Population Genetics and Phylogeny of the Bush Brown Butterfly in Genus *Mycalesis* Hübner, 1818 (Lepidoptera: Nymphalidae) in Peninsular Thailand

Sakiyah Morlor

A Thesis Submitted in Partial Fulfillment of the Requirements for the
Degree of Master of Science in Zoology
Prince of Songkla University
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I hereby certify that this work has not been accepted in substance for any degree, and is not being currently submitted in candidature for any degree.

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ชื่อวิทยานิพนธ์ พันธุศาสตร์ประชากรและวงศ์วานวิวัฒนาการของผีเสื้อตาลพุ่มในสกุล *Mycalesis* Hübner, 1818 (Lepidoptera: Nymphalidae) ในคาบสมุทรไทย
ผู้เขียน นางสาวซากียะ มอลอ
สาขาวิชา สัตววิทยา
ปีการศึกษา 2560

บทคัดย่อ

ประเทศไทยตั้งอยู่ในเขตร้อนชื้นซึ่งมีความหลากหลายทางชีวภาพสูงโดยเฉพาะบริเวณคาบสมุทรไทย เป็นบริเวณรอยต่อการแพร่กระจายของพันธุ์พืชและสัตว์บางชนิดระหว่างภูมิภาคอินโดจีนและภูมิภาคซุนดา ผีเสื้อตาลพุ่มในสกุล *Mycalesis* เป็นกลุ่มที่มีการแพร่กระจายในเขตภูมิภาคเอเชียตะวันออกเฉียงใต้และออสเตรเลีย ลักษณะเด่นของผีเสื้อกลุ่มนี้คือ มีรูปแบบของปีกที่แตกต่างกัน 2 รูปแบบได้แก่ รูปแบบในฤดูฝน และรูปแบบในฤดูแล้ง โดยรูปแบบปีกในฤดูแล้งมีการลดรูปของจุดตาของปีกด้านล่าง ซึ่งทำให้ยากต่อการจำแนกชนิด วัตถุประสงค์ของการศึกษาครั้งนี้เพื่อสำรวจและจำแนกชนิดผีเสื้อตาลพุ่ม ตรวจสอบความผันแปรทางพันธุกรรม และศึกษาความสัมพันธ์เชิงวิวัฒนาการของผีเสื้อตาลพุ่มในคาบสมุทรไทย โดยได้ทำการเก็บตัวอย่างผีเสื้อตาลพุ่มใน 6 จังหวัดตามแนวเทือกเขาในภาคใต้ ได้แก่ จังหวัดชุมพร จังหวัดสุราษฎร์ธานี จังหวัดนครศรีธรรมราช จังหวัดพังงา จังหวัดตรัง และจังหวัดนราธิวาส ตั้งแต่เดือนกุมภาพันธ์ 2558 ถึง เดือนกรกฎาคม 2559 โดยใช้สวิงจับแมลงและกับดักผลไม้ จากนั้นนำมาจัดรูปร่าง ถ่ายรูปตัวอย่างและจำแนกชนิดโดยใช้ลักษณะของปีกและอวัยวะสืบพันธุ์ นอกจากนี้ได้นำขาคู่กลางมาใช้ในการสกัดดีเอ็นเอเพื่อตรวจสอบความผันแปรทางพันธุกรรม และศึกษาความสัมพันธ์เชิงวิวัฒนาการระดับโมเลกุล โดยใช้ยีนในไมโทคอนเดรีย (*COI*) และยีนในนิวเคลียส (*EF-1α* และ *wingless*)

จากการศึกษาพบผีเสื้อตาลพุ่มทั้งหมด 214 ตัว สามารถจำแนกได้ 7 ชนิด ได้แก่ *Mycalesis intermedia*, *M. perseus*, *M. perseoides*, *M. visala*, *M. orseis*, *M. janardana* และ *M. mineus* ซึ่งพบรูปแบบปีกของรูปแบบในฤดูฝนและรูปแบบในฤดูแล้ง โดยการศึกษานี้ได้บรรยายลักษณะของอวัยวะสืบพันธุ์เพศผู้ของผีเสื้อตาลพุ่มทั้ง 7 ชนิด จากการศึกษาความผันแปรทางพันธุกรรมของผีเสื้อตาลพุ่มแต่ละชนิด พบว่ามีความแตกต่างกันในแต่ละยีน โดย *M. mineus* มีความผันแปรทางพันธุกรรมภายในชนิดต่ำทั้งสามยีน จากผลการศึกษาความสัมพันธ์เชิงวิวัฒนาการ

โดยการรวมยีนพบว่า ผีเสื้อตาลพุ่มในคาบสมุทรไทยมีบรรพบุรุษร่วมกันโดยสมาชิกใน *Mineus* group สามารถแบ่งได้สองเคลด จากผลการศึกษาครั้งนี้ยังแสดงให้เห็นว่า ผีเสื้อตาลพุ่มในคาบสมุทรไทยมีจุดกำเนิดในช่วงเวลา 32.47 ล้านปีในยุคโอลิโกซีน

Thesis Title Population Genetics and Phylogeny of the Bush Brown Butterfly in Genus *Mycalesis* Hübner, 1818 (Lepidoptera: Nymphalidae) in Peninsular Thailand

Author Miss Sakiyah Morlor

Major Program Zoology

Academic Year 2016

Abstract

Thailand is located in tropical rainforest with rich in biodiversity, especially peninsular Thailand, which is an important transition zone of fauna between the Indo-Chinese and Sundaic sub-regions. *Mycalesis* radiated spectacular in Southeast Asia and Australia, there are two distinct seasonal morphs (wet and dry season form). In dry season form, the submarginal ocelli pattern on the underside of wing is reduced that make difficult for identification. The aims of this study were observed species and identification, investigated genetic variation and phylogenetic relationships of *Mycalesis* in peninsular Thailand. The survey of *Mycalesis* in peninsular Thailand was conducted in 6 provinces, comprising of Chumphon, Surat Thani, Nakhon Si Thammarat, Phangnga, Trang and Narathiwat during February 2015 to July 2016. The adult specimens were collected by using insect nets and fruit-baited traps, then wing setting, photographs and genitalia dissections were carried out. Mitochondrial gene (*COI*) and two nuclear gene (*EF-1α* and *wingless*) were investigated to study the genetic variation and constructed phylogenetic relationships in *Mycalesis* populations.

Totally 214 *Mycalesis* specimens were collected, that could be identified to seven species; *M. intermedia, M. perseus, M. perseoides*, *M. visala, M. orseis, M. janardana* and *M. mineus*. In this study, two distinct seasonal morphs were found as wet and dry season forms, male genitalia also were described. Difference of genetic variation was found in each gene of *Mycalesis* species, but present as low in all genes of *M. mineus*. Phylogenetic relationships based on combined gene sequences indicated that the *Mycalesis* was monophyletic group, which Mineus group can be divided into two major clades. Estimating divergence time of *Mycalesis* in peninsular Thailand was 32.47 mya in Oligocene period.

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Sakiyah Morlor

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LIST OF ABBREVIATIONS AND SYMBOLS

AFLP = amplified fragment length polymorphism

pb = base pair (s)

°C = degree celcius

CH_3CO_2K = potassium acetate

CHP = Chumphon province

COI = cytochrome oxidase subunit I

DNA = deoxyribonucleic acid

EDTA = ethylenediamine tetraacetic acid

EF-1α = elongation factor 1 alpha

et al. = and others

F = forward

hr = hour

i.e. = id est (that is)

km = kilometer

KOH = potassium hydroxide

mM = millimolar

M = molar

min = minute

LIST OF ABBREVIATIONS AND SYMBOLS (Continued)

mtDNA = mitochondrial deoxyribonucleic acid

NaCl = sodium chloride

NST = Nakhon Si Thammarat province

NTW = Narathiwat province

PNG = Phang-Nga province

R = reward

RAPD = random amplified polymorphic DNA

rpm = revolution per minute

SDS = sodium dodecyl sulfate

SSCP = single strand conformation polymorphism

STN = Surat Thani province

TRG = Trang province

Tris-HCL = Tris-(hydroxymethyl)-aminomethane hydrochloric acid

µl = microliter

UnH = underside of hindwing

UpF = upperside of forewing

CHAPTER 1

GENERAL INTRODUCTION

Background and Rationale

Lepidoptera is a large order that the most economically important pests in the class Insecta (Ozden, 2003). Many schemes of classification exist for the Lepidoptera, some informal method divided the order into Microlepidoptera and Macrolepidoptera according to average body size of the included species. Another informal scheme divided the Lepidoptera into moths, butterflies, and skippers (Pedigo, 1996). Butterflies have been widely used as a bioindicator and model organisms to study the impact of habitat fragmentation, climate change and evolution (Benedick *et al*., 2007; Brakefield, 2012; Ghazanfar & Raza, 2015; Hill *et al*., 2006; Williams *et al*., 2003).

Butterflies of the subtribe Mycalesina (Nymphalidae; Satyrinae) are an emerging model in evo-devo, much has been studied about the development, genetic and evolution especially, African butterfly *Bicyclus anynana*. All species in this subtribe have a wing pattern element that appear to be eyespots (ocelli), they are very extensively in number, pattern, color, size and position (Brakefield, 2012). This group has distribute in Old World tropics, they have radiated successfully in almost all habitat types in Africa, Madagascar and Indo-Australian region. The most recent study of these group focused on revised classification and phylogenetic relationships among genus (Aduse-Poku *et al*., 2015).

Genus *Mycalesis* is one of the member in subtribe Mycalesina, comprises more than 100 taxa in the Oriental and the Australian regions, this group is in need of revision (Parsons, 1998; Tennent, 2000). This genus shows striking seasonal polymorphism in wing pattern, as a mechanism to survive the wet and dry seasonal changes in their habitats (Braby, 1994). Polyphenism is accompanied with behavioral, reproductive and habitat changes (Braby, 1994; Brakefield, 2012; Islam *et al*., 2010), these phenomena is characterized by the reduction of the eyespot in dry seasonal morph. This makes *Mycalesis* species identification difficult (Kondandaramaiah *et al*., 2010).

Thailand is situated in Southeast Asia, which lies between the northern Indochinese and Southern Sundaic biogeographical regions (Cobert & Hill, 1996). The Thai peninsular is the junction between two of the planet's biodiversity hotspots. Various part of peninsular Thailand have been submerged or isolated by water as sea levels rose and fell over the past, these change isolated many animals, plant species and peninsular populations of many butterfly species are recognized as separate from population elsewhere in mainland Southeast Asia (Ek-Amnuay, 2012).

The study is aimed to: investigate the species composition and distribution of *Mycalesis* population in peninsular Thailand and investigate the genetic variations and phylogenetic relationship of *Mycalesis* species in peninsular Thailand, inferred from mitochondrial and nuclear genes.

Research Questions

What is the phylogenetic relationships of butterfly in genus *Mycalesis* in peninsular Thailand?

1. Are there major genetic differences in the populations of *Mycalesis* in peninsular Thailand?
2. Are there *Mycalesis* in peninsular Thailand monophyly?

Review of Literatures

Mycalesis Hübner is a large tropical genus represented by many species in the Oriental and Australian regions (Braby, 1994; Common & Waterhouse, 1981; Corbet & Pendlebury, 1978; D'Abrera 1971, 1985).

Taxonomy and generalization

Order Lepidoptera
  Superfamily Papilionoidea
    Family Nymphalidae
      Subfamily Satyrinae
        Tribe Mycalesini
          Subtribe Mycalesina
            Genus *Mycalesis* (Hübner, 1818)

The butterflies of the *Mycalesis* group is an enormous genus of medium size (around 35-70 mm), species are characterized by the evenly rounded wings, the upperside (Up) of wings are mostly brown. There is a pale postdiscal band on the brighter underside of wings (Un) and a series of submarginal ocelli (eyespot) on both wings (Figure 1). On the forewing the base of vein 12 and the radius combined in strong swelling, and the bases of the cubitus and vein 1b are less strongly swollen. Sexes are usually more or less similar (Figure 2) (Pinratana, 1988; Monastyrskii, 2005). Males have secondary sexual character that comprises of a costal nacreous on the upperside of the hindwing (UpH), which has a patch of specialized scales covered by hair tuft and appear to be used in conjunction with a polished area nearly always containing a brand above the dorsum on the underside of the forewing (UnF) (Figure 1) (Monastyrskii, 2005).

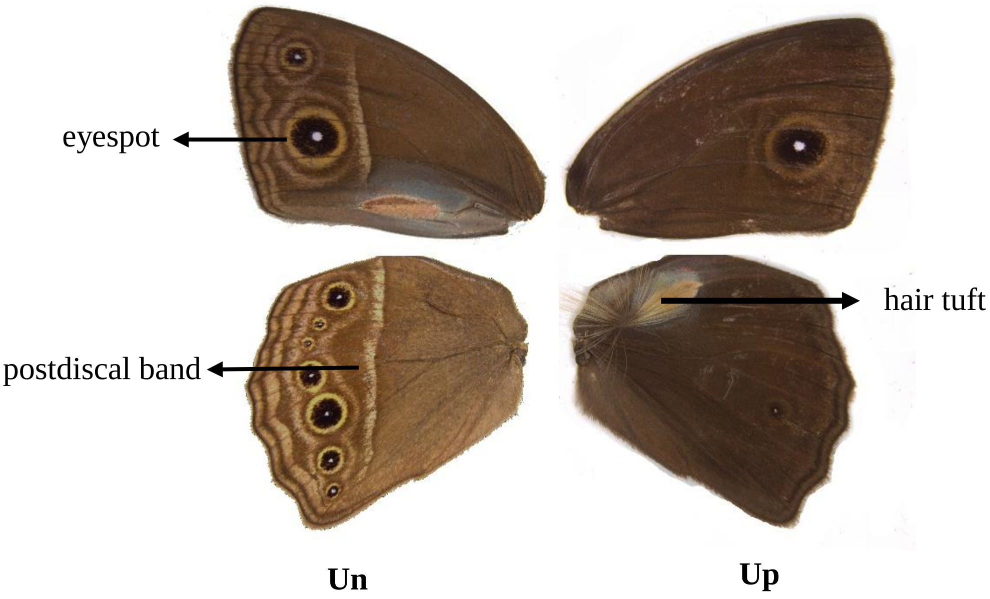

Figure 1 Character of eyespot (ocelli) and postdiscal band on the underside of wing (Un) and male sexual character on hindwing of genus *Mycalesis* (Up).

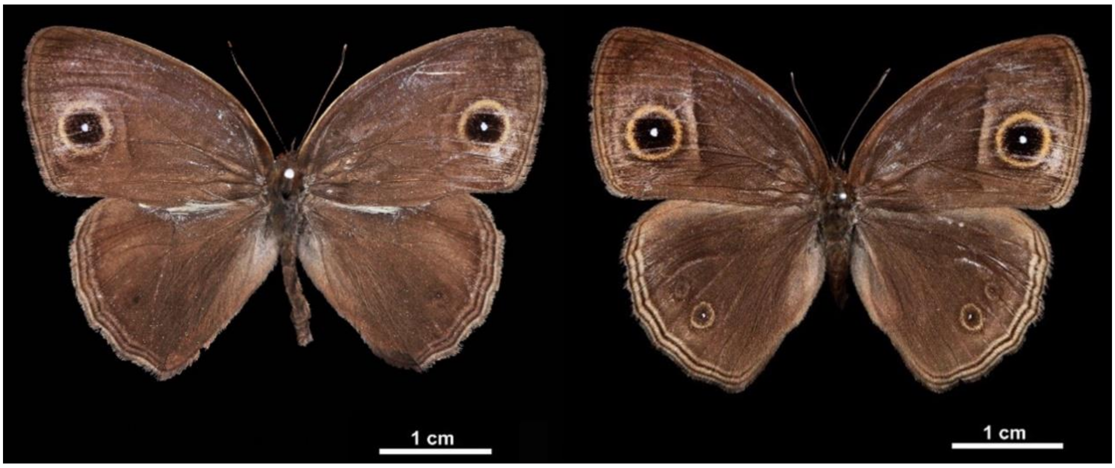

Figure 2 Male (left) and female (right) of genus *Mycalesis*.

Seasonal forms are strongly developed. The *Mycalesis*, show striking seasonal polyphenism in the Un wing pattern: the wet seasonal forms are characterized by conspicuous submarginal ocelli (eyespot) pattern on the underside of wing, in the dry seasonal forms are rather drab, being paler with greatly reduced ocelli (Braby, 1994; Brakefield & Reitsma, 1991; Corbet & Pendlebury 1978; Kirk, 1982). The phenotypic plasticity associated with marked changes in behavior and breeding status and associated changes in habitat favorability (Brakefield, 1987). The dry seasonal forms are usually reproductively dormant, less active, long-lived, aggregated in moist refugia and tent to rest amongst dead brown leaves, their wing pattern are thus well camouflaged against the resting background during the dormancy period (Braby, 1994; Brakefield, 1987; Brakefield & Reitsma, 1991). By contrast, the wet seasonal form tent to reproduce more directly, is more active, generally do not aestivate in refugia (Braby, 1994; Brakefield and Larsen, 1984) and the prominent ocelli possibly function as anti-predator devise, either to startle or to deflect attacks of predator from the vulnerable body (Braby, 1994; Brakefield & Larsen, 1984; Young, 1979). The majority of this genus prefers lowland habitats, low-flying species and preferring understory shade (Monastyrskii, 2005).

Life cycles

Mycalesis has a life cycle with four distinct phases: Eggs are generally spherical, whitish usually smooth and size 1.2-1.3 mm (Figure 3A). Egg are laid singly or in egg-masses. The majority of satyrid ovipositing activity occurs in the evening. Larvae (Figure 3B) of this genus feed on monocotyledon plant species belonging to the Poaceae and Cyperaceae (Monastyrskii, 2005). In the 5th stage of larva, body is pale cream-yellow at eclosion changing to light green after feeding, scattered primary setae; terminal abdominal segment with short bifid tail. Head capsule is shiny black, sometimes dark brown, with pair of prominent dorsal knobs and several long tapering setae, larva is long 2.0-3.0 mm (at eclosion) to 4.3 mm. Pupa (Figure 3C), with dull green or chocolate brown color, pupa is long 15-16 mm and suspended head downwards, they take along ten days to hatch to adult butterfly (Figure 3D).

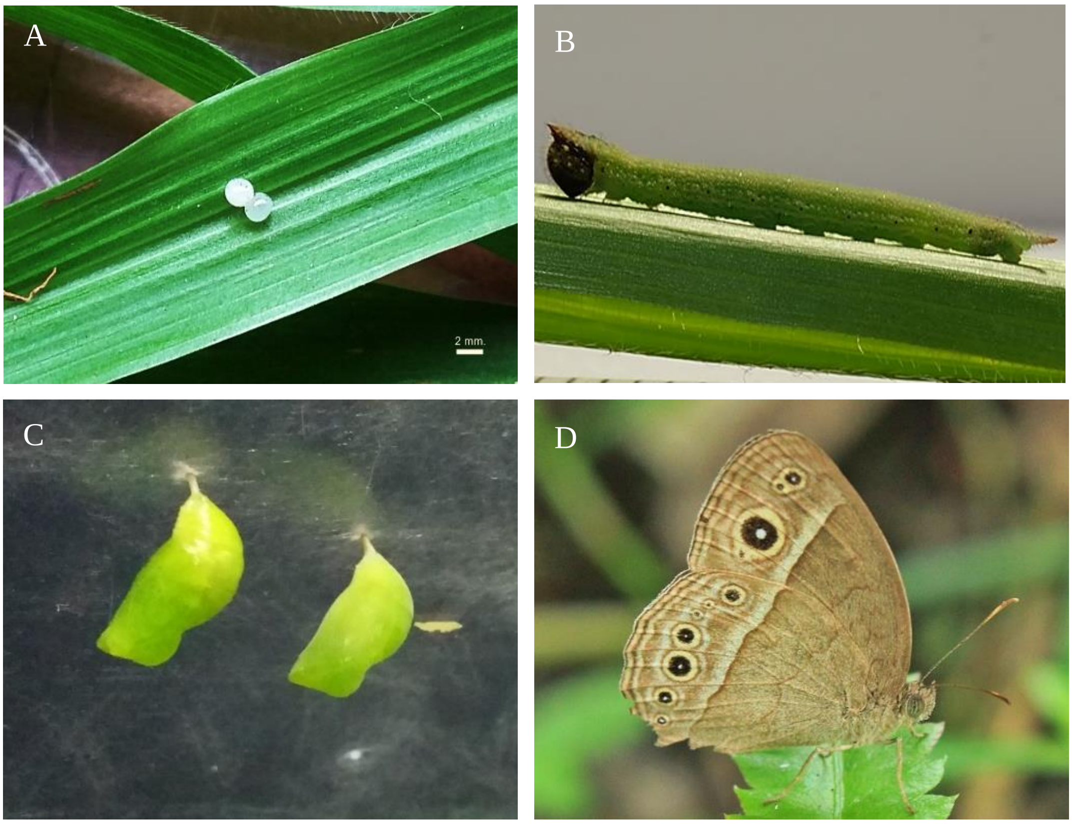

Figure 3 General life cycle of *Mycalesis* in each stage, A) egg B) larva C) pupa D) adult

The study of species distribution and ecology of genus *Mycalesis*

Mycalesis species are widely dispersed across Indo-Australian regions, including Sri Lanka, India, Southeast Asia, Australia, New Guinea and the East of Solomon Islands (Kodandaramaiah *et al*., 2010). There are many studies on *Mycalesis* as: Braby (1994) has studied seasonal polyphenism of several species of *Mycalesis* in northern Australia, Islam *et al*. (2010) studied on wet and dry season polymorphism of *Mycalesis mineus* in Bangladesh. *Mycalesis orseis* has been used to examine of habitat fragmentation on genetic diversity in Borneo. The genetic variation in *Mycalesis* based on mtDNA gene in Sri Lanka was studied by Goonesekera and Ranawaka (2013).

