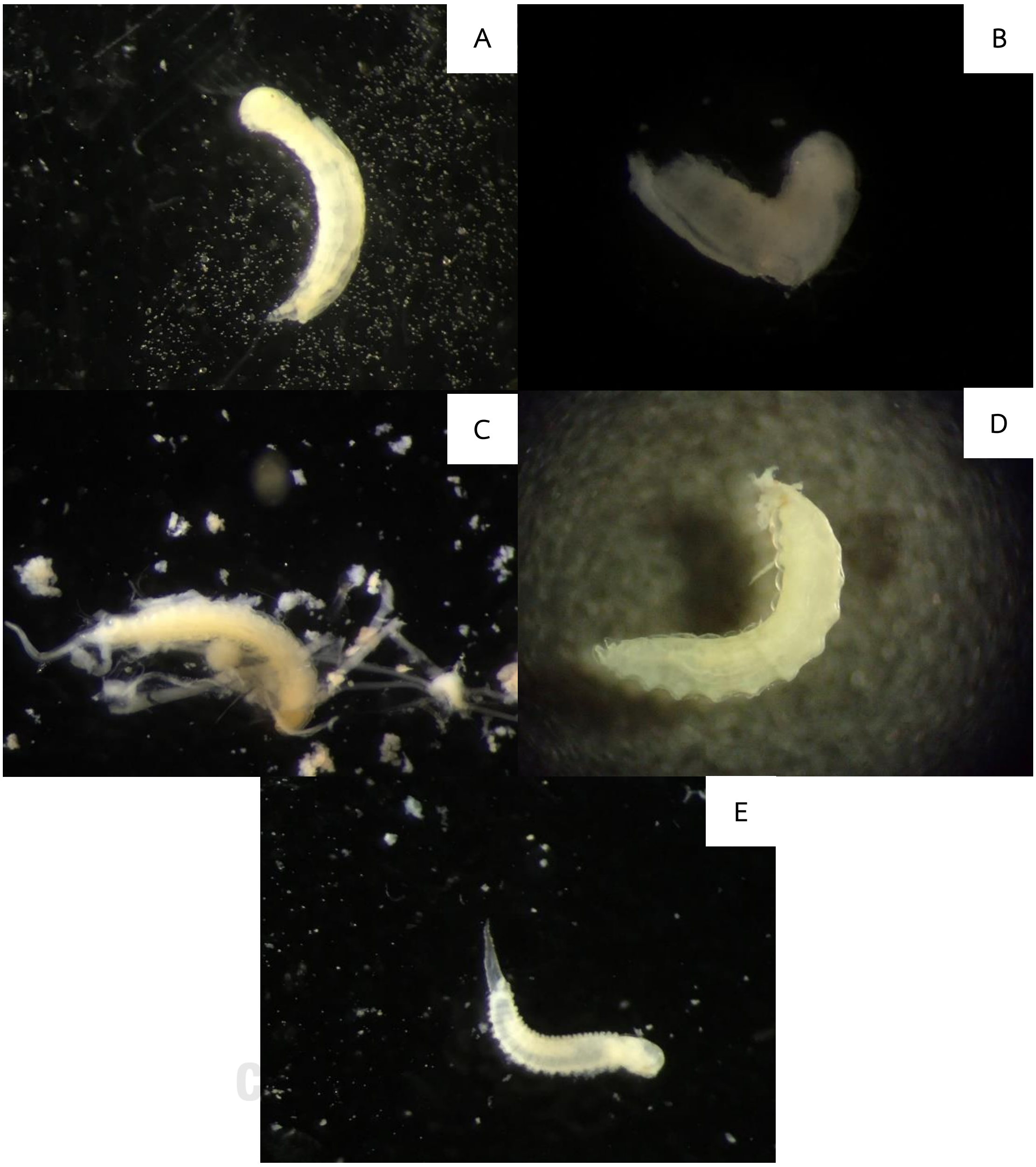

Figure D - 34 Photograph of the parasitoids in family Ichneumonidae; A, *Casinaria* sp.1; B, *Diadegma* sp.1; C, *Venturia* sp.1; D, *Holcojoppa* sp.1; E, *Enicospilus* sp.1

Figure D - 35 Photograph of the parasitoids in family Muscidea; A, *Potamia* sp.1