The study of butterflies in Thailand began in 1787, when Fabricius first described four species of butterflies from the country. Taxonomic research on Thai butterflies was continued by Druce in 1874 (Ek-Amnuay, 2012; Lekakul *et al*., 1977). Bro. Amnuay Pinratana published a set of six volumes entitled “Butterflies in Thailand” from 1981-1996. In addition, much work has been done by Japanese scientist, including a team of Osaka City University expedition during 1957-1958, Yata (1989-1995) published a revision of the pierid genus *Eurema*, Aoki & Uemura (1984) published “Studies on the genus *Ypthima* (Satyridae) in Thailand”, and Aoki & Yamagushi published “Notes on Butterflies of the genus *Mycalesis* (Satyridae) collected in Thailand, together with description of a new species”. A year later they described another new species of *Mycalesis* from northern Thailand (Ek-Amnuay, 2012).

Following to Ek-Amnuay (2012) reported that there are 27 species spreading throughout Thailand (Table 1). Among these, *M. fusca*, *M. janardana*, *M. perseus*, *M. mineus*, *M. visala*, *M. orseis* were restricted to the peninsular Thailand. Boonvano (1998) reported four species of *Mycalesis* at Ton Nga-Chang Wildlife Sanctuary, Songkla province, includings *M. fuscum*, *M. mineus, M. oroatis* and *M. janardana*. Wangthaveesup (2008) reported 12 species of *Mycalesis* in Hala - Bala forest , Yala and Narathiwat Provinces, consisted of *M. fusca fusca*, *M. perseus cepheus*, *M. mineus macromalayana*, *M. intermedia*, *M. anapita anapita*, *M. janardana sagittigera*, *M. anaxiodes*, *M. oroatis ustulata*, *M. orseis nautilus*, *M. mnasicles perna*, *M. maianeas maianeas* and *M. persoides*.

Population genetics

Population genetics is the study of genetic variation within and among populations and the evolutionary factors that explain this variation. Its foundation is the Hardy–Weinberg law, which is maintained as long as population size is large, mating is at random, mutation, selection and migration. Allele frequencies and genotype frequencies may change from one generation to the next. Variation in allele frequencies is found throughout the genome, and can be examined by genetic diversity and evolutionary patterns (Keats & Sherman, 2013).

Phylogenetic and Molecular technique

Phylogenetic is the study of the evolutionary history and relationships among individuals or groups of organisms (species or populations), these relationships are discovered through phylogenetic inference methods that observed heritable traits, such as DNA sequences or morphology under a model of evolution of these traits. The result of these analyses is a phylogeny or Phylogenetic tree (Yang & Rannala, 2012). Phylogenetic studies have been conducted on several insects such as, butterflies (Aduse-Poku *et al*., 2015; Kodandaramaiah *et al*., 2010; Pena *et al*., 2006; Torres *et al*., 2001), black flies (Sriphirom *et al*., 2014) and Mosquito (Fang *et al*., 2017; Sum *et al*., 2014).

There are many molecular technique for getting genetic information for example, DNA hybridization, Random amplified polymorphic DNA (RAPD), Amplified fragment length polymorphism (AFLP), single-strand conformational polymorphism (SSCP), microsatellite and DNA sequencing. Those technique also provide different results and use depends on time, cost and previous background information. For instance, microsatellite, RAPD and SSCP are powerful to resolve the genetic differences within study of species (Avise, 2004). Furthermore, DNA sequencing is widely used in many aspects because base alignments can compare explicit on intraspecific and interspecific variation in the population. Thus, nucleotide sequence with specific markers has been used in resolving taxonomic status and the genetic differences of populations (Wichachucherd, 2014).

Mitochondrial DNA (mtDNA) has been the most popular marker used to investigate the molecular diversity in animals (Galtier *et al*., 2009). Following Avise *et al*. (1987) and Moritz *et al*. (1987), population geneticists and molecular biologists have adopted this tool with little reserve. Virtually every molecular study of animals species in the field involves mtDNA haplotyping at some stage. Not surprisingly, a mitochondrial fragment, *COI*, was recently elected as the standardized tool for molecular taxonomy and identification (Galtier *et al*., 2009; Ratnasingham & Hebert 2007).

The reasons for the adoption of mtDNA as marker of choice are well-known. Experimentally, mtDNA is relatively easy to amplify because it appears in multiple copies in the cell. Mitochondrial gene content is strongly conserved across animals, with very few duplications, no intron, and very short intergenic regions (Gissi *et al*. 2008). Mitochondrial DNA is highly variable in natural populations because of its elevated mutation rate, which can generate some signal about population history over short time frames. Thus, *COI* was useful in fully resolving topologies within species of some butterfly species such as the *Chrysoritis* in Lycaenidae (Rand *et al*., 2000), as well as within groups of the Papilionidae (Caterino & Sperling, 1999). Included, the systematics and biogeography of Mycalesina (Aduse-Poku *et al*., 2015; Kodandaramaiah *et al*., 2010; Monteiro & Pierce, 2001).

However, nuclear gene also widely used for molecular study, which has shown utility in reconstructing species level to subfamily level relationships in some insects especially in Lepidoptera (Brower and DeSalle, 1998; Campbell *et al*., 2000). Previous studies (Campbell *et al*., 2000; Pena *et al*., 2006; Torres *et al*., 2001) indicated that *EF-1α* and *wingless* genes further resolved relationships among species groups within the same genus, also useful in resolving clades at subfamily level in Nymphalidae.

Therefore, analysis of sequence variations of mtDNA and nuclear gene is an outstanding approach to study the population genetics and the phylogenetic relationships within population of the butterfly genus *Mycalesis*.

Research objectives

1. To investigate the species composition and distribution of *Mycalesis* in peninsular Thailand
2. To examine the genetic variation and phylogenetic relationships of *Mycalesis* in peninsular Thailand

Table 1 Species list of *Mycalesis* in Thailand

Species	Distribution in Thailand	Distribution in the world
1. *M. anapita anapita* Moore,1858	TT	Thailand, India, Burma, Malay peninsula, Sumatra. A further subsp. in Borneo
2. *M. fusca fusca* (C. & R. Felder,1860)	PT	Peninsular Thailand, Malay peninsula, Sumatra. Other subsp.in Nais, Borneo, Java
3. *M. mnasicles* Hewitson, 1864		
3a. *M. mnasicles perna* Fruhstorfer, 1906	TT	Thailand, Burma, Vietnam, Malay peninsula. Nominate subsp. in Sumatra and Borneo
4. *M. janardaana* Moore,1858		
4a. *M. janardaana sagittigera* Fruhstorfer, 1908	PT	Peninsular Thailand, Malay peninsula, Sumatra. other subsp. throughout Sundaland Philippines and Sulawesi
5. *M. sangaica* Butler, 1877		
5*a. M. sangaica tunicula* Fruhstorfer, 1911	TT, except PT	Thailand, Burma, Laos, Vietnam. other subsp. in China and Taiwan
6. *M. perseus* (Fabricius, 1775)		
6a. *M. perseus blasius* (Fabricius, 1798)	N	Thailand, Assam (India), Burma
6b. *M. perseus cepheus* Butler, 1867	PT	Peninsular Thailand, Malay peninsula, Sumatra, Borneo, Java. Throughout Oriental region, extending to Australia
7. *M. mineus* (Linnaeus, 1758)		
7a. *M. mineus mineus* (Linnaeus, 1758)	TT, except PT	Thailand, north India, Burma, Vietnam, South China
7b. *M. mineus macromalayana* Fruhstorfer, 1911	PT	Peninsular Thailand, Malay Peninsula, Sumatra. other subsp. in Sri Lanka, Peninsular India, Nicobars and Taiwan
8. *M. intermedia* (Moore, 1892)	TT	Thailand, Burma, Vietnam, Malay peninsula
9. *M. thailandica* Aoki & Yamaguchi, 1984	TT, except PT	Thailand
10. *M. distanti* Moore, 1892	TT	Thailand, Vietnam, Burma, north Malay peninsula
11. *M. perseoides* (Moore,1892)	TT	Thailand, Assam (India), Burma, Vietnam, Malay peninsula
12. *M.* visala Moore, 1858		

Table 1 Continued.

Species	Distribution in Thailand	Distribution in the world
12a. *M. visala visala* (Moore, 1858)	TT, except PT	Thailand, Vietnam, Burma, north India
12b. *M. visala phamis* Talbot & Corbet, 1939	PT	Peninsular Thailand, Malay peninsula, other subsp. in peninsular India and Andaman Is
13. *M. orseis* Hewitson, 186		
13a. *M. orseis nautilus* Butler, 1867	PT	Peninsular Thailand, Malay peninsula, other subsp. in Sumatra, Nias, Borneo, Palawan
14. *M. francisca* Stoll, 1780		
14a. *M. francisca sanatana* Moore, 1858	TT	Thailand, north India, Burma, Vietnam. other subsp. in China, Taiwan, Japan
15. *M. inayoshii* Aoki & Yamaguchi, 1995	N	Thailand, Laos
16. *M. gotama* Moore,1858		
16a. *M. gotama charaka* Moore, 1875	N	Thailand, Assam (India), Burma, Vietnam. other subsp. in China, Taiwan, Japan
17. *M. anaxias* Hewitson, 1862		
17a. *M. anaxias aemate* Fruhstorfer, 1911	TT, except PT	Thailand, Burma, Laos, Vietnam. Other subsp. in India, Malay peninsula, Sumatra
18. *M. siamica* Riley & Godfrey, 1921	E	Thailand, Laos, Nominate subsp. from north Vietnam
19. *M. adamsoni* Watson, 1897	TT, except PT	Thailand, Assam (India), Burma
20. *M. anaxioides* Marshall, 1883	TT	Thailand, Burma, Malay peninsula
21. *M. maianeas maianeas* Hewitson, 1864	TT	Peninsular Thailand, Malay peninsula, Borneo. Further subsp. in Sumatra
22. *M. suaveolens* Wood - Mason & de Niceville, 1883		
22a. *M. suaveolens duguidi* Tytler, 1926	N	Thailand, Burma, Laos, Vietnam. Other subsp. in India, Taiwan
23. *M. nicotia* Westwood, 1850	N	Thailand, Burma, Laos, Vietnam, India
24. *M malsara* Moore, 1858	TT, except PT	Thailand, Burma, Vietnam, north India
25. *M. annamitica annamitica* Fruhstorfer, 1906	TT, except PT	Thailand, Vietnam. Further minor subsp. in Assam (India), Burma

Table 1 Continued.

Species	**Distribution in Thailand**	**Distribution in the world**
26. *M. lepcha* Moore, 1880		
26a. *M. lepcha kohimensis* Tytler, 1914	TT, except PT	Thailand, Burma, Laos. Further subsp. in India
27. *M. oroatis* Hewitson, 1864		
27a. *M. oroatis surkha* Marshall, 1882	TT, except PT	Thailand, Burma
27b. *M. oroatis ustulata* Distant, 1885	PT	Thailand, Burma, Australia

CHAPTER 2

Species composition of *Mycalesis* (Nymphalidae: Satyrinae) in peninsular Thailand with male genitalia description

Introduction

Mycalesis Hübner is a large tropical genus with more than 100 species distributed in the Oriental and Australian regions (Braby, 1994; Common & Waterhouse, 1981; Corbet & Pendlebury, 1978; D'Abrera 1971, 1985). This genus is characterised by evenly rounded wings, which is almost brown, and a series of subterminal ocelli (eyespots) on the underside of wing. The difference of structure in wing venation, eyespot and the genitalia separate the group from closely allied genera such as *Orsotriaena* Wallengren and the African *Bicyclus* Kirby and *Henotesia* Butler (Corbet & Pendlebury, 1978). *Mycalesis* are reported to display polyphenism with seasonal and geographical variation in morphology, they are two distinct seasonal morphs (wet and dry season form). In Thailand, according to Ek-Amnuay (2012) reported that there are twenty seven species, some species are restricted in some part of Thailand such as *M. gotama* are endemic in northern, *M. siamica* are restricted Eastern, *M. orseis* and *M. fusca* are only found in Peninsular Thailand.

Morphology and function of genitalia in subfamily Satyrinae have been actively carried out since 1930 (Klots & Rochester, 1931). Structure of male genitalia is a principle characteristic of most families of Lepidoptera. There are many studies and description on male genitalia of Papilionoidae including Satyrinae (Coutis, 1983; Dubatolov *et al*., 1994; Klalicek & Povolny, 1992; Lukhtonov, 1995; Parshall, 1989; Shirozu & Shima, 1979). The Asian Satyrinae was studied, for example in Malaysia and Vietnam (Corbet, Pendlebury & Eloit, 1978; Monastyrskii, 2005). However, there are a few studies in Thailand especially in genus *Mycalesis*. Therefore, this study aims to investigate the species composition and distribution of *Mycalesis* in peninsular Thailand with description of the male genitalia.

Materials and Methods

Selection of study site

Study sites were selected on the basis of the mountain ranges in peninsular Thailand consist of Chumphon province (CHP), Surat Thani province (STN), Nakhon Si Thammarat province (NST), Phang-Nga province (PNG), Trang province (TRG) and Narathiwat province (NTW) (Figure 1 – 2) details of each sampling site is given in Table 1. *Mycalesis* were collected during February 2015-July 2016 by using insect nets (Figure 3) and fruit-baited traps (Figure 4), which 10 fruit-baited traps were set along 1 km by line transect in each six sampling sites. Each traps was randomly placed on the line transect at a distance 100 m. The fruit-baited trap was sampled for seven consecutive days at each sampling site. Collected butterflies were immediately pressed the thorax carefully for minimizing damages to their external organs (scales, legs and wing veins) (Islam *et al*., 2010). *Mycalesis* was preserved in triangular paper envelopes and brought to the laboratory.

Species identification

Mycalesis specimens were identified to species level by using identification key, descriptions of Corbet, Pendlebury and Eloit (1978), Ek-Amnuay (2012), Monastyrskii (2005), Pinratana (1988) and Talbot (1947).

Genitalia dissection

The abdomen were detached from the thorax and placed in individual glass vials that contain about 500 µl of 10% KOH solution for 24 hr. Abdomen were transferred to a petri dich with distilled water and cleaned under the stereomicroscope by using a pair of straight forceps. EosinY was used for dying around 10 min and washed in 20% alcohol. After that they were dyed in Chlorozal black for 5 seconds and finally washed in 20% alcohol. Genitalia were separated from the abdomen and placed in 70% ethanol solution for cleaning. To preserve the genitalia immediately after the dissection, genitalia were preserved in a glycerin-filled small tube. Images of the genitalia were taken by using a Leica Microscope DM750. Images were adjusted with Adobe Photoshop CS6, only the neutralizing the background and balancing the contrast across samples. The structures were not edited (Muadsub, 2014).

Table 1 Details of each sampling sites

Study site	Province	Coordination	Description of study site
Ban Ta yang, Mueang	Chumphon	10°45.798’N 99°23.032’E	Open aria, oil palm agriculture, grass land
Ban Phumriang, Chaiya	Surat Thani	09°23.340’N 99°15.240’E	Open aria, oil palm agriculture, bamboo, grassland
Khlong Krabue, Pak phanang	Nakhon Si Thammarat	08°20.020’N 100°09.562’E	Open aria, oil palm agriculture, rice field, grassland
Ban Bang Yai, Takuapa	Phang-Nga	08°90.241’N 98°40.505’E	Open aria, oil palm agriculture, bamboo, grassland
Khao Chong , Na Yong	Trang	07°33.360’N 99°46.724’E	Closed canopy, open aria, oil palm agriculture, bamboo, grassland
Ban Kayu Khla, Waeng	Narathiwat	05°58.655’N 101°54.392’E	Open aria, rubber plantation, rice field, bamboo, grassland

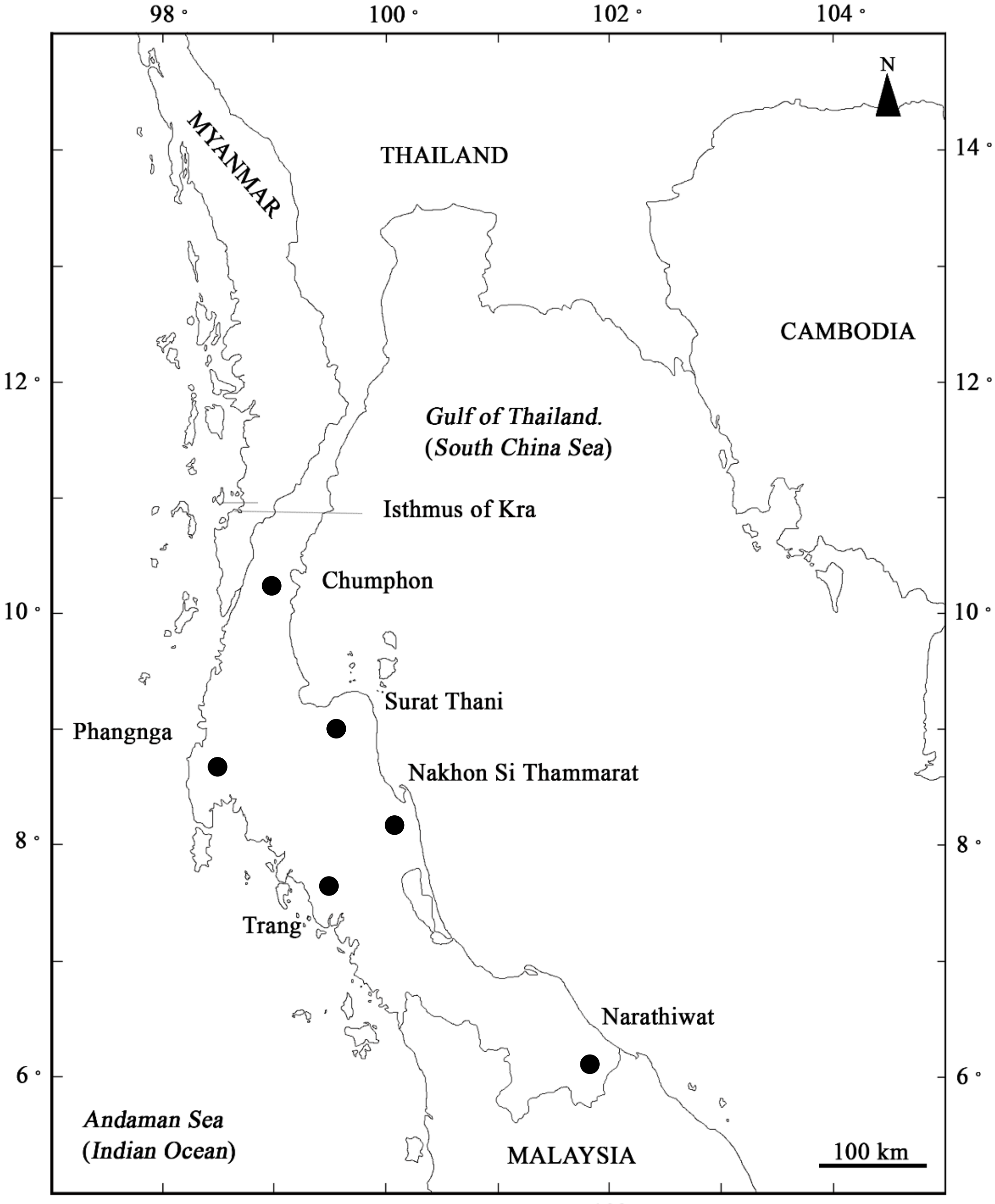

Figure 1 Map of peninsular Thailand showing locations of six sampling sites.