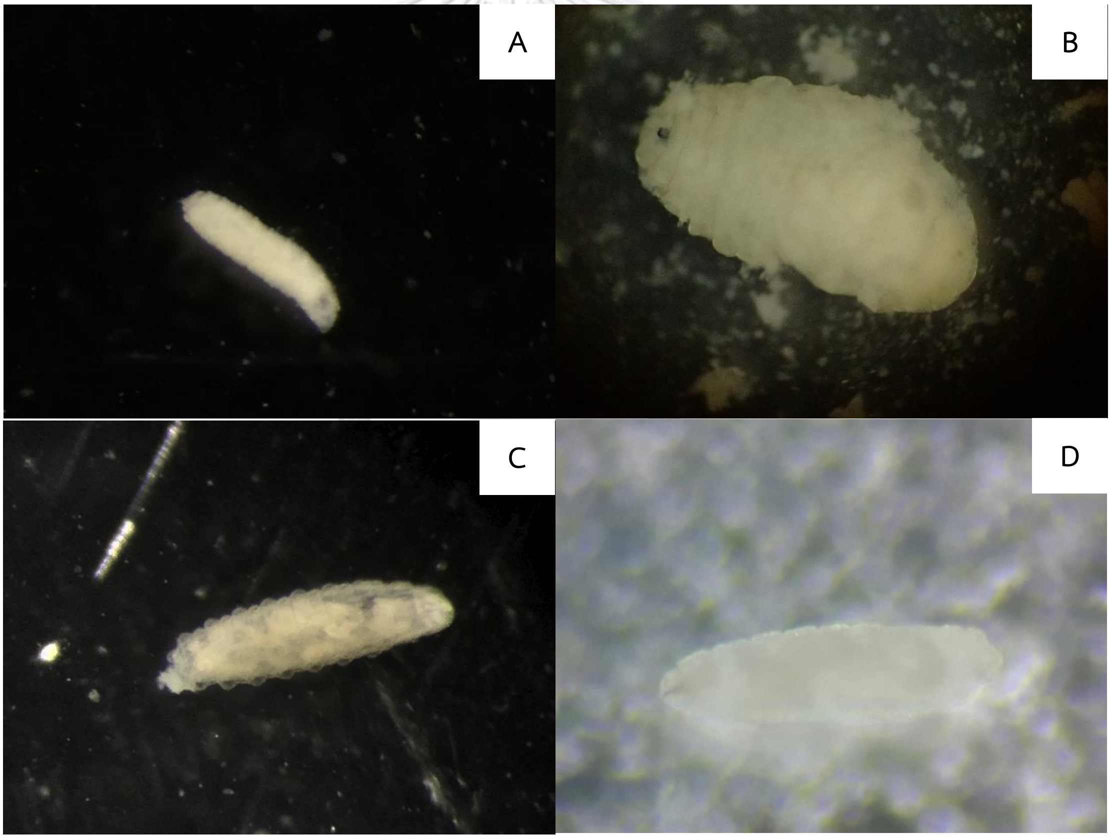

Figure D - 36 Photograph of the parasitoids in family Tachinidae; A, *Houghia* sp.1; B, *Belvosia* sp.1; C, *Belvosia* sp. 2; D, *Blepharella* sp.1