A) Ban Ta yang **B) Ban Phumriang**

C) Khlong Krabue **D) Ban Bang Yai**

E) Khao Chong **F) Ban Kayu Khla**

Figure 2 Habitat of collecting sites. A) Ban Ta yang, Chumphon province B) Ban Phumriang, Surat Thani province C) Khlong Krabue, Nakhon Si Thammarat province D) Ban Bang Yai, Phang-Nga province E) Khao Chong, Trang province and F) Ban Kayu Khla, Narathiwat province.

Figure 3 Butterfly sampling by using insect nets.

Figure 4 Butterfly sampling by using fruit-baited trap

Result

Species composition and distribution of *Mycalesis* in peninsular Thailand

The butterflies of genus *Mycalesis* were sampled, with a total of 214 individuals, described to seven species comprising of five members of *Mineus* group belonged to *M. intermedia*, *M. visala*, *M. perseoides*, *M. mineus* and *M. perseus*. The rest of *Mycalesis* were *M. orseis* of *Francisca* group and *M. janardana* of *Janardana* group (Table 2).

The result of Table 3 and Figure 5 showed that the species diversity, Chumphon province there are two *Mycalesis* species consisted of *M. perseoides* and *M. mineus,* there are three species composed of *M. perseoides, M. mineus* and *M. intermedia* were found in Surat Thani province. Four species, *M. perseus*, *M. intermedia*, *M. perseoides* and *M. visala* were found in Nakhon Si Thammarat province. Four *Mycalesis* species, *M. perseus M. mineus*, *M. perseoides,* and *M. visala* were found in Phang-Nga province. In addition, six species of *Mycalesis* consisted of *M. orseis*, *M. janardana*, *M. mineus*, *M. intermedia*, *M. perseoides* and *M. visala* were found in Trang province. However, five species, *M. mineus*, *M. intermedia*, *M. perseoides*, *M. visala* and *M. perseus,* occurred in Narathiwat province.

The result showed that high number of species was found at Trang province with six species, lowest number of species was found in Chumphon province with two species. Furthermore, *M. perseoides* was dominant species which found in all sampling sites across peninsular Thailand (Figure 5). *M. orseis* and *M. janardana* were found only one site from Trang province. In this study we found two distinct seasonal form (wet and dry season forms) in all site except Trang province.

Table 2 Species composition of *Mycalesis* in six sampling sites

Study site	**species**	**Number of individuals**			**Seasonal forms**	
		Male	**Female**	**Total**	**wsf.**	**dsf.**
Chumphon February, 2015	*M. mineus*	3	1	4	+	+
	M. perseoides	26	11	37	+	+
	Mycalesis sp.1	0	2	2	-	+
	Mycalesis sp.2	0	1	1	-	+
		29	**15**	**44**		
Surat Thani April, 2015	*M. mineus*	5	3	8	+	+
	M. intermedia	1	0	1	+	-
	M. perseoides	15	6	21	+	+
	Mycalesis sp.3	0	1	1	-	+
	Mycalesis sp.4	0	2	2	-	+
	Mycalesis sp.5	0	1	1	-	+
	Mycalesis sp.6	0	1	1	-	+
	Mycalesis sp.7	1	1	2	-	+
		22	**15**	**37**		
Nakhon Si Thammarat April, 2015	*M. intermedia*	2	0	2	+	-
	M. perseus	10	7	17	+	+
	M. perseoides	9	0	9	+	+
	M. visala	0	1	1	+	-
	Mycalesis sp.1	1	0	1	-	+
		22	**8**	**30**		
Phang-Nga February, 2015	*M. mineus*	6	1	7	+	+
	M. perseus	5	3	8	+	+
	M. perseoides	0	2	2	+	-
	M. visala	1	0	1	-	+
	Mycalesis sp. 1	1	1	2	-	+
	Mycalesis sp. 4	0	1	1	-	+
		13	**8**	**21**		

Table 2 (continued)

Study site	Species	Number of individuals			Seasonal form	
		Male	**Female**	**Total**	**wsf.**	**dsf.**
Trang June, 2015	*M. janardana*	1	1	2	+	-
	M. orseis	1	0	1	+	-
	M. intermedia	11	18	29	+	-
	M. mineus	0	2	2	+	-
	M. perseoides	1	0	1	+	-
	M. visala	2	1	3	+	-
		16	**22**	**30**		
Narathiwat May, 2015	*M. intermedia*	3	3	6	+	-
	M. mineus	5	3	8	+	-
	M. perseus	1	4	5	+	-
	M. perseoides	17	6	23	+	+
	M. visala	1	1	2	+	-
		27	**17**	**44**		
Total individuals		**129**	**85**	**214**		

Table 3 Species diversity and distribution of *Mycalesis* in six sampling sites.

Species	**Study site**					
	CHP	**STN**	**PNG**	**NST**	**TRG**	**NTW**
M. janardana	-	-	-	-	+	-
M. orseis	-	-	-	-	+	-
M. intermedia	-	+	+	+	+	+
M. mineus	+	+	+	-	+	+
M. perseus	-	-	+	+	-	+
M. perseoides	+	+	+	+	+	+
M. visala	-	-	+	+	+	+

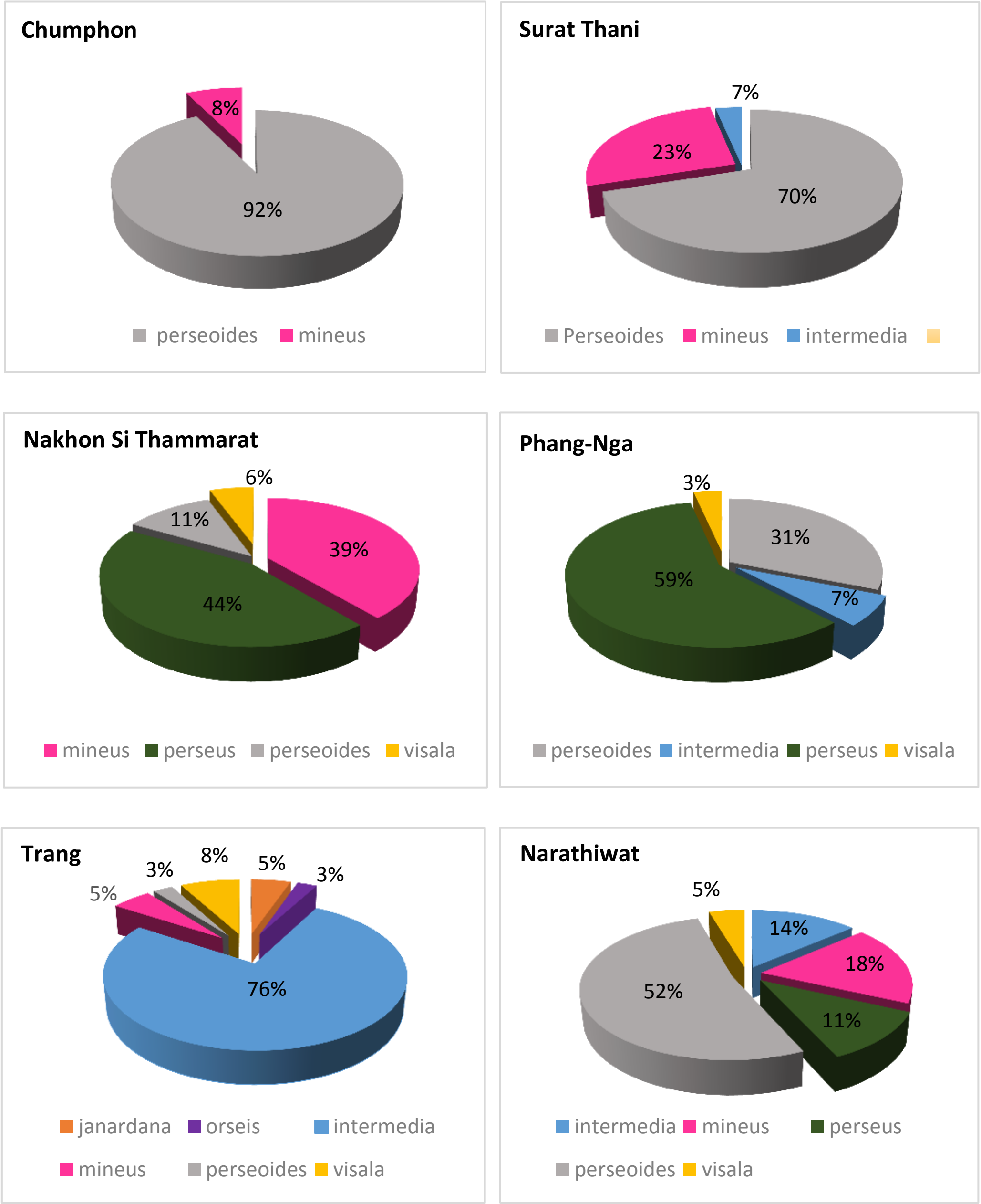

Figure 5 Species diversity and distribution of *Mycalesis* in each sampling sites.

Male genitalia description

The morphology of seven *Mycalesis* species were described. In general, the tegumen in lateral view of *M. orseis* and *M. janardana* formed a shallow dome and the rest of *Mycalesis* was flattened. The shape of tegumen in dorsal view was pentagonal. The width of combined length of the end of saccus to the tip of uncus varied from 0.2-0.4. The fenestrular was hardly defined in all species. The uncus was usually bent downward. The length of the gnathos was usually longer than uncus except *M. orseis* and *M. janardana*. The vinculum bent backward in all species. The saccus was elongated and bent upward or parallel to tegumen. The valva had a unique feather to the species

1. Mycalesis orseis Hewitson, 1864

Description: Tegumen in lateral view forming shallow dome; tegumen in dorsal view pentagonal, maximum width about 0.2 of combined length of the end of saccus to the tip of uncus. Fenestrula hardly defined; uncus elongate, slightly parallel, with short hook at tip, with moderately elongated gnathos; gnathos in lateral view moderately upward curve medially; gnathos in dorsal view bent inward at distal end; vinculum strongly bent backward; saccus elongate parallel to tegumen. Valva in lateral view convex outward and slightly longer than vinculum, sacculus weakly developed; distal half slightly tapered with pointed tip, aedeagus bent upward distal one-third and longer than vinculum; basal portion tapering (Figure 6).

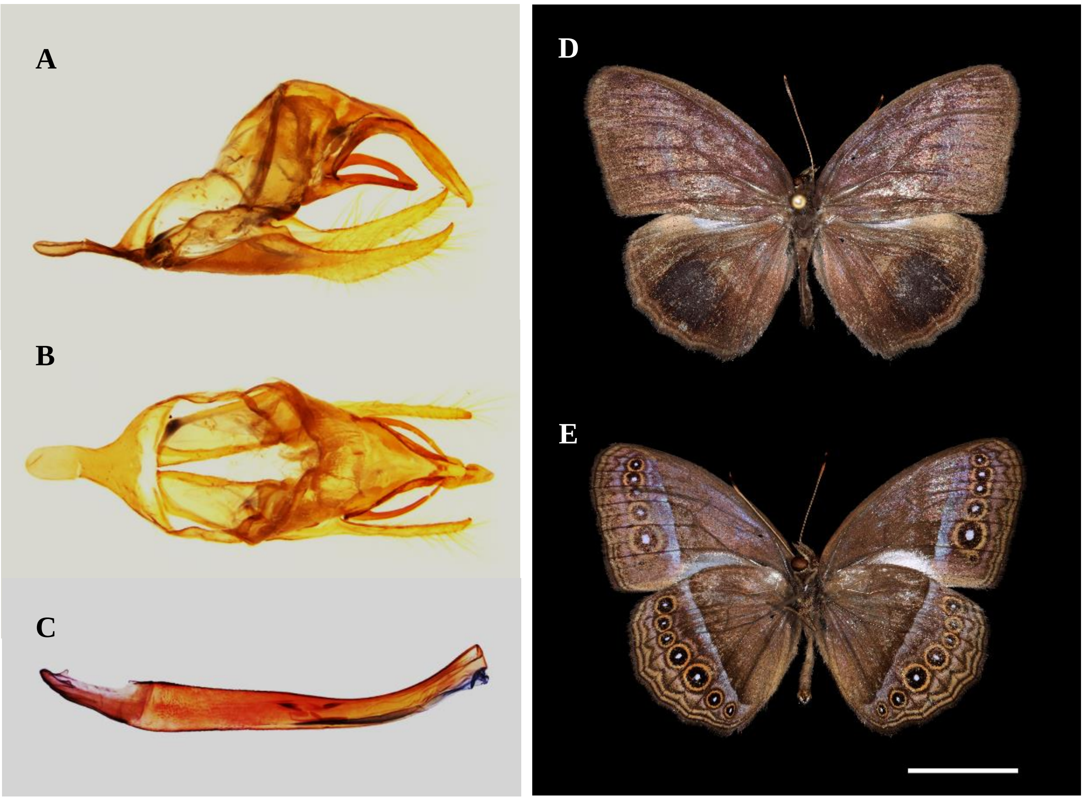

Figure 6 Male genitalia and adult of *M. orseis*; Genitalia, A) lateral view B) dorsal view C) aedeagus in lateral view. Adult, D) upperside E) underside (scale bar = 1cm).

2. *Mycalesis janardana* Moore, 1858

Description: Tegumen in lateral view forming dome; tegumen in dorsal view pentagonal, maximum width about 0.3 of combined length of the end of saccus to the tip of uncus. Fenestrula hardly defined; uncus elongate, basal tick, strongly tapering to bent downward apex, with rather slightly elongated gnathos; gnathos in lateral view bent downward; gnathos in dorsal view bent inward at distal end; vinculum strongly bent backward; saccus elongated and bent upward; valva in lateral view convex outward and bent inward at distal end, valva in lateral view slightly longer than vinculum; sacculus weakly developed; distal end of harpe slightly tapered and bent inward. Aedeagus bent upward distal end one-third and longer than vinculum, basal portion bent inward and tapering (Figure 7).

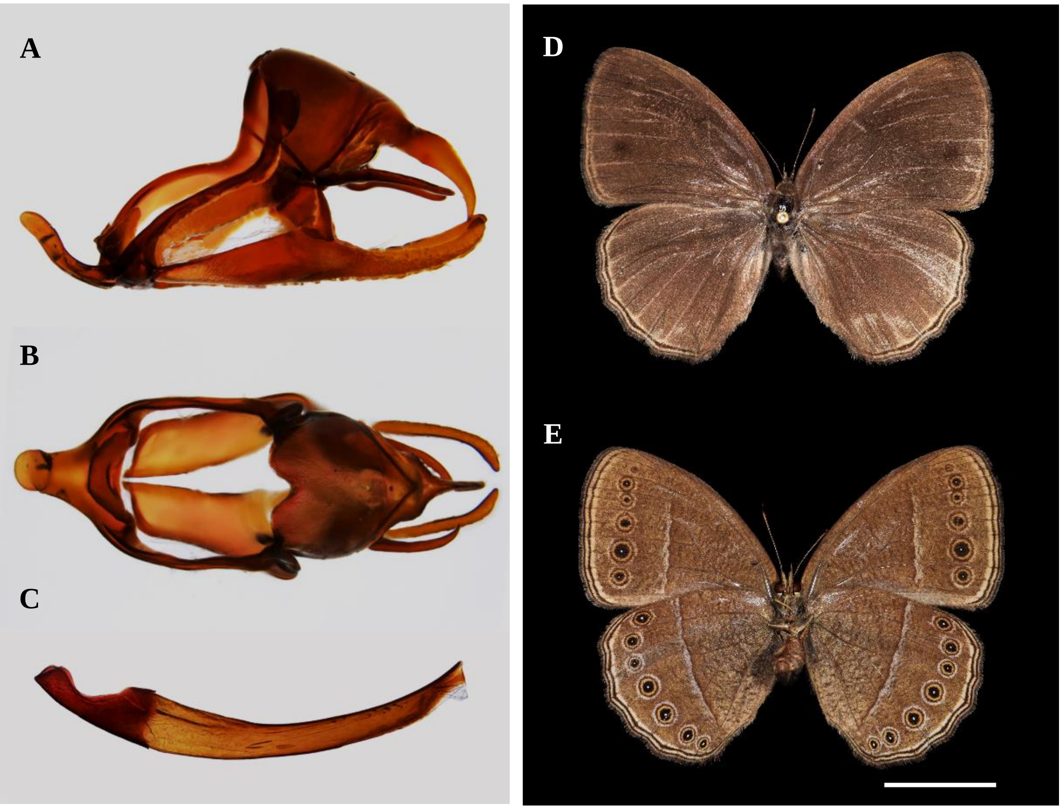

Figure 7 Male genitalia and adult of *M. janardana*; Genitalia, A) lateral view B) dorsal view C) aedeagus in lateral view. Adult, D) upperside E) underside (scale bar = 1cm).

3. Mycalesis mineus (Linnaeus, 1758)

Description: Tegumen in lateral view flat; tegumen in dorsal view pentagonal, maximum width about 0.4 of combined length of the end of saccus to the tip of uncus. Fenestrula hardly defined; uncus slightly elongate and bent downward apex, with elongated gnathos; gnathos in lateral view moderately curve upward at distal end, gnathos in dorsal view bent inward at distal end. Vinculum strongly bent backward; saccus elongated parallel to tegumen. Valva in lateral view with large sacculus subtriangular; neck distinct; cucullus with dorsal lobe subtriangular with posterior edge dentate, distal end long bifid, slightly dentate at tip; ventral margin round smooth with dense hair. Aedeagus bent upward distal end one-fourth with sub triangular at tip and longer than vinculum; basal portion with dorsal semi-circle (Figure 8).

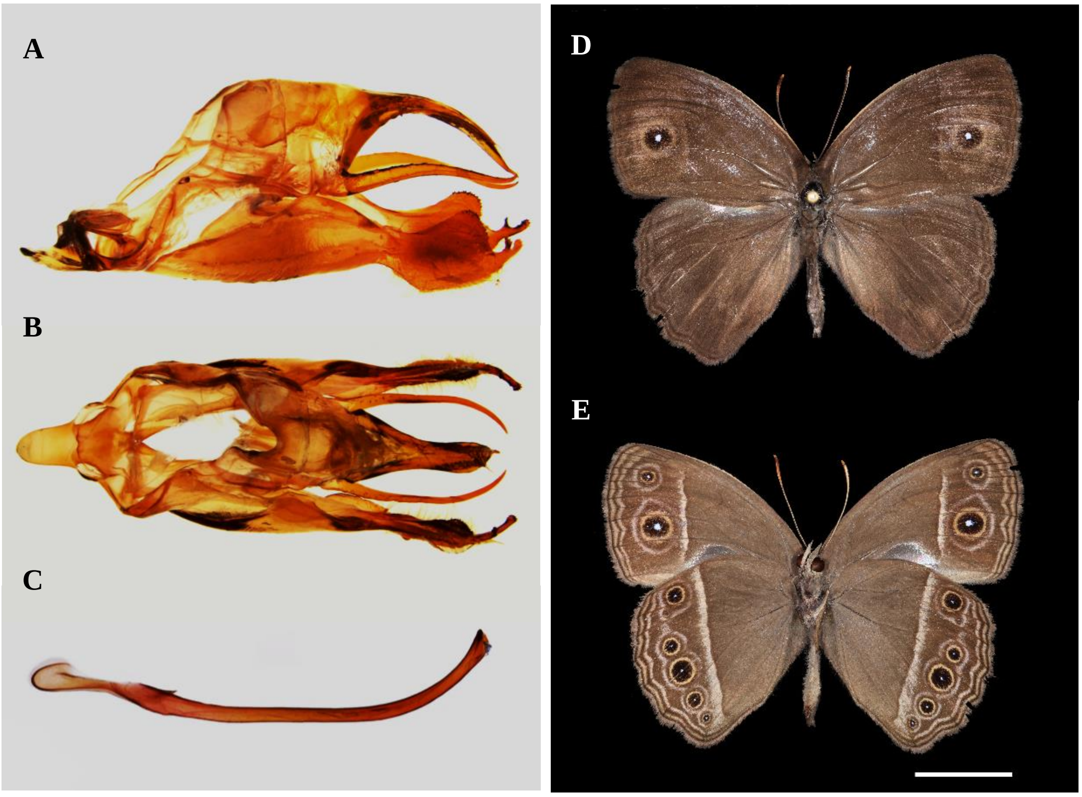

Figure 8 Male genitalia and adult of *M. mineus*; Genitalia, A) lateral view B) dorsal view C) aedeagus in lateral view. Adult, D) upperside E) underside (scale bar = 1cm).

4. Mycalesis perseus (Fabricius, 1775)

Description: Tegumen in lateral view flat; tegumen in dorsal view pentagonal, maximum width about 0.3 of combined length of the end of saccus to the tip of uncus. Fenestrula hardly defined; uncus elongate strongly tapering bent downward apex, with elongate gnathos; gnathos in lateral view moderately curve, weakly upward at distal end, gnathos in dorsal view bent inward at distal end, vinculum strongly bent backward, saccus elongated parallel to tegumen. Valva in lateral view with large sacculus subtriangular; neck distinct; cucullus with dorsal lobe subsemi-circle with posterior edge dentate, distal end short bifid, slightly dentate at tip; ventral margin round smooth with dense hair. Aedeagus bent upward distal end one-third and longer than vinculum; basal portion with dorsal subsemi-circle (Figure 9)

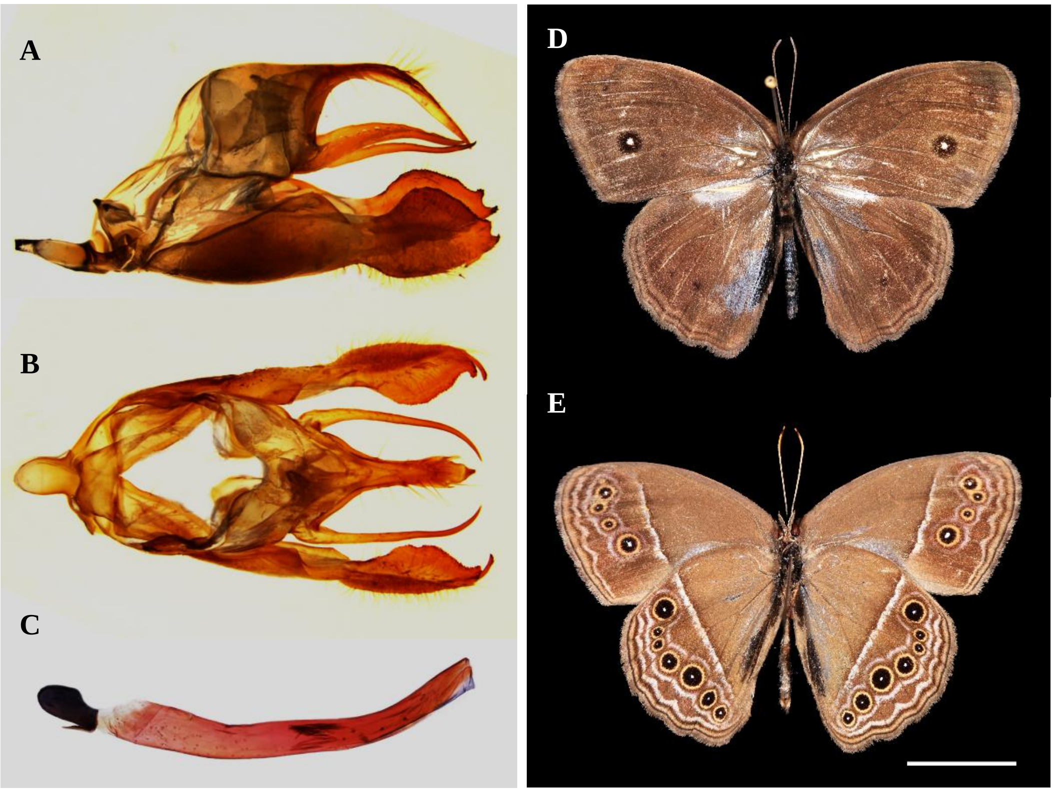

Figure 9 Male genitalia and adult of *M. perseus*; Genitalia, A) lateral view B) dorsal view C) aedeagus in lateral view. Adult, D) upperside E) underside (scale bar = 1cm).

5. *Mycalesis perseoides* (Moore, 1892)

Description: Tegumen in lateral view flat; tegumen in dorsal view pentagonal, maximum width about 0.3 of combined length of the end of saccus to the tip of uncus. Fenestrula hardly defined; uncus elongate, parallel to tegumen, strongly tapering bent downward apex, with elongated gnathos; gnathos in lateral view moderately curve upward, gnathos in dorsal view bent inward at distal end. Vinculum strongly bent backward; saccus elongated parallel to tegumen. Valva in lateral view with large sacculus subtriangle; neck distinct; cucullus with dorsal lobe subsemi-circle, with posterior edge dentate, distal end bifid with long tip, some saw tooth-like, slightly dentate at tip; ventral margin round, smooth with dense hair. Aedeagus bent upward distal end one-third with subtriangular tip and longer than vinculum; basal portion with dorsal semi-circle (Figure 10)

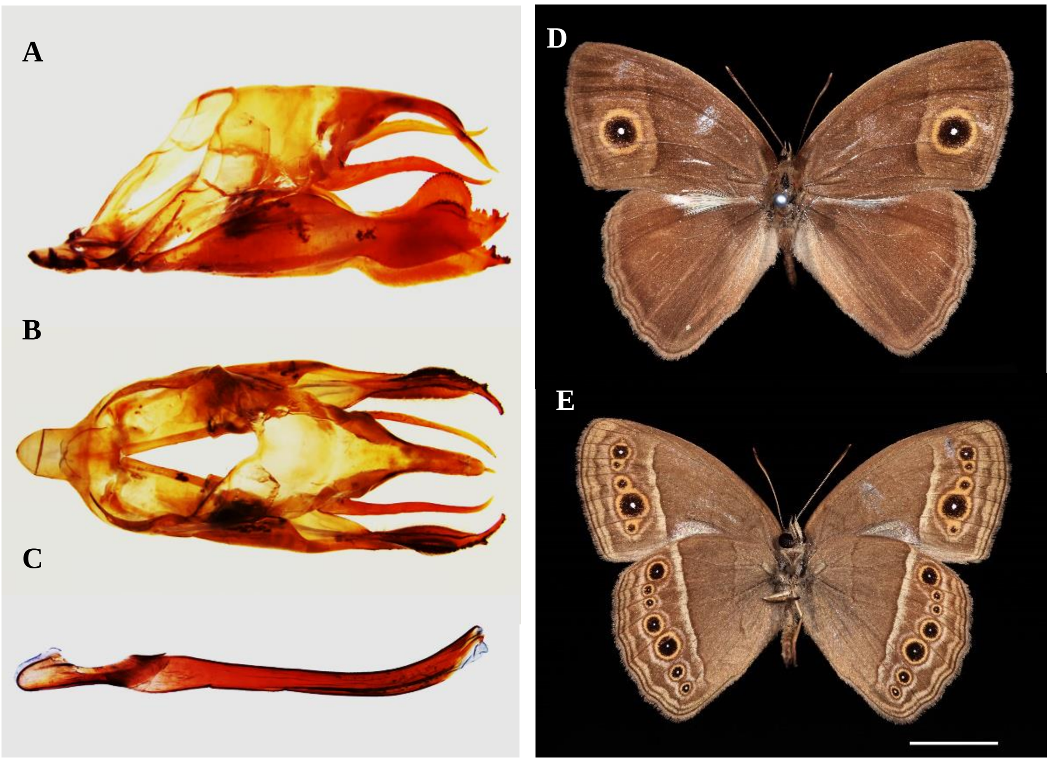

Figure 10 Male genitalia and adult of *M. perseoides*; Genitalia, A) lateral view B) dorsal view C) aedeagus in lateral view. Adult, D) upperside E) underside (scale bar = 1cm).

6. *Mycalesis visala* Moore, 1858

Description: Tegumen in lateral view flat; tegumen in dorsal view pentagonal, maximum width about 0.3 of combined length of the end of saccus to the tip of uncus. Fenestrula hardly defined; uncus elongate, parallel to tegumen, tapering bent downward apex, with elongated gnathos; gnathos in lateral view strongly curve upward medially, gnathos in dorsal view bent inward at distal end. Vinculum strongly bent backward; saccus elongate parallel to tegumen. Valva in lateral view with large sacculus subtriangle; neck distinct; cucullus with dorsal lobe subsemi-circle, with posterior edge dentate, distal end bifid with long tip some saw tooth-like, slightly dentate at tip; ventral margin round smooth with dense hair. Aedeagus bent upward distal end one-third, longer than vinculum, basal portion with dorsal semi-circle (Figure 11).

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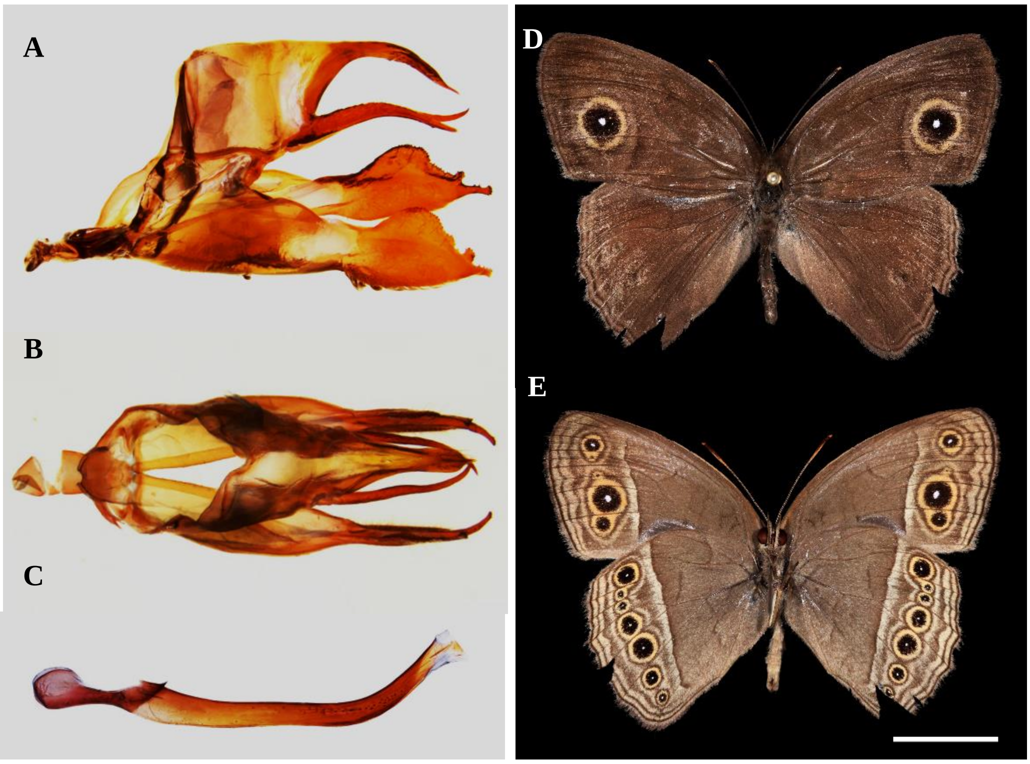

Figure 11 Male genitalia and adult of *M. visala*; Genitalia, A) lateral view B) dorsal view C) aedeagus in lateral view. Adult, D) upperside E) underside (scale bar = 1cm).

7. Mycalesis intermedia (Moore, 1892)

Description: Tegumen in lateral view flat; tegumen in dorsal view pentagonal, maximum width about 0.3 of combined length of the end of saccus to the tip of uncus. Fenestrula hardly defined; uncus elongate parallel to tegumen, strongly tapering bent downward apex, with elongated gnathos; gnathos in lateral view moderately curve upward medially, gnathos in dorsal view bent inward at distal end. Vinculum strongly bent backward; saccus elongated, bent backward. Valva in lateral view with large sacculus subtriangle; neck distinct; cucullus with dorsal lobe subsemi-circle, with posterior edge dentate, distal end bifid with long tip some saw tooth-like, slightly with hook at tip, ventral margin round, and smooth with dense hair. Aedeagus bent upward distal end one-third with sub triangular at tip and longer than vinculum, basal portion with dorsal semi-circle (Figure 12)

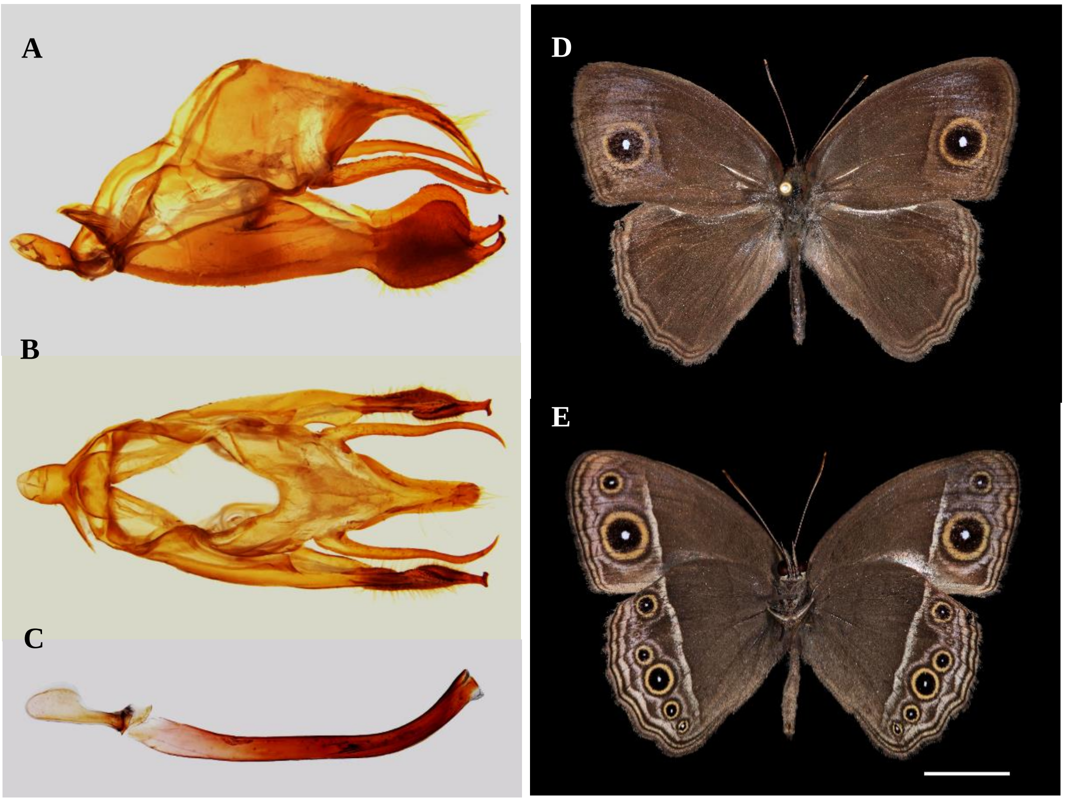

Figure 12 Male genitalia and adult of *M. intermedia*; Genitalia, A) lateral view B) dorsal view C) aedeagus in lateral view. Adult, D) upperside E) underside (scale bar = 1cm).

Discussion

According to previous report (Ek-Amnuay, 2012; Pinratana, 1988; Wangthaveesup, 2008) there are 15 species of *Mycalesis* distribute throughout peninsular Thailand, but in this study, a total of seven species were found. The result showed that *M. perseoides* is common species was found in all collecting sites. It was possible related with their host plant in each habitat type, this species can found several habitat such as open area, vegetation, grasslands, oil palm agriculture and bamboo forest (Lin, 2014). The food plant of *Mycalesis* is mainly in the family Poaceae and Cyperacae (Ackery, 1988). The study of *Mycalesis* host plant in Thailand were lack of knowledge, there are reported in some species such as, *Cyperus revifolius* has been recorded as larva host plant of *M. mineus*. *Axonopus compressus* has been recorded as larva host plant of *M. intermedia.* However, *Ottochloa nodosa* and *Ischaemum ciliare*, have been recorded as larva host plant of *M. perseoides* in Singapore (Tan, 2013).

The result in figure 5 showed that Khao Chong,Trang province have high species richness (number of species) with six species, associate with there are several microhabitat in collecting site (closed canopy, open aria, grass land, oil palm agriculture and bamboo forest) more than another collecting site. The finding was supported with Young *et al*. (2012) reported that the characteristic of vegetation cover led to different to microhabitat and might be a major factor the diversity of butterfly.

In this study, we collected the samples covered wet season and dry season. *Mycalesis* species were found into two seasonal form that wet and dry season forms. *M. orseis* and *M. janardana* were found only wet season form. The rest of, *M. perseoides*, *M.visala*, *M. perseus*, *M. intermedia* and *M. mineus* were found two distinct seasonal forms. According to Brakefield (1984) indicated that many species of Satyrinae and some others group of butterfly in tropical have a distinct seasonal forms. Braby, 1994 and Islam *et al*. (2010) reported that the development of seasonal morphs is determined by many physical factor such as temperature, humidity and photoperiod. In this study, those factor was not observed. However, previous study was suggested that temperature play an importance role in regulating wing phenotype in several Lepidoptera (Janzen, 1984)

Brakefield and Reitsma (1991) and Windig (1992) showed that different temperature in final instar larva of *Bicyclus safitza* induced different seasonal forms. Rienks (1985) and Jones *et al*. (1985) also demonstrate that small changes in photoperiod in conjunction with temperature can affect wing phenotype in two tropical Pieridae. Islam *et al*. (2010) report consistent with Brakefiled (1987) and Brakefield and Reitsma (1991) indicated that the turnover from dry season form to wet season form coincided with rising temperature when increase in humidity and food plant occur. In contrast, the turnover of wet season form to dry season form was found at declining temperature, low humidity and less food plant.

Braby (1994) and Brakefield (1984) proposed that the prominent eyespot pattern in wet season form possibly function as anti-predator devices. In contrast, dry season form butterflies have reduced ocelli and lack of eyespots this maybe probably for their survival. These type of phenotypic plasticity is associated with changes in habitat favorably (Braby, 1994; Islam *et al*., 2010).

CHARPTER 3

Genetic variation in *Mineus* group of *Mycalesis* (Nymphalidae: Satyrinae) in peninsular Thailand: inferred from mitochondrial and nuclear genes

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Original Article

Genetic variation in *Mineus* group of *Mycalesis* (Nymphalidae: Satyrinae) in peninsular Thailand: inferred from mitochondrial and nuclear genes

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Abstract

The aim of this study was to investigate genetic variation and phylogenetic relationships of the *Mineus* group of the genus *Mycalesis* in peninsular Thailand inferred by mitochondrial and nuclear gene markers (*COI*, *EF-1α* and *wingless*). The *Mycalesis* specimens were sampled from six provinces in peninsular Thailand. Seven species of the genus *Mycalesis* were identified. In this study, two distinct seasonal morphs were found as wet season and dry season forms. Phylogenetic relationships based on combined gene sequences indicated that the *Mineus* group of *Mycalesis* was monophyletic group. However, *M. intermedia*, *M. visala* and *M. perseoides* might be complex species. Five haplotype patterns were observed in *M. perseoides* indicating that Chumphon province was the origin of *M. perseoides*. Divergence time of the *Mineus* group was 23.03 mya during Oligocene in peninsular Thailand.

Keywords: *Mycalesis*, genetic differentiation, haplotype network, peninsular Thailand, phylogeny

Introduction

Butterflies of the subtribe Mycalesina (Nymphalidae: Satyrinae) were described into 7 genera based on molecular and morphological evidences consisting of genus *Lohora*, *Heteropsis*, *Mycalesis*, *Mydosama, Culapa*, *Bicyclus* and *Hallelesis* (Aduse-Poku *et al*., 2015). This subtribe is restricted in the Old World tropics in which *Mycalesis* is a dominant genus with over 100 estimated described species. Moreover, this genus has been widely dispersed in Indo-Australian region such as in Sri Lanka, India, Southeast Asia, Australia, New Guinea and the east of Solomon Islands (Kodandaramaiah *et al*., 2010). The majority of genus *Mycalesis* prefers lowland habitats and can be found in many kinds of habitat such as forest edges, grasslands and savannas. The butterflies are low-flight and prefer understory shade (Monastyrskii, 2005). The food plants were found in the family of Poaceae and Cyperaceae (Ackery, 1988; Torres *et al*., 2001).