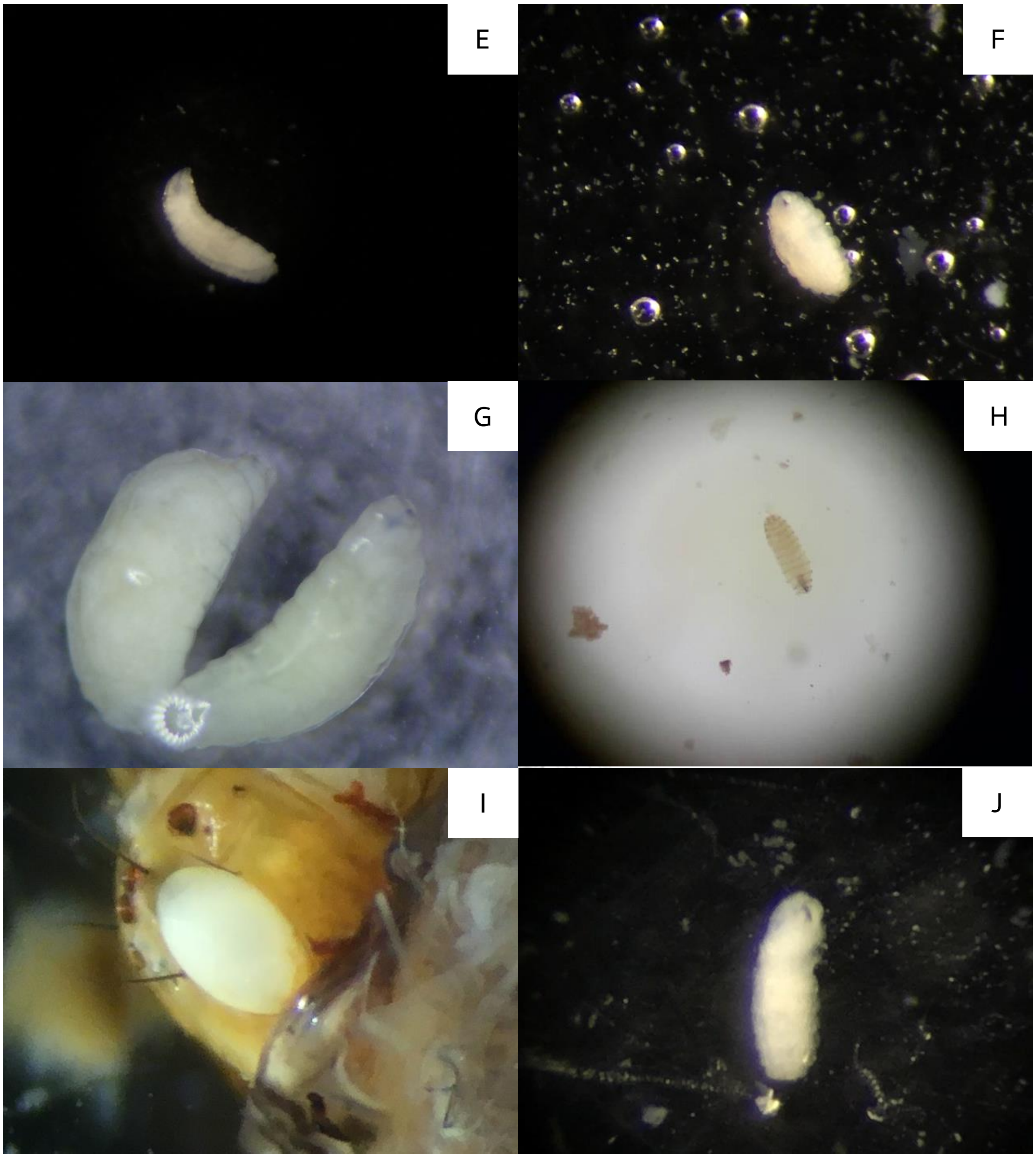

Figure D - 36 (cont.) Photograph of the parasitoids in family Tachinidae; E, *Chrysoexorista* sp.1; F, *Cyzenis* sp.1; G, *Drino inconspicua*; H, *Eumea* sp.1; I, *Exorista xanthaspis*; J, *Lespesia* sp.1

Figure D - 36 (cont.) Photograph of the parasitoids in family Tachinidae; K, *Pseudoperichaeta nigrolineata*; L, *Senometopia* sp.1; M, *Sturmia* sp.1; N, *Peribaea* sp.1; O, *Siphona* sp.1; P, *Chaetoglossa* sp.1

VITA

Mr. Pornthap Kerkig was born on July 2, 1990 in Bangkok, Thailand. He graduated Bachelor of Education Program in Science-Biology from Department of Biology, Faculty of Science, Srinakharinwirot University in 2014. After his graduation, he continued his study for Master's degree in Zoology at Department of Biology, Faculty of Science, Chulalongkorn University. He is interested in Entomology, therefore he chose to research on parasitoid insects, host-parasitoid relationships using DNA barcoding at Saraburi Province for his Master thesis. His work was supported by the CU Graduate School Thesis Grant, Chulalongkorn University.

Academic experiences

Poster presentations under the title of “DNA barcoding of lepidopteran hosts and their parasitoids at Chulalongkorn University Area Kaeng khoi District, Saraburi Province” in the theme of Biodiversity, Ecology and Systematics, the 21st Biological Sciences Graduate Congress (BSGC) 2016, at University of Malaya, Kuala Lumpur, Malaysia and then again in 2017 in the theme Biodiversity, Ecology and Environmental Biology at the 22nd Biological Sciences Graduate Congress (BSGC), National University of Singapore (NUS), Singapore.

Oral presentations and proceeding under the title of “DNA barcoding of lepidopteran hosts and their parasitoids at Chulalongkorn University Area Kaeng khoi District, Saraburi Province” in the theme of Biodiversity, the 43rd Congress on Science and Technology of Thailand (STT43) 2017, at Chulalongkorn University.