Butterflies in subtribe Mycalesina are an important model to understand the evolutionary study, ecology, development, genetics and phenotypic plasticity of tropical butterflies (Braby, 1994; Brakefield, 1984; 2012; Islam *et al*., 2010; Torres *et al*., 2001). For instance, the study of seasonal polymorphism of *Mycalesis* in Australia indicated the mechanism of survival between wet and dry seasonal change in their habitat (Braby, 1994). In addition, physical factors such as temperature, rainfall, humidity and photoperiod can determine the variation of wet and dry season forms (Islam *et al*., 2010). Interestingly, phenotypic variation of tropical butterfly in terms of morphological characters in the dry and wet seasonal forms are important. However, the phenotypic character in the dry seasonal form are not recognized, because the eyespots reduced. In a previous study, morphometric characterization of *Mycalesis* butterflies in Sri-Lanka showed that phenotypic characters are different, for examples, coloration of wings and dorsal forewing ocelli of adult *Mycalesis* species (Goonesekera, Poorten, & Ranawaka, 2014). Furthermore, genetic variation in *Mycalesis* from Sri Lanka based on analysis of *COI* gene indicated that the variation of haplotype network in *Mycalesis* was not different and also was restricted on their location. Genetic distances were significantly different among local species (Goonesekera & Rawanaka, 2013).

Peninsular Thailand is placed on the Sundaic shelf, which is an important transition zone between the Indo-Chinese and Sundaic sub-regions. Both sub-regions are separated by the Isthmus of Kra which was proposed a natural barrier for dispersal of fauna (Lohman *et al*., 2011). According to vegetation structure in the peninsular Thailand, two types of forest community consist of evergreen rain forest and mixed moist deciduous forest (the southern part of Thailand, Thai type) and evergreen rain forest (Kangar-Pattani line, Malayan type)(Santisook, 2012). However, the study on *Mycalesis* was not attended, especially in terms of diversity and abundance. Moreover, Ek-Amnuay (2012) and Pinratana (1988) reported that there are 27 species spreading throughout Thailand. Among these, *M. fusca*, *M. janardana*, *M. perseus*, *M. mineus*, *M. visala*, *M. orseis* were restricted to the peninsular Thailand. On the other hand, Evan (1932) divided *Mycalesis* species into five groups, i.e., *Gotama* group, *Mineus* group, *Oroatis* group, *Nicotia* group, and *Patnia* group. The members of *Mineus* group are *M. perseus*, *M. mineus*, *M. igilia*, *M. visala*, *M. perseoides*, *M. subtida*, *M. mercea*, *M. khasia*, *M. rama*, *M. evansii*, *M. mystes*, *M. adolphei*, *M. intermedia* and *M. oculus* (Evan, 1932; Talbot & Corbet, 1939). Nowadays, the phylogenetic relationship of the subtribe Mycalesina based on molecular data is established as monophyly. *Mycalesis* species are clustered into two clades as *Mycalesis* I consists of the taxa from mainland Southeast Asia and *Mycalesis* II belongs the taxa from Indo-Australia. However, both clusters are not monophyletic group (Aduse-Poku *et al*., 2015; Kodandaramaiah *et al*., 2010). In addition, there is lack of knowledge on phylogenetic relationships and genetic variation of *Mycalesis* (*Mineus* group) in peninsular Thailand.

This study aims to investigate the phylogenetic relationship and genetic variation of *Mycalesis* (*Mineus* group) inferred from one mitochondrial and two nuclear genes. Within the hypothesis of phylogenetic study, divergence times of *Mycalesis* group have been estimated. The finding of this study can contribute and clarify the *Mycalesis* (*Mineus* group) in peninsular Thailand.

Materials and Methods

Taxon sampling

Butterflies of the genus *Mycalesis* were collected in six provinces along the mountainous ranges of peninsular Thailand. Six sampling sites were at Chumphon province (CHP), Surat Thani province (STN), Nakhorn Si Thammarat province (NST), Phang-Nga province (PNG), Trang province (TRG) and Narathiwat province (NTW) during June 2015-July 2016. Adult butterflies were collected using insect nets and baited traps with 10 fruit-baited traps set up along 1 km line transect at each sampling site. Each trap was randomly placed on the line transect at a distance 100 m. The baited-trap was sampled during seven consecutively days at each sampling site. Adult butterflies were preserved in trianglular paper. A pair of middle legs were removed from the specimens and placed in 95% ethanol for DNA extraction. The rest of the specimens were in a box.

Species identification

Mycalesis species were identified to species level using identification keys descriptions and illustrations by Corbet, Pendlebury and Eloit (1978), Ek-Amnuay (2012), Monastyrskii (2005), Pinratana (1988) and Talbot (1947).

DNA extraction, PCR amplification and sequencing

Total DNA was extracted using applied protocol from Collins *et al*. (1987). The sample was homogenized with a pestles in a 1.5 micro centrifuge tube with 50 µl of lysis buffer including 0.8 M NaCl, 0.16 M sucrose, 0.06 M EDTA, 0.5% SDS and 0.1 M Tris-HCl pH 8.6. Two µl of Proteinase K was added and the homogenate was incubated at 65°C overnight. Seven µl of 8 M CH_3CO_2K was added and the tube was incubated for 30 min at -20°C. Then it was centrifuged at room temperature for 15 min at 13,400 rpm. Supernatant was removed to a sterile tube and 95% ethanol added and centrifuged again at 13,400 rpm for 15 min. After discarding supernatant, the pellet was washed with 70% ethanol and centrifuge again. The pellet was dried and suspended in 50 µl of TE buffer (10 mM Tris, 1 mM EDTA pH 8.0) and maintained at -20°C.

DNA was amplified from a mitochondrial gene Cytochrome Oxidase subunit I (*COI*) and two nuclear genes, Elongation factor 1 alpha (*EF-1α*) and *wingless* genes. The polymerase chain reaction was done using 2X Blue/Red mix DNA polymerase master mix (RBC Bioscience, Taiwan) following manufacturer's protocol. The primers of three genes follow Kodandaramaiah *et al*. (2010) with *COI* using primer LCO – HCO (LCO ; 5' GGTCAACAAATCATAAAGATATTGG 3' F and HCO : 5' TAAACTTCAGGGTGACCA AAAAATCA 3 'R) with following protocol : 95 °C 7 min for initial denature, 40 cycles for 95 °C 30 s, 50 °C 30 s and 72 °C 1 min, final extension at 72 °C for 10 min. *EF-1α* using primer Starsky-Luke (Starsky : 5'CACATYAACATTGTCGTSATYGG 3' F and Luke : 5'CATRTTGTCKCCGTGCCAKCC 3' R) with following protocol : 95 °C 7 min for initial denature, 40 cycles for 95 °C 30 s, 55 °C 30 s and 72 °C 1 min, final extension at 72 °C for 10 min. *wingless* using primer Wingnut 1A – Wingnut-3 (Wingnut 1A : 5'-GAAATGCGNCARGARTGYAA-3' F and Wingnut-3 : 5'-ACYTCRCARCACCARTGRAA-3' R) with following protocol : 80 °C 1 min for initial denature, 40 cycling for 94 °C 1 min, 52 °C 2 min and 72 °C 1 min, final extension at 72 °C for 10 min. PCR products were checked by 1.5% agarose gel electrophoresis and sent to sequencing with BIONEER (south Korea).

Genetic variation and phylogenetic analysis

Sequences were viewed by Chromas Lite version 2.5.1 software and aligned using Bioedit version 7.1.3 software (Hall, 1999). The aligned sequences were arranged by MEGA version 6.0 to analyze nucleotide composition and pairwise genetic distance (Tamura, Stecher, Peterson, Filipski, & Kumar, 2013). DnaSP version 5.10.01 (Rozas & Rozas, 1999) was use to estimate number of haplotype (*h*), haplotype diversity (*Hd*), nucleotide diversity (π), invariable site, parsimony informative site, number of polymorphic sites (*S*) and Tajima's *D* test (Nei & Kumar, 2000). Sequences were submitted to GenBank for accession numbers (Table 1).

Table 1 List of *Mycalesis* sequences were obtained for this study

Species	Localities	Coordinate	Accession Number		
			COI	*EF-1α*	*wingless*
M. perseoides	CHP	10°45.798’N	MG461862	MG461892	MG461922
		99°23.032’E	MG461863	MG461893	MG461923
			MG461864	MG461894	MG461924
			MG461865	MG461895	MG461925
M. perseoides	STN	09°23.340’N	MG461871	MG461901	MG461931
		99°15.240’E	MG461872	MG461902	MG461932
M. perseoides	NST	08°20.020’N	MG461875	MG461905	MG461935
		100°09.562’E	MG461880	MG461910	MG461940
M. perseoides	NTW	05°58.655’N	MG461887	MG461917	MG461947
		101°54.392’E	MG461891	MG461921	MG461951
M. intermedia	STN	09°23.340’N	MG461873	MG461903	MG461933
		99°15.240’E			
M. intermedia	NST	08°20.020’N	MG461874	MG461904	MG461934
		100°09.562’E	MG461877	MG461907	MG461937
M. intermedia	TRG	07°33.360’N	MG461882	MG461912	MG461942
		99°46.724’E	MG461885	MG461915	MG461945
			MG461886	MG461916	MG461946
M. intermedia	NTW	05°58.655’N	MG461888	MG461918	MG461948
		101°54.392’E	MG461889	MG461919	MG461949
			MG461890	MG461920	MG461950
M. mineus	STN	09°23.340’N	MG461869	MG461899	MG461929
		99°15.240’E	MG461870	MG461900	MG461930
M. visala	NST	08°20.020’N	MG461876	MG461906	MG461936
		100°09.562’E			
M. visala	TRG	07°33.360’N	MG461883	MG461913	MG461943
		99°46.724’E			
M. perseus	NST	08°20.020’N	MG461878	MG461908	MG461938
		100°09.562’E	MG461879	MG461909	MG461939
M. orseis	TRG	07°33.360’N	MG461881	MG461914	MG461944
		99°46.724’E			
M. janardana	TRG	07°33.360’N	MG461884	MG461911	MG461941
		99°46.724’E			

Genetic differentiation and phylogenetic tree of the butterfly genus *Mycalesis* in peninsular Thailand using *COI*, *EF-1α* and *wingless* genes were determined. Kimura 2-parameter model was used to calculate the genetic distance. Haplotype network of the *M. perseoides* was generated using TCS program version 1.7 (Clement, Posada, & Crandall, 2000). Phylogenetic analysis of the butterfly genus *Mycalesis* was conducted for *COI* sequence and for the combined dataset (*COI*, *EF-1α* and *wingless*). Bayesian analysis with MrBayes version 3.2.6 using General Time Reversible (GTR) model by GAMMA distribution was done for 10,000,000 generations with a sampling frequency of 100 generations (Huelsenbeck & Ronquist, 2001). Phylogeny was viewed and edited by FigTree version 1.3.1 (Rambaut, 2009). Species divergence time was investigated by the molecular clock using fossil record of *Lethe corbieri* by Neighbor-joining method (NJ) in MEGA program version 6.0.

Result

The butterflies of genus *Mycalesis* were sampled during February 2015 to July 2016 with a total of 214 individuals, Seven species were grouped into five members of *Mineus* group consisting of *M. intermedia*, *M. visala*, *M. perseoides*, *M. mineus* and *M. perseus*. The rest of *Mycalesis* were *M. orseis* and *M. janardana*. The *Mycalesis* species was found to be distributed in each province; Chumphon province (CHP) consisted of *M. mineus* and *M. perseoides*. Four *Mycalesis* species (*M. perseus, M. mineus, M. perseoides* and *M. visala*) were found in Phang-Nga province (PHG), Phuket mountain range. Three species, *M. mineus*, *M. intermedia* and *M. perseoides* were found in Surat Thani province (STN). Furthermore, four species, (*M. perseus, M. intermedia, M. perseoides* and *M. visala*), were found in Nakhon Si Thammarat province (NST). In addition, six species of *Mycalesis,* (*M. orseis*, *M. janardana*, *M. mineus, M. intermedia*, *M. perseoides* and *M. visala*), were found in Trang province (TRG), Nakhon Si Thammarat mountain range. However, five species, *M. mineus*, *M. intermedia*, *M. perseoides, M. visala* and *M. perseus,* occurred in Narathiwat province (NTW), San kala khiri mountain range. The result showed that *M. perseoides* was dominant species in all sampling sites across peninsular Thailand (Figure 1). Interestingly, *Mycalesis* species in peninsular Thailand showed two distinct seasonal morphs; wet season form and dry season form, were *M. mineus* and *M. perseoides*. This shows relationship between genetic variation and phenotypic plasticity (Figure 2). The phenotypic character of *M. mineus* and *M. perseoides* in the dry season form and the wet season form are different, especially in dry season forms they are difficult to be identified because the characters such as less colorations of wings and eyespots are reduced. On the other hand, for the wet season form, the colorations of wings and eyespots are prominent characters.

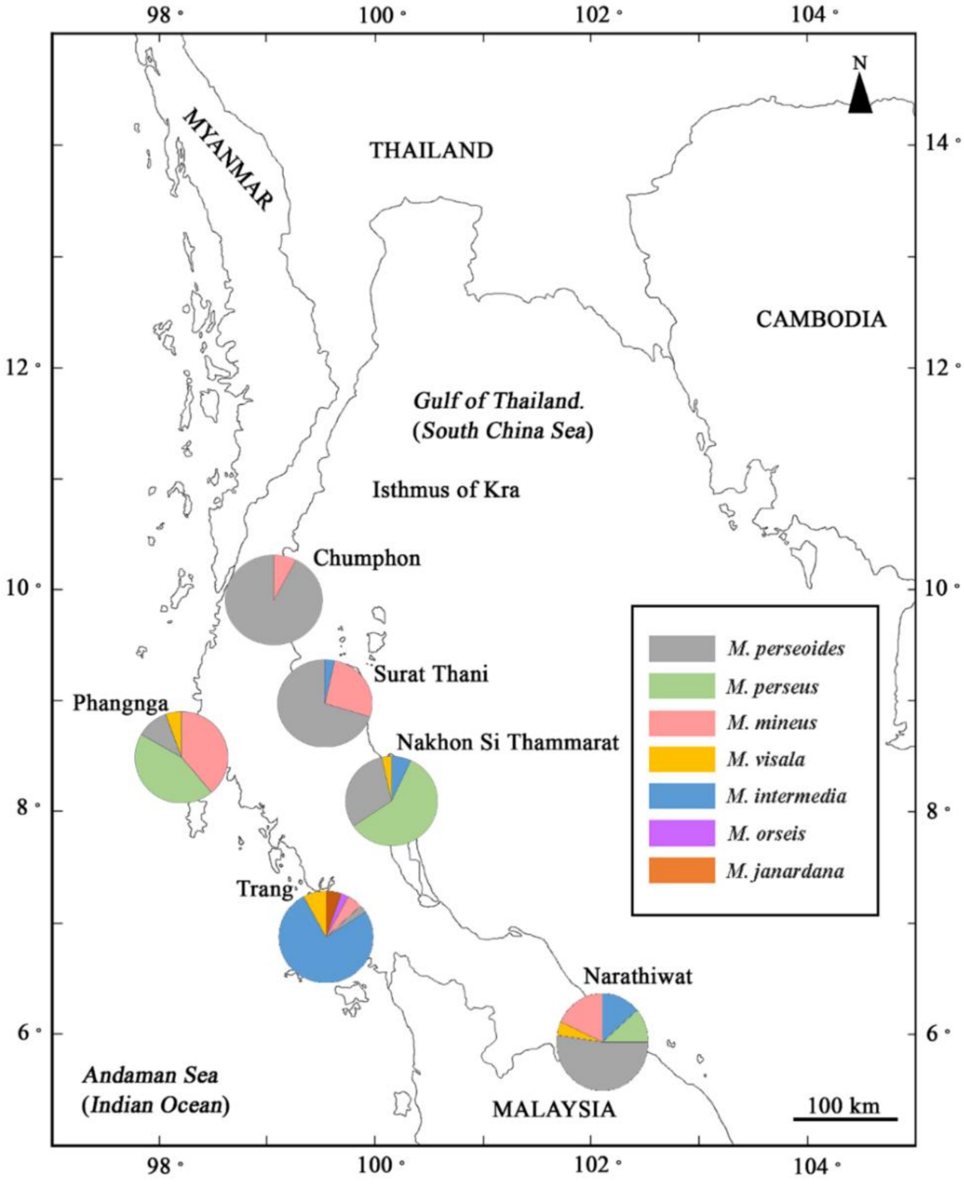

Figure 1 Distribution of *Mycalesis* species in six study sites of peninsular Thailand. Pie chart segments are proportional to the number of individuals collected at each location.

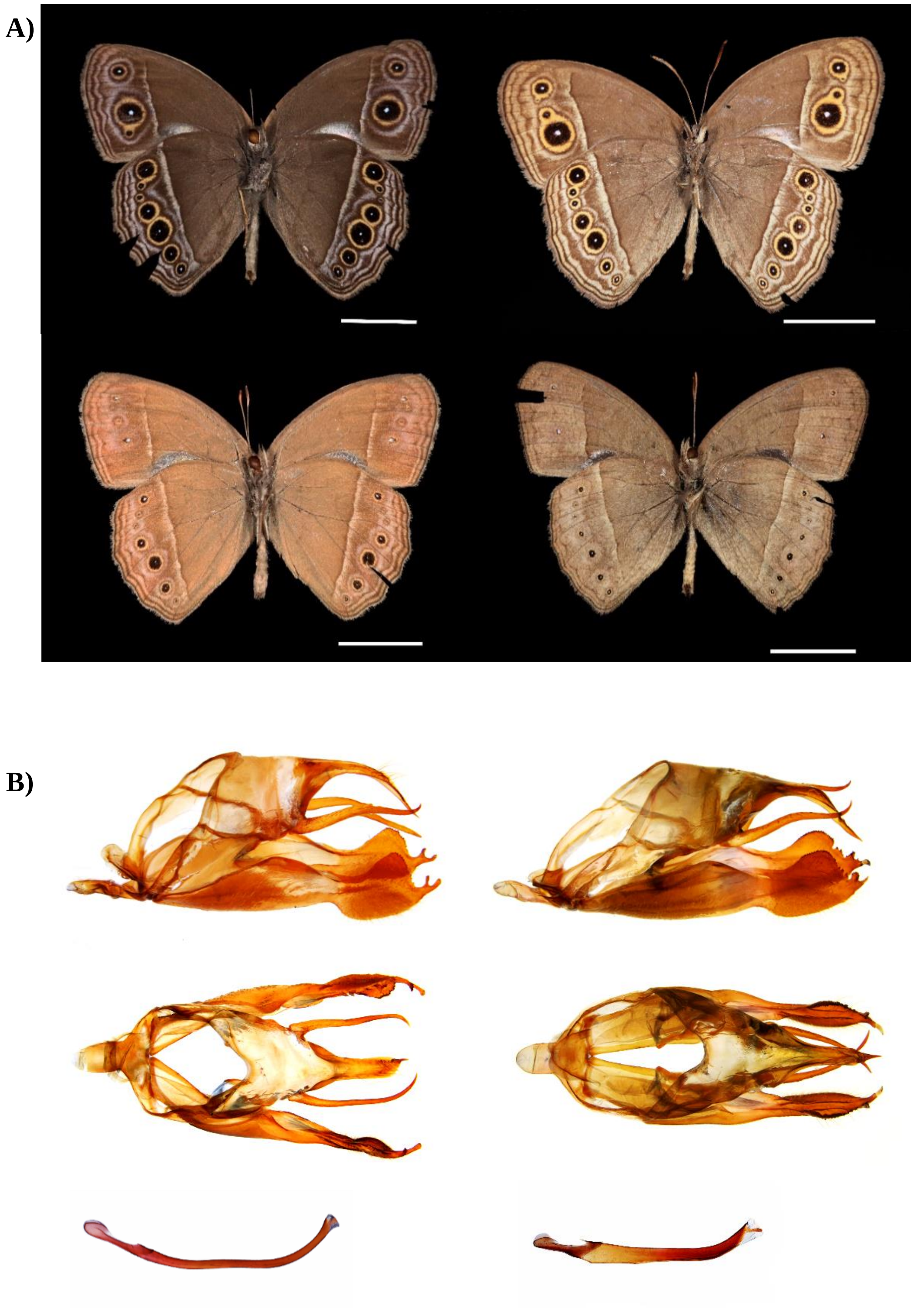

Figure 2 Two species of *Mycalesis* in peninsular Thailand: *M. mineus* (left column) and *M. perseoides* (right column); A) representative examples of wet season form (top row) and dry season form (bottom row); B) male genitalia and aedeagus. All specimens are males. Adult butterfly (scale bar = 1 cm).

Genetic variation

The aligned sequences were 632 bp (*COI*), 485 bp (*EF-1α*) and 379 bp (*wingless*). The *COI* sequence showed higher invariant sites than *EF-1α* and *wingless*. Among 632 bp of *COI* sequence, 73 sites were parsimony informative. The *EF-1α* sequence contained 24 variable parsimony informative sites while *wingless* contained only 16 variable parsimony informative sites. Genetic diversity indices of the three genes showed *COI* gene had 0.04019 nucleotide diversity (π), 25.32 average number of nucleotide differences (K) and 125 polymorphic sites (S). Furthermore, the nucleotide diversity, average number of nucleotide differences and number of polymorphic sites of *EF-1α* and *wingless* were 0.02293, 88, 10.93 and 0.01591, 52, 6.03 respectively. However, the number of haplotype (h) and haplotype diversity (Hd) were high in *wingless* gene, that belonging 23 and 0.980. The result of Tajima's D-test revealed that all genes were not significant (Table 2).

Table 2 Statistic for individual gene segments.

parameters	***COI***	***EF-1α***	***wingless***
Number of samples	29	29	29
Aligned positions	632	485	379
Polymorphic site			
- Invariable sites	505	389	327
- Singleton variable sites	52	64	36
- Parsimony informative sites	73	24	16
- Nucleotide diversity (π)	0.04019	0.02293	0.01591
- Number of polymorphic sites (S)	125	88	52
- Average number of nucleotide differences (K)	25.32	10.93	6.03
Haplotype diversity			
- Number of haplotype (h)	14	19	23
- Haplotype diversity (Hd)	0.771	0.887	0.980
Tajima's Test			
- Tajima's D	-1.23492*	-2.08307*	-2.20456*

Note: * not significant.

M. perseoides and *M. perseus* possessed the greatest intraspecific genetic differentiation in the nuclear gene (*EF-1α* values were 1.76 and 4.70, and *wingless* values were 0.80 and 1.10, respectively). However, intraspecific genetic divergence for *M. intermedia* and *M.visala* were high in *COI* gene (2.70 and 6.20, respectively) (Table 3).

Table 3 Intraspecific genetic divergence among the members of *Mycalesis Mineus* group in peninsular Thailand based on the Kimura 2-parameter model.

Species	***COI***	***EF-1α***	***Wingless***
M. perseoides	0.33 (0.000-0.006)	1.76 (0.000-0.042)	0.80 (0.003-0.013)
M. intermedia	2.70 (0.000-0.066)	1.00 (0.000-0.019)	0.67 (0.000-0.013)
M. mineus	0.25 (0.002-0.003)	0.40 (0.000-0.004)	0.65 (0.005-0.008)
M. visala	6.20 (0.000-0.062)	1.00 (0.002-0.015)	0.40 (0.003-0.005)
M. perseus	0.20 (0.002)	4.70 (0.047)	1.10 (0.011)

Note: The analyses involved 29 nucleotide sequences. All positions containing gaps and missing data were eliminated. There are a total of 360 positions for *COI*, 476 positions for *EF-1α* and 379 positions for *wingless*. All values are mean (%) (min.-max.). For *M. perseus* had only one value.

According to haplotype network of *Mycalesis* species in peninsular Thailand, the haplotype network of *M. perseoides* based on *EF-1α* gene in four provinces (CHP, STN, NST and NTW) was generated. The result showed that five haplotype patterns were found and the haplotype diversity was 0.667. Furthermore, number of polymorphic sites, nucleotide diversity and Average number of nucleotide differences were 22, 0.00949 and 4.556 respectively (Table 4).

Table 4 Statistic of *M. perseoides* based on *EF-1α* sequence.

parameters	***EF-1α***
Number of samples	10
Aligned positions	485
Polymorphic site	
- Invariable sites	458
- Singleton variable sites	21
- Parsimony informative sites	1
- Nucleotide diversity (*π*)	0.00949
- Number of polymorphic sites (*S*)	22
- Average number of nucleotide differences (*K*)	4.556
- Number of haplotype (*h*)	5
- Haplotype diversity (*Hd*)	0.667
- Tajima's D	-1.95824*

Note: * not significant.

The haplotype relationship of five haplotype is shown in Figure 3. Haplotype 1 of *M. perseoides* (n = 6) indicated that Chumphon province might be the origin of *M. perseoides* in peninsular Thailand. However, the haplotype of *M. perseoides* in Chumphon is different from the Surat Thani (haplotype 3, n = 1) in one mutation step of nucleotide substitution. Moreover, haplotype 4 (Nakhon Si Thammarat, n = 1) is 19 mutation steps of nucleotide substitution away from Chumphon haplotype pattern. However, the haplotype 5 (Narathiwat, n = 1) is different in two mutation steps of nucleotide substitution from Chumphon haplotype pattern.

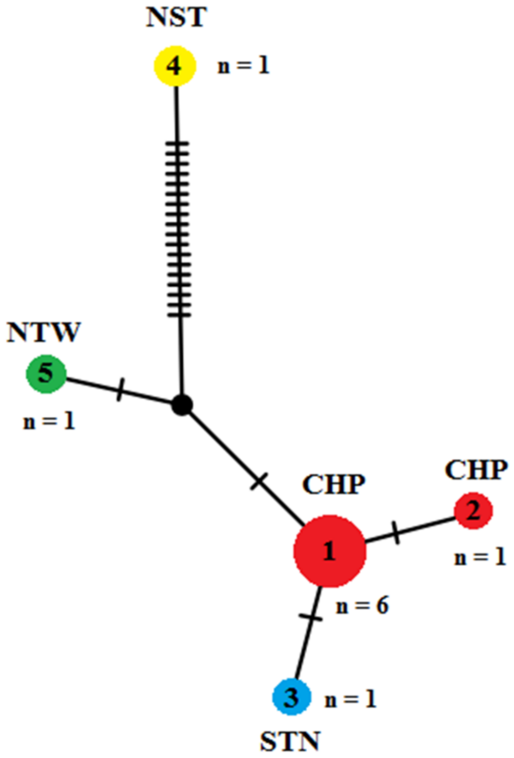

Figure 3 Haplotype network for *EF-1α* sequence of *M. perseoides* in peninsular Thailand**.** Solid lines on branches refer to mutation step.

Phylogenetic relationships

Phylogenetic analyses based on the combined dataset included 1,496 bp from 29 samples of *Mycalesis* species and one outgroup *O. medus* sequence from GenBank, DQ338766 (*COI*), DQ338906 (*EF-1α*) and DQ338633 (*wingless*). The phylogenetic tree of Bayesian approach showed that the *Mineus* group of *Mycalesis* in peninsular Thailand was monophyletic with a strong support (posterior probability, BI = 100). This tree was divided into two major clades, A and B (Figure 4).

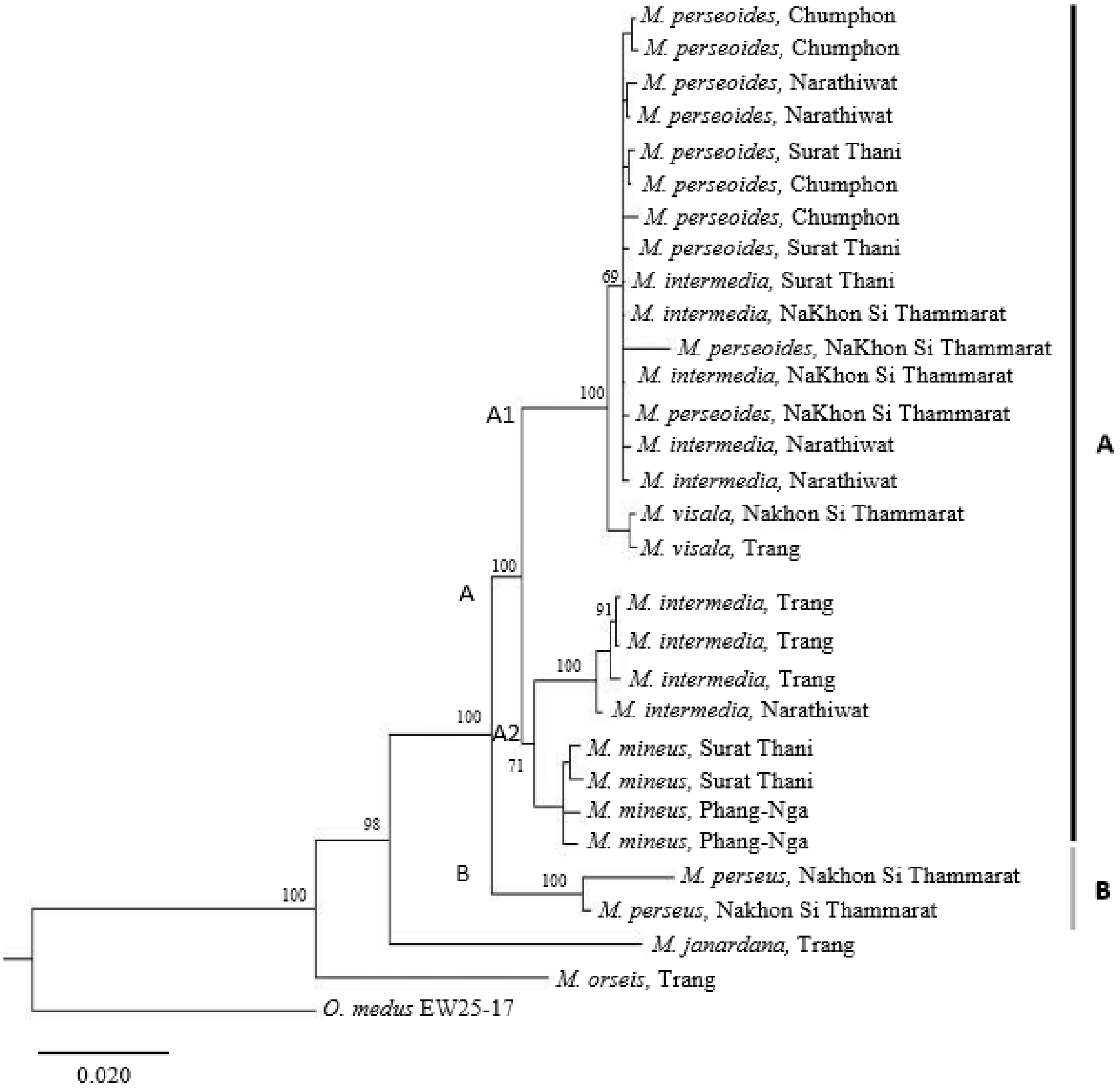

Figure 4 Bayesian tree for the combined dataset of *COI*, *EF-1α* and *wingless* sequences of *Mycalesis* species in peninsular Thailand. Posterior probabilities base on Likelihood ratio test for Maximum likelihood.

Clade A consisting of *M. perseoides*, *M. intermedia*, *M. visala* and *M. mineus* was strongly supported as monophyly (posterior probability, BI = 100). Clade A can be divided into two subclade: A1 and A2. In subclade A1, *M. visala* from Nakhon Si Thammarat province and Trang province were grouped together. However, the result indicated that *M. perseoides* from Chumphon, Surat Thani, Nakhon Si Thammarat and Narathiwat provinces and *M. intermedia* from Surat Thani, Nakhon Si Thammarat and Narathiwat provinces in subclade A1 were grouped together. The result indicated that this might be species complex of *Mineus* group. Sublcade A2 consisted of *M. intermedia* from Trang province and Narathiwat province and *M. mineus* from Surat Thani province and Phang-Nga province. The result showed that each species was clearly separated in different branch. Furthermore, clade B composed of *M. perseus* from Nakhon Si Thammarat province and it was strongly supported as monophyly (BI = 100). The rest of *Mycalesis* (*M. janardana* of *Janardana* group and *M. orseis* of *Francisca* group from Trang province) were collected.

Divergence time estimates

The divergence time in the genus *Mycalesis* in this study was estimated from age of fossil record of *Lethe corbieri* during the Oligocene in southeast France, approximately 28.4 to 23.03 million years ago (mya) (Nel, Nel, & Balme, 1993). The analysis in Neighbor-joining (NJ) indicated that *Mycalesis* in peninsular Thailand was diverged between 32.47 mya during Oligocene period (Figure 5). Initial split the *janardana* group and *Mineus* group arised ca. 23.03 mya during Oligocene period. The molecular phylogram showed that *Mineus* group it was divided into two clades (A and B) ca. 11.76 mya during Miocene period. In clade A, *Mycalesis* species were separated approximately 10.66 mya into two subclades (A1 and A2). Subclade A1 arised ca. 9.72 mya and is composed of *M. perseoides* from Chumphon, Surat Thani, Nakhon Si Thammarat and Narathiwat province, *M. intermedia* from Surat Thani, Nakhon Si Thammarat and Narathiwat provinces and *M. visala* from Nakhon Si Thammarat and Trang provinces colonizing around 0.78 mya during Pleistocene period. Subclade A2 consisted of *M. mineus* from Surat Thani and Phang-Nga provinces (0.65 mya) during Pleistocene. However, Clade B consisted of *M. intermedia* from Trang and Narathiwat provinces colonizing around 0.29 mya during Pleistocene period.

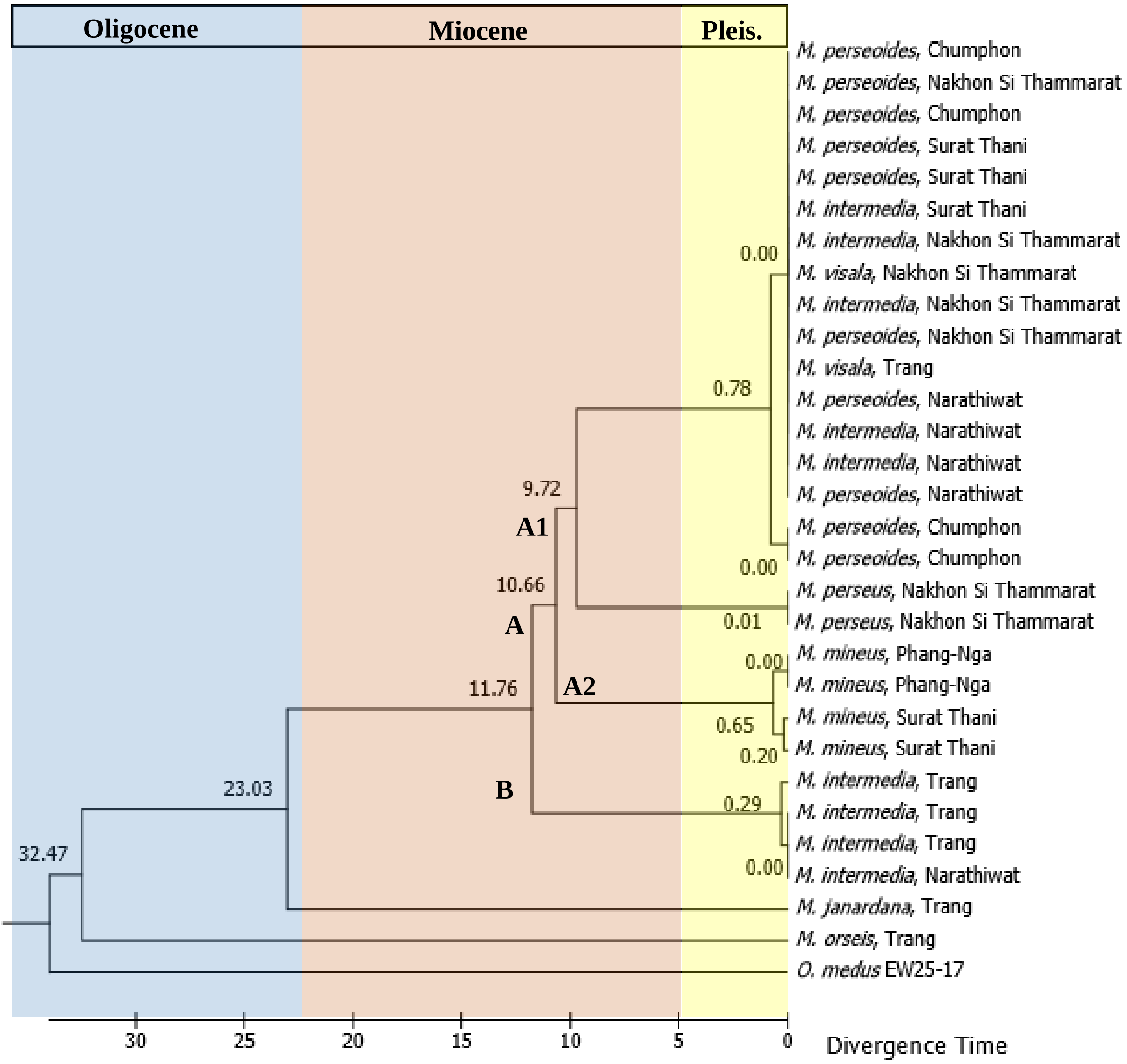

Figure 5 The neighbor-joining tree is obtained from *COI* gene of *Mycalesis* species and out group in peninsular Thailand. Values on branches refer to divergence times. Scale bar indicates million years ago (mya) for divergence time molecular clock.

Discussion

Molecular technique provides a powerful tool to investigate the population dynamics of organism and also enable more detailed understanding on the relationship between populations (Sum *et al*. 2014). Various genetic markers have been used to illustrate the genetic differentiation that occurs in butterfly populations, especially mitochondrial and nuclear gene markers. In this study, a good candidate gene marker is revealed as the mitochondrial gene (*COI*) with high variability in polymorphic sites (invariable sites, singleton variable sites, parsimony informative sites, nucleotide diversity, number of polymorphic sites and Average number of nucleotide differences of interspecific genetic differentiation). However, the number of haplotype and haplotype diversity were high in nuclear genes (*EF-1α* and *wingless*). Although, four *Mycalesis* (*Mineus* groups); *M. visala*, *M. intermedia*, *M. perseus* and *M. perseoides* were highly different in intraspecific genetic divergence in each gene. Intraspecific genetic variation of *M. visala* had high diversity in *COI* and *M. perseus* in *EF-1α* and *wingless*. *M. mineus* had low intraspecific genetic diversity in all genes, indicating high degree of gene flow within population.

Phylogenetic relationship of *Mycalesis* (*Mineus* group) in peninsular Thailand was monophyletic with strong support based on Bayesian analysis. *Mycalesis* (*Mineus* group) can be divided into two major clades (clade A and B). At species level, *M. mineus* of Surat Thani province and Phang-Nga province were grouped together in clade A2, consistent with intraspecific genetic distance which was low in all genes. Therefore, their genetic relationship is closely related within population. However, *M. Intermedia* and *M. perseoides* were species complex which were weakly supported (BI = 69). However, those species were not clearly related in this study. These three species were different in terms of morphological characters of male genitalia. On the other hand, the genetic divergence among species of *M. intermedia*, *M. perseoides* and *M. visala* was low. This result suggested that the gene introgression in mtDNA and nuclear gene likely happened during species expansion. According to species delimitation, their connecting populations have been influenced by gene flow. Intraspecific genetic differentiation (introgression) would affect species integrity. Recent studies have proposed that the correlation between intraspecific genetic differentiation and gene flow was a negative correlation. Therefore, species delimitation might be more effective with markers experiencing high degree of gene flow (Petit & Excoffier, 2009).

This finding of the monophyly of *Mineus* group in peninsular Thailand is consistent with the scenario of Kodandaramaiah *et al*. (2010) indicating that the *Mycalesis* species was clustered into two clades as *Mycalesis* I and *Mycalesis* II. *Mycalesis* I belonged to *Mycalesis* species from mainland Southeast Asia (China, Vietnam, Laos, Bangladesh and Thailand) and *Mycalesis* II belonged to the taxa from Indo-Australia (Indonesia, Australia, Papua New Guinea and Solomon Island). In this study, all members of *Mycalesis* in peninsular Thailand might be clustered in clade *Mycalesis* I. The finding of the monophyletic group of *Mycalesis* (*Mineus* group) in peninsular Thailand was supported by divergence time as well. The result showed that *Mycalesis* species in peninsular Thailand diverged ca. 32.47 mya during Oligocene period. *Mycalesis Mineus* group arised at approximately 23.03 mya in Oligocene period, consistent with the reported of Aduse-Poku *et al*. (2015) proposing that the butterfly subtribe Mycalesina and Lethina diverged from each other about 39.8 mya during Eocene period. Furthermore, divergence time of *Mycalesis* in Southeast Asia was observed to have occurred around the Oligocene and Eocene boundary, roughly at the same time as diverged the endemic African genera *Bicyclus* and *Hallesis*. Furthermore, the origin of the subtribe Mycalesina was in Asia and later distributed to other regions (Aduse-Poku *et al*., 2015). However, *Mycalesis Mineus* group was divided into two clades approximately 11.76 mya in mid Miocene period.

According to Pena and Wahlberg (2008), the fossil record of butterfly reconstructed a divergence time of subfamily Satyrinae and the result showed that subfamily Satyrinae might dispersed to other continental with their adaptive radiation of food plants approximately 25 mya during Oligocene epoch (Brakefield, 2012; Cerling *et al*., 1997; Sage, 2004). The larvae of these butterflies feed on grasses (Poaceae) that are dominant in shaded and open habitats, especially the tropical rain forest (Pena & Wahlberg, 2008). Interestingly, *M. perseoides* is a good example to answer the haplotype network and migration route of *Mycalesis* species. The haplotype network of the *EF-1α* sequence of *M. perseoides* suggested that the haplotype pattern of Chumphun (n = 6) is assumed to be the origin then it was divided into Surat Thani pattern (n = 1), Narathiwat pattern (n =1) and Nakhon Si Thammarat pattern (n = 1). In this study, the result indicated that *M. perseoides* have a genetic connectivity microhabitat between populations of *M. perseoides* in peninsular Thailand. Furthermore, this study has determined relationship between genetic variation and phenotypic plasticity of *Mycalesis* populations in Thailand. *Mycalesis* species in peninsular Thailand were found in two distinct seasonal morphs, wet and dry season forms such as in *M. mineus* and *M. perseoides*. The morphology of male genitalia was distinguishing character to identify species in this genus. The butterfly in subtribe Mycalesina is well known important model to understand development, genetics and evolutionary of phenotypic plasticity as a response to wet and dry seasonal environment in their habitat. This phenomena has been influenced on seasonal fluctuation and reproductive dormancy. Temperature and humidity play an important role to regulate diel activity (Islam *et al*., 2010). Furthermore, the dry season form was usually reproductively inactive, long-lived, and has less diel activity. By contrast, wet season form was reproductively active more diel activity (Braby, 1994; Islam *et al*., 2010).

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CHAPTER 5

CONCLUSION

From the result of this thesis, a total of 214 individuals adult *Mycalesis* were collected by insect nets and fruit-baited trap during February 2015 to July 2016. It can be identified to seven species. In this study, *M. perseoides* was most dominant and distributed at all collecting site along peninsular Thailand. Some species such as *M. orseis* and *M. janardana* were only found in Trang province (Figure 5, Chapter 2). We found two seasonal forms of wing pattern (wet and dry season forms) in all collecting sites except Khao Chong at Trang province was found only wet season form. Morphological variation of wing pattern in two seasonal forms can occur in *Mycalesis* species because of phenotypic plasticity that associated with environment conditions such as temperature, humidity and photoperiod in their habitat. Morphology of male genitalia were also described here.

We used different markers to reveal genetic diversity and genetic variation of *Mycalesis* in peninsular Thailand, as different markers have different level of variations (Hind & Saunders, 2013; Whichachucherd, 2014). The result of our study using the three molecular markers (*COI*, *EF-1α* and *wingless*), revealed as mtDNA with high variability in polymorphic sites such as invariable sites, parsimony informative sites, nucleotide diversity, number of polymorphic sites and average number of nucleotide differences. Haplotype diversity and number of haplotype were high in nuclear markers, but Tajima's *D* test were negative in all gene. Intraspecific genetic divergence of some *Mycalesis* species low, that could be have genetic connectivity (gene flow) among species, consistent with the scenario of Petit and Excoffier (2009) proposed that the correlation between intraspecific genetic differentiation and gene flow was negative correlation.

Aduse-Poku *et al*., (2015) proposed that Asia as the area of origin of *Mycalesis* and later distributed to Indo-Australian region, includes Brunei, Indonesia, Malaysia, Papua New Guinea, Singapore and peninsular Thailand. The result of the haplotype network of *EF-1α* sequence of *M. perseoides* showed that the haplotype pattern of Chumphon is assume to be the origin and it was divided into Surat Thani, Nakhon Si Thammarat and Narathiwat (Figure 3, Chapter 3) . This result suggested that the gene introgression likely happened during species radiation. *M. perseoides,* is a good candidate to answer the migration route of *Mycalesis* species in peninsular Thailand.

Phylogenetic results using the combined dataset clearly indicated that *Mycalesis* in peninsular Thailand as monophyletic group. For *Mineus* group it can be divided into two major clades, although the result showed monophyly of *Mycalesis* in *Mineus* group, *M. perseoides* and *M. intermedia* in clade A1 were still unclear (Figure 4, Chapter 3). According to previous reported of Kodandaramaiah *et al*. (2010) indicated that *Mycalesis* was clustered into two clades (*Mycalesis* I and *Mycalesis* II). *Mycalesis* I belonged to *Mycalesis* species from mainland Southeast Asia (China, Vietnam, Laos, Bangledesh and Thailand), consists *M. gotama, M. francisca, M. orseis, M. anaxias, M. mynior, M. perseus, M. perseoides, M. intermedia, M. visala* and *M. mineus*. Therefore, all members of *Mycalesis* in this study might be clustered in *Mycalesis* I. As well as the divergence time of *Mycalesis* was estimated and the result showed that *Mycalesis* in peninsular Thailand diverged around 32.47 mya during Oligocene period (Figure 5, Chapter 3). According to Pena and Wahlberg (2008) proposed that the butterflies might be dispersed with their adaptive radiation of food plant during Oligocene epoch. The larva of these butterflies feed on Poaceae (grasses) that are dominant in shaded and open habitats, especially the tropical rain forest.

However, further research are needed, with large sample sizes representing more locations covering the different elevation and climatic zone. More replicate samples collecting in each site are required to determine the species diversity and distribution in Southeast Asia. Moreover, to investigate the gene expression of *wingless* gene in wet and dry season forms of *Mycalesis* species in Thailand.

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APPENDIX

APPENDIX A Intraspecific genetic diversity of *Mycalesis perseoides* among population in peninsular Thailand

population	**N**	***S***	***K***	***π***
Chumphon	4	1	0.500	0.00103
Surat thani	2	1	1.000	0.00206
Nakhon Si Thammarat	2	19	19.000	0.03958
Narathiwat	2	2	2.000	0.00414
All	10	23	4.556	0.00949

N: Number of sequences, S: Number of polymorphic sites, K: Average number of nucleotide differences, ***π***: Nucleotide diversity

APPENDIX B Nucleotide composition of *Mycalesis* species for individual’s gene segment**.**

Species	***COI***					***EF-1α***					***Wingless***				
	T(U)	C	A	G	Total	T(U)	C	A	G	Total	T(U)	C	A	G	Total
M. janardana	40.5	15.5	29.6	14.4	632	21.2	28.0	25.4	25.4	485	14.7	32.1	20.8	32.4	379
M. orsies	39.1	16.3	30.4	14.1	632	20.6	27.6	24.7	27.0	485	16.4	30.3	22.2	31.1	379
M. intermedia	39.6	15.6	31.0	13.8	632	20.0	28.2	25.3	26.6	485	14.5	31.9	20.0	33.6	379
M. minues	40.8	14.1	31.0	14.1	632	19.7	28.6	24.9	26.8	485	14.7	31.7	20.0	33.6	379
M. persues	39.6	15.2	31.0	14.3	632	21.2	27.5	25.6	25.6	485	14.8	31.7	20.3	33.3	379
M. perseoides	39.6	15.4	31.3	13.6	632	20.2	27.7	25.6	26.5	485	14.6	32.0	20.0	33.4	379
M. visala	39.6	15.5	31.2	13.7	632	20.1	28.2	25.3	26.4	485	14.4	32.0	20.2	33.4	379
Avg.	39.8	15.4	30.8	14.0	632	20.4	28.0	25.3	26.3	485	14.9	31.7	20.5	33.0	379

APPENDIX C Interspecific genetic divergence of *Mycalesis* among population for individual’s gene segment

COI

Species	**1**	**2**	**3**	**4**	**5**	**6**	**7**
1. *M. janardana*							
2. *M. orseis*	0.113						
3. *M. perseus*	0.095	0.116					
4. *M. mineus*	0.084	0.113	0.048				
5. *M. intermedia*	0.097	0.117	0.052	0.043			
6. *M. perseoides*	0.098	0.119	0.054	0.046	0.057		
7. *M. visala*	0.097	0.117	0.052	0.040	0.059	0.056	

EF-1α

Species	**1**	**2**	**3**	**4**	**5**	**6**	**7**
1. *M. janardana*							
2. *M. orseis*	0.067						
3. *M. perseus*	0.074	0.071					
4. *M. mineus*	0.064	0.061	0.019				
5. *M. intermedia*	0.067	0.064	0.022	0.008			
6. *M. perseoides*	0.071	0.067	0.025	0.011	0.011		
7. *M. visala*	0.064	0.061	0.019	0.005	0.003	0.005	

Wingless

Species	1	2	3	4	5	6	7
1. *M. janardana*							
2. *M. orseis*	0.065						
3. *M. perseus*	0.113	0.096					
4. *M. mineus*	0.055	0.045	0.072				
5. *M. intermedia*	0.062	0.052	0.082	0.015			
6. *M. perseoides*	0.109	0.101	0.131	0.017	0.061		
7. *M. visala*	0.065	0.045	0.066	0.002	0.015	0.017	

APPENDIX D List of *Mycalesis* species ware used in this study and submitted to Genbank

Seq.	Species	Localities	Specimen N.	Isolate
1	*M. perseoides*	CHP	CH5	MpersdS011
2	*M. perseoides*	CHP	CH22	MpersdS012
3	*M. perseoides*	CHP	CH30	MpersdS013
4	*M. perseoides*	CHP	CH33	MpersdS014
5	*M. mineus*	PNG	PH7	MminS021
6	*M. mineus*	PNG	PH10	MminS022
7	*M. mineus*	STN	ST4	MminS031
8	*M. mineus*	STN	ST5	MminS032
9	*M. perseoides*	STN	ST8	MpersdS031
10	*M. perseoides*	STN	ST19	MpersdS032
11	*M. intermedia*	STN	ST25	MintS031
12	*M. intermedia*	NST	NK4	MintS041
13	*M. perseoides*	NST	NK6	MpersdS041
14	*M. visala*	NST	NK9	MvisS041
15	*M. intermedia*	NST	NK12	MintS042
16	*M. perseus*	NST	NK22	MpersS041
17	*M. perseus*	NST	NK23	MpersS042
18	*M. perseoides*	NST	NK28	MpersdS042
29	*M. janardana*	TRG	TR1	MjanS051
20	*M. intermedia*	TRG	TR2	MintS051
21	*M. visala*	TRG	TR3	MvisS051
22	*M. orseis*	TRG	TR15	MorsS051
23	*M. intermedia*	TRG	TR19	MintS052
24	*M. intermedia*	TRG	TR21	MintS053
25	*M. perseoides*	NTW	NR13	MpersdS061
26	*M. intermedia*	NTW	NR21	MintS061

APPENDIX D (Cont.)

Seq.	Species	Locatities	Specimen N.	Isolate
27	*M. intermedia*	NTW	NR25	MintS062
28	*M. intermedia*	NTW	NR30	MintS063
29	*M. perseoides*	NTW	NR39	MpersdS062

APPENDIX E Nucleotide sequencing of *Mycalesis* individual’s gene segment for this study

COI **gene**

Seq1 [organism=Mycalesis perseoides] [isolate=MpersdCOIS011]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGTAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq2 [organism=Mycalesis perseoides] [isolate=MpersdCOIS012]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAATATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAACTTA

AATACTTCTTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

seq3 [organism=Mycalesis perseoides] [isolate=MpersdCOIS013]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

seq4 [organism=Mycalesis perseoides] [isolate=MpersdCOIS014]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAATATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAACTTA
AATACTTCTTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

seq5 [organism=Mycalesis mineus] [isolate=MminCOIS021]

ATAGTAGGTACTTCTTTAAGTCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATTGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTTCCTC
GTATAAATAATATAAGATTTTGACTTTTACCTCCTTCTTTAGTACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATATC
CCCCCCTTTCATCAAATATTGCCCATGGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATTAATTT
TATTTCAACAATTATTAATATACGAATTAATAGTATAACTTATGATCAAAT
ACCCCTTTTTGTATGAGCTGTTGGAATTACAGCTCTATTACTATTATTATCT

TTACCTGTTTTAGCTGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCTTTTTTTGATCCAGCTGGAGGAGGAGATCCTATCCTTTATCAA
CATTTATTTTGATTTTT

Seq6 [organism=Mycalesis mineus] [isolate=MminCOIS022]

ATAGTAGGTACTTCTTTAAGTCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATTGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTTCCTC
GTATAAATAATATAAGATTTTGACTTTTACCTCCTTCTTTAGTACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATATC
CCCCCCTTTCATCAAATATTGCCCATGGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATTAATTT
TATTTCAACAATTATTAATATACGAATTAATAGTATAACTTATGATCAAAT
ACCCCTTTTTGTATGAGCTGTTGGAATTACAGCTCTATTACTATTATTATCT
TTACCTGTTTTAGCTGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCTTTTTTTGATCCAGCTGGAGGAGGAGATCCTATCCTTTATCAA
CATTTATTTTGATTTTT

Seq7 [organism=Mycalesis mineus] [isolate=MminCOIS031]

ATAGTAGGTACTTCTTTAAGTCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATTGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTTCCTC
GTATAAATAATATAAGATTTTGACTTTTACCTCCTTCTTTAGTACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATATC
CCCCCCTTTCATCAAATATTGCCCATGGCGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATTAATTT
TATTTCAACAATTATTAATATACGAATTAATAGTATAACTTATGATCAAAT
ACCCCTTTTTGTATGAGCTGTTGGAATTACAGCTCTATTACTATTATTATCT
TTACCTGTTTTAGCTGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCTTTTTTTGATCCAGCTGGAGGAGGAGATCCTATCCTTTATCAA
CATTTATTTTGATTTTT

Seq8 [organism=Mycalesis mineus] [isolate=MminCOIS032]

ATAGTAGGTACTTCTTTAAGTCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATTGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTTCCTC
GTATAAATAATATAAGATTTTGACTTTTACCTCCTTCTTTAGTACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATATC
CCCCCCTTTCATCAAATATTGCCCATGGCGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATTAATTT
TATTTCAACAATTATTAATATACGAATTAATAGTATAACTTATGATCAAAT

ACCCCTTTTTGTATGAGCTGTTGGAATTACAGCTTTATTACTATTATTATCT
TTACCTGTTTTAGCTGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCTTTTTTTGATCCAGCTGGAGGAGGAGATCCTATCCTTTATCAA
CATTTATTTTGATTTTT

Seq9 [organism=Mycalesis perseoides] [isolate=MpersdCOIS031]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq10 [organism=Mycalesis perseoides] [isolate=MpersdCOIS032]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq11 [organism=Mycalesis intermedia] [isolate=MintCOIS031]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT

TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq12 [organism=Mycalesis intermedia] [isolate=MintCOIS041]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq13 [organism=Mycalesis perseoides] [isolate=MpersdCOIS041]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq14 [organism=Mycalesis visala] [isolate=MvisCOIS041]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA

TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq15 [organism=Mycalesis intermedia] [isolate=MintCOIS042]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq16 [organism=Mycalesis perseus] [isolate=MpersCOIS041]

ATAGTAGGAACCTCTCTAAGCCTTATTATTCGAACAGAATTAGGAAACCC
AGGATTTTTAATTGGAGATGATCAAATTTATAACACTATTGTAACAGCACA
TGCTTTTATTATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGATTC
GGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCT
CGTATAAATAATATAAGATTTTGACTTTTACCACCTTCTTTAATGCTTTTAA
TTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATAT
CCCCCTCTTTCATCAAATATTGCTCATGGAGGATCTTCAGTAGATTTAGCA
ATTTTTTCATTACATTTAGCGGGAATTTCTTCAATTTTAGGAGCTATTAATT
TTATTTCAACAATTATTAACATACGAGTTAATAATATATCTTATGATCAAA
TACCTCTTTTCGTATGAGCTGTTGGAATTACAGCTTTATTACTTTTACTATC
TTTACCTGTTTTAGCTGGAGCTATTACTATATTATTAACAGATCGAAATTT
AAATACTTCTTTTTTTGATCCAGCCGGAGGAGGAGACCCTATTCTTTATCA
ACATTTATTTTGATTTTT

Seq17 [organism=Mycalesis perseus] [isolate=MpersCOIS042]

ATAGTAGGAACCTCTCTGAGCCTTATTATTCGAACAGAATTAGGAAACCC
AGGATTTTTAATTGGAGATGATCAAATTTATAACACTATTGTAACAGCACA
TGCTTTTATTATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGATTC
GGAAATTGATTAGTACCTTTAATATTAGGAGCTCCTGATATAGCTTTCCCT
CGTATAAATAATATAAGATTTTGACTTTTACCACCTTCTTTAATGCTTTTAA
TTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATAT

CCCCCTCTTTCATCAAATATTGCTCATGGAGGATCTTCAGTAGATTTAGCA
ATTTTTTCATTACATTTAGCGGGAATTTCTTCAATTTTAGGAGCTATTAATT
TTATTTCAACAATTATTAACATACGAGTTAATAATATATCTTATGATCAAA
TACCTCTTTTCGTATGAGCTGTTGGAATTACAGCTTTATTACTTTTACTATC
TTTACCTGTTTTAGCTGGAGCTATTACTATATTATTAACAGATCGAAATTT
AAATACTTCTTTTTTTGATCCAGCCGGAGGAGGAGACCCTATTCTTTATCA
ACATTTATTTTGATTTTT

Seq18 [organism=Mycalesis perseoides] [isolate=MpersdCOIS042]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq19 [organism=Mycalesis janardana] [isolate=MjanCOIS051]

ATAGTAGGAACTTCTTTAAGTTTAATTATTCGAACAGAATTAGGAAATCCT
GGATTTTTAATTGGTGATGATCAAATTTATAATACTATTGTAACCGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAATTCCTTTAATATTAGGAGCTCCTGACATAGCATTTCCAC
GAATAAATAATATAAGATTTTGACTATTACCCCCCTCATTAGTACTTTTAA
TTTCAAGAAGTATCGTAGAAAATGGAGCCGGTACAGGATGAACAGTTTAT
CCCCCTCTTTCATCTAATATTGCTCATGGAGGCTCCTCTGTTGATTTAGCA
ATTTTCTCTTTACATTTAGCCGGTATTTCATCAATTTTAGGGGCTATTAATT
TTATTTCCACAATTATTAATATACGAATTAATAGTATATCCTATGATCAAA
TACCTCTTTTTGTTTGAGCTGTGGGAATCACAGCTTTATTACTTTTATTATC
ATTGCCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTT
AAATACCTCTTTTTTTGATCCTGCTGGAGGAGGAGACCCTATTTTATACCA
ACATTTATTTTGATTTTT

Seq20 [organism=Mycalesis intermedia] [isolate=MintCOIS051]

ATAGTAGGTACTTCATTAAGTCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTACAATACTATTGTAACAGCCCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCACTAATACTAGGAGCTCCTGATATAGCTTTTCCCC
GTATAAATAATATAAGATTTTGACTTTTACCTCCTTCCTTAATACTTTTAAT

TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTTTATC
CCCCTCTTTCATCAAATATTGCTCATGGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCTCTGCATTTAGCGGGAATTTCTTCAATTTTAGGAGCTATTAATTT
TATTTCAACAATTATTAATATACGAATTAACAATATAACTTACGATCAAAT
ACCTCTTTTCGTATGAGCTGTTGGAATTACAGCTCTATTACTTTTATTATCT
TTACCTGTTTTAGCCGGAGCTATTACTATGTTATTAACAGATCGAAATTTA
AATACTTCTTTTTTTGACCCAGCTGGAGGAGGAGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq21 [organism=Mycalesis visala] [isolate=MvisCOIS051]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq22 [organism=Mycalesis orseis] [isolate=MorsCOIS051]

ATAAAAAGTACTTCTTTGGGGNAAATTTTTCGAACAGAATTAGGAAAACC
AGGATTTTTAATTGGAGATGATCAAATTTATAATACTATTGTTACAGCTCA
TGCTTTTATCATAATTTTTTTTATGGTTATACCTATTATAATTGGAGGATTT
GGAAATTGATTAGTGCCTCTAATATTAGGAGCTCCAGATATAGCCTTCCCC
CGAATAAATAATATAAGTTTTTGACTTTTACCCCCCTCATTAATTTTATTAA
TTTCAAGTTCTATTGTAGAAAATGGAGCAGGAACAGGATGAACAGTGTAT
CCCCCCCTTTCATCTAATATTGCTCACAGAGGATCCTCTGTTGACTTAGCA
ATTTTTTCTCTTCATTTAGCTGGAATTTCCTCAATTTTAGGAGCTATTAATT
TTATTTCCACAATTATTAATATACGAATTAATAATATATCATATGATCAAA
TACCTCTTTTTGTATGAGCAGTAGGTATTACAGCTTTATTACTTTTATTATC
TCTACCTGTACTAGCAGGAGCTATTACTATACTTCTTACAGATCGAAATTT
AAATACCTCTTTTTTTGACCCTGCAGGAGGAGGAGATCCAATTCTTTATCA
ACATTTATTTTGATTTTT

Seq23 [organism=Mycalesis intermedia] [isolate=MintCOIS052]

ATAGTAGGTACTTCATTAAGTCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGACGATCAAATTTACAATACTATTGTAACAGCCCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCACTAATACTAGGAGCTCCTGATATAGCTTTTCCCC

GTATAAATAATATAAGATTTTGACTTTTACCTCCTTCCTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTTTATC
CCCCTCTTTCATCAAATATTGCTCATGGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCTCTGCATTTAGCGGGAATTTCTTCAATTTTAGGAGCTATTAATTT
TATTTCAACAATTATTAATATACGAATTAACAATATAACTTACGATCAAAT
ACCTCTTTTCGTATGAGCTGTTGGAATTACAGCTCTATTACTTTTATTATCT
TTACCTGTTTTAGCCGGAGCTATTACTATGTTATTAACAGATCGAAATTTA
AATACTTCTTTTTTTGACCCAGCTGGAGGAGGAGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq24 [organism=Mycalesis intermedia] [isolate=MintCOIS053]

ATAGTAGGTACTTCATTAAGTCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGACGATCAAATTTACAATACTATTGTAACAGCCCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCACTAATACTAGGAGCTCCTGATATAGCTTTTCCCC
GTATAAATAATATAAGATTTTGACTTTTACCTCCTTCCTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTTTATC
CCCCTCTTTCATCAAATATTGCTCATGGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCTCTGCATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATTAATTT
TATTTCAACAATTATTAATATACGAATTAACAATATAACTTACGATCAAAT
ACCTCTTTTCGTATGAGCTGTTGGAATTACAGCTCTATTACTTTTATTATCT
TTACCTGTTTTAGCCGGAGCTATTACTATGTTATTAACAGATCGAAATTTA
AATACTTCTTTTTTTGACCCAGCTGGAGGAGGAGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq25 [organism=Mycalesis perseoides] [isolate=MpersdCOIS061]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq26 [organism=Mycalesis intermedia] [isolate=MintCOIS061]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG

GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq27 [organism=Mycalesis intermedia] [isolate=MintCOIS062]

ACAGAAGGTACTTCATTAGGTCTTATTATTCGAACAGAATTAGGAAATCC
AGGATTTTTAATTGGAGACGATCAAATTTACAATACTATTGTAACACCCCA
TGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTT
GGAAATTGATTAGTACCACTAATACTAGGAGCTCCTGATATAGCTTTTCCC
CGTATAAATAATATAAGATTTTGACTTTTACCTCCTTCCTTAATACTTTTAA
TTTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTTTAT
CCCCCTCTTTCATCAAATATTGCTCATGGAGGATCTTCAGTAGATTTAGCA
ATTTTTTCTCTGCATTTAGCGGGAATTTCTTCAATTTTAGGAGCTATTAATT
TTATTTCAACAATTATTAATATACGAATTAACAATATAACTTACGATCAAA
TACCTCTTTTCGTATGAGCTGTTGGAATTACAGCTCTATTACTTTTATTATC
TTTACCTGTTTTAGCCGGAGCTATTACTATGTTATTAACAGATCGAAATTT
AAATACTTCTTTTTTTGACCCAGCTGGAGGAGGAGATCCTATTCTTTATCA
ACATCTATTTTGATTTTT

Seq28 [organism=Mycalesis intermedia] [isolate=MintCOIS063]

ATAGTAGGTACCTCTTTANGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT
GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

Seq29 [organism=Mycalesis perseoides] [isolate=MpersdCOIS062]

ATAGTAGGTACCTCTTTAAGCCTTATTATTCGAACAGAATTAGGAAATCCA
GGATTTTTAATTGGAGATGATCAAATTTATAATACTATCGTAACAGCTCAT

GCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTG
GAAATTGATTAGTACCATTAATATTAGGAGCTCCTGATATAGCTTTCCCTC
GTATAAATAACATAAGATTTTGACTCCTACCCCCTTCTTTAATACTTTTAAT
TTCAAGAAGTATTGTAGAAAATGGAGCTGGAACAGGATGAACAGTATACC
CTCCTCTCTCATCAAATATTGCTCATAGAGGATCTTCAGTAGATTTAGCAA
TTTTTTCATTACATTTAGCAGGAATTTCTTCAATTTTAGGAGCTATCAATTT
TATTTCAACAATTATTAATATACGAATTAATAATATAACTTATGATCAAAT
ACCTCTTTTTGTATGAGCTGTTGGAATTACAGCCTTATTACTTTTATTATCC
TTACCTGTTTTAGCAGGAGCTATTACTATATTATTAACAGATCGAAATTTA
AATACTTCCTTTTTTGATCCAGCTGGAGGAGGTGATCCTATTCTTTATCAA
CATCTATTTTGATTTTT

EF-1α gene

Seq1 [organism=Mycalesis perseoides] [isolate=MpersdEF-1alphaS011]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq2 [organism=Mycalesis perseoides] [isolate=MpersdEF-1alphaS012]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

seq3 [organism=Mycalesis perseoides] [isolate=MpersdEF-1alphaS013]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATTAAAAACATG

ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

seq4 [organism=Mycalesis perseoides] [isolate=MpersdEF-1alphaS014]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

seq5 [organism=Mycalesis mineus] [isolate=MminEF-1alphaS021]

ACGTACCATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGCAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTCTGGAAGTTCGAGACGGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAGAACATG
ATCACCGGAACCTCGCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq6 [organism=Mycalesis mineus] [isolate=MminEF-1alphaS022]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGCAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAGAACATG
ATCACTGGAACCTCGCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTTGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq7 [organism=Mycalesis mineus] [isolate=MminEF-1alphaS031]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGCAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAGAACATG
ATCACCGGAACCTCGCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACTGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq8 [organism=Mycalesis mineus] [isolate=MminEF-1alphaS032]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGCAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAGAACATG
ATCACCGGAACCTCGCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq9 [organism=Mycalesis perseoides] [isolate=MpersdEF-1alphaS031]

GCGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq10 [organism=Mycalesis perseoides] [isolate=MpersdEF-1alphaS032]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA

AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq11 [organism=Mycalesis intermedia] [isolate=MintEF-1alphaS031]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq12 [organism=Mycalesis intermedia] [isolate=MintEF-1alphaS041]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq13 [organism=Mycalesis perseoides] [isolate=MpersdEF-1alphaS041]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGAATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACAGA
ATCACCGAAACATCTCAGGCCAATTGTGCGGTGTTGATCGTGGCCGCCGG
ACCGGGTAAGTTCAAGGCCGGTATCTCCAAGAACGCCCGGACCCGGGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCNATACAGTGAGTCCCGTTTCGAGGA
ATCNNAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTNACAACCCAG
CTGCCGTCGCTTTCGTACCCATATCTGGCTGGCACG

Seq14 [organism=Mycalesis visala] [isolate=MvisEF-1alphaS041]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGCAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAAAACATG

ATCACCGGAACCTCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCTACTGAGCCCCCATACAGTGAGTCACGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAT
CTGCTGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq15 [organism=Mycalesis intermedia] [isolate=MintEF-1alphaS042]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq16 [organism=Mycalesis perseus] [isolate=MpersEF-1alphaS041]

ACGTACTATCGAGAAGGNCGAGAAGGAGGTTCAAGAAATGCGCAAAGGT
TCCTTCAAATACATCTGGATGTTGGANAAACGAAAGGCTGAGCGCGAGCT
CTCTATCACCATCGACCTTGTTCTGTCCAAGTTCGAGACTGCTAAATTGTA
CGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAGAACATGA
TCACTGGAACCTCGCAGGCCGATTGTGCCGTGCTGATCGTTGCCGCCGGT
ACCGGTGAGTTCGAGGCAGGTATCTCCAAGAACGGCCAGACTCGTGAGCA
CGCGCTACTCGCCTTCACCCTCGGTGTCAAGCAGCTGATCGTGGGCGTCA
ACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGAA
ATCAAAAAGGAAGTGTCCTCATACATCAAGAAGATTGGTTACAACCCAGC
TGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq17 [organism=Mycalesis perseus] [isolate=MpersEF-1alphaS042]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCTCAGGAAATGGGCAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACTGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAGAACATG
ATCACTGGAACCTCGCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCAGGTATCTCCAAGAACGGCCAGACTCGTGAGC
ACGCGCTACTCGCCTTCACCCTCGGTGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCATACATCAAGAAGNTTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq18 [organism=Mycalesis perseoides] [isolate=MpersdEF-1alphaS042]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGANGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq19 [organism=Mycalesis janardana] [isolate=MjanEF-1alphaS051]

ACGTTCTATTGAGAAGTTCGAGAAGGAGTTCCAGGAAATGGGCAAAGGCT
CCTTCAAATATGCCTGGGTATTGGACAAACTAAAGGCTGAGCGCGAGCGT
GGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACTGCCAAATACTA
CGTCACCATCATCGACGCTCCTGGGCACAGAGATTTCATCAAGAACATGA
TCACCGGAACCTCACAGGCCGATTGCGCCGTGCTGATCGTCGCCGCCGGT
ACTGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAAACCCGTGAGCA
CGCTCTGCTCGCCTTCACCCTCGGTGTCAAACAGCTGATCGTGGGCGTTAA
CAAAATGGACTCCACTGAGCCCCCATACAGCGAGTCTCGTTTCGAGGAAA
TCAAGAAGGAAGTGTCCTCCTACATCAAGAAAATCGGTTACAACCCAGCT
GCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq20 [organism=Mycalesis intermedia] [isolate=MintEF-1alphaS051]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGCAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAGAACATG
ATCACCGGAACCTCGCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCTACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq21 [organism=Mycalesis visala] [isolate=MvisEF-1alphaS051]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACCTCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCTACTGAGCCCCCATACAGTGAGTCACGTTTCGAGGA

AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAT
CTGCTGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq22 [organism=Mycalesis orseis] [isolate=MorsEF-1alphaS051]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGCAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTGAAGGCTGAGCGCGAGCG
TGGTATCACCATCGATATCGCTCTGTGGAAGTTCGAGACTGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAGAACATG
ATCACTGGAACCTCACAGGCCGATTGCGCCGTGCTGATCGTCGCCGCAGG
TACCGGCGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGTTGTTGGCCTTCACCCTCGGTGTCAAGCAGCTGATCGTGGGCGTCA
ACAAAATGGACTCCACTGAGCCCCCGTACAGTGAGCCTCGTTTCGAGGAA
ATCAAGAAGGAAGTGTCCTCCTACATCAAGAAGATTGGTTACAACCCAGC
TGCTGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq23 [organism=Mycalesis intermedia] [isolate=MintEF-1alphaS052]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGCAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAGAACATG
ATCACCGGAACCTCGCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq24 [organism=Mycalesis intermedia] [isolate=MintEF-1alphaS053]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGCAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAGAACATG
ATCACCGGAACCTCGCAGGCAGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCTACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq25 [organism=Mycalesis perseoides] [isolate=MpersdEF-1alphaS061]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG

ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACGGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCTTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq26 [organism=Mycalesis intermedia] [isolate=MintEF-1alphaS061]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCTTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq27 [organism=Mycalesis intermedia] [isolate=MintEF-1alphaS062]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGCAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTCACCATCATCGACGCTCCCGGACACAGAGATTTCATCAAGAACATG
ATCACCGGAACCTCGCAGGCAGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq28 [organism=Mycalesis intermedia] [isolate=MintEF-1alphaS063]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Seq29 [organism=Mycalesis perseoides] [isolate=MpersdEF-1alphaS062]

ACGTACTATCGAGAAGTTCGAGAAGGAGGCCCAGGAAATGGGAAAAGGT
TCCTTCAAATACGCCTGGGTGTTGGACAAACTAAAGGCTGAGCGCGAGCG
TGGTATCACCATCGACATCGCTCTGTGGAAGTTCGAGACGGCCAAATACT
ACGTTACCATCATCGACGCTCCTGGACACAGAGATTTCATCAAAAACATG
ATCACCGGAACATCTCAGGCCGATTGTGCCGTGCTGATCGTCGCCGCCGG
TACCGGTGAGTTCGAGGCCGGTATCTCCAAGAACGGCCAGACCCGTGAGC
ACGCGCTGCTCGCCTTCACCCTCGGCGTCAAGCAGCTGATCGTGGGCGTC
AACAAAATGGACTCCACTGAGCCCCCATACAGTGAGTCCCGTTTCGAGGA
AATCAAAAAGGAAGTGTCCTCGTACATCAAGAAGATTGGTTACAACCCAG
CTGCCGTCGCTTTCGTACCCATTTCTGGCTGGCACG

Wingless gene

Seq1 [organism=Mycalesis perseoides] [isolate=MpersdwinglessS011]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TTGACGGGGCGTCGCGGGTCATGATGCCCAACACCGAGGTGGAGGCGCCG
TCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGGT
ACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGTC
AAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACCC
CAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACCAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq2 [organism=Mycalesis perseoides] [isolate=MpersdwinglessS012]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGATGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACCAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

seq3 [organism=Mycalesis perseoides] [isolate=MpersdwinglessS013]

GATGAGGCTGCCGACTTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCCCGGGTCATGATGCCCAACACCGAGGTGGAGGCGCCG
TCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGGT
ACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGTC
AAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACCC
CAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACTAGCA
TCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGACC
GAGACCATGTTCGTGGTGGAGCGCTGCAAC

seq4 [organism=Mycalesis perseoides] [isolate=MpersdwinglessS014]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGATGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACTAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

seq5 [organism=Mycalesis mineus] [isolate=MminwinglessS021]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGATGCCCAATACCGAGGTGGAGGCGCCG
TCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGATCGGTA
CAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGTCA
AGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACCCC
AGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACGAGCA
TCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGACC
GAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq6 [organism=Mycalesis mineus] [isolate=MminwinglessS022]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGATGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCATAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACGAG
CATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGA
CCGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq7 [organism=Mycalesis mineus] [isolate=MminwinglessS031]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGAGCGTCGCGGGTCATGATGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACGAG
CATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGA
CCGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq8 [organism=Mycalesis mineus] [isolate=MminwinglessS032]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGATGCCCAATACCGAGGTGGAGGCGCCG

TCACAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGGT
ACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGTC
AAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACCC
CAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACGAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq9 [organism=Mycalesis perseoides] [isolate=MpersdwinglessS031]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACCAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq10 [organism=Mycalesis perseoides] [isolate=MpersdwinglessS032]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TTGACGGGGCGTCGCGGGTCATGATGCCCAACACCGAGGTGGAGGCGCCG
TCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGGT
ACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGTC
AAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACCC
CAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACCAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq11 [organism=Mycalesis intermedia] [isolate=MintwinglessS031]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACCAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq12 [organism=Mycalesis intermedia] [isolate=MintwinglessS041]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACTAGC

ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq13 [organism=Mycalesis perseoides] [isolate=MpersdwinglessS041]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACTAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq14 [organism=Mycalesis visala] [isolate=MviswinglessS041]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACTAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq15 [organism=Mycalesis intermedia] [isolate=MintwinglessS042]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACCAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq16 [organism=Mycalesis perseus] [isolate=MperswinglessS041]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGATAGCT
TCGACGGGGCATCGCGGGTCATGATGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCACGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAACCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCATCGCCGGGTTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACGAG
CATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGA
CCGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq17 [organism=Mycalesis perseus] [isolate=MperswinglessS042]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGATAGCT
TCGACGGGGCGTCGCGGGTCATGATGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAACCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCACCGGGTTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACGAG
CATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGA
CCGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq18 [organism=Mycalesis perseoides] [isolate=MpersdwinglessS042]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TTGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACTAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq19 [organism=Mycalesis janardana] [isolate=MjanwinglessS051]

GATGAGGTTGCCGACGTTCCGATCTGTAGGCGACGCCCTCAAAGACAGCT
TCGACGGGGCGTCGCGGGTCATGATGCCCAACACGGAGGTAGAGGCGCC
GTCCCAGCGAAACGACGCCGCGCCCCACCGGGTGCCGCGACGGGACCGG
TACAGATTCCAACTTCGGCCGCACAACCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTATACTTGGAATCGTCGCCGGGCTTCTGCGAGAAGAACC
CCAGGCTGGGCATTCCCGGTACGCACGGGCGTGCCTGCAACGACACGAGC
ATCGGCGTCGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACAGGAC
TGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq20 [organism=Mycalesis intermedia] [isolate=MintwinglessS051]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAATGACACGAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq21 [organism=Mycalesis visala] [isolate=MviswinglessS051]

GATGAGGCTGCCGACGTTCCGATCTGTATGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT

CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACTAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq22 [organism=Mycalesis orseis] [isolate=MorswinglessS051]

GATGAGGCTGCCGACGTTCAGATCTGTAGGCGATGCCCTAAAAGACAGCT
TCGACGGGGCGTCGCGGGTCATGATGCCCAACACCGAGGTAGAAGCGCC
GTCTCAACGGAACGACGTTGCACCTCATAGGGTCCCGCGACGAGACCGGT
ACAGATTTCAACTTCGGCCGCACAACCCTGACCACAAAACACCCGGGGTC
AAGGACCTAGTATACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACCC
CAGGCTGGGCATTCCGGGTACGCACGGGCGTGCCTGCAACGACACGAGTA
TCGGCGTCGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGACC
GAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq23 [organism=Mycalesis intermedia] [isolate=MintwinglessS052]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACGAG
CATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGA
CCGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq24 [organism=Mycalesis intermedia] [isolate=MintwinglessS053]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGATGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCATGGGCGCGCCTGCAACGACACGAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq25 [organism=Mycalesis perseoides] [isolate=MpersdwinglessS061]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGACTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACCAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq26 [organism=Mycalesis intermedia] [isolate=MintwinglessS061]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGTCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACCAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq27 [organism=Mycalesis intermedia] [isolate=MintwinglessS062]

GATGAGGCTGCCGACGTTCCGATCTGTTTGCGACGCCCTGAATGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGGCTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACGAG
CATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGA
CCGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq28 [organism=Mycalesis intermedia] [isolate=MintwinglessS063]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGATGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGACTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACCAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

Seq29 [organism=Mycalesis perseoides] [isolate=MpersdwinglessS062]

GATGAGGCTGCCGACGTTCCGATCTGTAGGCGACGCCCTGAAGGACAGCT
TCGACGGGGCGTCGCGGGTCATGAAGCCCAACACCGAGGTGGAGGCGCC
GTCGCAGCGGAACGACGCCGCACCTCACCGGGTGCCGCGACGAGACCGG
TACAGGTTTCAACTTCGGCCGCACAATCCTGACCACAAAACACCCGGGGT
CAAGGACCTAGTGTACTTGGAATCGTCGCCGGGCTTCTGCGAAAAGAACC
CCAGACTGGGCATTCCGGGCACGCACGGGCGCGCCTGCAACGACACCAGC
ATCGGCGTGGACGGCTGCGACCTCATGTGCTGCGGCCGCGGGTACCGGAC
CGAGACCATGTTCGTGGTGGAGCGCTGCAAC

VITAE

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